Morphological and molecular determination of *Fucus* (Fucales, Heterokontophyta) biogeography across North American shores

by

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ABSTRACT

The genus *Fucus* (Phaeophyceae) has nine commonly accepted species, six of which inhabit North American shores: *F. gardneri, F. serratus, F. distichus, F. evanescens, F. vesiculosus*, and *F. spiralis*. *Fucus* inhabit the intertidal zones of the Atlantic, Pacific and Arctic Oceans and due to their highly plastic and morphologically simple phenotypes, are valuable candidates for molecular phylogenetic research. Furthermore, *Fucus* species are valuable for biogeographic investigations due to their relatively slow migration, limited dispersal range, and easily collected distribution.

The closest ancestral species to the genus is a Pacific endemic *Hesperophycus californicus* supporting a North Pacific origin of the species (Serrão *et al.* 1999). However, a closer relationship between Atlantic and Arctic *Fucus* has been described casting doubt on the Pacific origins of the genus (Lindstrom 2001, Dunton 1992). The investigation of *Fucus* across this area is necessary to elucidate the apparent contradiction in the origin of the genus. Samples were collected from 79 locations across North American waters. The amplification of the divergent mtDNA spacer region was performed to assess taxonomic placement of 55 collected species and reconstruct the biogeography of North American *Fucus* species. Morphological analysis was also completed based on 21 measured characteristics in an attempt to support molecular analysis.

Results of the study indicate two distinct lineages among collected samples. One lineage (*F. spiralis* and *F.* vesiculosus) with a distinct Atlantic origin and the second lineage (*F. distichus* and *F. serratus*) with a widely distributed *F. distichus,* and the Atlantic *F. serratus.* Morphological analysis and statistical support for these lineages was determined through discriminant analysis of the collected samples. Overall results determined

biogeographic influences in the *F. distichus* species complex across Arctic, Pacific, and Atlantic regions with little apparent biogeographical influence within *F. vesiculosus, F. serratus* and *F. spiralis*. Closer phylogenetic relationships between Arctic and Atlantic samples were apparent as suggested by Lindstrom (2001) and Dunton (1992).

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1.0 INTRODUCTION

1.1 GENERAL INTRODUCTION

Brown algae (Phaeophyceae) are one of the most abundant intertidal macroalgae on rocky shorelines within the eulittoral (intertidal) zone of cold North American waters. Species within this class can exhibit variable distributions such as a few individuals on soft-bottomed shores as well as abundant populations along rocky shorelines (Seed & O'Connor 1981, Druehl 2000, Coyer *et al.* 2006a, Lindstrom 2001, Lindstrom 2006). The genus *Fucus* (order Fucales) is within this brown algal class and is an important member of intertidal communities (Figure 1; Adl *et al.* 2005, Deutsch & Voss 2006, Steneck *et al.* 2004) in the eastern and western North Atlantic, Arctic Ocean, and the North Pacific regions (Lindstrom 2001). In high Arctic and temperate latitudes, *Fucus* is often an integral part of the marine ecosystem and helps mitigate the effects of over-fishing, pollution, and decreased availability of nutrients (Steneck *et al.* 2002). For example, these seaweeds provide surface area for attachment of epiphytic algal species and sessile organisms; shelter for organisms during both high and low tides; near shore structure to slow or stop near shore sediment runoff into pelagic regions; and food for near shore grazing species (Seed & OConnor1981).

The morphology of *Fucus* varies considerably dependent on external stimuli such as wave action, light exposure, and habitat. Hence, this plasticity has been the subject of many studies (Lindstrom 2001, Coyer *et al.* 2006b, Fowler-Walker *et al.* 2006). Historically, habitat characteristics and phenotypic analyses were used to delineate species within this genus; however, for the reasons noted above these taxonomic criteria were often problematic

Figure 1. Brown algae (Phaeophyceae) *Fucus* genus attached to intertidal rocky substrate at Bauline Newfoundland, Canada (K. Müller June 4, 2006).



and result in questionable identifications and non-monophyletic groupings (Fowler-Walker *et al.* 2006, Billard *et al.* 2005). Hence, members of this genus are logical candidates for molecular phylogenetic research. In addition, their abundance, slow migration, and limited near shore dispersal range provides further incentive to use this genus in studies attempting to elucidate evolutionary patterns of Arctic intertidal seaweeds (Lindstrom 2001).

The biological history of the North American Arctic region is of particular evolutionary interest due to recent re-population and possible relict species following the last ice age as well as the relative lack of human influence on the area. As a result, the biogeography of organisms present in the arctic can tell us a great deal about movement of species between the Atlantic and Pacific, as well as the impact of historical water level changes on organisms in this region. For example, the Bering Strait has played a major role in influencing the distribution of organisms in the arctic region and is referred to by Gladenkov *et al.* (2002) as "among the most globally significant regions for paleogeography and biogeography." The Bering Strait, direction of water flow in the northern arctic and the biogeography of *Fucus* in this region provide a framework to investigate evolutionary questions with respect to the history of this genus in both the Atlantic and Pacific basins and connections among these populations via the Arctic ocean.

1.2 FUCUS TAXONOMY

The order Fucales is within the class Phaeophyceae and contains the genus *Fucus* (Adl *et al.* 2005) which includes nine commonly accepted species (Table 1): *F. distichus* L., *F. gardneri* P.C. Silva, *F. evanescens* C. Agardh, *F. serratus* L., *F. vesiculosus* L., *F. virsoides* J. Agardh, *F. spiralis* L., *F. ceranoides* L., and *F. cottonii* M.J. Wynne & Magne (Guiry & Guiry 2007).

Table 1. A list of *Fucus* species with their geographic distribution and authority.

Name	Location	Authority
F. ceranoides	Iceland, Norway, Europe	Linnaeus, C. (1753). *Species plantarum* , exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Vol. 2 pp. [i], 561-1200, [1-30, index], [i, err.]. Holmiae [Stockholm]: Impensis Laurentii Salvii.
F. cottonii	Britian, Norway, Europe	Wynne, M.J. & Magne, F. (1991). Concerning the name Fucus muscoides (Cotton) J. Feldmann et Magne. Cryptogamie, Algologie 12: 55-65.
F. distichus	Canadian Arctic, Norway, North America (Maine, Massachusetts and New Hampshire), Alaska	Linnaeus, C. (1753). *Species plantarum* , exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Vol. 2 pp. [i], 561-1200, [1-30, index], [i, err.]. Holmiae [Stockholm]: Impensis Laurentii Salvii.
F. evanescens	Canadian Arctic, North American East Coast, Iceland, Norway	Agardh, C.A. (1820). *Species algarum* rite cognitae, cum synonymis, differentiis specificis et descriptionibus succinctis. Vol. 1, Part 1 pp. [i-iv], [1]-168. Lund: Berling.
F. gardneri	Alaska, British Columbia, Washington, Oregon	Silva, P.C. (1953). The identity of certain *Fuci* of Esper. *Wasmann Journal of Biology* 11: 221-232.
F. serratus	Canada (Maritime Provinces), Norway, Europe, Iceland	Linnaeus, C. (1753). *Species plantarum* , exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Vol. 2 pp. [i], 561-1200, [1-30, index], [i, err.]. Holmiae [Stockholm]: Impensis Laurentii Salvii.
F. spiralis	Maine, Washington, Norway, United Kingdom, Europe, Africa	Linnaeus, C. (1753). *Species plantarum* , exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Vol. 2 pp. [i], 561-1200, [1-30, index], [i, err.]. Holmiae [Stockholm]: Impensis Laurentii Salvii.
F. vesiculosus	Canadian Arctic, Norway, North America (Maine, Massachusetts and New Hampshire), Greenland	Linnaeus, C. (1753). *Species plantarum* , exhibentes plantas rite cognitas, ad genera relatas, cum differentiis specificis, nominibus trivialibus, synonymis selectis, locis natalibus, secundum systema sexuale digestas. Vol. 2 pp. [i], 561-1200, [1-30, index], [i, err.]. Holmiae [Stockholm]: Impensis Laurentii Salvii.
F. virsoides	Adriatic Sea and Surrounding Area	Agardh, J.G. (1868). Bidrag till kännedomen om Spetsbergens alger. Tilläg till föregående afhandling. *Kungliga Svenska Vetenskapsakademiens Handlingar* 7: 27-49, 1 table.
F. radicans	Baltic Sea	Bergström L, Tatarenkov A, Johannesson K, Jonsson RB, Kautsky L (2005) Genetic and morphological identification of Fucus radicans sp Nov (Fucales, Phaeophyceae) in the brackish Baltic Sea. *Journal of Phycology,* 41, 5, 1025-1038.

In addition, two other species, *F. radicans* Lena Bergström & Lena Kautsky and *F. lutarius* (Chauvin, Kützing) Sauv., have also been described (Bergström *et al.* 2005, Leclerc *et al.* 1998, Wallace *et al.* 2004). Bergström *et al.* (2005) described *F. radicans* as a distinct species from a sample present in the brackish waters of the Baltic Sea. *Fucus lutarius*, is an ecad, which is a free floating algae that does not attach to substrate through a holdfast, and can often be observed as an epiphytic form (Wallace *et al.* 2004). In the past, *F. lutarius* has been described as a distinct species, but has also been considered a variety of *F. vesiculosus* (Leclerc *et al.* 1998). Mathieson *et al.* (2006) identified *F. lutarius* in Maine salt marshes and determined that when *F. spiralis* was transplanted into the same salt marsh habitats as *F. lutarius* the two species became phenotypically indistinguishable. As such, Mathieson *et al.* (2006) designated *F. lutarius* as an ecad of *F. spiralis* and noted that this is similar to Taylor (1957) when he listed *lutarius* as a variety of *F. spiralis* (Mathieson *et al.* 2006). *Fucus distichus, F. evanescens,* and *F. gardneri* are currently considered three distinct species, however several molecular phylogenetic studies (Coyer *et al.* 2006a, Lindstrom 2001, Lindstrom 2006) have suggested their combination into a single species with three distinct subspecies. It is clear that due to the high degree of morphological variation within a species, reliable taxonomic separation and determination of species within the *Fucus* genus is difficult.

1.3 MORPHOLOGY

The considerable variation of morphology in *Fucus* as well as closely related species has been the subject of many studies that hypothesized that the influence of external stimuli such as wave action, light exposure, and habitat can dramatically impact morphology (Coyer *et al.*

2006a, Lindstrom 2001, Fowler-Walker *et al.* 2006). In one such study, Billard *et al.* (2005) evaluated the reliability of the taxonomic identification using morphology and geographic location within the species *F. vesiculosus*, *F. spiralis*, and *F. ceranoides* along the Atlantic Ocean coast of France. Samples were evaluated using microsatellite markers and a large morphological variation among samples within each species was reported and also showed high genetic variability among *F. vesiculosus* samples (Billard *et al.* 2005).

Robertson and Coyer (2004) conducted a morphological study of *Eisenia arborea* Aresch. (Laminariales, Heterokontophyta) across different sites along the California coast that were either open or sheltered from wave action but similar in all other variables (e.g. light, nutrients etc.). Microsatellites were then used to determine genetic relationships among the varying morphologies of *Eisenia arborea* and determined significant genetic variation between wave swept and wave sheltered sites. This in combination with clear phenotypic morphological variation and the separation of the two sites by approximately 40 to 80 km indicate clear morphological variation within the species.

Another member of the Laminariales, *Egregia menziesii* (Turner) Aresch., also having variable morphology, was the subject of study by Blanchette *et al.* (2002). Initially they noted that there were morphological differences among individuals in low wave action areas (longer, thinner stipes with many fronds) compared to high wave action areas (shorter and thicker stipes with fewer fronds; Blanchette *et al.* 2002). Blanchette *et al.* (2002) then transplanted thalli from high and low wave action areas and placed them in the opposite environment following which there appeared to be no clear morphological change in response to the different environments (Blanchette *et al.* 2002). The authors suggested that the two distinct morphologies, one in the low wave action environment and the other in the

high wave action environment, provide advantages in survival, growth, and reproduction within their respective native habitats and hence were selected for in the respective habitats though no genetic evaluation of samples was conducted. Hence it is not clear as to whether or not morphological variation within *Egregia menziesii* is due to phenotypic plasticity or a change in genotype. In the Baltic Sea, Russell *et al.* (1998) transplanted *F. vesiculosus* in two distinct locations that differed in water turbidity but had similar wave action, habitat, and water temperatures. They noted little phenotypic during transplantation and an overall low morphological plasticity among samples and did not observe a significant change in the production of chlorophyll or other photosynthetic pigments across the different light conditions (Russell *et al.* 1998). Although the results are interesting and suggest that *F. vesiculosus* does not display a high morphological plasticity, the four-month duration of the experiment may not have been sufficient to draw definitive conclusions and as suggested by the authors (Russell *et al.* 1998).

Other transplantation studies have noted variation of *Fucus* morphology across a saline gradient. Ruuskanen and Bäck (2002) recorded *F. vesiculosus* having smaller total size in low salinity [approximately 2 practical salinity units (psu)] compared to a larger plant and frond size in higher salinity conditions (approaching 24 psu). In addition, when *F. vesiculosus* individuals are exposed to salinity variations the resulting osmotic pressure could effect gamete dispersal, gamete survival, and nutrient uptake (Russell *et al.* 1998). Furthermore, high wave action also appeared to have a larger impact on the width and length of the *F. vesiculosus* fronds when combined with the salinity pressures, already influencing the *Fucus,* yielding smaller vegetative individuals (Russell *et al.* 1998). Kalvas and Kautsky (1993) drew similar conclusions to the previous study when they noted morphological

variation in *F. vesiculosus* features including individual length and weight, thallus diameter, and the number of receptacles, their weight and total branching of the fronds in response to wave action. Other studies have investigated similar phenotypic diversity within the species *F. spiralis* (Scott *et al.* 2001), in which morphology varied among areas of differing wave exposure (Scott *et al.* 2001, Kalvas & Kautsky1993).

Rice and Chapman (1985) investigated both *F. distichus* and *F. evanescens* across the North Atlantic shores of North America and described clear phenotypic variation among the samples within each of the species (Rice *et al.* 1985). *Fucus gardneri* displayed variable morphology in different habitats with varying light, salinity and wave action (Ruuskanen & Nappu 2005). These authors noted morphological differences in *F. gardneri* between high wave action North Pacific shores and more southerly shores with an overall gentler wave action. They also point out that other factors influence morphology of the species and that although wave action has a large influence on *Fucus*, the overall environmental pressures of a region must also be considered (Ruuskanen & Nappu 2005). Ruuskanen and Nappu (2005) suggested that morphological variation may not be due simply to plasticity but could be accompanied by genetic variation, hence, species adaption to the differing environments.

The occurrence of species hybridization presents a further difficulty with using geographic location and morphological traits as identification. The hybridization of European *F. serratus* and *F. evanescens* across a zone of species contact has been observed among Denmark populations (Coyer *et al.* 2002). With overlapping geographic locations and difficult morphological identification due to plasticity, products of hybridization present difficulties in establishing to which species they belong. Hybridizations in North American *Fucus* have also been identified (Wallace *et al.* 2004). Wallace *et al.* (2004) discussed a

possible intermediate species between *F. spiralis* and *F. vesiculosus* in salt marshes along the North Atlantic shorelines. The product of this *F. spiralis* and *F. vesiculosus* crossing resulted in what the authors describe as a "muscoides" or ecad individual (Engel *et al.* 2006). Engel *et al.* (2004) suggested that the ability of this hybridization is due to an intermediate species and reinforces Wallace *et al.* (2004) observations of difficult species identifications due to hybridization.

There are few studies that combine an analysis of morphological data with that of genetic information (Scott *et al.* 2001, Kalvas & Kautsky1993). As noted previously, environmental factors can contribute to variation in morphology for *Fucus* species, and hence accurate species identifications are complex. This difficulty is particularly noticeable in the Arctic region where varying water temperatures, increased pressures such as variation in water salinity and wave exposure due to freeze and thaw, and decreased nutrients also play a role (Adey & Steneck 2001, Brittain & Milner 2001, Oechel & Vourlitis 1994).

1.4 GEOGRAPHIC DISTRIBUTION OF THE GENUS FUCUS

Members of the genus *Fucus* have a wide distribution with locations on both the eastern and western North Atlantic, the Arctic Ocean and Pacific shores from Russia (in the north) to Japan (in the south) and stretching as far down as northern California in the Pacific (Lindstrom 2001). The Mediterranean Sea also contains the endemic *Fucus* species, *F. virsoides,* which is not present on North American shores (Serrão *et al.* 1999). *Fucus distichus* L. is the one species in this genus that has been collected across all three of these oceans (Lindstrom 2001). Similar to Lindstrom (2001), Coyer *et al.* (2006) carried out an extensive investigation into the various species of *Fucus* in the arctic area and observed *F.*

distichus in both the Pacific and Atlantic. The difference between the two studies is that Coyer *et al.* (2006a) considered *F. distichus* and *F. evanescens* as a single species where Lindstrom (2001) also included *F. gardneri* in this group. *Fucus gardneri* is a North Eastern Pacific species inhabiting the mid and high intertidal zones of the rocky shores from Oregon to British Columbia (Edwards *et al.* 2006). However, *F. gardneri* does not inhabit Atlantic coasts in contrast to *F. evanescens* on both the Atlantic and Pacific shores. *Fucus gardneri* has been treated as both a separate species as well as a subspecies of *F. distichus* (Coyer *et al.* 2007, Lüning *et al.* c1990).

Fucus vesiculosus is only observed in the North Atlantic and is distributed from North Carolina extending up into the Arctic and with a European distribution that ranges from the southern coast of France into areas of the Russian Arctic coasts (Billard *et al.* 2005, Engel *et al.* 2003, Jormalainen & Honkanen 2004). The species *Fucus spiralis* is observed across the North-eastern Atlantic shores and has also been collected on the North American Atlantic coast in Maine and also on the Pacific coast in Washington (Coyer *et al.* 2006a, Romera *et al.* 2008, Lindstrom 2001, Coleman 2008). The presence of this species in the Pacific may be due to vector-assisted transport and may be a recent introduction (Coyer *et al.* 2006a, Coleman & Muhlin 2008). *Fucus serratus* is commonly observed in the Northwest Atlantic coastline near the Gulf of St. Laurence (Engel *et al.* 2003) and is also observed on Northeastern Atlantic shores from Russia to Spain, the United Kingdom and Iceland (Lüning *et al.* c1990).

1.5 SPECIES CONCEPTS

There are a myriad of different concepts being used to define species, including, Ecological, Evolutionary, Biological, Morphological, and Phylogenetic species concepts (Manhart *et al.* 1992, de Queiroz 1998). Historically, habitat and morphological characteristics were used to delineate algal species; however, these were often problematic due to high phenotypic plasticity, particularly in macroalgae (Fowler-Walker *et al.* 2006). Some species concepts, such as the biological and morphological, are common in literature and practice; however, their utility in genera such as *Fucus* is questionable. A clear species definition is necessary to effectively evaluate the biogeography of any given organism or group of organisms.

The Biological Species Concept (BSC) is a concept widely occurring in literature and at the centre of the species concept debate (Garnett & Christidis 2007). It is the most commonly used species concept among studies of complex organisms such as those in the kingdom Animalia (Garnett & Christidis 2007). The BSC uses the sexual success, as measured by production of fertile offspring, between two distinct populations to define a separation into two species (Mayr 1942). The BSC does present some challenges in application among algae. Using the BSC to separate algal species creates difficulties due to recorded interspecies hybridizations (Manhart *et al.* 1992). One example of this can be seen in the *F. serratus* and *F. evanescens* populations along Norwegian coasts (Coyer *et al.* 2002). Coyer *et al.* (2002) describe a clear and distinct region of hybridization separating two populations of *F. serratus* and *F. evanescens*. In this case application of the BSC would suggest that this hybridization indicates a single species of these two distinct populations.

Manhart *et al.* (1992) argue that in cases such as this the use of sexual compatibility as the primary indicator of species may not always be reliable, as is seen in the Coyer *et al.*

(2002) study, as sexual compatibility is a primitive trait. Furthermore there are many algal species with the ability to reproduce asexually, including *F. spiralis* (Engel *et al.* 2005) for which the BSC (and other concepts that use sexual reproduction as the foundation of species determination e.g. Isolation Species Concept) is not easily applied (Bergström *et al.* 2005, Manhart *et al.* 1992, Tatarenkov *et al.* 2005, Templeton 1989).

The Ecological Species Concept delineates species based on the survival of organisms within a particular niche emphasizing the natural selection pressures of the environment on the delineation of species (de Queiroz 1998). The changing habitat and location of *Fucus* over time would create difficulties in the application of this species concept with this genus. The Evolutionary Species Concept lessens the impact of the location of organisms as a primary determinant of species by requiring that a species be represented as a distinct group or population of organisms that have shared a similar "evolutionary fate" over time (de Queiroz 1998, Templeton 1989). An advantage of the Evolutionary Species Concept is that it can be applied to extant and extinct species and also those that reproduce sexually or asexually (Templeton 1989).

The Morphological Species Concept has been the primary method of species classification leading up to the 19th century and is still in use today (Manhart *et al.* 1992). The Morphological Species Concept uses comparative anatomy across visible similarities and differences of organisms for taxonomic identification (Hillis 1987). Similar to the BSC, the exclusive use of the Morphological Species Concepts presents problems with taxonomic identification among algae because of environmental factors making morphological evaluations difficult due to high phenotypic plasticity among *Fucus*. The morphological plasticity of macroalgae, and in particular *Fucus,* has been well documented (Coyer *et al.*

2006a, Lindstrom 2001, Fowler-Walker *et al.* 2006). Marine diatoms, traditionally separated through morphological identifications, have been the subjects of investigations questioning the accuracy of exclusive divisions using morphological evaluations (Amato *et al.* 2007). Furthermore, fundamental characters of species may not be seen through phenotypic evaluations. Hillis (1987) suggests that reproductive isolation can occur across organisms without changes in morphology but by simple chemical changes.

A method that can be used to further support morphological identifications is cladistics. Cladistics is a process that estimates the evolutionary history of organisms by creating a phylogenetic tree based on their shared derived characters (synapomorphies) (Manhart *et al.* 1992, Freeman & Herron 2004, Lomolino *et al.* 2006). The Phylogenetic Species Concept delineates species using cladistics where all species represented in the analysis are monophyletic in relation to each other (Manhart *et al.* 1992). Monophyly is a clade, on a phylogenetic tree, that consists of an ancestor and all its descendants (Freeman & Herron 2004). Although only a single shared derived character is necessary to distinguish between two species, either morphological, chemical or molecular, molecular data provides a greater number of informative characters and are the predominant choice in current phylogenetics (Garnett & Christidis 2007, Manhart *et al.* 1992, Vogler & Monaghan 2007). Although, morphological identifications and cladistics based on non-molecular shared derived characters are valuable in providing initial taxonomic separations they are not always sufficient when used as the sole method of taxonomic evaluation.

The Phylogenetic Species Concept, specifically using molecular data termed molecular phylogenetics, can identify and confirm taxonomic separations made using other species concepts (Manhart *et al.* 1992, de Queiroz 1998). A further advantage to using

molecular phylogenetics is although other concepts separate species into taxonomic groups, using molecular information can suggest the relationship between members within the same group (Zink 2006). This intraspecies evaluation is achieved because molecular data provides large amounts of information from a genetic region where a single nucleotide change can represent a shared derived character across a data set (Ricklefs 2007).

There are cautions with the use of molecular data, one of which is that researchers must choose the appropriate region of interest to represent the species during analysis in order to gain reliable information from the procedure (Manhart *et al.* 1992). The ribosomal DNA small and large subunits (rDNA-SSU, LSU) have been used to evaluate the relationships among genera at the family level Fucaceae (Lee *et al.* 1999). The use of nuclear ribosomal internal transcribed spacer (ITS) DNA is another region that has been used for evaluation of genera within the Fucaceae (Leclerc *et al.* 1998). For the evaluation of *Fucus* species Coyer *et al.* (2006) used a mitochondrial intergenic spacer region. All of these studies use molecular phylogenetics, which take into consideration evolutionary concepts when establishing a phylogeny. One final method of confirming separation of samples into groups using molecular information is through the use of molecular barcoding (Vogler & Monaghan 2007).

Molecular phylogenies are most valuable when used as a secondary method of species delineation where taxonomic results are verified using ecology, habitat, behaviour, and other traits, where appropriate (Rundle *et al.* 2001). This type of application of the molecular phylogenetics can also lead to reinterpretations of taxonomic lineages and discovery of cryptic species (Vogler & Monaghan 2007). The use of a molecular

phylogenetics species definition for the evaluation of *Fucus* is the most informative of the discussed methods and as such will be the definition of choice for the purposes of this thesis.

1.6 CRYPTIC SPECIES

Cryptic species, also know as sibling species, are morphologically similar species that are difficult to distinguish (Freeman & Herron 2004, Lomolino *et al.* 2006, Knowlton 1993, Bickford *et al.* 2007). Until recently species descriptions have been based largely on morphology (Bickford *et al.* 2007). The definition of cryptic species, which is strongly linked to the Morphological Species Concept, is that divergent traits such as songs, odours, chemical content and signaling, and other traits not immediately visible may contribute to lumping of species and creation of cryptic species (Scott *et al.* 2001, Freeman & Herron 2004, Bickford *et al.* 2007).

Cryptic species are particularly evident when considering marine organisms due to differing species concepts and evaluation techniques, difficult sample collection, and organism plasticity (Knowlton 1993). In addition, species within marine environments can display divergence across habitat characteristics of depth, salinity, exposure or water temperature (Knowlton 1993). The assessment of cryptic species is greatly dependant on the species concept used for taxonomic identification. Studies attempting to elucidate cryptic species rely on the original taxonomic separation and a subsequent study method to provide further evidence from other species concepts (Bickford *et al.* 2007, McGovern & Hellberg 2003, Morales 2003, Zuccarello & West 2004, Pruett & Winker 2008). The investigation and confirmation of *Fucus* species delineated using morphology and then subsequently examined using molecular phylogenetics may elucidate any potential cryptic species

Bickford (2007) suggests that recent speciation events may result in two species with similar morphologies. These similar characteristics across two or more species may lead to cryptic species as determined by morphological characters (Bickford *et al.* 2007). Furthermore, cryptic species may also be present in species with large distributions. Ingolfsson (1993) noted high similarities among marine near shore plant species from North American coasts and European coasts. This large allopatric separation with the inability for non-motile species to exchange genetic information resulting in two or more distinct gene pools may hide cryptic species (Wares & Cunningham 2001, Ingolfsson 1992). Wares *et al.* (2001) also describe possible cryptic species between North American and European shores among the small marine crustacean *Idotea Balthica*.

Zones of hybridization and the ability of two species to have sexual reproduction can also yield difficult species distinctions leading to the possibility of cryptic species (Hewitt 1996). Arctic *Daphnia* species have also displayed the ability to hybridize, potentially hiding cryptic species among others already described (Colbourne *et al.* 1998). Members within the Phaeophyceae have also been discovered with the ability to hybridize among species (Coyer *et al.* 2006b, Coyer *et al.* 2002, Kraan & Guiry 2000). *Alaria* species maintain the ability to hybridize although they are separated geographically across American Pacific and Atlantic shores (Kraan & Guiry 2000). Coyer *et al.* (2002) described a zone of *F. serratus* and *F. evanescens* hybridization that they estimated to be approximately 100 years old. The stability of this zone is interesting and may suggest cryptic species among the *F. serratus* and *F. evanescens* (Coyer *et al.* 2006b, Coyer *et al.* 2002). The ability of two species to hybridize in nature may suggest a close relationship among the species but further methods

of species delineation should be used, especially among morphologically plastic species, in an attempt to minimize the number of cryptic species described (Kraan & Guiry 2000).

Determination of cryptic species in marine arctic and northern cold water environments is important due to the large and varying number of species which contribute toward community structure and to elucidating geographical historical impacts on species within the region (Bickford *et al.* 2007, Morales 2003). The use of molecular data and phylogenetic techniques will play a large role in the determination of *Fucus* cryptic species on North American shores (Palumbi 1997).

1.7 BIOGEOGRAPHY

When constructing a model of the distribution or biogeography of a species across a given region (Lomolino *et al.* 2006), there are numerous factors to be considered. For example, with marine organisms, water temperature and salinity fluctuations are important factors as both exert pressures on sexual reproduction and gamete dispersal of *Fucus* species. Life history characteristics and geographic barriers are also important to consider when forming a robust biogeographic model (Adey & Steneck 2001, Arrontes 2002). The influence of water temperatures, particularly warm water on the cold water *Fucus* species, cannot be overlooked as a factor influencing species survival, movement, and dispersal (Adey & Steneck 2001). Furthermore, the influence of water temperature is a major factor attributed to the overall Northern biogeography of the *Fucus* genus (Briggs 2003, Magnasco 2001, Dunton 1992). The determination of temperature pressures on species can help to predict past distributions using climate data and fossil records (Lüning 1984). An accurate determination of the

current number and locations of *Fucus* species is needed to effectively elucidate temperature influences and biogeographic regions.

In addition, vicariance in the North Pacific, Arctic, and North Atlantic Oceans, which are, considered to be part of an arctic biotic region (Briggs 2003), have greatly impacted the distribution of organisms within the region (Van Oppen, M. J. H. *et al.* 1995). Glaciation and shifts in continental landmasses, specifically the separation of Eurasia from North America, and the opening of the Bering Strait, created the Arctic region we recognize today (Dunton 1992, Van Oppen, M. J. H. *et al.* 1995, Marincovich & Gladenkov 1999).

1.8 HISTORICAL LANDMASS MOVEMENTS AND GLACIATIONS

During historical Arctic glacial periods, glacial ice dramatically reduced the sea level, in some cases up to 120m, resulting in land bridges separating marine habitats and also reducing the amount of available water (Hewitt 2000, Lindstrom 2001, McElwain & Punyasena 2007). The Bering land bridge is one historically reoccurring example of this effect (Gladenkov *et al.* 2002). The Bering Strait, with varying water flow over the last 120 million years, is of special interest for the potential access that it has allowed organisms between the Pacific, Arctic, and Atlantic Oceans (Lawver *et al.* 1990). After the Cretaceous, the Atlantic continued to open which also resulted in the closing of the Bering Strait 80 million years ago leading to the isolation of the Pacific from the Arctic Ocean during establishment of the Bering Land Bridge (Zonenshain & Natapov 1989). Reopening of the Bering Strait occurred 17 mya and has had several opening and closings over this time. The most recent opening of the Bering Strait, 7.4 to 4.1 million years ago allowed North Pacific and Arctic oceanic exchange (Gladenkov *et al.* 2002, Hoarau *et al.* 2007). Although

currently the water flow and arctic currents run from the North Pacific to the Arctic through the Bering Strait and out to the Atlantic, this may not have always been the case (Lindstrom 2001). An open Panamanian Isthmus from 6.4 to 3.5 mya would have resulted in a possible change in Arctic water flow from North Atlantic to North Pacific through the Arctic Ocean (Lindstrom 2001). The forming of the connection between North and South America 3.5 mya, isolating the Pacific and Atlantic Oceans, at what is now the Panama Canal, influenced Pacific and Atlantic water currents (Lindstrom 2001). This closing of the Panamanian Isthmus resulted in the change of oceanic currents to the Pacific to Atlantic flow present today (Lindstrom 2001, Marincovich & Gladenkov 1999).

Following the most current glacial retreat, beginning approximately 18000 years ago, the Arctic area once covered with ice was left exposed leaving wide unpopulated regions available for invading species (Van Oppen, M. J. H. *et al.* 1995). From a marine perspective it was not until the glacial retreat uncovered the shallow water environment with an underlying hard substratum that the shallow water marine organisms were able to survive (Adey & Steneck 2001). From an evolutionary perspective, this glacial retreat occurred very close to the opening of the Bering Strait (Gladenkov *et al.* 2002, Sher 1999). Fluctuations in near shore environment due to changing water levels, an increased area of permafrost resulting in less water run off, lower temperatures, and reduced water availability all influenced distributional changes in species (Hewitt 2004). With respect to the marine environment, the reduction of sea water and freezing of a large portion of the sea, has had the major impact on the evolutionary history of marine organisms, and has caused five aquatic mass extinction events through the earth's history by loss of habitat through freezing (McElwain & Punyasena 2007). The continued survival of species through the length of a

glacial period would be dependant on the fitness of the organisms and the availability of liquid water (Vincent *et al.* 2004).

Freezing seawater concentrates solutes such as sodium chloride in small water pools, which facilitates the maintenance of liquid water at below freezing temperatures causing higher absorption of sunlight do to reduced albedo (Vincent *et al.* 2004). This process results in available pools of liquid water through glaciations supporting organisms by providing the much-needed water for survival (Vincent *et al.* 2004). For some macroalgal species reduced water may not have played a significant role to their survival through glaciations (Lüning 1984). Lüning (1984) note that the species *F. vesiculosus,* which when dehydrated by approximately 30%, has an increased heat tolerance by nearly 5 °C. This change in temperature tolerance mechanism could have also contributed to species survival during glacial periods of reduced water.

The Arctic region and its ability to support organisms is relatively young (Dayton *et al.* 1994). These young traits show a direct relationship to the Pliocene glaciations between approximately 5 million to 18 000 years ago (Adey & Steneck 2001, Dunton 1992). Comparisons between the Arctic and Antarctic provide evidence of these relatively young characteristics (Piepenburg 2005). The Croll-Milankovitch theory has suggested a link to the Earth's orbit and an estimate of world glacial oscillations, including the glaciations during the Pleistocene at about every 100 thousand years (Hewitt 2000).

The extension of the northern ice sheet, at the last glacial maximum approximately 18000 years ago (Van Oppen, M. J. H. *et al.* 1995), was between 52 and 47 N latitude in Europe, approaching the current Iberian peninsula coast. The North American glacier had a

costal extension to approximately 42 N latitude and was a major influence as it covered a large area of habitat previously occupied by many species (Hewitt 2004, Coyer *et al.* 2003).

1.9 GLACIAL REFUGIA

A glacial refuge is an area of habitable environment where organisms survive during large-scale glacial events (Hoarau *et al.* 2007). During glacial expansion, ice sheets advanced and large climate changes resulted in shifting species distributions into refugial areas (Seddon *et al.* 2001). These pockets of surviving organisms have contributed to the current North American biogeography. The presence of a glacial refuge may be due to several factors such as historical climates and climate fluctuations, geothermal surface heat, species movement toward the equator, or areas of less water subsequently having less potential for ice (Vincent *et al.* 2004).

Presumably during this ice covered time, species with higher cold tolerance occupied more northern refugia where species adapted to warmer temperatures occupied more southern refugia as is seen in current fossil records (Hewitt 2004). Briggs (2006) attributes the success or failure of an organism to the incidence of cold-water pressures as opposed to warm water pressures. Adey and Steneck (2001) also point out the importance of water temperatures as an influence on marine macroalgae and the existence of marine biogeographic regions with scientific writings to support this dating back to Darwin and Wallace (Wallace *et al.* 2004, Darwin 1859). Temperature, particularly winter temperatures, often influences the distribution and overall community structure of marine organisms including coral reefs and kelp (Adey & Steneck 2001, Kröncke *et al.* 1998). Intertidal *Fucus* in particular are influenced by this cold winter season as sexual reproductive success of cold

water *Fucus* species decreases with increased temperature and low tide situations expose individuals to the possibility of desiccation in warm temperatures (Coleman & Brawley 2005).

The underlying principle when evaluating glacial refugia is that more recently colonized regions would contain a lower genetic diversity then ones which have existed longer (Widmer & Lexer 2001). Species currently observed in cold temperature environments, like *Fucus*, red algae of the genus *Leptophytum*, and Arctic Char (Lindstrom 2006, Athanasiadis 2008, Leder 2002), may exist due to the direct effects of the last ice age with its colder temperature influences creating more pressures for species of the region. When the ice receded the species continued to survive in the habitat retreating toward the poles leading to the cold adapted species and cold adapted endemic species we see today (Vincent *et al.* 2004).

Endemic species are often used as possible indicators of refugia through glacial cycles (Lomolino *et al.* 2006). The existence of such endemic species suggests their adaptation to their endemic location where they have had a long-standing presence through glacial extinctions (Adey & Steneck 2001). Beringia is an area with strong evidence to support past refugia through the last glaciation with terrestrial areas of high endemism such as the old growth forests of the Alexander Archipelago (Cook *et al.* 2001), and many described endemic algae (including *Asterocolax hypophyllophila* M.J. Wynne, *Compsonema tenue* Setchell et N.L. Gardner, *Orculifilum denticulatum* S.C. Lindstrom, *Pleonosporium pedicellatum,* S.C. Lindstrom, M.J. Wynne, et N.I. Calvin) (Lindstrom 2006, Wisely *et al.* 2008). This clear increase in both terrestrial and aquatic organisms with adaptations to survival in the region including red and brown algae and (Hewitt 2004, Avise 2000).

Lindstrom (2006) noted that these endemic seaweeds occurring in the Alaskan Beringia area indicates the presence of one or more past glacial refugial areas. The indication of refugial areas is not limited to the Alaskan area, there are also many proposed aquatic and terrestrial refugial areas throughout Europe, both large and small covering Arctic and near Arctic regions with narrows and straits similar to Beringia (Huntley & Birks 1983).

In these glacial areas, once the ice had receded, refugial species were free to populate the newly exposed habitat. The colonization of an unpopulated habitat is less demanding for a species then the colonization into an area already populated with increased competition for resources (Hewitt 2004). This competition for resources was not a factor for species of refuge because they were uniquely situated near receding ice with barren habitat to colonize (Hewitt 2004). However, due to the mixture of various refugial zones during glacial oscillations genetic diversity is not simple to evaluate (Comps *et al.* 2001). Furthermore, the distance between pre-glaciated distributions and areas of refuge during glacial cycles could also have had a major impact on the genetic diversity of the refugial regions. Less distant migrations generally yield larger final populations and therefore a higher overall genetic diversity within that population (Hewitt 2004).

Addison and Hart (2005) used DNA microsatellites to evaluate genetic variation in green sea urchins in the North Atlantic and North Pacific to evaluate past biogeography during glaciations. The study concluded *Strongylocentrotus droebachiensis* inhabiting the North West Atlantic was more closely related to those of the Pacific than the samples from North East Atlantic (Addison & Hart 2005). Hence, the use of the microsatellites in this study was very useful in evaluating the potential glaciations of the North Atlantic and the movement of the Sea Urchins. Barnosky (2008), however, brought up two interesting

problems associated with using current DNA to hypothesize historical species distribution. First, how are distributions and the genetic divergence of species affected in areas of glaciation? Secondly, if we could determine the length of time of the glacial periods and their impact on the genetic divergence how can we be sure that the same effect would occur in the absence of the glaciations? These two questions are very difficult to answer since we assume that the genetic differentiations in areas once glaciated are from the most recent glacial period. Evaluating species historical biogeography from the current DNA, a very small sample in the overall time of living organisms, is exceedingly difficult and, in many cases, leads to questionable final conclusions (Barnosky 2008). However, the estimates of refugial zones and species divergence are useful and informative when using appropriate techniques based on good evidence like fossil records and DNA fossil evidence (Graur & Martin 2004).

Unfortunately fossil records are not present for all organisms (including a soft bodied seaweed such as *Fucus*) to provide structure for inferring molecular divergence and areas of glacial refugia (Hoarau *et al.* 2007, Barnosky 2008). Most vertebrates with soft bodies do not have extensive fossil records and comprise a full one third of all animal phyla lacking accurate fossil record (Blair Hedges & Kumar 2004). Without the presence of fossil records it becomes necessary to estimate the rate of genetic divergence of species using a method that incorporates an evolutionary hypothesis (Barnosky 2008). A molecular clock is one example of a method used for analysis to estimate the rate of genetic divergence (Blair Hedges & Kumar 2004). When evaluating the biogeography of North American *Fucus* species consideration of possible refugial zones must be considered.

1.10 CLIMATE

Marine organisms of the Arctic region, including algae, are largely influenced by changing climate (Kröncke *et al.* 1998). Understanding the influence of historical climates and climate changes in the Arctic region can help us to elucidate the current relationships of algae in the Arctic. Temperatures, particularly winter temperatures, often influence the distribution and overall community structure of near shore marine organisms including coral reefs and kelp (Adey & Steneck 2001, Kröncke *et al.* 1998). Rapid Pleistocene climate changes had major influences on the intertidal zones with freeze thaws causing movement of the near shore intertidal zones had (Adey & Steneck 2001). This disruption and changing of water temperatures and water movements has certainly altered the thermal definition of the Arctic intertidal (Adey & Steneck 2001).

Environmental pressures that affect species survival, through both glacial and inter-glacier periods, include the expansion of year round permafrost, lower mean annual temperatures and the overall reduction of water availability (Hewitt 2004). Bennet (1997) also points out the importance of the reflective nature of the increased surface area of ice and snow (called albedo) in the creation of robust climatic models. Albedo could have had a significant impact on the overall climate of a region during high glacial periods. This could have lead to temperature variation and potential varied distribution of species (Bennett 1997). Historical information on physical factors in the region and paleoclimate data has shown that large scale climate changes have effected Arctic organisms for time periods lasting anywhere from years to decades (Schumacher & Kruse 2005).

Current climate conditions are also a concern for the Arctic Region (Piepenburg 2005). Climate changes directly affect water temperatures and therefore directly affect

Arctic near shore marine environments (Kröncke *et al.* 1998). The creation of models to estimate environmental conditions through time is one method used to help understand and explain both past and present species distributions. Recently a global warming effect has caused an increase in atmospheric temperatures as much as 4^{o}C in portions of the Arctic region (Oechel & Vourlitis 1994). Oechel and Vourlitis (1994) predict that the Arctic region will see an increase in the presence of temperate organisms if these regional temperatures continue to increase or stay consistent. This increase in temperature causes ground thaw resulting in more water absorption by the soil and less water run off, decreasing the movement of soil nutrients to the near shore zone (Oechel & Vourlitis 1994).

Coleman *et al.* (2005) agrees with the importance of climate on the marine environment and examined different *Fucus* species (*F. distichus and F. evanescens*) to determine the effect of water r temperature fluctuations on bimodal annual reproduction. Samples were collected (including herbarium material) and the number of reproductive fronds on each plant was counted and compared to historical water temperature data over the same relative locations and time periods. The resulting data supported the conclusion that water temperature fluctuations caused variations in annual reproductive activity, which can lead to unsuccessful reproduction and increased selfing. This further suggests the importance of water temperatures, and water fluctuations from climatic variation, to reproductive success in *Fucus* species (Coleman & Brawley 2005).

1.11 ARCTIC ALGAL PARADOX

Speculation on the existence of an Arctic algal paradox has also been suggested (Dunton 1992). Dunton (1992) discussed how the majority of the Arctic marine flora, and specifically

algal species, appear to have distinct Atlantic affinities compared to few examples of Arctic flora with Pacific affinities. It was noted that the direction of Arctic water flow has been from North Pacific to Arctic and finally Atlantic for nearly 5.5 million years (Dunton 1992). The paradox is further examined in that there are few endemic algal species in the Arctic, a region of a distinctly young species (Dunton 1992, Dayton *et al.* 1994). Dunton (1992) also mentions that the fauna, both benthic and near shore terrestrial species, are predominately from the Pacific coast (Dunton 1992). The combination of these factors, as mentioned by Dunton (1992), makes up the Arctic algal paradox.

On the other hand, Lindstrom (2001) disagrees with the Arctic paradox and suggests that species are varying in origins because of migration of species from both oceans, multiple glaciations where some species may have survived in small refuges, and the intermittent opening and closing of the Bering strait. Lindstrom's argument of small ice-free areas during the Pleistocene has also been proposed on the European coasts of Scotland and Norway (Van Oppen, M. J. H. *et al.* 1995). Gladenkov *et al.* (2002) noted that the first opening of the Bering Strait ending terrestrial migrations for a time 5.5 to 5.4 million years ago. This could support Lindstrom's (2001) argument indicating that the Arctic near land and land animals have a higher evolutionary relation to Pacific coast land animal species because they had an earlier migration for a longer duration then the other aquatic species.

Another possible factor influencing biota in the Arctic Ocean region is that although the Bering Strait opened, there may not have been significant water volume exchange due to the relatively shallow nature of the Strait (Briggs 2003). The shallow nature of the strait may have reduced the movement of water from the North Pacific into the Arctic Ocean but this shallow nature may also have assisted in the movement of benthic organisms. The near shore

biota in the North Pacific would not have been able to move as easily into the Arctic across the entire Bering Strait if it were too deep. And conversely, the deep-water fauna and ostracods that live and thrive below the 50-meter depth may not have had opportunity to migrate across the shallow strait (Dunton 1992). The direct influence of historical land mass movements and the shallow nature of the strait would have allowed movement of near shore algae further supporting Lindstrom (2001) argument that Arctic species are more equally distributed from Pacific and Atlantic.

1.12 THESIS OBJECTIVES

Examine the genetic relationship and biogeography among the North Pacific, North Atlantic and Arctic Ocean *Fucus* species to ascertain their genetic variation and phylogenetic position.

The amplification and analysis of the divergent mtDNA spacer region was performed to assess taxonomic placement of 52 collected species and reconstruct the biogeography of North American *Fucus* species. These sequences were then compared to current literature using the same region of mtDNA to gain a better understanding of population distributions in the context of global collections *Fucus* species.

Determine if the current morphological species concept agrees with genetic information and phylogenetic analyses.

Using 21 measured morphological characters of 158 samples, clustering analysis was performed to determine if the measured characters are informative and sufficient to separate

collected samples into groups. Resulting groups from the hierarchical clustering were then evaluated based on the geographic collection location, level of exposure to open ocean at the point of collection, season of collection, and molecular phylogenetic analysis groupings to determine character reliability in separating samples. Finally, discriminant function analysis was performed using the above groups as grouping variables and the reliable characters within the data set for separation into informative groups were determined.

2.0 MATERIALS AND METHODS

2.1 COLLECTION AND STORAGE

Samples of *Fucus* were collected from the Pacific, Arctic and Atlantic Oceans and sample locations are noted in Figure 2. Corresponding location names and coordinates of these samples are listed in Table 2. A full listing of all collected samples at each site is included in Appendix A. Specimens were collected from high to mid intertidal areas predominately along shorelines of rocky substrate from cold-water marine environments similar to that seen in Figure 3.

After collection, samples were placed in plastic bags, sealed and stored in cool dark conditions until return to the laboratory. Some specimens were also dehydrated using silica gel when collection trips were longer than one week. Upon return to the laboratory, fresh samples were immediately stored at 4^{o}C. Over three days, these samples were individually rinsed three times in a 3% salt deionizing water solution to remove excess compounds and epiphytic organisms. A final rinse in an eliminating polysaccharide buffer wash consisting of 20% ethanol and 0.5 M potassium acetate (KAc) was conducted to eliminate excess polysaccharides (Jobes *et al.* 1995, Wang *et al.* 2005). This last rinse was conducted due to an abundance of polysaccharides interfering with the extraction of intact DNA from the brown algae (Wang *et al.* 2005). A potassium acetate rinse causes a precipitation of polysaccharides, which reduces the total amount of interfering polysaccharides (Jobes *et al.* 1995). Following this rinse, *Fucus* plants were air-dried and a small portion was clipped from the main portion of each plant, ground in liquid nitrogen, and stored at -80^{o}C for later molecular analyses. The remaining algal material was then mounted on herbarium sheets for later morphological analysis.

Figure 2. A map of North America indicating sites of collection. In some cases multiple samples from a single population were collected. There were also sites with multiple collections among different populations from the same area with the samples having variation in morphology. Collection location numbers correspond to collection locations in Table 2.

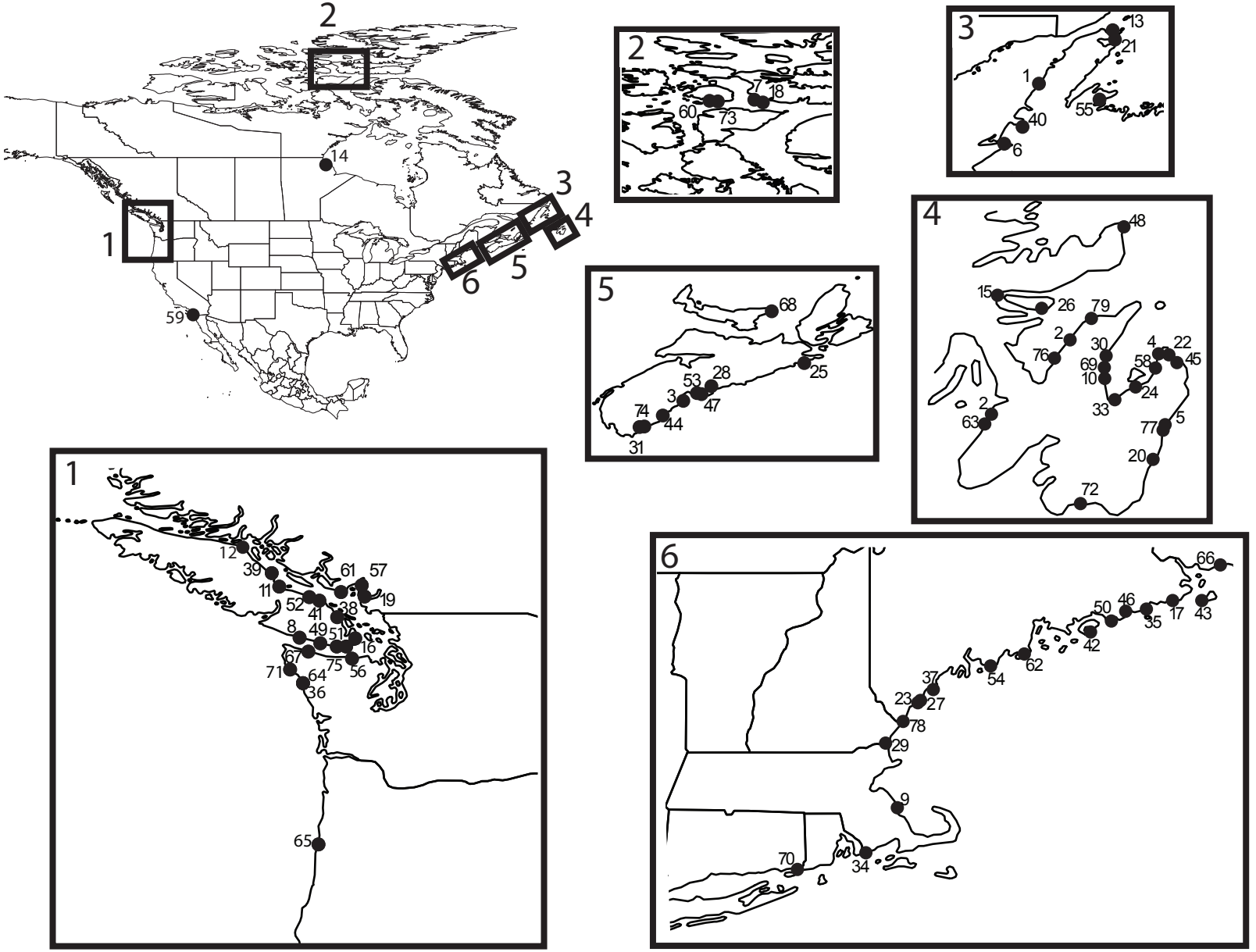

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Table 2. A listing of samples sites with corresponding longitude and latitude coordinates. Sample numbers match map points in Figure 2.

Number	Collection Location	Long.	Lat.
1	Arches Provincial Park Newfoundland Canada	50.16	-57.62
2	Argentia Newfoundland Canada	47.29	-53.99
3	Battery Point Breakwater, Lunenburg Nova Scotia Canada	44.36	-64.30
4	Bauline Newfoundland Canada	47.72	-52.83
5	Bay Bulls Newfoundland Canada	47.31	-52.81
6	Bear Cove Newfoundland Canada	48.54	-58.56
7	Beechy Island NWT Canada	74.70	-91.81
8	Botany Bay British Columbia Canada	48.53	-124.45
9	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65
10	Brigus Newfoundland Canada	47.54	-53.20
11	Bukley's Bay British Columbia Canada	49.53	-124.85
12	Campbell River British Columbia Canada	48.03	-125.24
13	Cape Onion Newfoundland Canada	51.61	-55.62
14	Churchill Manitoba Canada	58.77	-94.13
15	Clarenville Newfoundland Canada	48.16	-53.96
16	Cordoba Bay B.C. Canada	48.52	-123.37
17	Cutler Naval Base Maine USA	44.67	-67.25
18	Devon Island NWT Canada	74.67	-91.70
19	Dunderave Park West Vancouver B.C. Canada	49.33	-123.18
20	Ferryland Newfoundland Canada	47.03	-52.89
21	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56
22	Flatrock Newfoundland Canada	47.71	-52.71
23	Fortune Rocks Maine USA	43.43	-70.38
24	Foxtrap Newfoundland Canada	47.52	-52.99
25	Georges Ledge, Tor Bay Nova Scotia Canada	45.20	-61.39
26	Goose Berry Cove Newfoundland Canada	48.03	-53.64
27	Goose Rocks Beach Maine USA	43.40	-70.41
28	Halifax Nova Scotia Canada	44.65	-63.58
29	Hampton Beach New Hampshire	42.90	-70.81
30	Harbour Grace Newfoundland Canada	47.70	-53.21
31	Harts Point, Shelburne Nova Scotia Canada	43.73	-65.34
32	Hearts Desire Newfoundland Canada	47.81	-53.44
33	Holyrood Newfoundland Canada	47.39	-53.13
34	Horseneck Beach Massachusetts	41.51	-71.06
35	Just Past Jonesport Maine USA	44.56	-67.57
36	Kalaloch Beach Washington USA	47.64	-124.39
37	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22
38	Kin Beach Cowichen B.C Canada	48.93	-123.72
39	Kitty Coleman Provincial Park B.C. Canada	49.79	-125.00
40	L'anseaut Meadows Newfoundland Canada	49.00	-58.06
41	Lantzville British Columbia Canada	49.25	-124.07
42	Long Point, Cranberry Island Maine USA	44.26	-68.27
43	Lubec Maine USA (under boarder crossing)	44.67	-66.98
44	Massacre Island, off Port Mouton Nova Scotia Canada	43.93	-64.82
45	Middle Cove Newfoundland Canada	47.65	-52.70
46	Millbridge Maine USA	44.54	-67.88
47	Myra Island Skerry, Blind Bay Nova Scotia Canada	44.51	-63.84
48	Nameless Cove Newoundland Canada	48.62	-53.01
49	Near Jordan River Hwy 14 Vancouver Island B.C. Canada	48.42	-124.05
50	On the road to Corea Maine USA	44.41	-68.01
51	Parker Bay British Columbia Canada	48.36	-123.54
52	Parksville British Columbia Canada	49.32	-124.26
53	Peggy's Cove Nova Scotia Canada	44.49	-63.92
54	Pemaquid Point Maine USA	43.84	-69.51

Number	Collection Location	Long.	Lat.
55	Perry Cove Newfoundland Canada	49.73	-55.98
56	Port Angeles Washington USA	48.12	-123.43
57	Porteau Provincial Park B.C. Canada	49.55	-123.24
58	Portugal Cove Newfoundland Canada	47.63	-52.86
59	Pt. Lona California USA	32.67	-117.25
60	Resolute Town NWT Canada	74.68	-94.90
61	Roberts Creek, British Columbia Canada	49.42	-123.64
62	Rockland Maine USA	44.10	-69.11
63	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93
64	Ruby Beach Washington USA	47.64	-124.39
65	Seal Rock Orgeon USA	44.49	-124.08
66	Sealys Bay New Brunswick Canada	45.08	-66.65
67	Sekui Washington USA	48.26	-124.28
68	Singing Sands PEI Canada	46.38	-62.11
69	Spaniards Bay Newfoundland Canada	47.61	-53.28
70	Stonington Connecticut USA	41.33	-71.91
71	Teahwhit Washington USA	47.91	-124.64
72	Trespassey Newfoundland Canada	46.73	-53.37
73	West end of Assistance Bay southside of Cornwallis NWT Canada	74.65	-94.36
74	Western Way, Shelburne Nova Scotia Canada	43.76	-65.32
75	Whiffin Spit Park British Columbia Canada	48.36	-123.73
76	Whiteway Newfoundland Canada	47.69	-53.49
77	Witless Bay Newfoundland Canada	47.28	-52.83
78	York Point Maine USA (In park near Lighthouse)	43.17	-70.59
79	Hants Harbour Newfoundland Canada	48.02	-53.27

Figure 3. Intertidal zone with *Fucus* attached to the rocky substrate in Brant Rock Massachusetts, USA (November 30, 2006).



2.2 MORPHOLOGICAL EVALUATIONS

Herbarium samples of collected *Fucus* from the Pacific, Arctic and Atlantic Oceans and sample locations are noted in Figure 4 and Table 3. In order to determine the presence of any morphologically defining species characteristics, morphological characters were selected and measured on a total of 158 herbarium specimens. Where possible a total of 21 characters were measured for each plant. The selection of measured characters was based on *Fucus* morphological studies by Rice *et al.* (1985), Bäck (1993), and Ruuskanen and Nappu (2005). All continuous characters were measured, using standard 15 and 30 cm rulers, to an accuracy of 1 mm and non-continuous characters were recorded as integers. For each sample, measurements and counts were recorded and placed in a table for statistical analysis (Appendix B). The methodologies of measurements are listed in Table 4. Where possible five measurements were taken for each character and the average of these five values was used in the morphological analyses: Each measurement number in Table 4 corresponds to measurement numbers in Figure 5.

- Plant length (PLTLG) - measured from the holdfast to the distal frond tip.
- Plant width (PLTWD) - widest point from frond tip to frond tip of the plant on a line across the plant nearly perpendicular to the stipe.
- The number of stipes (STPNUM) emanating from the holdfast.
- Stipe length (STPLG) - measurement from the holdfast to the oldest dichotomy or the one closest to the holdfast.
- Stipe width (STPWD) - the widest point on the stipe between the holdfast and the oldest dichotomy.

Figure 4. A map of North America indicating sites of herbarium samples. In some cases multiple samples from a single location are present. Collection location numbers correspond to collection locations in Table 3.

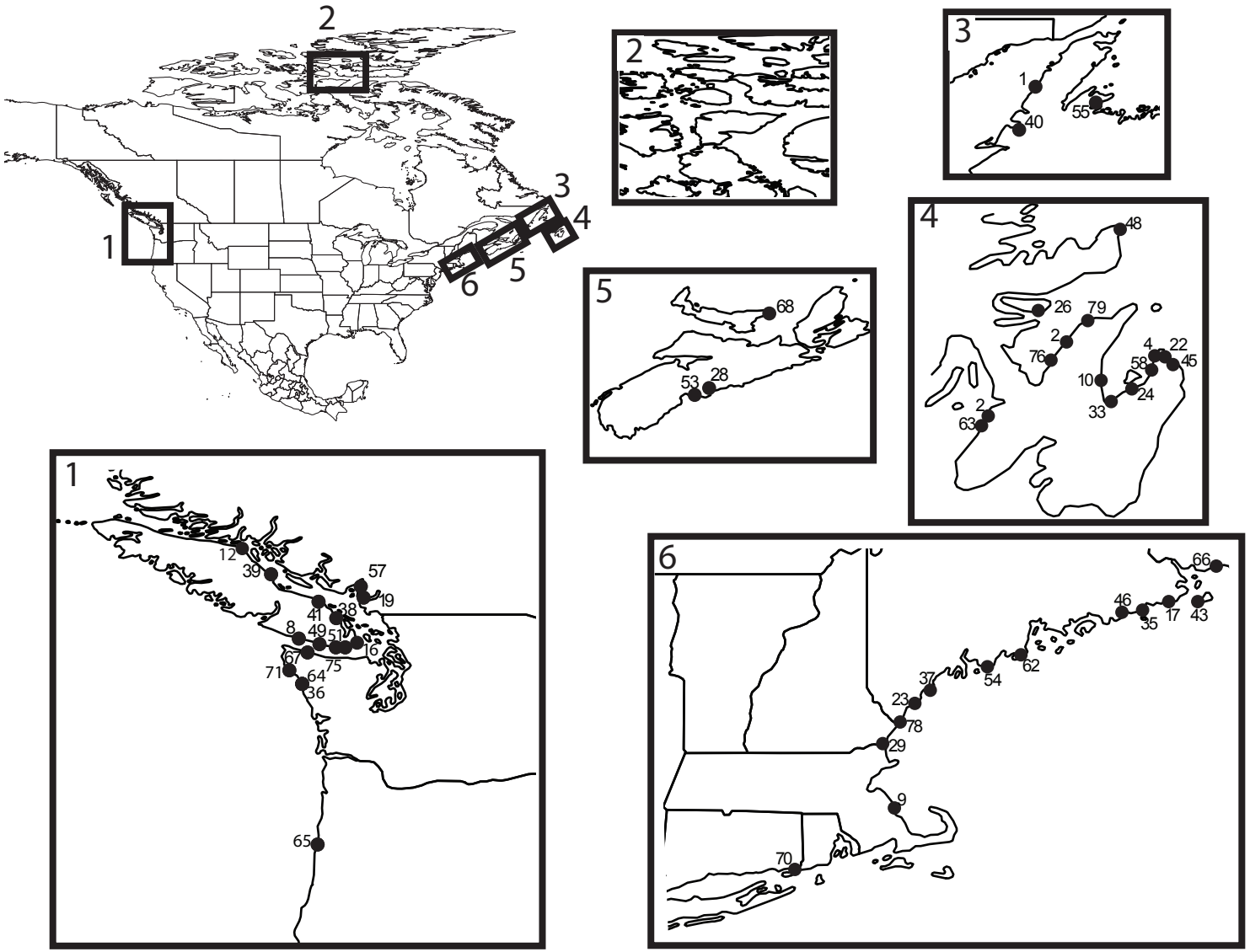

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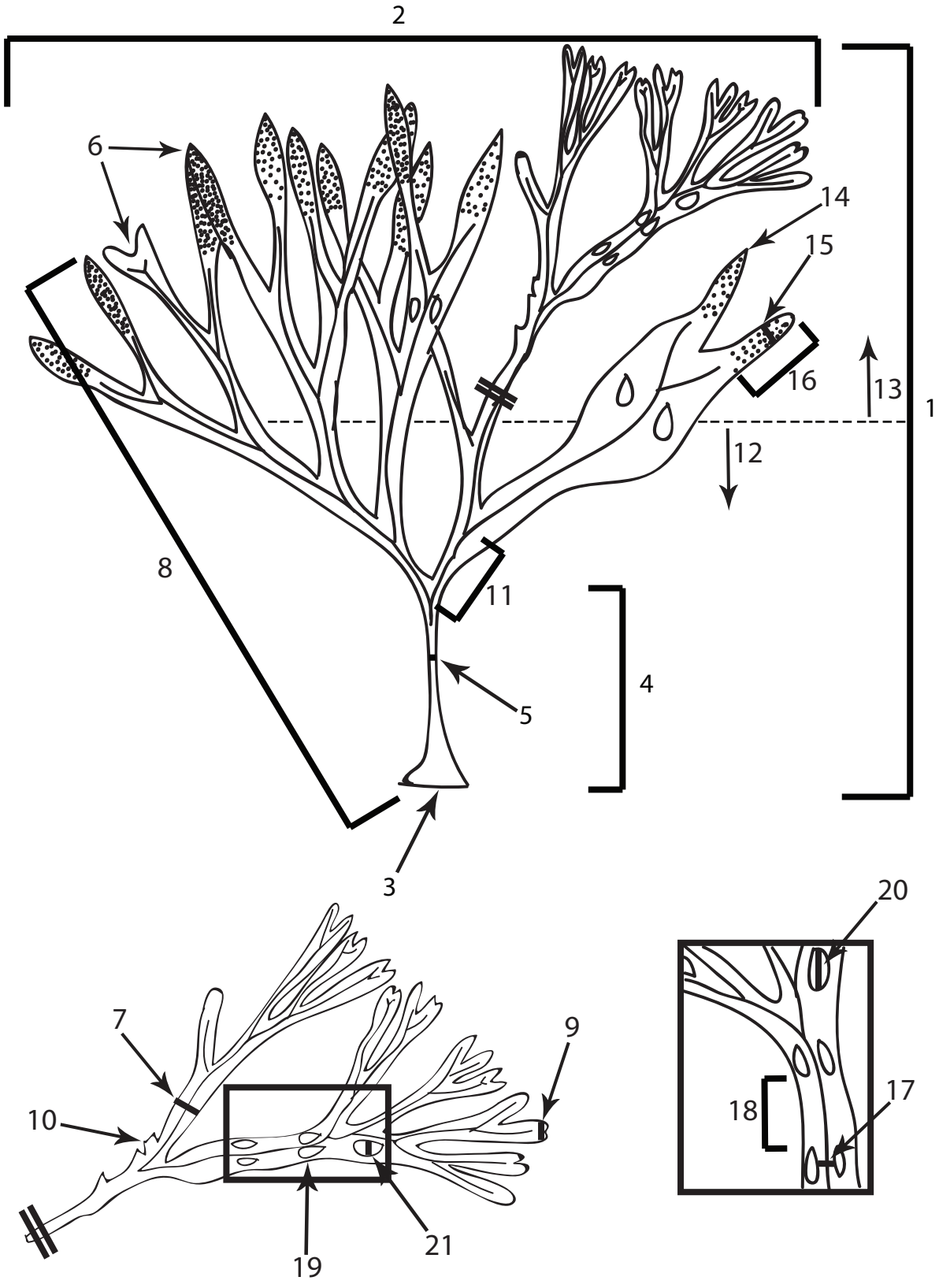
Table 3. A listing of herbarium sample sites with corresponding longitude and latitude coordinates. Sample numbers match map points in Figure 4.

Number	Collection Location	Long.	Lat.
1	Arches Provincial Park Newfoundland Canada	50.16	-57.62
2	Argentia Newfoundland Canada	47.29	-53.99
4	Bauline Newfoundland Canada	47.72	-52.83
8	Botany Bay British Columbia Canada	48.53	-124.45
9	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65
10	Brigus Newfoundland Canada	47.54	-53.20
12	Campbell River British Columbia Canada	48.03	-125.24
16	Cordoba Bay B.C. Canada	48.52	-123.37
17	Cutler Naval Base Maine USA	44.67	-67.25
19	Dunderave Park West Vancouver B.C. Canada	49.33	-123.18
22	Flatrock Newfoundland Canada	47.71	-52.71
23	Fortune Rocks Maine USA	43.43	-70.38
24	Foxtrap Newfoundland Canada	47.52	-52.99
26	Goose Berry Cove Newfoundland Canada	48.03	-53.64
28	Halifax Nova Scotia Canada	44.65	-63.58
29	Hampton Beach New Hampshire	42.90	-70.81
32	Hearts Desire Newfoundland Canada	47.81	-53.44
33	Holyrood Newfoundland Canada	47.39	-53.13
35	Just Past Jonesport Maine USA	44.56	-67.57
36	Kalaloch Beach Washington USA	47.64	-124.39
37	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22
38	Kin Beach Cowichen B.C Canada	48.93	-123.72
39	Kitty Coleman Provincial Park B.C. Canada	49.79	-125.00
40	L'anseaut Meadows Newfoundland Canada	49.00	-58.06
41	Lantzville British Columbia Canada	49.25	-124.07
43	Lubec Maine USA (under boarder crossing)	44.67	-66.98
45	Middle Cove Newfoundland Canada	47.65	-52.70
46	Millbridge Maine USA	44.54	-67.88
48	Nameless Cove Newoundland Canada	48.62	-53.01
49	Near Jordan River Hwy 14 Vancouver Island B.C. Canada	48.42	-124.05
51	Parker Bay British Columbia Canada	48.36	-123.54
53	Peggy's Cove Nova Scotia Canada	44.49	-63.92
54	Pemaquid Point Maine USA	43.84	-69.51
55	Perry Cove Newfoundland Canada	49.73	-55.98
57	Porteau Provincial Park B.C. Canada	49.55	-123.24
58	Portugal Cove Newfoundland Canada	47.63	-52.86
62	Rockland Maine USA	44.10	-69.11
63	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93
64	Ruby Beach Washington USA	47.64	-124.39
65	Seal Rock Orgeon USA	44.49	-124.08
66	Sealys Bay New Brunswick Canada	45.08	-66.65
67	Sekui Washington USA	48.26	-124.28
68	Singing Sands PEI Canada	46.38	-62.11
70	Stonington Connecticut USA	41.33	-71.91
71	Teahwhit Washington USA	47.91	-124.64
75	Whiffin Spit Park British Columbia Canada	48.36	-123.73
76	Whiteway Newfoundland Canada	47.69	-53.49
78	York Point Maine USA (In park near Lighthouse)	43.17	-70.59
79	Hants Harbour Newfoundland Canada	48.02	-53.27

Table 4. A listing and description of the 21 vegetative characters used to measure *Fucus* samples. Measurements were made to an accuracy of 1mm on all plants where morphological characters were present. (Note measurement identification numbers correspond to those in Figure 5)

Measurement Identification Number	Morphometric Character	Name Abbreviation	Description
1	Plant Length	PLTLG	Holdfast to most distal frond tip
2	Plant Width	PLTWD	Widest point on plant approximately 90 degrees to holdfast
3	Stipe Number	STPNUM	Number of stipe emanating from a single holdfast
4	Stipe Length	STPLG	Measured from the holdfast to the oldest dichotomy. Mean of 5 measurements where possible.
5	Stipe Width	STPWD	Widest point on stipe between holdfast and oldest dichotomy. Mean of 5 measurements where possible.
6	Number of Fronds	FRNDNUM	Total Number
7	Frond width	FRNDWD	Measured at base of dichotomies. Mean of 5 measurements where possible.
8	Frond Length	FRNDLG	Measured from holdfast to tip of fronds. Mean of 5 measurements where possible.
9	Width of frond at distal point	FRNDDISTWD	Measured at widest point distally on the frond before apex. Mean of 5 measurements where possible.
10	Number of serrations on Frond	SERNUM	Total Number
11	Average distance between dichotomies	BRCHDIST	Mean of 5 measurements where possible starting with measurement from oldest dichotomy to more recent dichotomies.
12	Number of lower dichotomies	BRCHLOW	Number of dictotomies from holdfast to 1/2 plant height
13	Number of upper dichotomies	BRCHUP	Number of dictotomies from 1/2 plant height toward frond tips
14	Number of recepticals	RECNUM	Total Number
15	Width of recepticals	RECWD	Mean of 5 measurements where possible.
16	Length of recepticals	RECLG	Mean of 5 measurements where possible.
17	Distance between two in a pair of vesicles	VESDISTBT2	Mean of 5 measurements where possible.
18	Distance between two pairs of vesicles	VESDISTBTPRS	Mean of 5 measurements where possible.
19	Number of vesicles	VESNUM	Total Number
20	Length of Vesicles	VESLG	Mean of 5 measurements where possible.
21	Width of Vesicles	VESWD	Mean of 5 measurements where possible.

Figure 5. Morphometric characters displayed as measured on collected specimens of *Fucus*. For a description of measurement methodology see Table 4. 1. Plant Length (mm), 2. Plant Width (mm), 3. Stipe Number (integer), 4. Stipe Length (mm), 5. Stipe Width (mm), 6. Number of Fronds (integer), 7. Frond width (mm), 8. Frond Length (mm), 9. Width of frond at distal point (mm), 10. Number of serrations on Frond (integer), 11. Average distance between dichotomies (mm), 12. Number of lower dichotomies (integer), 13. Number of upper dichotomies (integer), 14. Number of receptacles (integer), 15. Width of receptacles (mm), 16. Length of receptacles (mm), 17. Distance between two in a pair of vesicles (mm), 18. Distance between two pairs of vesicles (mm), 19. Number of vesicles (integer), 20. Length of Vesicles (mm), 21. Width of Vesicles (mm).


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- Total number of fronds (FRNDNUM) - the total number of distal vegetative or reproductive tips where separation by a mid rib was apparent.
- Frond width (FRNDWD) - measured on the plant at the widest point directly before a dichotomous division.
- Frond length (FRNDLG) - was measured in the same manner as plant height and where possible four measurements were recorded from four quadrants on the plant, as established by the plant width, while not repeating the plant height measurement.
- Frond distal width (FRNDDISTWD) - measured by taking the widest point distally on the frond before apex and after separation from sister fronds.
- Mean number of serrations per frond (SERNUM) - determined by the clear points emanating from jagged edges on both sides of a given frond.
- Average distance between dichotomies (BRCHDIST) - the distance from the division of midrib of the oldest dichotomy to the division of midrib of the next oldest dichotomy continuing distally along the plant.
- Total number of lower dichotomous branches (BRCHLOW) - The lower half of the plant was determined as the measurement from holdfast to one half the height of the plant. The remaining dichotomous branching was counted as the number of upper branching (BRCHUP) events on the plant.
- Total number of apical receptacles (RECNUM) on the plant.
- Width of the receptacle (RECWD) - the widest part of the receptacle perpendicular to the midrib of the frond from which it emanates.

- Length of receptacle (RECLG) - the longest part of the receptacle parallel to the midrib.
- Total number of air vesicles (VESNUM) present on the plant.
- Distance between paired air vesicles (VESDISTBT2) – when air vesicles occurred in pairs.
- Mean distance between pairs of vesicles (VESDISTBTPRS) - when multiple pairs of vesicles occur on a single frond.
- Vesicle width (VESWD) - the widest part of the vesicle perpendicular to the midrib of the frond from which it was located.
- Length of vesicle (VESLG) - the longest part of the vesicle parallel to the midrib.

Recorded measurements (Appendix B) in the matrix were subjected to various analyses including basic statistical analyses, hierarchical clustering, and discriminant analyses. All statistical analyses were completed with Systat version 10 for Windows operating system (SPSS Inc. 2000). Statistical analyses were only completed using samples with reproductive characters to eliminate the possibility of having non-mature plants, and therefore containing no reproductive receptacles, skewing results. Basic statistics including, total number of cases, minimum, maximum, median, mean, and standard deviation were obtained for all measured characters in the data set using only reproductive samples. Hierarchical clustering was conducted using Euclidian distance for collected samples with reproductive bodies. Hierarchical clustering using Euclidian distance was also conducted where only the total number of vesicles per plant (VESNUM) was used for vesicle data

across the reproductive sample set in an attempt to determine if the lack of vesicle data for all samples was affecting clustering results.

The lack of an accepted treatment for use in the identification of North American *Fucus* species does not allow for the use of morphologically identified samples to be subjected to discriminant analysis. As such four different *a priori* groups were chosen for use in the discriminant analysis of the morphological data matrix. These four groups were 1) season of collection, 2) geographical collection locations (Pacific versus Atlantic), 3) direct exposure to ocean, and 4) clades of tree structure based on molecular analyses.

A discriminant analysis was undertaken to determine statistically significant differences among *a pirori* groups using all specimens exhibiting reproductive characters. Characters that were most useful in separating the samples based on season of collection, geographical location, exposure to open ocean, and clades of tree structure based on molecular analyses were determined first by stepwise discriminant analysis and recorded. A stepwise discriminant analysis was also conducted using the same specimens with only the number of vesicles (VESNUM) included for vesicle data. This was performed to determine if the lack of data for some samples for vesicle measurements was creating a bias in the discriminant analyses.

Using discriminant functions, samples in the data set were assigned to groups *a posteriori.* These groups were tested through statistical probabilities (Wilks' λ, Piallai's trace, and Hotelling-Lawley trace) based on distance between group centroids in N-dimensional hyperspace. Geisser assignment probabilities were also used to determine placement of samples in to the *a posteriori* groupings based on Mahalanobis distances in N-dimensional hyperspace and F statistics based on the distances. Classificatory analysis was

completed using these placements of samples in to the *a priori* groups. This analysis was subjected to jack-knife resampling to provide support for classification of samples. Geisser probabilities were evaluated to ensure correct *a posteriori* placement of samples with low assignment probabilities did not display grouping based on weak separation of samples.

2.3 DNA ISOLATION

DNA extraction is difficult for many macroalgae due to the high concentration of polysaccharides, tannins, and proteins (Wang *et al.* 2005, Hu *et al.* 2004, Mayes *et al.* 1992, Phillips *et al.* 2001, Varela-Alvarez *et al.* 2006). Early DNA extraction attempts were performed using various extraction methods including the Qiagen DNeasy Plant Mini Kit (Qiagen, Canada), Promega Wizard DNA Extraction Kit (Promega, USA), MOBIO PowerSoil DNA Extraction Kit (MOBIO, Canada), and a nuclear DNA extraction procedure (Varela-Alvarez *et al.* 2006). These early extraction attempts yielded poor quality DNA and insufficient yields for subsequent successful PCR amplifications. The Saunders (1993) phenol/chloroform procedure was noted to extract sufficient quantities of DNA (Mayes *et al.* 1992, Saunders 1993) and hence this procedure was used with several modifications to enhance the quantity and quality of the DNA yields. For example, the lysis buffer was modified with final concentrations of 0.1M Tris HCl, 1.5% Sodium Dodctyl Sulfate (SDS), 1.5M NaCl (Apt & Grossman 1993), 1% weight per volume of polyvinylpyrrolidone (PVP) (Wang *et al.* 2005), and 2% beta-mercaptoethanol (Varela-Alvarez *et al.* 2006). Furthermore, when fresh ground material was added to the lysis buffer the quantity of the ground material was increased from that used in the Saunders (1993) procedure to approximately 2g of ground material for each extraction to increase the overall yield of DNA

(Hong *et al.* 1995). After incubation in lysis solution 1/3 volume of 5M KAc was added to the extracts and the samples were kept on ice for thirty minutes to further precipitate polysaccharides from the extract solutions (Wang *et al.* 2005). These steps were altered in an attempt to increase the DNA yield while minimizing the amount of interfering compounds in the final extracts. Finally, the number phenol/chloroform/isoamyl alcohol extraction rounds, following the lysis portion of the procedure, was increased from 3 to between 12 and 15 in an attempt to reduce contaminates within the final extract solutions.

Although the modified Saunders (1993) procedure did yield DNA of sufficient quality for PCR amplification, the results were not consistent and there were many samples that did not produce a sufficient DNA yield for further analysis. This fact, in combination with the time intensive extraction (due to the numerous rounds of phenol/chloroform/isoamyl alcohol required) and cost of reagents for the procedure resulted in an overall inefficient procedure. Hence, these problems created a need for a more effective and efficient method of extraction. The Invisorb® Spin Plant Mini Kit (Invitek, Germany) was then utilized and provided the most consistent DNA yields from any previously attempted procedure and was used for all future extractions.

2.4 DNA AMPLIFICATION AND SAMPLE PREPARATION

Amplification of the mitochondrial 23S ribosomal RNA gene-23S ribosomal RNA-tRNA-Val intergenic spacer region (23S mtDNA) was completed using forward primer 5‘ CGTTTGGCGAGAACCTTACC 3’ and reverse primer 5’ TACCACTGAGTTATTGCTCCC 3’(Coyer *et al.* 2006a) on an Eppendorf Mastercycler® Gradient 5331 (Eppendorf, Canada). PCR amplification was performed in 50 µl volume

reactions with 100mM reaction buffer, 25mM $MgCl_2$, 0.25mM of each dNTP, 4mM of each primer (Sigma-Aldrich, Canada), 1.0 unit of Fisherbrand™ Taq polymerase (Fisher Scientific, Canada), 0.3µl of bovine serum albumin (BSA) at 10mg/ml, and 1µl of template DNA. The thermocycler amplification was conducted with the following protocol: denaturation at 94°C for 4 minutes, followed by 30 cycles of denaturation at 94°C for 30 seconds, annealing at 45°C for 30 seconds, elongation at 72°C for 30 seconds, and concluding with a final elongation step of 72°C for 5 minutes.

After PCR amplification a portion of the PCR product (5µL) was loaded into a 1.5% agarose gel along side a HaeIII digested Lambda phage ladder (New England Biolabs, Canada) for fragment size estimation. Electrophoresis was performed in a FisherBrand electrophoresis apparatus containing TBE buffer (0.089M Tris, 0.089M Boric Acid, 0.02mM EDTA pH 8). Gel electrophoresis was then carried out at 120V for 45 minutes; the agarose gel was removed and then placed in TBE buffer with ethidium bromide (1µg/ml) for staining. After approximately 30 minutes gels were visualized using the Syngene BioImaging System (Synoptics Limited© 2000).

PCR products were deemed successful if a band of DNA was visible near the 600 to 800 base pair region on the agarose gel. Successful amplifications were purified using the QiaQuick PCR purification kit (Qiagen, Canada). Purified samples were sequenced using an Applied Biosystems 3130XL Genetic Analyzer at the University of Waterloo Molecular Biology Core Facility and an Applied Biosystems 3730 DNA Analyzer at the University of Guelph Advanced Analysis Centre. Both systems employ a dye termination method of DNA sequencing. Sequence chromatograms were viewed and sequences were manually edited using the BioEdit alignment editor program (www.mbio.ncsu.edu/BioEdit/bioedit.html). In

addition to the 52 sequences obtained through laboratory procedures, 44 sequences for the region of interest were also obtained from NCBI's GenBank (http://www.ncbi.nlm.nih.gov/) as well as one *Hesperophycus californicus* P.C. Silva sequence for use as an outgroup (Table 5; Coyer *et al.* 2006a).

2.5 MOLECULAR DATA ANALYSIS

An overall sequence alignment, including new sequences as well as sequences obtained from NCBI, was conducted in three steps. All sequence alignment steps were conducted using the MUSCLE multiple sequence alignment program version 3.6 (Edgar 2004). First, all new sequence data was aligned and saved as a multiple sequence alignment (MSA). Secondly, the NCBI sequences were also aligned in the same manner as the new sequences. Finally, MUSCLE was used to construct a profile alignment with the previous two alignments to yield an overall multiple sequence alignment.

At each of the three steps, the multiple sequence alignments were manually edited. On the final alignment, regions at both 5' and 3' ends of the overall sequence alignment were truncated to remove areas of unreliability where there were many unknown nucleotide positions and unreliable chromatogram peaks. Furthermore, during manual sequence editing 16 nucleotide bases of the sequence alignment was removed from a non-informative region between nucleotides 135 and 151.

The final alignment was then analyzed using the program PAUP version 4.0 (Phylogenetic Analysis Using Parsimony) to score the data (Swofford 1998). This scoring information was used with the Modeltest (Posada & Crandall 1998) program to provide a model of evolution. Four separate analyses were then conducted on the multiple sequence

alignment: neighbor-joining (using PAUP), maximum likelihood (using PhyML), and Bayesian analysis (PAUP). Finally, the Splitstree (Huson & Bryant 2006) program was used to construct a phylogenetic network from the sequence alignment using neighbor-net and Split Decomposition methods. The freely available tree viewing program, FigTree Version 1.1.2, was used to view phylogenetic trees for later editing and creation of figures (http://tree.bio.ed.ac.uk/software/figtree/).

Table 5. GenBank accession numbers and reference for samples used in the phylogenetic analysis to supplement experimentally obtained sequences.

GenBank Accession Number	*Species*	Reference
AY494079	*Fucus vesiculosus*	Secq *et al.* (2006)
AY659874	*Fucus serratus*	Coyer et al. (2006)
AY659876	*Fucus serratus*	Coyer et al. (2006)
AY659877	*Fucus serratus*	Coyer et al. (2006)
AY659878	*Fucus serratus*	Coyer et al. (2006)
AY659879	*Fucus serratus*	Coyer et al. (2006)
AY659880	*Fucus serratus*	Coyer et al. (2006)
AY659881	*Fucus serratus*	Coyer et al. (2006)
AY659882	*Fucus serratus*	Coyer et al. (2006)
AY659883	*Fucus serratus*	Coyer et al. (2006)
AY659884	*Fucus distichus*	Coyer et al. (2006)
AY659885	*Fucus distichus*	Coyer et al. (2006)
AY659887	*Fucus distichus*	Coyer et al. (2006)
AY659888	*Fucus distichus*	Coyer et al. (2006)
AY659889	*Fucus evanescens*	Coyer et al. (2006)
AY659890	*Fucus evanescens*	Coyer et al. (2006)
AY659891	*Fucus distichus*	Coyer et al. (2006)
AY659892	*Fucus distichus*	Coyer et al. (2006)
AY659893	*Fucus evanescens*	Coyer et al. (2006)
AY659894	*Fucus evanescens*	Coyer et al. (2006)
AY659895	*Fucus evanescens*	Coyer et al. (2006)
AY659896	*Fucus gardneri*	Coyer et al. (2006)
AY659897	*Fucus gardneri*	Coyer et al. (2006)
AY659898	*Fucus vesiculosus*	Coyer et al. (2006)
AY659901	*Fucus vesiculosus*	Coyer et al. (2006)
AY659902	*Fucus vesiculosus*	Coyer et al. (2006)
AY659903	*Fucus vesiculosus*	Coyer et al. (2006)
AY659904	*Fucus vesiculosus*	Coyer et al. (2006)
AY659905	*Fucus vesiculosus*	Coyer et al. (2006)
AY659906	*Fucus virsoides*	Coyer et al. (2006)
AY659907	*Fucus spiralis*	Coyer et al. (2006)
AY659909	*Fucus spiralis*	Coyer et al. (2006)
AY659910	*Fucus spiralis*	Coyer et al. (2006)
AY659911	*Fucus spiralis*	Coyer et al. (2006)
AY659912	*Fucus spiralis*	Coyer et al. (2006)
AY659913	*Fucus cottoni*	Coyer et al. (2006)
AY659914	*Fucus spiralis*	Coyer et al. (2006)
AY659915	*Hesperophycus sp.*	Coyer et al. (2006)
AY941092	*Fucus gardneri*	Coyer et al. (2006)
AY941093	*Fucus gardneri*	Coyer et al. (2006)
AY941094	*Fucus gardneri*	Coyer et al. (2006)
EU309506	*Fucus vesiculosus*	Muhlin and Brawley (Unpublished)
EU309509	*Fucus vesiculosus*	Muhlin and Brawley (Unpublished)
EU309510	*Fucus vesiculosus*	Muhlin and Brawley (Unpublished)

3.0 RESULTS

3.1 MORPHOLOGICAL ANALYSIS

Initial visual inspection showed large morphological variation among collections of *Fucus*. For example, Figure 6 depicts several herbarium samples highlight this, with noticeable variations in the size of the samples as well as the width and shape of the fronds. Statistical analyses were completed using samples with reproductive characters to eliminate non-mature, and therefore containing no reproductive receptacles, plants from skewing results. Table 6 contains basic statistics on the morphological data across reproductive samples. The large variation in the data can be seen across many of the measured variables. Standard deviations for the number of dichotomous branchings, both upper and lower, are high at 47.9 and 18.4 respectively, compared to their means of 34.1 and 14.8. With a mean number of receptacles of 17.5 and a standard deviation of 20.2 across the data set, the large difference in the standard deviation compared to the mean suggests variability among receptacle data maybe useful in clustering analysis.

Measurements in relation to plant stipes also display variation among measured samples. The number of stipes emanating from a single holdfast has a mean value of 1.9 across the data set but with a standard deviation of 2.7. Furthermore, the stipe length and width had large variation between the samples with stipe length mean of 3.1 and standard deviation of 2.6 and a stipe width mean of 0.3 and standard deviation of 0.2.
Hierarchical clustering did not provide well-established clustering across the entire sample set exhibiting reproductive characters and provided little information for the separation of the samples into groups (Figure 7). With a total Euclidian distance of 60, the majority of the *Fucus* samples, 80 of the 86 sample set, only separated toward the distal portion of the tree

Figure 6. Demonstration of highly variable morphology among collected *Fucus* samples. Scale bar for all pictures is 10cm length x 1cm width. A-Arches Provincial Park Nfld *Fucus* 1*;* B-Whiteway Nfld *Fucus* 3*;* C-Pemaquid Pt. Maine *Fucus* 2A*;* D-Millbridge Maine *Fucus* 1B*;* E-Singing Sands PEI *Fucus serratus;* F-Lubec Maine *Fucus* 1A*;* G-Rocky Beach Hwy 100 Nfld *Fucus* 3B*;* H-Whiffin Spit Park BC *Fucus* 1


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K. M. Müller Herbarium
Species:
Location:
Collector:
GPS - N:

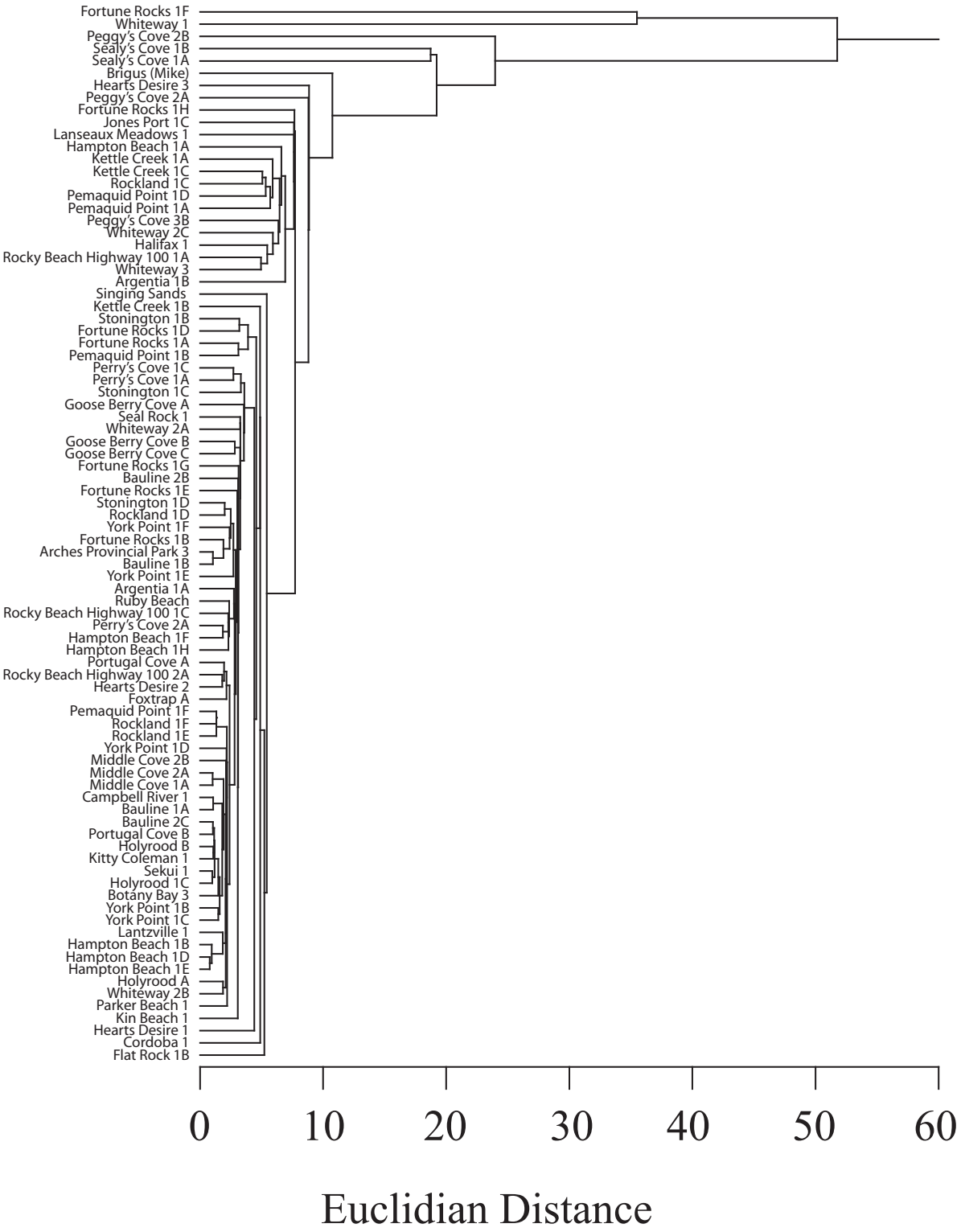
Table 6. Basic statistic of morphometric characters as measured on all collected *Fucus* specimens with reproductive bodies. Values used in the descriptor column were either measurements of continuous characters in millimeters (mm) or integer count values (int). Discriminant analysis characters were selected among: Plant length (PLTLG), Plant width (PLTWD), Number of stipes (STPNUM), Stipe length (STPLG), Stipe width (STPWD), Total number of fronds (FRNDNUM), Frond width (FRNDWD), Frond length (FRNDLG), Frond distal width (FRNDDISTWD), Mean number of serrations per frond (SERNUM), Mean distance between dichotomies (BRCHDIST), Number lower dichotomous branches (BRCHLOW), Number of upper branching (BRCHUP), Number of apical receptacles (RECNUM), Width of the receptacle (RECWD), Length of receptacle (RECLG), Number of air vesicles (VESNUM), Distance between paired air vesicles (VESDISTBT2), Mean distance between pairs of vesicles (VESDISTBTPRS), Air vesicle width (VESWD), Air vesicle length (VESLG) For a description of original measurement methodology see Figure 5 and Table 4. For a full listing of measured values see Appendix B.

Statistic	PLTLG (mm)	PLTWD (mm)	STPNUM (int)	STPLG (mm)	STPWD (mm)	SERNUM (int)	FRNDNUM (int)
Number of Cases	86	86	86	86	86	86	86
Minimum	3.3	2	1	0.1	0.1	0	7
Maximum	44.9	34.5	16	14.3	2.1	13	344
Median	15.75	12.65	1	2.25	0.265	0	34
Arithmetic Mean	17.215	14.723	1.942	3.169	0.306	0.151	52.919
Standard Deviation	8.538	7.079	2.775	2.601	0.251	1.402	57.71

Statistic	FRNDWD (mm)	FRNDLG (mm)	FRNDDISTWD (mm)	BRCHDIST (mm)	BRCHLOW (int)	BRCHUP (int)	RECNUM (int)
Number of Cases	86	86	86	86	86	86	86
Minimum	0.22	2.82	0.12	0.4	1	1	1
Maximum	2.64	41.8	1.44	6.06	131	358	97
Median	0.535	13.68	0.36	2.18	8	21	9.5
Arithmetic Mean	0.66	15.093	0.42	2.319	14.872	34.14	17.547
Standard Deviation	0.415	7.779	0.21	0.987	18.405	47.91	20.267

Statistic	RECWD (mm)	RECLG (mm)	VESDISTBT2 (mm)	VESDISTBTPRS (mm)	VESNUM (int)	VESLG (mm)	VESWD (mm)
Number of Cases	86	86	86	86	86	86	86
Minimum	0.16	0.28	0	0	0	0	0
Maximum	1.4	7.42	0.78	0.34	149	1	0.9
Median	0.42	0.825	0	0	0	0	0
Arithmetic Mean	0.5	1.167	0.028	0.025	3.802	0.107	0.09
Standard Deviation	0.243	1.107	0.128	0.074	18.721	0.255	0.211

Figure 7. Hierarchical clustering of reproductive specimens based on morphological characters using Euclidian distance. Clustering analysis includes all measured morphological characters among samples displaying reproductive characters. For a description of original measurement methodology and list of characters used in the clustering analysis see Figure 5 and Table 4. For a full listing of measured values see Appendix B.


Fortune Rocks 1F
Whiteway 1
Peggy's Cove 2B
Sealy's Cove 1B
Sealy's Cove 1A
Brigus (Mike)
Hearts Desire 3
Peggy's Cove 2A
Fortune Rocks 1H
Jones Port 1C
Lanseaux Meadows 1
Hampton Beach 1A
Kettle Creek 1A
Kettle Creek 1C
Rockland 1C
Pemaquid Point 1D
Pemaquid Point 1A
Peggy's Cove 3B
Whiteway 2C
Halifax 1
Rocky Beach Highway 100 1A
Whiteway 3
Argentia 1B
Singing Sands
Kettle Creek 1B
Stonington 1B
Fortune Rocks 1D
Fortune Rocks 1A
Pemaquid Point 1B
Perry's Cove 1C
Perry's Cove 1A
Stonington 1C
Goose Berry Cove A
Seal Rock 1
Whiteway 2A
Goose Berry Cove B
Goose Berry Cove C
Fortune Rocks 1G
Bauline 2B
Fortune Rocks 1E
Stonington 1D
Rockland 1D
York Point 1F
Fortune Rocks 1B
Arches Provincial Park 3
Bauline 1B
York Point 1E
Argentia 1A
Ruby Beach
Rocky Beach Highway 100 1C
Perry's Cove 2A
Hampton Beach 1F
Hampton Beach 1H
Portugal Cove A
Rocky Beach Highway 100 2A
Hearts Desire 2
Foxtrap A
Pemaquid Point 1F
Rockland 1F
Rockland 1E
York Point 1D
Middle Cove 2B
Middle Cove 2A
Middle Cove 1A
Campbell River 1
Bauline 1A
Bauline 2C
Portugal Cove B
Holyrood B
Kitty Coleman 1
Sekui 1
Holyrood 1C
Botany Bay 3
York Point 1B
York Point 1C
Lantzville 1
Hampton Beach 1B
Hampton Beach 1D
Hampton Beach 1E
Holyrood A
Whiteway 2B
Parker Beach 1
Kin Beach 1
Hearts Desire 1
Cordoba 1
Flat Rock 1B
0
10
20
30
40
50
60
Euclidian Distance

between 0 and 10. Furthermore, there were only two larger clusters apparent on the dendrogram, both of which occurred in the 0 to 10 range. These close divisions suggest that the use of all measured morphometric characters on plants exhibiting reproductive traits are ineffective in separating groups of samples in a clustering analysis. The lack of larger clusters of samples toward the root of the tree suggests the inability for the morphological characters used to establish meaning clusters for grouping samples. With only two large clusters present on the dendrogram, the smaller cluster comprised of 12 samples, the larger cluster containing 63 samples, and the remaining 11 samples in individual branches, there is little information to separate samples into groups. Also, no meaningful clustering of samples into *a priori* groups, such as seasonal collection, geographical location, or level of exposure to open ocean is apparent.

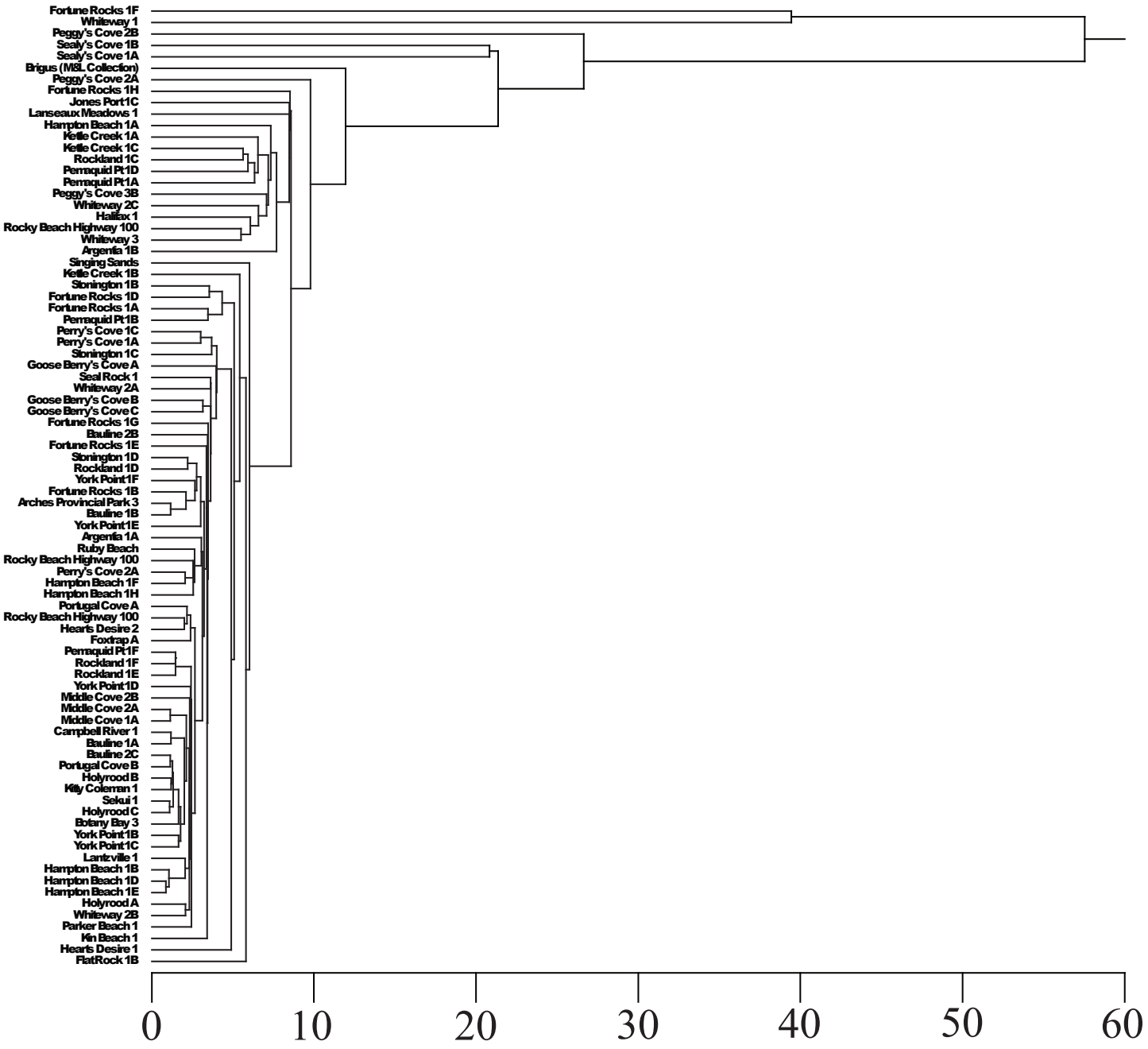
The inability of samples to form clusters based on geographical location and exposure is highlighted with samples from Hampton Beach (NH). Hampton Beach (NH) samples A-F and H, all collected from the same sampling location, are separated on the dendrogram. Samples from a single location scattered across the dendrogram is not limited to Hampton Beach (NH). York Pt. (ME), Fortune Rocks (ME), and Whiteway (NL) samples are also scattered throughout the dendrogram. Also, the hierarchical clustering of seasonal collections has not occurred, and collections from both seasons have grouped within the same cluster. Two Atlantic samples, Perry Cove 2A (NL) and Hampton Beach 1F (NH), collected during different seasons, are clustering together at the most distal point on the dendrogram. Close clustering also occurs between the summer collection Botany Bay 3 (BC) and the winter collection of York Pt. 1B (ME).

As not all samples contained air vesicle data, hierarchical clustering was conducted using only the total number of vesicles to eliminate potential bias on samples where no air vesicle data existed. This clustering provided little information for the separation of the samples into groups (Figure 8). As was seen in the clustering analysis using all vesicle data, the majority of the samples, 80 of the 86 plant sample set, only separated toward the distal portion of the tree between 0 to 10 where the tree has a total tree distance of 60. Similar to the clustering using all of the vesicle data there were only two larger clusters apparent on the dendrogram, both of which occurred in the 0 to 10 range. These close divisions again suggest that the use of these measured morphometric characters on plants exhibiting reproductive traits are ineffective in separating groups of samples with a clustering analysis.

The lack of larger clusters of samples toward the root of the tree suggests the inability for the morphological characters to establish clusters for grouping samples. With only two large clusters present on the dendrogram, there is little information to separate samples into groups and no meaningful clustering of samples into the *a priori* groups seasonal collection, geographical location, or level of exposure to open ocean is apparent. Furthermore, the overall dendrogram structures between the reproductive hierarchical clustering and the dendrogram from the clustering analysis using only the number of vesicles for vesicle data were nearly identical.

The step-wise discriminant analysis using all specimens exhibiting reproductive bodies in to the *a priori* groups season of collection, ocean of origin, and exposure to open ocean yielded the most useful characters, based on F statistic values. Characters with a high

Figure 8. Hierarchical clustering using Euclidian distance of reproductive specimens based on all morphological characters excluding characters distance between two vesicles in a pair (VESDISTBT2), distance between pairs of vesicles (VESDISTBTPRS), average vesicle length (VESLG), and the average vesicle width (VESWD). For a description of original measurement methodology and list of characters used in the clustering analysis see Figure 5 and Table 4. For a full listing of measured values see Appendix B.


Fortune Rocks 1F
Whiteway 1
Peggy's Cove 2B
Sealy's Cove 1B
Sealy's Cove 1A
Brigus (M&L Collection)
Peggy's Cove 2A
Fortune Rocks 1H
Jones Port1C
Lanseaux Meadows 1
Hampton Beach 1A
Kettle Creek 1A
Kettle Creek 1C
Rockland 1C
Pennaquid Pt1D
Pennaquid Pt1A
Peggy's Cove 3B
Whiteway 2C
Halifax 1
Rocky Beach Highway 100
Whiteway 3
Argentia 1B
Singing Sands
Kettle Creek 1B
Stonington 1B
Fortune Rocks 1D
Fortune Rocks 1A
Pennaquid Pt1B
Perry's Cove 1C
Perry's Cove 1A
Stonington 1C
Goose Berry's Cove A
Seal Rock 1
Whiteway 2A
Goose Berry's Cove B
Goose Berry's Cove C
Fortune Rocks 1G
Bauline 2B
Fortune Rocks 1E
Stonington 1D
Rockland 1D
York Point1F
Fortune Rocks 1B
Arches Provincial Park 3
Bauline 1B
York Point1E
Argentia 1A
Ruby Beach
Rocky Beach Highway 100
Perry's Cove 2A
Hampton Beach 1F
Hampton Beach 1H
Portugal Cove A
Rocky Beach Highway 100
Hearts Desire 2
Foxtrap A
Pennaquid Pt1F
Rockland 1F
Rockland 1E
York Point1D
Middle Cove 2B
Middle Cove 2A
Middle Cove 1A
Campbell River 1
Bauline 1A
Bauline 2C
Portugal Cove B
Holyrood B
Kitty Coleman 1
Sekui 1
Holyrood C
Botany Bay 3
York Point1B
York Point1C
Lantzville 1
Hampton Beach 1B
Hampton Beach 1D
Hampton Beach 1E
Holyrood A
Whiteway 2B
Parker Beach 1
Kin Beach 1
Hearts Desire 1
FlatRock 1B
0
10
20
30
40
50
60
Euclidian Distance

F value (greater then ± 1) were recorded and are listed in Table 7 for analyses with all characters as well as analyses excluding all vesicle data except the number of vesicles (VESNUM). Hierarchical clustering for each set of useful characters obtained resulted in no apparent groupings on the dendrograms for any of the *a priori* groups using their selected useful characters. In each case the resulting dendrograms were very similar to the original clustering dendrograms in Figure 7 and Figure 8.

The stepwise discriminant analysis using all measured characteristics selected a single character, the average vesicle length (VESLG), across all three *a priori* groupings, season of collection, ocean of origin, and exposure to open ocean (Table 7). A total of eight characters (Table 7) were selected from the analysis using the ocean of origin (Pacific and Atlantic) as a grouping variable: PLTLG, FRNDWD, FRNDLG, FRNDDISTWD, VESDISTBTPRS, VESNUM, and VESLG. Using these characters the statistical probabilities, Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, indicate a significant separation of the two, Pacific and Atlantic, group centroids (Table 8). All three statistical analyses had a probability value of ($P = 0.001$) and successfully separate the two *a priori* groups of Pacific collections and Atlantic collections based on the eight selected characters. Therefore the null hypothesis of samples being members of the same group is rejected.

Geisser assignment probabilities were also determined for all samples and based on this probability each samples was placed in to one of the two groups *a posteriori* to create a classification matrix (Table 9). A jack-knifed resampling method, based on the original classifications, was also conducted and placed in a matrix to support the original classificatory analysis (Table 9). Classificatory analysis resulted in 77% correct *a posteriori* placement of samples and a jack-knifed resampling value of 74%. Twenty of the 86

Table 7. A table of informative characters as determined through discriminate functions analysis of all samples exhibiting reproductive structures. Three a priori groups are represented: season of collection summer or winter (SUMVWINT); exposure to open ocean compared to more sheltered sites (EXPOSE); ocean of origin (GEOG). Table A contains analyses using all measured morphological characters. Table B contains results from analyses excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD. Values appearing in the characters column were either measurements of continuous characters in millimeters (mm) or integer count values (int). Discriminant analysis characters were selected among: Plant length (PLTLG), Plant width (PLTWD), Number of stipes (STPNUM), Stipe length (STPLG), Stipe width (STPWD), Total number of fronds (FRNDNUM), Frond width (FRNDWD), Frond length (FRNDLG), Frond distal width (FRNDDISTWD), Mean number of serrations per frond (SERNUM), Mean distance between dichotomies (BRCHDIST), Number lower dichotomous branches (BRCHLOW), Number of upper branching (BRCHUP), Number of apical receptacles (RECNUM), Width of the receptacle (RECWD), Length of receptacle (RECLG), Number of air vesicles (VESNUM), Distance between paired air vesicles (VESDISTBT2), Mean distance between pairs of vesicles (VESDISTBTPRS), Air vesicle width (VESWD), Air vesicle length (VESLG) Marked characters (✔) were used in the discriminant analyses. For a description of original measurement methodology see Figure 5 and Table 4. For a full listing of measured values see Appendix B.

Table A

Characters	All Characters GEOG	All Characters SUMVWINT	All Characters EXPOSE
PLTLG	✔	-	-
PLTWD	-	✔	-
STPNUM	✔	-	-
STPLG	-	-	-
STPWD	-	-	✔
SERNUM	-	✔	✔
FRNDNUM	-	-	✔
FRNDWD	✔	-	-
FRNDLG	-	-	-
FRNDDISTWD	✔	-	-
BRCHDIST	✔	-	-
BRCHLOW	-	-	✔
BRCHUP	-	-	-
RECNUM	-	-	-
RECWD	-	-	-
RECLG	-	-	-
VESDISTBT2	-	✔	-
VESDISTBTPRS	✔	✔	-
VESNUM	✔	-	-
VESLG	✔	✔	✔
VESWD	-	✔	-

Table B

Characters	All Characters GEOG	No Vesicle Specs SUMVWINT	No Vesicle Specs EXPOSE
PLTLG	✔	-	-
PLTWD	-	-	-
STPNUM	✔	-	-
STPLG	-	-	-
STPWD	-	-	✔
SERNUM	-	✔	✔
FRNDNUM	-	-	-
FRNDWD	-	-	-
FRNDLG	-	-	-
FRNDDISTWD	✔	-	-
BRCHDIST	✔	✔	-
BRCHLOW	-	-	✔
BRCHUP	-	-	✔
RECNUM	-	-	✔
RECWD	-	-	-
RECLG	-	✔	-
VESNUM	✔	-	✔

Table 8. Multivariate statistics and F approximations analysis of all reproductive samples. The Wilks' λ, Piallai's trace, and Hotelling-Lawley trace tests for the discriminant analysis for the: A. seasonal collection (SUMVWINT) using all characters; B. ocean of origin (GEOG) using all characters; C. exposure (EXPOSE) using all characters; D. seasonal collection excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; E. ocean of origin (GEOG) excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; and F. exposure (EXPOSE) excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD.

A. Seasonal Collection (SUMVWINT)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.4030	19.478	79	0.0000
Pillai's Trace	0.5970	19.478	79	0.0000
Lawley-Hotelling Trace	1.4790	19.478	79	0.0000

B. Ocean of origin (GEOG)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.8540	7.103	83	0.0010
Pillai's Trace	0.1460	7.103	83	0.0010
Lawley-Hotelling Trace	0.1710	7.103	83	0.0010

C. Exposure to open Ocean (EXPOSE)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.6380	6.312	78	0.0000
Pillai's Trace	0.3620	6.312	78	0.0000
Lawley-Hotelling Trace	0.5660	6.312	78	0.0000

D. Seasonal Collection (SUMVWINT)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.4030	19.478	79	0.0000
Pillai's Trace	0.5970	19.478	79	0.0000
Lawley-Hotelling Trace	1.4790	19.478	79	0.0000

E. Ocean of origin (GEOG)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.8540	7.103	83	0.0010
Pillai's Trace	0.1460	7.103	83	0.0010
Lawley-Hotelling Trace	0.1710	7.103	83	0.0010

F. Exposure to open Ocean (EXPOSE)

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.7590	6.426	81	0.0000
Pillai's Trace	0.2410	6.426	81	0.0000
Lawley-Hotelling Trace	0.3170	6.426	81	0.0000

Table 9. Classification matrix and jackknifed classification matrix of all samples with reproductive bodies. Samples with reproductive characters, using a stepwise discriminate function of: A. seasonal collections using all characters; B. ocean of origin using all characters; C. exposure using all characters; D. seasonal collections excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; E. ocean of origin excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; and F. exposure excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD . Characters used for final discriminate analysis are listed in Table 7. The first value represents the classification based on Geisser assignment probabilities while the second is the jackknifed resampling value.

A. Seasonal Collection (SUMVWINT)

	Number of Samples		
Group	Summer	Winter	% Correct
Summer	49 / 48	2 / 3	96 / 94
Winter	5 / 6	30 / 29	86 / 83
Total	54 / 54	32 / 32	92 / 90

B. Ocean of origin (GEOG)

	Number of Samples		
Group	Pacific	Atlantic	% Correct
Pacific	8 / 8	2 / 2	80 / 80
Atlantic	18 / 20	58 / 56	74 / 76
Total	26 / 28	60 / 58	77 / 74

C. Exposure to open Ocean (EXPOSE)

	Number of Samples		
Group	Sheltered	Exposed	% Correct
Sheltered	37 / 37	8 / 8	82 / 82
Exposed	9 / 11	32 / 30	78 / 73
Total	46 / 48	40 / 38	80 / 78

D. Seasonal Collection (SUMVWINT)

	Number of Samples		
Group	Summer	Winter	% Correct
Summer	49 / 48	2 / 3	96 / 94
Winter	5 / 6	30 / 29	86 / 83
Total	54 / 54	32 / 32	92 / 90

E. Ocean of origin (GEOG)

	Number of Samples		
Group	Pacific	Atlantic	% correct
Pacific	8 /8	2 / 2	80 / 80
Atlantic	18 / 20	58 / 56	76 / 74
Total	26 / 28	60 / 58	77 / 74

F. Exposure to open Ocean (EXPOSE)

	Number of Samples		
Group	Sheltered	Exposed	% Correct
Sheltered	33 / 33	12 / 12	73 / 73
Exposed	10 / 11	31 / 30	76 / 73
Total	43 / 44	43 / 42	74 / 73

samples used in the discriminant analysis were misclassified during *a posteriori* placement. Fifty-six of the samples were classified based on Geisser probabilities between 50% and 90%. A mere ten of the eighty-six samples were correctly placed with high probability of 90% or better based on the eight selected characters.

Analysis using season of collection as grouping variables yielded a total of six useful characters: PLTWD, SERNUM, VESDISTBT2, VESLG, and VESWD (Table 7). Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, statistical probabilities indicate a significant separation of samples between the two collection seasons summer and winter (Table 8). All three statistical analyses indicate significant ($P < 0.001$) to separate samples in to the *a priori* groups of summer and winter collections based on the six selected characters.

Geisser probability assignments were used to construct a classification matrix through the placement of samples in to seasonal groupings *a posteriori* (Table 9). A jack-knifed resampling method, based on the original classifications, was also conducted and a matrix was created to support the original classificatory analysis (Table 9). Classificatory analysis resulted in high *a posteriori* placement of samples at 92%. Furthermore, the jack-knifed resampling classification matrix also produced high placement with a value of 90%. The majority of the Geisser probabilities assigning placement of samples were high with 70 of the 86 samples being placed with a 70 to 100% probability. Only 9 samples were placed in the 50 to 70% range with the remaining 7 samples being placed in the incorrect groups ranging from 20 to 50%.

Analysis using exposure to open ocean as grouping variables resulted in five useful characters: STPWD, SERNUM, FRNDNUM, BRCHLOW, and VESLG (Table 7). The statistical probabilities of Wilks' λ, Piallai's trace, and Hotelling-Lawley trace indicate a

significant separation of samples between the two collections and the null hypothesis of a single group regardless of exposure at the site of collection is rejected. All three statistical analyses indicate a significant probability ($P < 0.001$) to separate samples in to the *a priori* groups of exposed and sheltered collections using the five selected characters (Table 8).

Classificatory analyses were constructed using Geisser probabilities to assign samples into seasonal groupings *a posteriori* (Table 9). A jack-knifed resampling method, based on the original classifications, was also conducted and a matrix was created to support the original classificatory analysis (Table 9). Classificatory analysis resulted in correct *a posteriori* placement of samples at 80% with a jack-knifed resampling classification value of 78%. Of the 86 sample data set a 69 of the samples had a Geisser probability assignment greater then a 50% Geisser assignment. In addition to a large number of the samples having grater then 50% Geisser probability placement, 32 of the 86 samples had an 80% or greater Geisser probability placement.

Analyses only using only the number of vesicles (VESNUM) character for vesicle data had little effect on the outcomes from the ocean of origin and the seasonal collection discriminant analyses. There were few changes in useful characters determined from the analysis, with the obvious exclusion of the other four vesicle characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD. Only a single character (FRNDWD) was dropped in the ocean of origin analysis and only two changes occurred in the season of collection analysis with PLTWD being dropped and BRCHDIST being added as a useful character (Table 7). All classificatory analyses (Table 9) and Geisser probability distributions produced using these two sets of grouping variables had identical values. Moreover,

statistical probability results for the Wilks' λ, Piallai's trace, and Hotelling-Lawley trace yielded identical values compared to the discriminant analyses using all characters (Table 8).

Discriminant analysis, using the *a priori* grouping of exposure to open ocean with the number of vesicles (VESNUM) as the only vesicle data, displayed a number of differences compared to the analysis using all characters. Analysis with all characters yielded five informative characters, however using only the number of vesicles the number of fronds (FRNDNUM) character was dropped as a significant character and three characters were added that were not included as significant during the analysis using all characters: BRCHUP, RECNUM, and VESNUM. The total number of useful characters in this analysis was six including: STPWD, SERNUM, BRCHLOW, BRCHUP, RECNUM, and VESNUM (Table 7).

Although Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, probabilities are statistically supported with $P < 0.001$, all three raw values and the associated F ratio values were different compared to the analysis completed with all characters (Table 8). The value changes, which did not occur across the other two analyses, suggest a strong relationship between level of exposure and the vesicle data. Classificatory analysis also changed when vesicle data was excluded (Table 9). The percent of correct *a posteriori* placements decreased from 80% with all characters to 74% using only the number of vesicles. The jack-knifed classification matrix also decreased from 78% to 73%. Furthermore, the distribution of the Geisser probabilities differed significantly with 50 of the 86 samples being placed in to a *posteriori* classifications based on 40% to 70% Geisser assignment probabilities. These results suggest that vesicle data is necessary to separate *Fucus* samples based on level of exposure.

Because collection methods were biased toward particular regions (Atlantic shore collections from Connecticut to Maine occurring exclusively during the winter and north Pacific sample collections occurring during summer), ocean of origin discriminant analysis using winter samples was unreliable due to insufficient sample sizes. Discriminant analysis of summer samples using the ocean of origin as the grouping variable resulted in a total of twelve characters selected as grouping variables: PLTLG, STPNUM, STPLG, STPWD, SERNUM, FRNDNUM, FRNDWD, RECNUM, RECWD, RECLG, VESDISTBT2, VESDISTBTPRS. Using these characters the statistical probabilities, Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, indicate a significant separation of the two, Pacific and Atlantic, group centroids. All three statistical analyses have a probability value of ($P = 0.003$) and successfully separate the two *a priori* groups of Pacific collections and Atlantic collections based on the twelve selected characters.

Geisser probability *a posteriori* placement of samples had 15 of the 49 samples being placed under 50% with 13 samples having a greater then 80% placement. Classificatory analysis and jack-knifed resampling both resulted in a 69% correct placement of samples in to *a posteriori* groups. As with the ocean of origin analysis using all seasonal collections the analysis using only vesicle numbers for vesicle data resulted in the exact same Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistics and classificatory results. The characters selected for use in the discriminant analysis were slightly different with the PLTLG character being dropped and the addition of the two characters, branch distance (BRCHDIST) and number of lower branches (BRCHLOW).

The discriminant analysis of winter samples with exposure as a grouping variable yielded similar collection bias difficulties as the ocean of origin analysis and as such

discriminant analysis using winter samples was not conducted due to lack of specimens. Analysis of summer collections using exposure as a grouping variable resulted in a total of nine useful characters: PLTLG, STPNUM, STPLG, STPWD, SERNUM, FRNDNUM, FRNDWD, RECNUM, RECWD, RECLG, VESDISTBT2, VESDISTBTPRS. Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistics indicated significant differences between the two seasonal groups with a probability of less then 0.001 for all three tests. The classification matrix and the jack-knifed resampling matrix both resulted in an 84% correct placement of samples in to *a posteriori* groups. Geisser probability *a posteriori* placement to achieve the classification matrices had 8 of the 49 samples under a 50% with 32 samples having a greater then 70% placement and 23 with over 80%.

Discriminant analysis using only the vesicle number for vesicle data and the grouping variable of exposure with summer collections resulted in the selected characters: Plant length (PLTLG), number of upper branches (BRCHUP), receptacle number (RECNUM), and receptacle width (RECWD). Using these characters the statistical probabilities, Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, indicate a statistical support for the separation of the two, Pacific and Atlantic, group centroids with a probability of $P = 0.014$ across all three statistical analyses. Geisser probability *a posteriori* placement of the 49 samples had 12 samples under a 50% probability with 27 samples having between 60% and 70% placement and only 2 with over 70%. Classificatory analysis and jack-knifed resampling both resulted in a 76% correct placement of samples in to *a posteriori* groups. Again similar to the analyses using all collection seasons with reduced vesicle characters to only the number of vesicles, the significant differences in results across all analyses indicates the influence of exposure on vesicle data exclusively in summer growth seasons.

Collections biases were also apparent between Pacific and Atlantic samples where only eight samples exhibiting reproductive bodies were present from Pacific shores. Due to this small sample size discriminant analysis only using samples of Pacific origin was unreliable and was not conducted. Discriminant analysis of Atlantic reproductive samples with seasonal collection as a grouping variable produced five useful characters from the stepping summary: VESDISTBT2, VESDISTBTPRS, VESWD, VESLG, AND SERNUM. With these characters Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistical probabilities indicated a significant probability ($P<0.001$) to distinguish the two *a priori* seasonal groups of winter and summer Atlantic collections. Geisser probability *a posteriori* placement of samples had 67 of the 72 samples being placed with over 50% probability of placement and of those 50 samples had a greater then 80% placement. Classificatory analysis and jack-knifed resampling resulted in a 93% and 89% correct placement respectively of samples in to *a posteriori* groups.

As with the ocean of origin analysis using all seasonal collections the analysis only using vesicle numbers for vesicle data resulted in the exact same Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistics and classificatory results. The characters selected for use in the discriminant analysis were significantly different as four of the original selected characters were measurements of a plants vesicle. The number of serrations character (SERNUM) again selected and in addition the receptacle length characters were also selected.

Like the previous analysis the discriminant analysis of Pacific Ocean samples with exposure as a grouping variable had an insufficient samples size and was not conducted. Analysis of Atlantic Ocean collections using exposure as a grouping variable resulted in a

total of seven useful characters: PLTWD, FRNDNUM, BRCHLOW, BRCHUP, RECNUM, RECLG, VESLG. Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistics indicated significant differences between the two seasonal groups with a probability of less then 0.001 for all three tests. The classification matrix resulted in an 83% placement value based on Geisser *a posteriori* probability placement. The Jack-knifed resampling of this classification matrix resulted in an 82% placement value. Geisser probability *a posteriori* placement to achieve the classification matrices had 12 of the 72 samples under a 50% and 24 of the samples with a value of between 50% and 70% probability placement. There were 22 samples with a high (above 90% Geisser probability placement) value.

Discriminant analysis using only the vesicle number for vesicle data and the grouping variable of exposure with Atlantic Ocean collections resulted in the nine selected characters: STPNUM, STPWD, SERNUM, FRNDNUM, FRNDLG, BRCHUP, RECNUM, RECLG, VESNUM. Wilks' λ, Piallai's trace, and Hotelling-Lawley trace discriminant statistics using these characters resulted in a high probability ($P>0.999$) that the data represents two distinct groups of highly exposed and more sheltered samples. Classification of the samples based on Geisser probabilities resulted in a classificatory and jack-knifed resampling classificatory probability placement of 71%. Geisser probability *a posteriori* placement of the 72 samples resulted in 60 samples under a 70% probability and only 12 with over 70%. These low classificatory analyses placements and significant difference from the analysis including all vesicle data indicates a strong influence of exposure on vesicle data.

3.2 MOLECULAR PHYLOGENETIC ANALYSIS

Successful amplification of 52 sequences were obtained from Pacific, Arctic, and Atlantic shores (Figure 9 and Table 10). The mitochondrial 23S ribosomal RNA-tRNA-Val intergenic spacer region (23S mtDNA) alignment of these sequences displayed variation in the form of large alignment gaps from insertion-deletion (indel) events, and a number of smaller nucleotide changes of both transversions and transitions. Two large insertion-deletion regions occurred approximately between the nucleotides 179 and nucleotides 334 and again with a smaller region between nucleotides 555 and 655. It is these two regions where the insertion-deletion events are present in the multiple sequence alignment that establishes the two major phylogenetic divisions (Figure 10). The outcome of model testing, through the ModelTest program, on the multiple sequence alignment was the transversional model with rate variation among sites. Although this was the output from Modeltest, the PAUP program was not programmed to accept this model so a similar model, the General Time Reversible (GTR) model, was used in its place. General time reversible transition and transversion rates of [A-C] = 0.5895, [A-G] = 1.2014, [A-T] = 0.3711, [C-G] = 0.7170, [C-T] = 1.2014, and [G-T] = 1.0000, were used with a gamma distribution parameter of 0.7054.

Phylogenetic analysis of the 52 sequences of samples included in this study and an additional 44 GenBank sequences are shown on the maximum likelihood tree in Figure 10. This tree (Figure 10) includes neighbor-joining bootstrap values (NJB; Appendix D) and Baysian posterior probabilities (BPP; Appendix E) as support. Two clades are evident toward the root of the tree that group with the *Hesperophycus californicus* sequence. The first of these two minor clades (clade 4 in Figure 10) contained the sequences for Seal Rock 1 (OR) (e-value 4e-69),

Figure 9. North American map indicating sites represented by molecular sequence from collected specimens. Some locations have multiple sequences from a single population. Collection location numbers correspond to collection locations in Table 12.

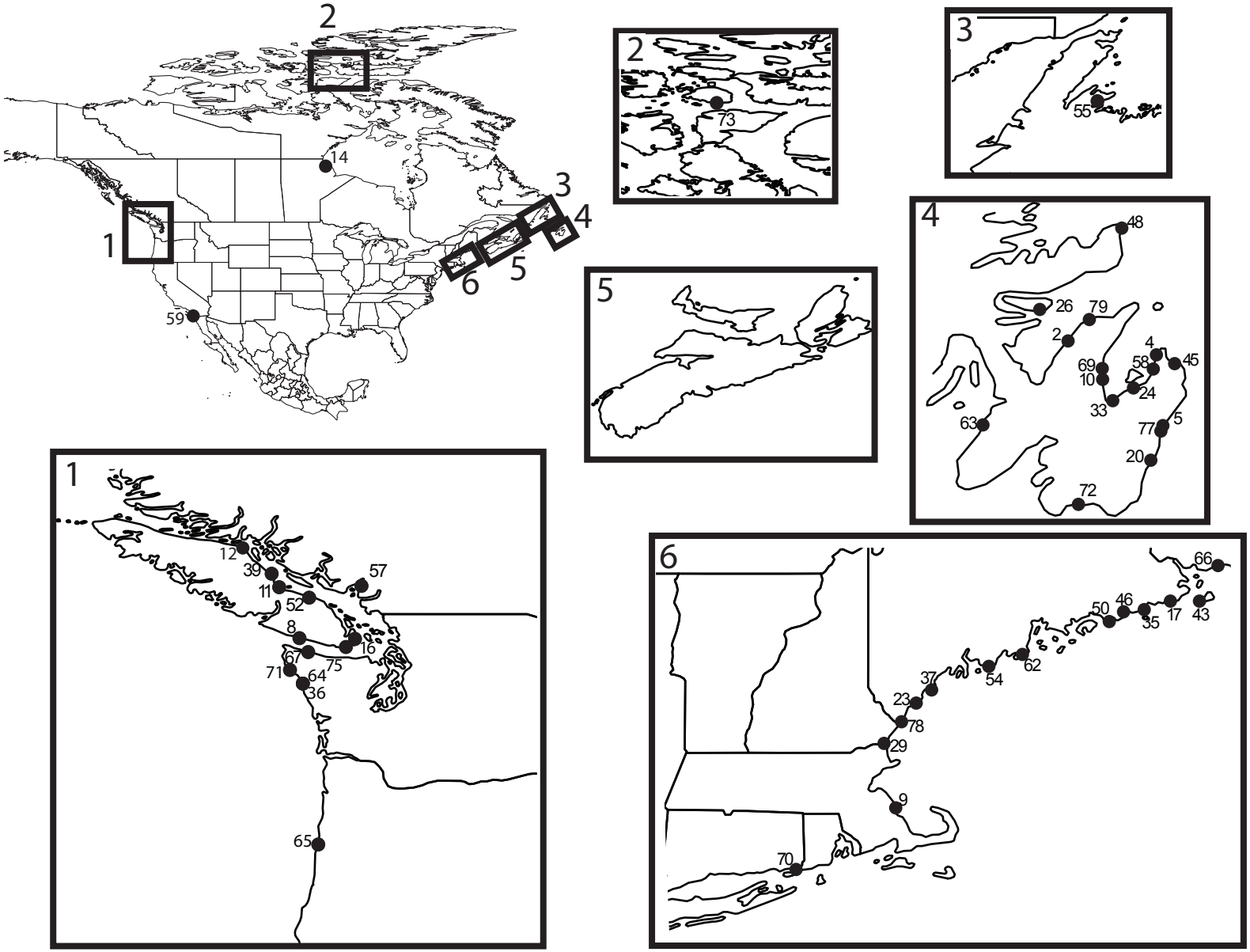
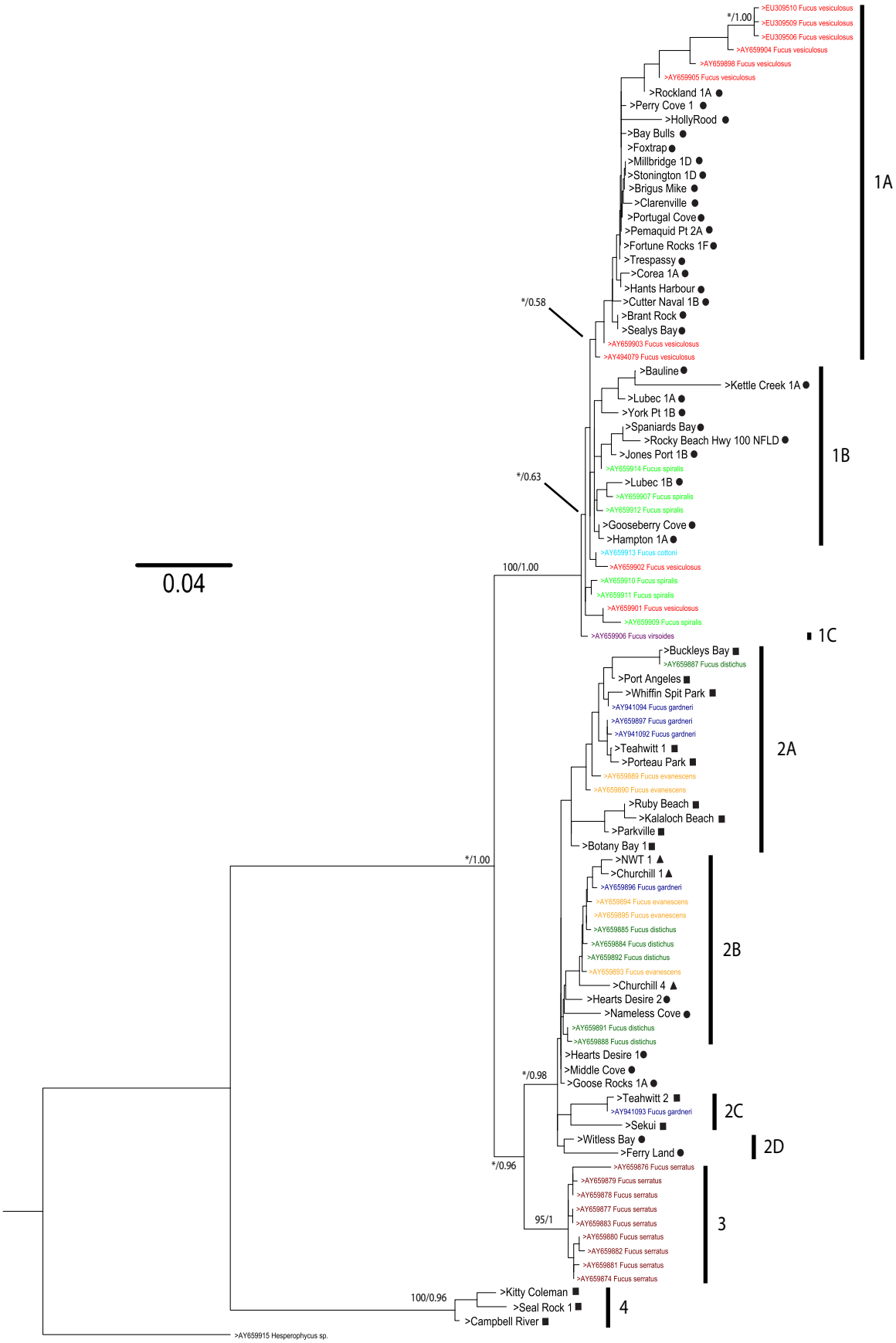

2
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3
4
6
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14
59
2
73
3
55
4
48
26
79
2
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69
58
45
10
24
33
63
77
5
20
72
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1
12
39
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11
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70

Table 10. A list of collection sites represented by molecular sequence from collected specimens with corresponding longitude and latitude coordinates. Some locations have multiple sequences. Collection location numbers correspond to collection locations in Figure 9.

Number	Collection Location	Long.	Lat.
4	Bauline Newfoundland Canada	47.72	-52.83
5	Bay Bulls Newfoundland Canada	47.31	-52.81
8	Botany Bay British Columbia Canada	48.53	-124.45
9	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65
10	Brigus Newfoundland Canada	47.54	-53.20
11	Bukley's Bay British Columbia Canada	49.53	-124.85
12	Campbell River British Columbia Canada	48.03	-125.24
14	Churchill Manitoba Canada	58.77	-94.13
15	Clarenville Newfoundland Canada	48.16	-53.96
16	Cordoba Bay B.C. Canada	48.52	-123.37
17	Cutler Naval Base Maine USA	44.67	-67.25
20	Ferryland Newfoundland Canada	47.03	-52.89
23	Fortune Rocks Maine USA	43.43	-70.38
24	Foxtrap Newfoundland Canada	47.52	-52.99
26	Goose Berry Cove Newfoundland Canada	48.03	-53.64
29	Hampton Beach New Hampshire	42.90	-70.81
32	Hearts Desire Newfoundland Canada	47.81	-53.44
33	Holyrood Newfoundland Canada	47.39	-53.13
35	Just Past Jonesport Maine USA	44.56	-67.57
36	Kalaloch Beach Washington USA	47.64	-124.39
37	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22
39	Kitty Coleman Provincial Park B.C. Canada	49.79	-125.00
43	Lubec Maine USA (under boarder crossing)	44.67	-66.98
45	Middle Cove Newfoundland Canada	47.65	-52.70
46	Millbridge Maine USA	44.54	-67.88
48	Nameless Cove Newoundland Canada	48.62	-53.01
50	On the road to Corea Maine USA	44.41	-68.01
52	Parksville British Columbia Canada	49.32	-124.26
54	Pemaquid Point Maine USA	43.84	-69.51
55	Perry Cove Newfoundland Canada	49.73	-55.98
57	Porteau Provincial Park B.C. Canada	49.55	-123.24
58	Portugal Cove Newfoundland Canada	47.63	-52.86
59	Pt. Lona California USA	32.67	-117.25
62	Rockland Maine USA	44.10	-69.11
63	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93
64	Ruby Beach Washington USA	47.64	-124.39
65	Seal Rock Orgeon USA	44.49	-124.08
66	Sealys Bay New Brunswick Canada	45.08	-66.65
67	Sekui Washington USA	48.26	-124.28
69	Spaniards Bay Newfoundland Canada	47.61	-53.28
70	Stonington Connecticut USA	41.33	-71.91
71	Teahwhit Washington USA	47.91	-124.64
72	Trespassey Newfoundland Canada	46.73	-53.37
73	West end of Assistance Bay southside of Cornwallis NWT Canada	74.65	-94.36
75	Whiffin Spit Park British Columbia Canada	48.36	-123.73
77	Witless Bay Newfoundland Canada	47.28	-52.83
78	York Point Maine USA (In park near Lighthouse)	43.17	-70.59
79	Hants Harbour Newfoundland Canada	48.02	-53.27

Figure 10. Maximum Likelihood phylogenetic tree based on mtDNA intergenic spacer sequences obtained from North American shores (See Figure 9 and Table 12). Included in the analysis are selected GenBank sequences with accession number and species identifications. Nodal values are neighbor joining bootstrap values (1000 replicates) and Bayesian posterior probabilities respectively. Where support values are not listed tree structure was not resolved across all three phylogenetic methods. Where an "*" is present no support value could be determined from the tree structures.


*/1.00
>EU309510 Fucus vesiculosus
>EU309509 Fucus vesiculosus
>EU309506 Fucus vesiculosus
>AY659904 Fucus vesiculosus
>AY659898 Fucus vesiculosus
>AY659905 Fucus vesiculosus
>Rockland 1A
>Perry Cove 1
>HollyRood
>Bay Bulls
>Foxtrap
>Millbridge 1D
>Stonington 1D
>Brigus Mike
>Clarenville
>Portugal Cove
>Pemaquid Pt 2A
>Fortune Rocks 1F
>Trespassy
>Corea 1A
>Hants Harbour
>Cutter Naval 1B
>Brant Rock
>Sealys Bay
>AY659903 Fucus vesiculosus
>AY494079 Fucus vesiculosus
1A
*/0.58
>Bauline
>Kettle Creek 1A
>Lubec 1A
>York Pt 1B
>Spaniards Bay
>Rocky Beach Hwy 100 NFLD
>Jones Port 1B
>AY659914 Fucus spiralis
1B
*/0.63
>Lubec 1B
>AY659907 Fucus spiralis
>AY659912 Fucus spiralis
>Gooseberry Cove
>Hampton 1A
>AY659913 Fucus cottoni
>AY659902 Fucus vesiculosus
>AY659910 Fucus spiralis
>AY659911 Fucus spiralis
>AY659901 Fucus vesiculosus
>AY659909 Fucus spiralis
>AY659906 Fucus virsoides
1C
0.04
100/1.00
>Buckleys Bay
>AY659887 Fucus distichus
>Port Angeles
>Whiffin Spit Park
>AY941094 Fucus gardneri
>AY659897 Fucus gardneri
>AY941092 Fucus gardneri
>Teahwitt 1
>Porteau Park
>AY659889 Fucus evanescens
>AY659890 Fucus evanescens
2A
>Ruby Beach
>Kalaloch Beach
>Parkville
>Botany Bay 1
*/1.00
>NWT 1
>Churchill 1
>AY659896 Fucus gardneri
>AY659894 Fucus evanescens
>AY659895 Fucus evanescens
>AY659885 Fucus distichus
>AY659884 Fucus distichus
>AY659892 Fucus distichus
>AY659893 Fucus evanescens
>Churchill 4
>Hearts Desire 2
>Nameless Cove
>AY659891 Fucus distichus
>AY659888 Fucus distichus
2B
>Hearts Desire 1
>Middle Cove
>Goose Rocks 1A
*/0.98
>Teahwitt 2
>AY941093 Fucus gardneri
2C
>Sekui
>Witless Bay
>Ferry Land
2D
*/0.96
>AY659876 Fucus serratus
>AY659879 Fucus serratus
>AY659878 Fucus serratus
>AY659877 Fucus serratus
>AY659883 Fucus serratus
95/1
>AY659880 Fucus serratus
>AY659882 Fucus serratus
>AY659881 Fucus serratus
>AY659874 Fucus serratus
3
100/0.96
>Kitty Coleman
>Seal Rock 1
>Campbell River
4
>AY659915 Hesperophycus sp.

Kitty Coleman (BC) (e-value 6e-62), and Campbell River (BC) (e-value 5e-78) and were identified through GenBank MegaBlast program and determined to be members of the genus *H. californicus*. Two larger terminal clades are present and are well supported on a maximum likelihood tree with (89% NJB; BPP = 1). The first of these two major clades (clade 1 in Figure 10) contains the species *F. vesiculosus, F. spiralis, F. virsoides*, and *F. cottonii*. The second clade (2 and 3 in Figure 10) contains the species *F. distichus, F. virsoides, F. gardneri*, and *F. serratus*. These two large separations are in agreement with Coyer *et al.* (2006) whose study of *Fucus* species employed the same region of the mitochondrial spacer for phylogenetic analysis and was the source for many of the GenBank sequences used in this thesis. More terminal branches on the phylogenetic tree (Figure 10) do not have support values included as the bootstrapping and Baysian posterior probabilities were low (NJB< 50; BPP < 1), or the topology was inconsistent across the methodologies. Absent Baysian posterior probability values were not recoded more distally as tree topology was not consistent with the maximum likelihood results in (Figure 10).

The first of the two larger clades contains sub clades 1A, 1B, and 1C where groups 1A and 1B are grouping together and 1C is separate (Figure 10). The separation of subclades A and B with subclade C is well supported with 100% NJB and BPP of 1. The separation of *F. virsoides*, an European endemic (Rindi & Battelli 2005), from subclades A and B into subclade C (Figure 10) is phylogenetically supported as a distinct species. The lack of grouping of non-GenBank sequences with this group is expected, as North American collections of the European endemic would not exist. The remaining sub clades A and B of this region on the phylogenetic tree are composed of the species *F. vesiculosus, F. spiralis,* and *F. cottonii.* The species *F. cottonii* is an endemic to the European region and as such this

GenBank sequence is not directly grouping among any thesis samples sequenced. (Caram & Jónsson 1972, Rueness 1997, Wynne & Magne 1991). There are several European *F. vesiculosus* samples, which are grouping in well supported (100% NJB and BPP of 1) clade 1A at the most distal clade on the phylogenetic tree (Figure 10). The *F. vesiculosus* sequences in this clade may not be correctly placed. Correct identification of these sequences cannot be verified because the sequences were submitted to GenBank as unpublished data. Clade 1A consists entirely of Atlantic North American collected samples and *F. vesiculosus* GenBank samples creating a clearly defined separation of all *F. vesiculosus*. Although *F. vesiculosus, F. cottonii,* and *F. spiralis* are all present in clade 1B, North American thesis collection sequences within this clade grouped exclusively with *F. spiralis* GenBank samples.

The second major clade, contains clades 2 and 3 where clade 2 is not as clearly defined with samples from Atlantic, Pacific and Arctic Oceans and GenBank samples of three different species, *F. gardneri, F. distichus, F. evanescens.* The separation of clade 3 from the larger clade containing clades 2 and 3 (Figure 10) is more defined and is comprised entirely of GenBank *F. serratus* sequences. The large geographic distribution and separation of sequences within this clade 2 (Figure 10) are a possible consequence of geographic influences and biogeographic trends. Clade 2A (Figure 10) contains GenBank sequences from all three species and thesis sequences from Arctic and Atlantic shores. In contrast to clade 2A, thesis sequences in clade 2B and clade 2C (Figure 10) are entirely Pacific in origin.

GenBank sequences present in the clade 2 (Figure 10) are intermixed among all thesis sequences. Within this intermingled clade all GenBank *F. distichus* samples are of North Atlantic origin and all *F. gardneri* are of Pacific origin. Finally, with the exception of one, a

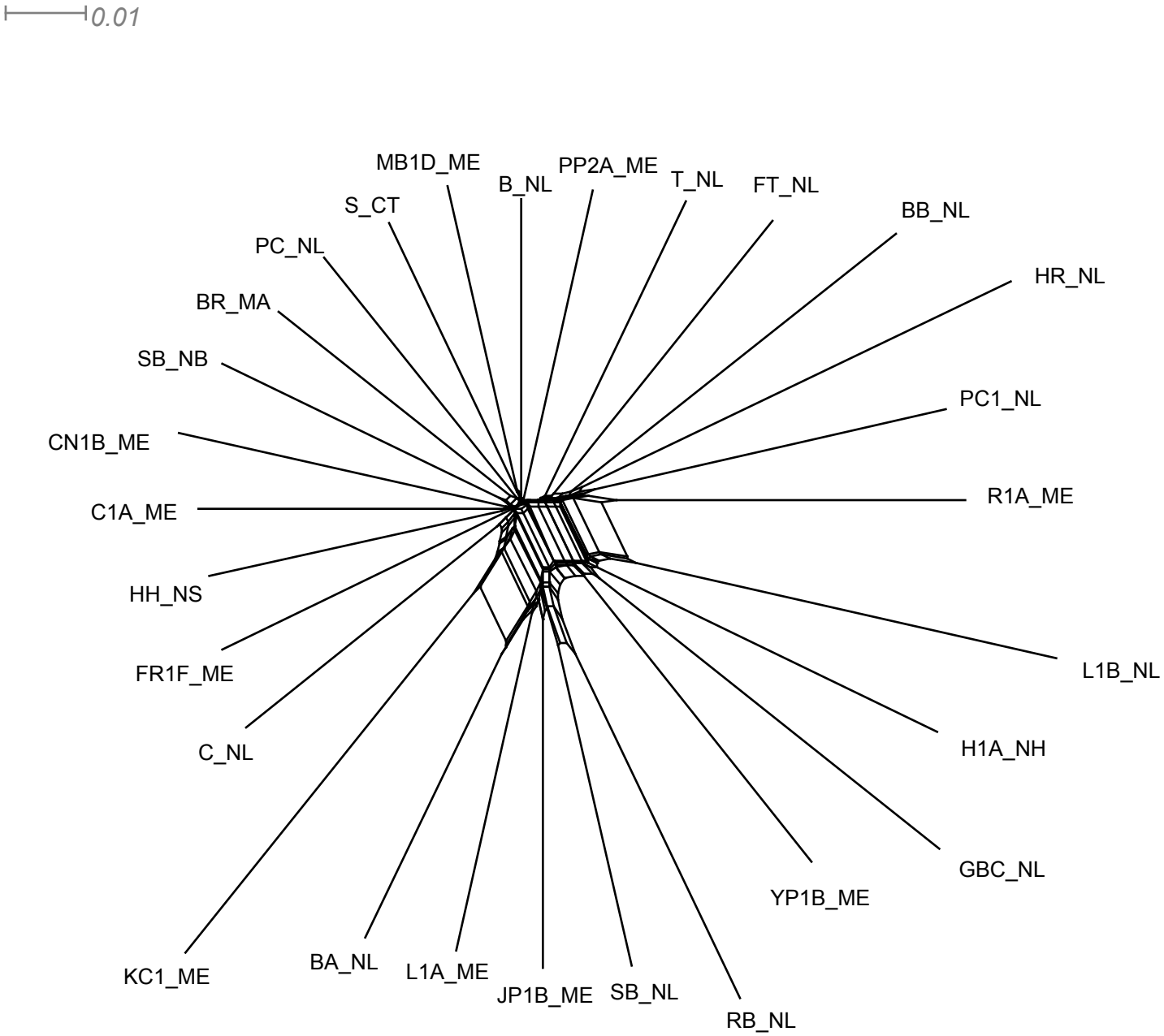
F. evanescens collected from Maine, all GenBank *F. evanescens* sequences were of European origins. GenBank sequences and thesis sequences from all three oceans are intermingled throughout clade 2 (Figure 10); all samples closely grouping with *F. gardneri* are of Pacific and Arctic origin. The close relationship of these samples is in agreement with the geographic distribution of the species, an endemic of the Pacific Ocean (Scagel *et al.* 1989, Hansen *et al.* 1997). Although, the *F. gardneri* sequences are closely related to sequences of Pacific origin, *F. gardneri* sequences do not make up a large group and are instead present in several areas of clade 2 on the phylogenetic tree (Figure 10). Furthermore, the *F. distichus* and *F. evanescens* are not grouping in any particular region of clade 2 (Figure 10) and do not appear to have a relationship with any region of collection within the phylogenetic tree.

3.3 MOLECULAR NETWORK ANALYSIS

Network analysis was completed using split decomposition, parsimony, and neighbor-net methods, and although general topology of networks was the same, neighbor-net provided more informative networks when evaluating the close relationships among samples. Therefore all networks included in the results and discussion sections were created using the neighbor-net method. Networks were created using the General Time Reversible method with the same transition and transversion rates that were used in the phylogenetic tree construction.

Two networks were created using neighbor-net with each network concentrating on a different region of the phylogenetic tree. The first of these two was a network using samples from clade 1 excluding NCBI samples (Figure 11). Network analysis (Figure 11) of

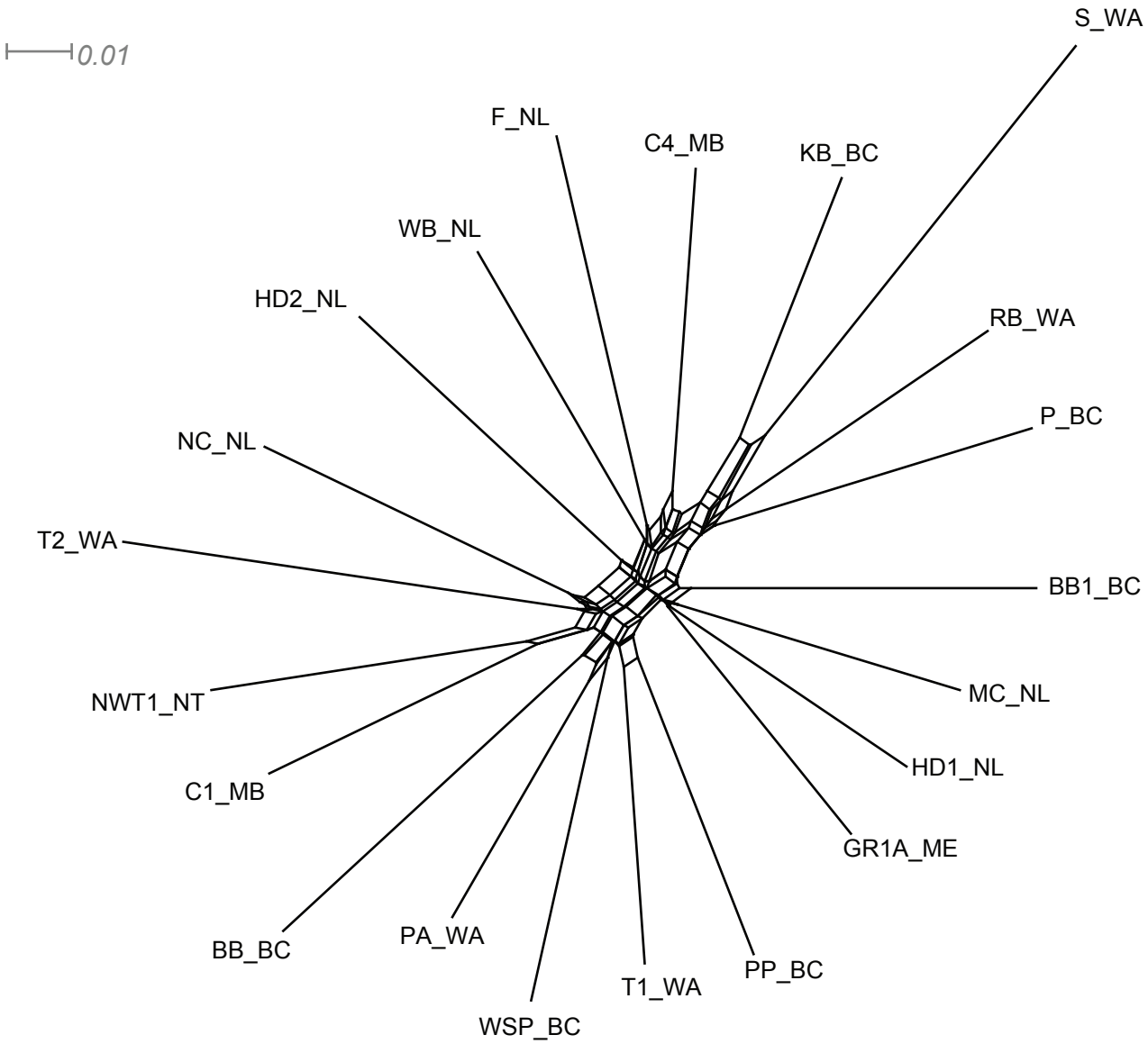
Figure 11. Phylogenetic network using neighbor-net construction method of samples taken from phylogenetic tree (Figure 11) clades 1A and 1B. Samples on the network are indicated with a sample and location code where the first set of characters represents the specific location and the second represents the state or province of collection. Sample and sample abbreviations are as follows: Millbridge 1D Maine (MB1D_ME), Portugal Cove Newfoundland (PC_NL), Brigus Newfoundland (BR_NL), Trespassy Newfoundland (T_NL), Perry Cove 1 Newfoundland (PC1_NL), Rockland 1A Maine (R1A_ME), Bay Bulls Newfoundland (BB_NL), Holyrood Newfoundland (HR_NL), Foxtrap Newfoundland (FT_NL), Pemaquid Pt. 2A Maine (PP2A_ME), Brant Rock Massachusetts (BR_MA), Fortune Rocks 1F Maine (FR1F_ME), Hants Harbour Nova Scotia (HH_NS), Corea 1A Maine (C1A_ME), Cutler Naval 1B Maine (CN1B_ME), Sealys Bay New Brunswick (SB_NB), Clarenville Newfoundland (C_NL).Stonington Connecticut (S_CT), Hampton 1A New Hampshire (H1A_NH), Lubec 1A Maine (L1A_ME), Bauline Newfoundland (BA_NL), Kettle Creek 1A Maine (KC1A_ME), Jones Port 1B Maine (JP1B_ME), Spaniards Bay Newfoundland (SB_NL), Rocky Beach Hwy 100 Newfoundland (RB_NL), York Pt. 1B Maine (YP1B_ME), Gooseberry Cove Newfoundland (GBC_NL), Lubec 1B Maine (L1B_NL).


0.01
MB1D_ME
B_NL
PP2A_ME
T_NL
FT_NL
S_CT
BB_NL
PC_NL
HR_NL
BR_MA
SB_NB
PC1_NL
CN1B_ME
R1A_ME
C1A_ME
HH_NS
L1B_NL
FR1F_ME
H1A_NH
C_NL
GBC_NL
YP1B_ME
KC1_ME
BA_NL
L1A_ME
JP1B_ME
SB_NL
RB_NL

samples from clades 1 on the maximum likelihood phylogenetic tree (Figure 10) are reinforced with two distinct clades appearing in both the network and phylogenetic tree analyses. However, the relationship between the two groups compared to the overall relationships among samples is small and as such the network has relatively equal relationships among all samples. Despite this overall close relationship, the two distinct upper and lower groups on the phylogenetic network correspond to the maximum likelihood phylogenetic analysis. The upper group in the network analysis is entirely composed of samples occurring in subclade 1A on the phylogenetic tree. The lower group of samples on the phylogenetic network consists of samples in clade 1B on the phylogenetic tree (Figure 10).

The network of clade 2 (Figure 12) sequences from the maximum likelihood phylogenetic tree (Figure 10), again have large distances from the samples to the central node with only small relationships among samples closer to the central node (Figure 11). Although the genetic distances between the samples near the central node of the network are small, there are clear groupings of samples between east and west coast origins. These several distinct groups within the network do not always agree with the phylogenetic tree (Figure 10). The close grouping Churchill 1 (MB) and North West Territories 1 (NT) samples from the arctic region is interesting in that they are not also close on the phylogenetic network to the third sample, Churchill 4 (MB). The samples Teahwitt 2 (BC) and Nameless Cove (NL), one west coast sample and one east coast, are also showing a greater relationship on the phylogenetic network then what they have on the phylogenetic tree (Figure 10).

Figure 12. Phylogenetic network using neighbor-net construction method of samples taken from phylogenetic tree (Figure 11) clades 2 and 3. Samples on the network are indicated with a sample and location code where the first set of characters represents the specific location and the second represents the state or province of collection. Sample and sample abbreviations are as follows: Buckleys Bay British Columbia (BB_BC), Teahwitt 1Washington (T1_WA), Porteau Park British Columbia (PP_BC), Goose Rocks 1A Maine (GR1A_ME), Hearts Desire 1 Newfoundland (HD1_NL), Middle Cove Newfoundland (MC_NL), Botany Bay 1British Columbia (BB1_BC), Ruby Beach Washington (RB_WA), Parkville British Columbia (P_BC), Kalaloch Beach Washington (KB_WA), Sekui Washington (S_WA), Hearts Desire 3 Newfoundland (HD3_NL), Churchill 4 Manitoba (C4_MB), Ferry Land Newfoundland (F_NL), Witless Bay Newfoundland (WB_NL), Hearts Desire 3 Newfoundland (HD3_NL, Nameless Cove Newfoundland (NC_NL), Teahwitt 2 Washington (T2_WA), NWT 1 Northwest Territories (NWT1_NT), Churchill 1 Manitoba (C1_MB), Whiffinspit Park British Columbia (WSP_BC), Port Angeles Washington (PA_WA)


0.01
S_WA
F_NL
C4_MB
KB_BC
WB_NL
HD2_NL
RB_WA
P_BC
NC_NL
T2_WA
BB1_BC
NWT1_NT
MC_NL
HD1_NL
C1_MB
GR1A_ME
BB_BC
PA_WA
PP_BC
T1_WA
WSP_BC

3.4 MORPHOLOGICAL ANALYSIS USING MOLECULAR GROUPINGS

General statistics on molecular based *a priori* groups (Table 11) revealed large differences across variables and large standard deviations compared to character means suggesting that the data may be useful in clustering analyses. Both of the variables upper dichotomous branching (BRCHUP) and lower dichotomous branching (BRCHLOW) had large standard deviations of 50.292 and 13.387 respectively compared to their means of 34.508 and 12.651. Also the character of number of plant stipes had a large standard deviation compared to its mean with the standard deviations of 2.601 and means of 1.905. Finally, the receptacle number (RECNUM) and receptacle length (RECLG) characters also displayed large standard deviations at 16.474and 1.117 compared to their means 13.286 and 1.098.

Hierarchical clustering using Euclidian distance (Figure 13) produced a dendrogram with a total distance of 80 and having the majority of divisions in the dendogram occurs from 0 to 10. These close divisions and the lack of large clustering does not provide support for the separation of samples into molecular groupings based on morphological data. Clustering analysis only using the number of vesicles for vesicle data resulted in the same dendrogram with the same topology and distances.

Step-wise discriminant analysis results using the major phylogenetic divisions from the maximum likelihood phylogenetic tree (Figure 10) yielded the most useful characters, based on F statistic values (greater then ± 1). Based on this analysis, four useful characters, stipe length (STPLG), number of upper branches (BRCHUP), number of receptacles (RECNUM), and the length of the receptacles (RECLG) were determined (Table 12). Discriminant analyses using clades 1 and 2 (Figure 10) from the maximum likelihood

Table 11. Basic statistic of morphometric characters as measured on all collected *Fucus* specimens with molecular data and reproductive bodies. Values used in appearing in the descriptor column were either measurements of continuous characters in millimeters (mm) or integer count values (int). Discriminant analysis characters were selected among: Plant length (PLTLG), Plant width (PLTWD), Number of stipes (STPNUM), Stipe length (STPLG), Stipe width (STPWD), Total number of fronds (FRNDNUM), Frond width (FRNDWD), Frond length (FRNDLG), Frond distal width (FRNDDISTWD), Mean number of serrations per frond (SERNUM), Mean distance between dichotomies (BRCHDIST), Number lower dichotomous branches (BRCHLOW), Number of upper branching (BRCHUP), Number of apical receptacles (RECNUM), Width of the receptacle (RECWD), Length of receptacle (RECLG), Number of air vesicles (VESNUM), Distance between paired air vesicles (VESDISTBT2), Mean distance between pairs of vesicles (VESDISTBTPRS), Air vesicle width (VESWD), Air vesicle length (VESLG) For a description of original measurement methodology see Figure 5 and Table 4. For a full listing of measured values see Appendix B.

Statistic	PLTLG (mm)	PLTWD (mm)	STPNUM (int)	STPLG (mm)	STPWD (mm)	SERNUM (int)	FRNDNUM (int)
Number of Cases	63	63	63	63	63	63	63
Minimum	3.3	2	1	0.1	0.1	0	7
Maximum	44.9	29.2	15	9.2	0.5	0	329
Median	17	11.8	1	2.3	0.2	0	33
Arithmetic Mean	18.224	14.005	1.905	2.994	0.262	0	47.206
Standard Deviation	9.108	6.605	2.601	2.234	0.113	0	50.772

Statistic	FRNDWD (mm)	FRNDLG (mm)	FRNDDISTWD (mm)	BRCHDIST (mm)	BRCHLOW (int)	BRCHUP (int)	RECNUM (int)
Number of Cases	63	63	63	63	63	63	63
Minimum	0.22	2.82	0.14	0.4	1	1	1
Maximum	2.34	41.8	1.44	6.06	55	358	97
Median	0.53	14.68	0.36	2.34	7	18	8
Arithmetic Mean	0.627	16.01	0.423	2.383	12.651	34.508	13.286
Standard Deviation	0.361	8.316	0.224	1.042	13.387	50.292	16.474

Statistic	RECWD (mm)	RECLG (mm)	VESDISTBT2 (mm)	VESDISTBTPRS (mm)	VESNUM (int)	VESLG (mm)	VESWD (mm)
Number of Cases	63	63	63	63	63	63	63
Minimum	0.16	0.28	0	0	0	0	0
Maximum	1.4	7.42	0.78	0.34	149	0.9	0.7
Median	0.4	0.74	0	0	0	0	0
Arithmetic Mean	0.48	1.098	0.029	0.032	4.571	0.13	0.108
Standard Deviation	0.255	1.117	0.129	0.084	21.325	0.267	0.217

Figure 13. Hierarchical clustering of specimens with molecular data based on morphological characters using Euclidian distance for all measured samples with reproductive characters. Clustering analysis includes all measured morphological characters among samples displaying reproductive characters. For a description of original measurement methodology and list of characters used in the clustering analysis see Figure 5 and Table 4. For a full listing of measured values see Appendix B.

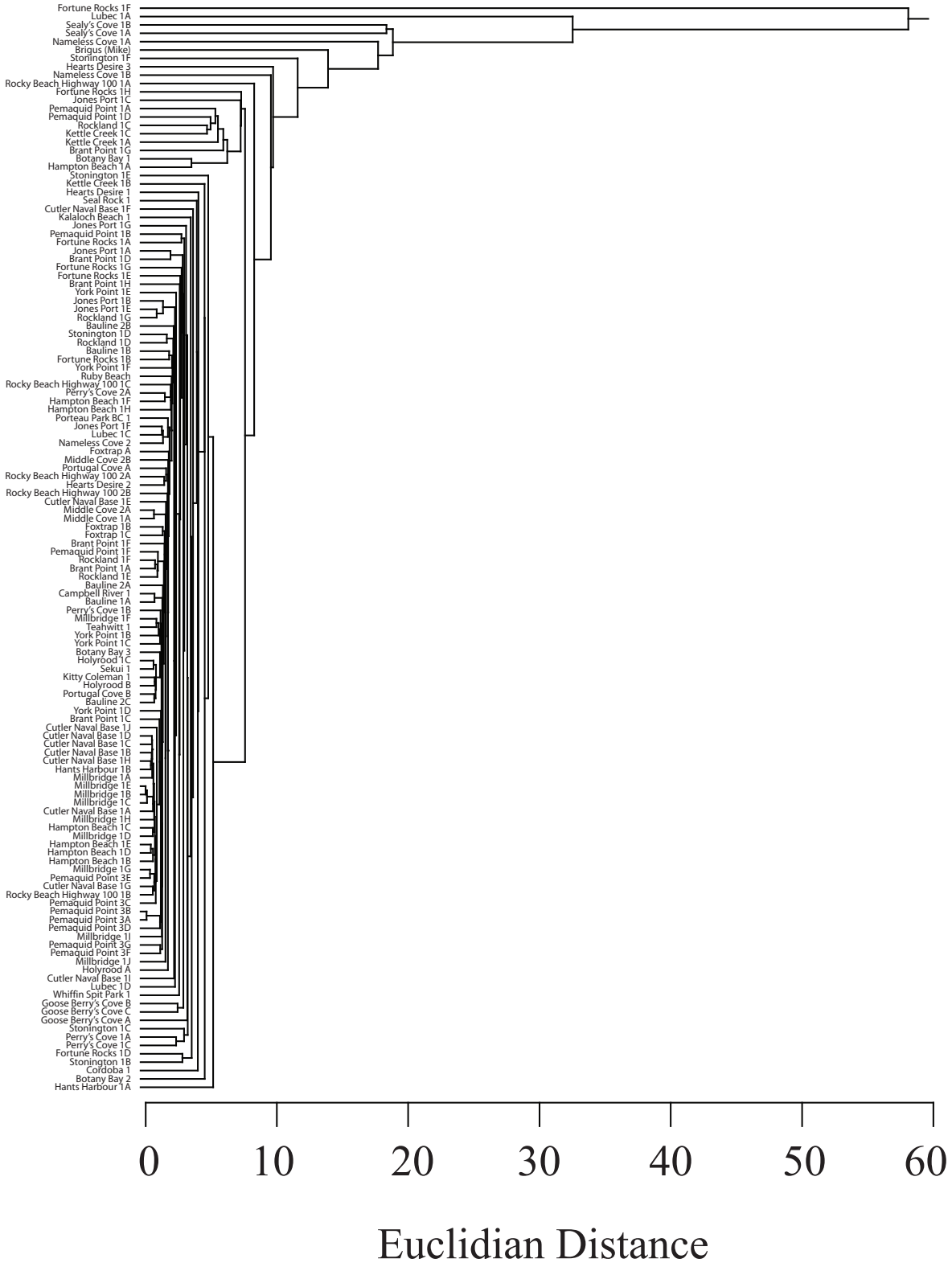

Fortune Rocks 1F
Lubec 1A
Sealy's Cove 1B
Sealy's Cove 1A
Nameless Cove 1A
Brigus (Mike)
Stonington 1F
Hearts Desire 3
Nameless Cove 1B
Rocky Beach Highway 100 1A
Fortune Rocks 1H
Jones Port 1C
Pemaquid Point 1A
Pemaquid Point 1D
Rockland 1C
Kettle Creek 1C
Kettle Creek 1A
Brant Point 1G
Botany Bay 1
Hampton Beach 1A
Stonington 1E
Kettle Creek 1B
Hearts Desire 1
Seal Rock 1
Cutler Naval Base 1F
Kalaloch Beach 1
Jones Port 1G
Pemaquid Point 1B
Fortune Rocks 1A
Jones Port 1A
Brant Point 1D
Fortune Rocks 1G
Fortune Rocks 1E
Brant Point 1H
York Point 1E
Jones Port 1B
Jones Port 1E
Rockland 1G
Bauline 2B
Stonington 1D
Rockland 1D
Bauline 1B
Fortune Rocks 1B
York Point 1F
Ruby Beach
Rocky Beach Highway 100 1C
Perry's Cove 2A
Hampton Beach 1F
Hampton Beach 1H
Porteau Park BC 1
Jones Port 1F
Lubec 1C
Nameless Cove 2
Foxtrap A
Middle Cove 2B
Portugal Cove A
Rocky Beach Highway 100 2A
Hearts Desire 2
Rocky Beach Highway 100 2B
Cutler Naval Base 1E
Middle Cove 2A
Middle Cove 1A
Foxtrap 1B
Foxtrap 1C
Brant Point 1F
Pemaquid Point 1F
Rockland 1F
Brant Point 1A
Rockland 1E
Bauline 2A
Campbell River 1
Bauline 1A
Perry's Cove 1B
Millbridge 1F
Teahwitt 1
York Point 1B
York Point 1C
Botany Bay 3
Holyrood 1C
Sekui 1
Kitty Coleman 1
Holyrood B
Portugal Cove B
Bauline 2C
York Point 1D
Brant Point 1C
Cutler Naval Base 1J
Cutler Naval Base 1D
Cutler Naval Base 1C
Cutler Naval Base 1B
Cutler Naval Base 1H
Hants Harbour 1B
Millbridge 1A
Millbridge 1E
Millbridge 1B
Millbridge 1C
Cutler Naval Base 1A
Millbridge 1H
Hampton Beach 1C
Millbridge 1D
Hampton Beach 1E
Hampton Beach 1D
Hampton Beach 1B
Millbridge 1G
Pemaquid Point 3E
Cutler Naval Base 1G
Rocky Beach Highway 100 1B
Pemaquid Point 3C
Pemaquid Point 3B
Pemaquid Point 3A
Pemaquid Point 3D
Millbridge 1I
Pemaquid Point 3G
Pemaquid Point 3F
Millbridge 1J
Holyrood A
Cutler Naval Base 1I
Lubec 1D
Whiffin Spit Park 1
Goose Berry's Cove B
Goose Berry's Cove C
Goose Berry's Cove A
Stonington 1C
Perry's Cove 1A
Perry's Cove 1C
Fortune Rocks 1D
Stonington 1B
Cordoba 1
Botany Bay 2
Hants Harbour 1A
0
10
20
30
40
50
60
Euclidian Distance

Table 12. A table of informative characters as determined through discriminate functions analysis of all samples with molecular data. Three a priori groups are represented: season of collection summer or winter (SUMVWINT); exposure to open ocean compared to more sheltered sites (EXPOSE); ocean of origin (GEOG). Table A contains analyses using all measured morphological characters. Table B contains results from analyses excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD. Values appearing in the characters column were either measurements of continuous characters in millimeters (mm) or integer count values (int). Discriminant analysis characters were selected among: Plant length (PLTLG), Plant width (PLTWD), Number of stipes (STPNUM), Stipe length (STPLG), Stipe width (STPWD), Total number of fronds (FRNDNUM), Frond width (FRNDWD), Frond length (FRNDLG), Frond distal width (FRNDDISTWD), Mean number of serrations per frond (SERNUM), Mean distance between dichotomies (BRCHDIST), Number lower dichotomous branches (BRCHLOW), Number of upper branching (BRCHUP), Number of apical receptacles (RECNUM), Width of the receptacle (RECWD), Length of receptacle (RECLG), Number of air vesicles (VESNUM), Distance between paired air vesicles (VESDISTBT2), Mean distance between pairs of vesicles (VESDISTBTPRS), Air vesicle width (VESWD), Air vesicle length (VESLG) Marked characters (✔) were used in the discriminant analyses. For a description of original measurement methodology see Figure 5 and Table 4. For a full listing of measured values see Appendix B.

Characters	All Characters	Only Vesicle Number (VESNUM)
PLTLG	-	-
PLTWD	-	-
STPNUM	-	-
STPLG	✔	✔
STPWD	-	-
SERNUM	-	-
FRNDNUM	-	-
FRNDWD	-	-
FRNDLG	-	✔
FRNDDISTWD	-	-
BRCHDIST	-	✔
BRCHLOW	-	-
BRCHUP	✔	-
RECNUM	✔	-
RECWD	-	-
RECLG	✔	-
VESDISTBT2	-	
VESDISTBTPRS	-	
VESNUM	-	-
VESLG	-	
VESWD	-	

phylogenetic tree as grouping variables were conducted with all reproductive characters. The Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistical probably tests indicate a significant separation of the two groups, clade 1 (Figure 10) containing *F. vesiculosus, F. spiralis,* and *F. cottonii* species and clade 2 (Figure 10) containing *F. distichus, F. evanescens,* and *F. gardneri* (Table 13). All three statistical analyses have a probability value of ($P < 0.001$) and successfully separate the two *a priori* molecular phylogenetic groups based on the four selected characters.

Geisser probabilities classification matrix and jack-knifed resampling resulted in 92% correct *a posteriori* placement of samples with a jack-knifed resampling value of 90% (Table 14). With 58 of the 63 samples classified with an *a posteriori* placement of 50% or higher. Fifty-two of the samples were classified based on Geisser probabilities between 90% and 100% strongly supporting the classification matrices.

Discriminant analysis using only the vesicle number for vesicle data and the molecular grouping variables resulted in the three selected characters: stipe length (STPLG), frond length (FRNDLG), and distance between branches (BRCHDIST; Table 12). Using these characters the statistical probabilities, Wilks' λ, Piallai's trace, and Hotelling-Lawley trace, indicate a statistical support for the grouping of samples in to the two phylogenetic clades (Figure 10) with a probability of $P < 0.001$ across all three (Table 13). Geisser probability *a posteriori* placement of the 63 samples had 8 samples classified with less then 50% Geisser probability support and 55 samples having over 70% placement with 51 of those samples having over 90%. Classificatory analysis and jack-knifed resampling both resulted in an 87% correct placement of samples in to *a posteriori* groups (Table 14). Although there are changes in the useful characters determined for the analysis using all

Table 13. Multivariate statistics and F approximations of all samples with molecular data. The Wilks' λ, Piallai's trace, and Hotelling-Lawley trace tests for the discriminant analysis for the: A. seasonal collection (SUMVWINT) using all characters; B. ocean of origin (GEOG) using all characters; C. exposure (EXPOSE) using all characters; D. seasonal collection excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; E. ocean of origin (GEOG) excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; and F. exposure (EXPOSE) excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD.

A. Molecular grouping with all characters

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.482	15.577	58	0.0000
Pillai's Trace	0.518	15.577	58	0.0000
Lawley-Hotelling Trace	1.074	15.577	58	0.0000

B. Molecular groupings with only vesicle numer for vesicle data

Statistic	Value	Approx. F-ratio	df	p-value
Wilks's Lambda	0.466	13.06	57	0.0000
Pillai's Trace	0.534	13.06	57	0.0000
Lawley-Hotelling Trace	1.146	13.06	57	0.0000

Table 14. Classification matrix and jackknifed classification matrix of all samples with molecular data. Samples with reproductive characters, using a stepwise discriminate function of: A. seasonal collections using all characters; B. ocean of origin using all characters; C. exposure using all characters; D. seasonal collections excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; E. ocean of origin excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD; and F. exposure excluding the characters VESDISTBT2, VESDISTBTPRS, VESLG, and VESWD. Characters used for final discriminate analysis are listed in Table 7. The first value represents the classification based on Geisser assignment probabilities while the second is the jackknifed resampling value.

A. Molecular grouping with all characters

Group	Number of Samples		% Correct
	F. vesiculosus, F. cotonii, F. spiralis	*F. distichus, F. gardneri, F. evanescens*	
F. vesiculosus, F. cotonii, F. spiralis	50 / 49	3 / 4	94 / 92
F. distichus, F. gardneri, F. evanescens	2 / 2	8 / 8	80 / 80
Total	52 / 51	11 / 12	92 / 90

B. Molecular groupings with only vesicle number for vesicle data

Group	Number of Samples		% Correct
	F. vesiculosus, F. cotonii, F. spiralis	*F. distichus, F. gardneri, F. evanescens*	
F. vesiculosus, F. cotonii, F. spiralis	47 / 47	6 / 6	89 / 89
F. distichus, F. gardneri, F. evanescens	2 / 2	8 / 8	80 / 80
Total	49 / 49	14 / 14	87 / 87

characters compared to only using the number of vesicles for vesicle data the overall results indicate support for two separate groups in both analyses.

4.0 DISCUSSION

4.1 MORPHOLOGICAL

Plasticity among *Fucus* species and morphological variation across study samples indicates that some of the measured morphological characters used in this thesis are not sufficient to delineate collected *Fucus* samples. Analysis using the total data set including all characters was ineffective in separating samples based on *a priori* groupings. Clustering analysis using all samples and characters produced a dendrogram (Figure 7) that had no clear groupings of samples based on geographical location, season of collection, or degree of exposure. The largest grouping of samples occurs between two clusters in the tree, the first from Flat Rock 1B (NL) at the top to Singing Sands (PE) near the bottom and the second from Argentia 1B (NL) to Fortune Rocks 1H (ME). Not only were there no discernable groups, such as geographical location or level of exposure that can be discerned from this dendrogram, but also members contained between these two groups are significantly similar. For example, Pemaquid Pt. (ME). Samples 1A and 1D are contained in the second and lower cluster where Pemaquid Pt. (ME) samples 1B and 1F are in the larger upper cluster. This suggests the unreliability of the dendrogram as these samples are all taken from the same site, at the same time from the same small population of *Fucus*. This situation is also true of Fortune Rocks (ME), Jones Port (ME), and Hampton Beach (NH) samples between the two large clusters within the dendogram. This lack of clustering maybe due to limited sample size, background noise in the analysis due to ineffective characters, or lack of independent characters.

Although clustering analysis was ineffective to distinguish samples based on the measured characters, discriminant analyses based on the grouping variables geographical location, wave exposure, and season of collection were effective in statistically separating the

collected samples. This separation of samples based on multivariate statistics is in agreement with other studies (Bergström *et al.* 2005, Rice *et al.* 1985, Ruuskanen & Nappu 2005). For example, Rice and Chapman (1985) provide statistical evidence for the separation of *F. distichus* and *F. evanescens* across 1279 samples from 51 populations. They note that the ability for their study to effectively separate the species was due to the large data set across the entire range of the two species (Rice *et al.* 1985). Rice and Chapman (1985) also highlighted the presence of morphologically distinct populations within each species across the distributional range.

Although discriminant analyses using all characters and the three grouping variables ocean of collection, season of collection, and level of exposure to open ocean at the site of collection produced were stastically significant the results did display variation. This variation among the results was apparent across all three groups and all analysis results including the clustering analyses, the classificatory analyses, and discriminant analyses. These variations are most likely due to the variation in original data including collection times and locations. The high statistical probability values with a low classificatory values and large variation among Geisser assignment probabilities could be because the most crucial characters lacked the low within group variance and high between group variance ideal in diagnostic traits. The variation in the useful characters across all three grouping supports this with few characters appearing in more then one analysis (Table 7).

Finally, as indicated by Rice and Chapman (1985) the lack of sufficiently large enough data set may not have provided a sufficient enough sample size for all analyses employed in this thesis leading to variation among results from the various grouping variables and statistical tests. Furthermore, the possibility of up to six species present on

North American shores further limits the possibility of the overall number of each species within the entire collection being sufficient to obtain statistically significant results. Small sample sizes results in higher variances. Finally, the presence of morphologically distinct populations within species, as described by Rice and Chapman (1985) and Bäck (1993), would only contribute to the lack of resolution with the analysis of morphological characters.

Although, the sample size used in this thesis is small the separation of distinct levels of exposure has been achieved in other studies with a data set of approximately 150 samples using a subset of the same characters used in this study (Bäck 1993). Although, Bäck (1993) did describe a noticeable division of samples into distinct groups based on geographical location and wave exposure, the final conclusion of the Bäck (1993) study was that morphology was insufficient to accurately determine taxonomic divisions among the collected samples.

The collection of samples within the broad description of intertidal zone could have introduced variation among collected samples. *Fucus* species distribution through the intertidal zone has been reported in many species descriptions, studies, and keys (Bergström *et al.* 2005, Wynne & Magne 1991, Sears 1998, Villalard-Bohnsack July 1995, Gabrielson 2000). Approaches like Bäck (1993) where all sample collections were made in water depths of 1 to 2 meters, are still influenced by the slope of the near shore environment, variation in substrate, and the size of the intertidal area. Furthermore, near shore collection of North American species in the high to mid intertidal zone would not have excluded species based on collection methodology. *Fucus distichus* and *F. evanescens* inhabit at the high to low intertidal (Sears 1998, Villalard-Bohnsack July 1995), *F. gardneri* occurs in the mid to upper intertidal (Gabrielson 2000), *F. vesiculosus* is present on mid to low intertidal areas (Sears

1998, Villalard-Bohnsack July 1995), *F. serratus* inhabits the upper to mid intertidal zone (Sears 1998), and *F. spiralis* is present in the upper intertidal (Wynne & Magne 1991, Sears 1998, Gabrielson 2000). Methods of *Fucus* collection used in this thesis from mid to high intertidal areas would include the intertidal habitat of all North American species.

Moving down the intertidal zone from terrestrial area toward benthic area, the impact of wave action on substrate attached algal species is lessened and this is more apparent in areas with small intertidal zones or tideless shores (Kalvas & Kautsky1993). The methodology employed in this thesis with the consistent collection of samples in the high to mid intertidal contributed to a standardized collection method while allowing the influence of wave action on samples to achieve a collection consistent with the morphological variation of *Fucus* species. Although collections were not conducted on a standard measurement from the high tide mark toward low tide this in itself may not have been appropriate. It is not likely that any two collection locations would have the same near shore influences, and as collections were made from a variety of sites with variation of near shore slope and surface substrate as one moved down the intertidal space, the use of a standard measurement from the high tide mark would not be effective.The overall morphology and survival of *Fucus* in the upper to mid intertidal area is influenced by the relative exposure of the sites to open ocean. Small changes in wave exposure have been determined to greatly affect the morphology of some *Fucus* species, including Baltic *F. vesiculosus* and North Atlantic *F. spiralis* (Ruuskanen & Nappu 2005). Ruuskanen and Nappu (2005) provide statistical evidence for morphological variation across wave exposed and sheltered sites but indicated that factors other than wave action are involved. Rice *et al.* (1985) also suggested that large

morphological variations are influenced by a biotic factors such as temperature, salinity, and exposure to light (Rice *et al.* 1985).

The results from the discriminant analyses with the removal of data for the vesicle characters, distance between two vesicles in a pair (VESDISTBT2), distance between two pairs of vesicles (VESDISTBTPRS), average vesicles length (VESLG), and average vesicle width (VESWD), support the conclusions of Ruuskanen and Nappu (2005). In all discriminant analyses where these vesicle characters were removed and exposure was used as a grouping variable there were significant changes in the classificatory results and the statistical tests. Further study of the relationship among samples of a single known species are necessary to support the removal of vesicle data as a important character in the taxonomic identification of samples. However, the use of vesicle the four vesicle characters indicates that the separation of collected samples based on the season of collection and ocean of collection using this information is not reliable.

The large number of winter collection in the North Atlantic may have resulted in the increased collection of morphology simplistic samples. *Fucus* plants grow at approximately 1mm per day in the late spring, summer and early fall and this growth is reduced to one third of that during cold weather conditions (Lüning *et al.* c1990). *Fucus* species are generally not fertile until after one full season of growth and survive for 2 to 3 years, (with some exceptions such as *F. vesiculosus* where specimens living as long as 7 or 8 years have been reported in Barents Sea; Lüning *et al.* c1990). The winter collections of these Atlantic samples may have selected specimens in their first or second winter season having experienced only one full growth season. Also, collections over differing seasons may also subject the samples to varying amounts of wave exposure because in some regions wave

action can vary significantly from one season to another (Ruuskanen & Nappu 2005). Furthermore, during winter months older and larger plants are more susceptible to desiccation and destruction from wave action, ice formation, and weathering (Rice *et al.* 1985, Lüning *et al.* c1990). As a result, winter collections may have a bias toward the collection of immature plants due to desiccation and destruction during early harsh winter conditions. Sample collection bias due to winter collections was not apparent in the collections of this thesis. A total of 158 collections were made of which 80 samples were collected during winter months and 78 during summer, and of these a total of 86 samples exhibited reproductive characters. The percentage of collected samples exhibiting reproductive characters did differ slightly with 44% of winter collections exhibiting reproductive characters compared to 65% of summer collections.

Although this discrepancy does not justify the exclusion of winter samples based on season of collection, results using multivariate statistics suggest otherwise. Discriminant analysis using summer samples compared to analysis using collections from both seasons displayed a clear drop in the statistical support from $P = 0.003$ to $P<0.001$ for Wilks' λ, Piallai's trace, and Hotelling-Lawley trace statistics. Although this change is not statistically significant the small difference could be due to the overall small sample size or the seasonal collection bias toward Pacific and Atlantic collections. In addition to the drop in statistical significance the classificatory analysis correct placement percentages significantly changed when using collections from both seasons with both exposure and ocean of collection grouping variables. Analysis with exposure as a grouping variable increased from 78% jack-knifed classificatory analysis using both seasons to 84% using only summer samples. This change could also be due to a change in the weather and wave action patterns between

seasons, which would only support the collection of samples during summer samples to remove added unknown factor.

The use of mature plants, as determined by the presence of reproductive bodies, has been described as a necessary procedure to eliminate the large effects of age on morphological characters (Rice *et al.* 1985, Bäck 1993). The collection and inclusion of samples that were not mature and did not have the ability to display all characters, like reproductive bodies and vesicles, may have created variation within the data set. Results of discriminant analysis using only samples with reproductive bodies should have removed the possibility of having non-reproductive sample collections interfering with the separation of samples into groups.

Future sample collections to accompany the present data set should attempt to balance all possible reported biases. An attempt to make sample collections during opposing seasons as well as collections of both reproductive and non-reproductive samples at all sites of collection. Finally, the measurement of sample sites and the application of cartographical methods to place significance on variation of wave exposure would reduce the potential unknown degree of wave action influencing morphological plasticity (Ruuskanen & Nappu 2005, Bäck 1993).

4.2 MOLECULAR

The molecular phylogenetic maximum likelihood analysis of the mitochondrial 23S mtDNA (Figure 10) identified 4 distinct monophyletic groups, clade 1, clade 2, clade 3, and clade 4. Clade 1 (Figure 10) consists of *F. vesiculosus, F. spiralis, F. cottonii*, and *F. virsoides*. The second clade (clade 2 Figure 10) contained the species *F. gardneri, F. distichus,* and *F.*

evanescens. Clade 3 (Figure 10) composed entirely of *F. serratus*. The remaining clade, clade 4 (Figure 10), exclusively consists of *Hesperophycus* samples. These five groups are in general agreement with Serrão *et al.* (1999) evaluation of the members of *Fucus* using the ITS-1 and ITS-2 region of the nuclear ribosomal DNA (nrDNA). Serrão *et al.* (1999) described two distinct lineages, the first of which consist of *F. serratus, F. gardneri, F. distichus,* and *F. evanescens* and is representative of clades 2 and 3 in the present thesis. Serrão *et al.* (1999) also describe a second lineage comprised of *F. vesiculosus, F. spiralis, F. cottonii*, and *F. virsoides* and is similar to clade 1 in this thesis (Serrão *et al.* 1999). Bayesian posterior probabilities and neighbor-joining bootstrap values also support the large division in to the two clades 1 and 2 on the maximum likelihood tree (Figure 10). Slightly lower NJB values may be due to the two large indels in the multiple sequence alignment resulting in resampling outcomes with little information.

4.2.1 HESPEROPHYCUS CALIFORNICUS OUTGROUP

The use of *Hesperophycus californicus* as an outgroup for the study of *Fucus* is accurate as *H. californicus* is a direct and common ancestor to all *Fucus* species (Serrão *et al.* 1999). This relationship has been confirmed by Serrão *et al.* (1999) who evaluated all genera in the Fucaceae family using sequences of the internal transcribed spacer regions of nuclear ribosomal DNA. Coyer *et al.* (2006) also effectively used *H. californicus* as an outgroup in a molecular study of *Fucus* species predominantly inhabiting European shores using the 23S mtDNA, the same region used in this thesis.

The *H. californicus* samples have clear sequence divergent from all other samples in the alignment consisting of transitions and transversions but with few insertion deletion areas

across all four *H. californicus* samples compared to the entire alignment. What is interesting is not the variation of the four *H. californicus* samples compared to all other samples in the multiple sequence alignment, but the variation among the *H. californicus* samples. Seal Rock 1 (OR), Kitty Coleman (BC), and Campbell River (BC) sequences all group together on the maximum likelihood tree (Figure 10) and share an extremely high degree of identity (80 to 90%) among the three theses samples in the multiple sequence alignment compared to low identity among all four aligned sequences of (45to 55%). However, the sequence of *H. californicus* from GenBank (AY659915) does not group with these three samples and has 24 transitional, 30 transversional, and 2 single nucleotide indelshas two large insertion-deletion areas from nucleotide 163 to 342 and again from nucleotide 481 to 495. This separation of these collections of *H. californicus* sequences is interesting as there is currently only one described species for the genus, *Hesperophycus californicus* P.C. Silva. The insertion deletion region of the sequence alignment with all four samples certainly decreased the identity among all samples. When the indel regions are removed there is still a significant difference between percent identity among all samples where the GenBank sequences only has between 85 and 90% identity compared to all other samples and the Seal Rock 1 (OR), Kitty Coleman (BC), Campbell River (BC) cluster shares a minimum of 97.5% identity. It is unclear as to the reason for such a large variation between the GenBank *H. californicus*, collected from Pacific Grove California (Coyer *et al.* 2006a), and the group of Seal Rock 1 (OR), Kitty Coleman (BC), and Campbell River (BC) sequences. Further samples are necessary to fully evaluate this genetic separation and determine if this variation represents the presence of a second species within the genus or if this variation is due to the biogeography of *H. californicus* on the Pacific coast.

Furthermore, when the indel regions are removed from the full data set the variation in nucleotide identity between the GenBank *H. californicus* (AY659915) and all *Fucus* samples is between 60 and 70% where the identity between the three *H. californicus* thesis samples and all *Fucus* sequences is only 10% lower between 50 and 60% identity. In comparison the variation among all *Fucus* samples is between approximately 20 and 100% with an average identity of 82%.

The larger genetic separation among *H californicus* samples compared to the separation among *Fucus* samples on the maximum likelihood phylogenetic tree (Figure 10) is further verified through the low identity between *H californicus* samples and the *Fucus* samples the established phylogenetic position of *H californicus* as ancestral to the genus *Fucus* (Serrão *et al.* 1999). In addition to the sequence identity variations the lack of grouping among the *H californicus* species using hierarchical clustering based on morphological characters suggests two possible reasons. The first is that *H californicus,* like *Fucus,* is morphologically plastic and recognition of the genus among *Fucus* specimens is more difficult. The secondly that perhaps the lack of clustering is representative of two *H californicus* species present on the Pacific coast. Further sampling of the species is necessary to elucidate these questions.

4.2.2 Fucus spiralis, vesiculosus, and virsoides Lineage (clade 1)

Clade 1, consisting of subclades 1A, 1B, and 1C, is a monophyletic clade present in the molecular phylogenetic maximum likelihood tree (Figure 10). This larger clade 1 is entirely composed of thesis samples from the North Atlantic region covering the entire collection range from Connecticut at the southern point to Newfoundland at the northern point. With

the exception of *F. virsoides*, (1C Figure 10), the remaining subclades 1A and 1B are paraphyletic with *F. vesiculosus* occurring in both lineages. The low sequence variability among samples in clade 1 suggests a recent radiation (Serrão *et al.* 1999 using nrDNA-ITS, Coyer *et al.* 2006 using mtDNA; Leclerc *et al.* 1998). The well-supported (BPP = 1) separation of the endemic *F. virsoides*, the only *Fucus* species in the Mediterranean and Adriatic Seas, is a direct result of glacial refugia and speciation due to allopatric isolation from the last glacial maximum (Coyer *et al.* 2006a, Rindi & Battelli 2005, Furnari *et al.* 1999). This species is within a distinct monophyletic clade and its unique geographic habitat indicates that it is a separate species within clade 1 (Figure 10)

The presence of the largely separated *F. vesiculosus* in clade 1A (Figure 10), the grouping of *F. spiralis* in clade 1B, and the lack of thesis samples grouping with the European endemics (*F. cottonii* and the already mentioned *F. virsoides*), suggests two distinct species: *F. vesiculosus* in clade 1A and *F. spiralis* in clade 1B (Caram & Jónsson 1972, Rueness 1997, Wynne & Magne 1991). The low support values for the separation of subclades 1A and 1B (Figure 10) and the phylogenetic mixture of the two species in both sub clades 1A and 1B suggest that their distinction as species *F. spiralis* and *F. vesiculosus*, may not be sufficient information to conclusively delineate the species using this DNA region due to the large indel regions. The thesis samples collected across the North Atlantic shores are not grouping within geographical regions and the small genetic distance between samples within each of the subclades in clade 1 (Figure 10) does not support the presence of *F. spiralis* or *F. vesiculosus* biogeographic regions.

The physical near shore separation of the species *F. spiralis* and *F. vesiculosus* in clade 1 (Figure 10) is another possible factor influencing molecular phylogenetic topology

present in the maximum likelihood tree (Figure 10). The intertidal distribution of *F. vesiculosus,* from mid to low intertidal (Sears 1998, Villalard-Bohnsack July 1995), and *F. spiralis,* in the high intertidal region (Wynne & Magne 1991, Sears 1998, Gabrielson 2000), further supports results of the phylogenetic analysis (Figure 10) and the distinction of these two subclades (1A and 1B) as individual species. Variations in the active reproductive season of *F. vesiculosus* and *F. spiralis* has been recorded (Serrão *et al.* 1999) between non-overlapping summer and fall periods, resulting in reproductively isolated populations and increased molecular divergence resulting in the separation of the clades on the maximum likelihood tree (Figure 10). Microsatellite studies using allele frequencies have identified a genetic basis for the maintenance of the species *F. vesiculosus* and *F. spiralis* (Billard *et al.* 2005). Furthermore, the phylogenetic network of thesis samples (Figure 11) present in clades 1A and 1B (Figure 10) provides a clear division among groups of samples or between individual samples for the continued support of *F. vesiculosus* and *F. spiralis*.

The difference in the organization of sexual characters between *F. vesiculosus* (diecious) and *F. spiralis* (monoecious) further supports the presence of two distinct species (Coyer *et al.* 2006a). However, the hybridization of *F. vesiculosus* and *F. spiralis* species has been reported and likely contributes to difficult taxonomic division and potential polyphyly among these species (Billard *et al.* 2005). Furthermore, the suggestion that the ability to hybridize between these two species indicates that the organization of sexual characters is not crucial for successful reproduction and therefore should not be considered a vital indicator for the distinction of these two species (Coyer *et al.* 2006a, Billard *et al.* 2005, Wallace *et al.* 2004, Engel *et al.* 2005). The variation in reproductive seasons among populations and hybridization of *F. vesiculosus* and *F. spiralis*, along with the recent

radiation of the *Fucus* genus, has lead to questionable non-monophyletic phylogenetic analysis of the *F. vesiculosus, F. spiralis, F. ceranoides, F. cottonii* complex.

The close genetic relationship among sequences within the sub-clades 1A and 1B (Figure 10) requires further molecular analysis to effectively separate members into clearly defined species. In addition to further molecular study, the species level placement of thesis samples through expert identification using morphological characters can confirm the taxonomic separation of samples among GenBank samples. Current information and phylogenetic analysis supports the distinction of three separate species within clade 1 (Figure 10), the monophyletic *F. virsoides* in subclade 1C, *F. vesiculosus* in clade 1A, with the remaining clades 1B representing *F. spiralis.*

4.2.3 Fucus distichus and F. serratus Lineage (clades 2 and 3)

The second monophyletic lineage consists of two distinct clades (Figure 10). The first of which, clade 2, contains three subclades 2A, 2B, 2C, and 2D (Figure 10). The third and final clade of *Fucus* on the maximum likelihood tree, originates from the second monophyletic lineage and is sister to clade 2 containing *F. distichus, F. evanescens, and F. gardneri* and contains the GenBank sequences for *F. serratus* (Figure 10). A lack of neighbor joining bootstrap values for the separation of these two clades is most likely due to the sequence alignment insertion deletion and neighbor joining bootstrap resampling methods as discussed above. High Baysian support (BPP=0.96) for the separation of these two lineages (clades 2 & 3; Figure 10) and topological agreement between Baysian and maximum likelihood trees indicate a well placed and supported *F. serratus* (Figure 10).

4.2.4 BIOGEOGRAPHY OF F. DISTICHUS LINEAGE (CLADE 2)

Clade 2 (Figure 10), consisting of subclades 2A, 2B, 2C, and 2D, is a monophyletic clade with a poor neighbor-joining bootstrap value (63% NJB) and a well-supported Baysian posterior probability (BPP = 0.98). This clade is comprised of three main subclades the first of which is divided in to the labeled clades 2A and 2B (Figure 10). The two other clades are sister to the larger sub clade containing 2A and 2C and are labeled 2C and 2D (Figure 10). The three larger clades of these four clades are polyphyletic with GenBank *F. gardneri* in all three and *F. distichus* and *F. evanescens* in subclades 2A and 2B. The study by Coyer *et al.* (2006) of the same species supports this polyphyletic relationship.

The structure of the maximum likelihood tree (Figure 10) for clade 2 does not support the presence of three *Fucus* species (*F. distichus, F. evanescens,* and *F. gardneri*). The clades short evolutionary distance, 0.05 from the node to the most distal sample, indicates very little evolutionary change among samples within the clade. The combination of these three species into a single *F. distichus* has been well supported in the literature for over 30 years (Coyer *et al.* 2006a, Lindstrom 2001, Lindstrom 2006, Serrão *et al.* 1999, Lüning *et al.* c1990, Abbott & Hollenberg 1976).

The current taxonomic separation between that of *F. distichus* and *F. evanescens* with *F. gardneri* is largely based on habitat (Silva 1953). *Fucus gardneri*, described as an endemic species of the North West Pacific (Ruuskanen & Nappu 2005, Serrão *et al.* 1999), is not distinguishable as a species using mtDNA on the maximum likelihood tree (Figure 10). Furthermore, the overlapping habitat between *F. distichus* and *F. gardneri* has been reported in the North Pacific and Atlantic coasts of Alaska (Scagel *et al.* 1989, Taylor 1957). In addition, reproductive structures and methods are nearly identical across all three species

providing further evidence for the lack of support for these three species. All three species, *F. distichus*, *F. evanescens*, and *F. gardneri* are monoecious with both male and female gametes present in conceptacles of a single plant and with recorded hybridizations across all three species in both laboratory and natural settings (Rice *et al.* 1985, Serrão *et al.* 1999, Lüning *et al.* c1990). In addition, the region of growth within the intertidal zone has significant overlap across all three species, with *F. distichus* and *F. evanescens* inhabiting the entire intertidal space from low to high, and *F. gardneri* being most abundant in the mid-intertidal (Lüning *et al.* c1990, Sears 1998, Villalard-Bohnsack July 1995, Gabrielson 2000). Hence, with this significant overlap in near shore habitat, hybridization between species is more probable.

The continued acceptance of the three species *F. distichus*, *F. evanescens*, and *F. gardneri* based on available literature and thesis data is not supported with any of the discussed species concepts. The data concerning the members of clade 2 (Figure 10) is not supported by the phylogenetic species concept due to the lack of support from resampling methods and lack of monophyletic clades representing each individual species. The biological species concept is not supported because there appear to be no distinct reproductive barriers, either due to incompatible sexual characteristics or physical barriers among the three species. The ecological species does not provide sufficient cause to keep all three species, as all three species are located on temperate rocky intertidal shores. Finally, the morphological species concept (as mentioned above) was unable to distinguish species based on measured characters and therefore is not viable as a concept among *Fucus* species. Due to the conclusions noted above, for the remainder of this thesis all samples within clade 2 will be treated as members of a single species, *F. distichus.*

The variation within clade 2 (Figure 10) does not support the separation of species, however, there are clear biogeographic trends. For example, there are three distinct groups of samples with a geographic relationship (Figure 10). The first group is the entire subclade 2A. This clade contains the samples Port Angeles (WA), Buckley's Bay (BC), Whiffinspit Park (BC), Teahwitt 1 (WA), Porteau Park (BC), Botany Bay 1 (BC), Ruby Beach (WA), Kalaloch Beach (WA), and Parkville (BC) all collected from north East Pacific shores. Clade 2B is comprised of the samples NWT 1 (NT), Churchill 1 (MB) and Churchill 4 (MB) from Arctic region and Nameless Cove (NL) and Hearts Desire 2 (NL from the north Atlantic region. The distinct geographic distribution of these samples is further supported because the Arctic samples are clearly grouping together in a more recently evolved clade sister to the Newfoundland samples. Again these samples appear to be grouping in a more distant clade than that of northern Atlantic samples from Hearts Desire 1 (NL), Middle Cove (NL), and Goose Rocks 1A (ME) which have not grouped with any of the mentioned clades and instead stand alone sister to clades 2A and 2B (Figure 10). The final region on the maximum likelihood tree (Figure 11) displaying a biogeographic cluster is cluster 2C and is comprised of the samples Teahwitt 2 (WA) and Sekui (WA). The clear grouping of Teahwitt 2 (WA) and Sekui (WA), two samples on the western shores of Washington State reinforces the biogeographic trends of the clade. With clear biogeographic trends present among *F. distichus* samples the strict application of the maximum likelihood hypothetical evolutionary metric is well supported with clades belonging entirely to specific regions. Relationships among Pacific, Arctic, and Atlantic Oceans, appears to be biogeographically supported in the maximum likelihood phylogenetic tree with the separation of the Pacific clades 2A and 2C (Figure 10) from that of the Atlantic clade 2D and the Arctic/Atlantic clade 2B.

Finally, seasonal reproductive variation among *F. distichus* (reported among *F. evanescens, F. gardneri,* and *F. distichus* (Coyer *et al.* 2006a, Serrão *et al.* 1999) has contributed to the genetic isolation between populations and further supports the existence of biogeographic trends. The presence (Figure 10) of these clearly defined biogeographic patterns further supports the recognition of a single *F. distichus* species influenced by the presence of biogeographic regions.

4.2.5 Fucus SERRATUS LINEAGE (CLADE 3)

Clade 3 (Figure 10) is a well-supported (95% NJB; BPP = 1) monophyletic clade consisting of collections of *F. serratus*. These high support values are valid for all of the sequences obtained from GenBank. The majority of the sequences obtained from GenBank were obtained from European and Icelandic locations with only the AY659874 *F. serratus* representing collections made on the shores of Nova Scotia (Coyer *et al.* 2006a). Furthermore, Coyer *et al.* (2006) did not note any distinguishable biogeography among samples of the *F. serratus* clade (clade 3 Figure 10).

The usually morphologically difficult genus of *Fucus* due to high phenotypic plasticity and a lack of reliable morphological characters, as discussed earlier in this thesis, are not as apparent with *F. serratus.* The distinct serrations on the frond make it clearly distinguishable from all other *Fucus* species (Sears 1998). Morphological evaluations of collected samples indicate a single collection of *F. serratus* from Singing Sands (PEI) (Figure 6E).

Although no sequences from this thesis were identified as *F. serratus*, the morphologically distinct species and separation of GenBank sequences from Coyer *et al.* (2006) provide evidence of a strongly supported monophyletic clade and the presence of a

distinct species. The closely related *F. serratus* clade across the wide geographic distribution including north Atlantic European coasts and north Atlantic American coasts, can be explained by anthropogenic introductions to north American coasts in the 1880's (Coyer *et al.* 2006c). Support for *F. serratus* as a distinct species has been extensively supported in the literature (Leclerc *et al.* 1998, Coyer *et al.* 2002, Serrão *et al.* 1999, Engel *et al.* 2003, Hoarau *et al.* 2007, Coyer *et al.* 2006c, Chapman *et al.* 2002, Coyer *et al.* 2004, Coyer *et al.* 2002).

4.3 Morphological Analysis Based on Molecular Phylogenetics

Morphological analysis using samples with molecular data was not able to separate *Fucus* samples into molecular phylogenetic clades. Initial hierarchical clustering using this data set produced a dendrogram (Figure 18) that did not provided clear groupings of samples based on geographical location, season of collection, degree of exposure, or molecular phylogenetic groupings. The largest cluster present on the dendrogram occurs between samples Stonington 1E and Hants Harbour 1A and contains a total of 110 of the 130 samples. In addition to the high number of samples contained within the single clade the total Euclidian distance for this clade was less then 10 of a total dendrogram length of 60. The lack of clear clustering into geographical location, season of collection, and degree of exposure was expected as the data set used in this clustering analysis (63) was a subset of the total data set (86) used in hierarchical clustering (Figure 7). In addition to these three groups there was no apparent clustering based on molecular phylogenetic analyses. For example, Sekui (WA) and Holyrood 1C (NL) are grouping next to each other but belong to completely separate phylogenetic groups, clade 2C and 1A (Figure 11) respectively.

Numerous studies on the morphological variation among species have been conducted (Rice *et al.* 1985, Ruuskanen & Nappu 2005, Bäck 1993). However, to our knowledge no known study on the molecular and morphological analysis of all species in the *Fucus* genus has been conducted. As such no direct comparison to current literature can be made. Through discriminant analysis important characters from both the analysis using all characters and the analysis using only the number of vesicles as vesicle data displayed only a single substantive character stipe length (STPLG). As the original analysis using all measured morphological characters did not include vesicle data the combination of the two analyses yields a potential 6 informative characters in total for use in the separation of samples based on taxonomic classification, specifically in to the two described phylogenetic clades 1 and clades 2 & 3 (Figure 10). These characters, stipe length (STPLG), frond length (FRDLG), average branch length (BRCHDIST), number of upper branches (BRCHUP), number of receptacles (RECNUM), and average length of receptacles, are further supported for their use in delineation between species through reliable statistical tests Wilks' λ, Piallai's trace, and Hotelling-Lawley trace probabilities of less then 0.001. Furthermore, with both the total character set and the reduced set there was a high Geisser assignment probability for all samples placed in the classificatory analysis with 52 and 51 over 90% respectively.

Because these two sets of characters are further supported with high classificatory placements their use as distinguishing characters for in phylogenetic keys is maybe recommended. However, with a total *Fucus* collection of 228 samples, 158 were not damaged and were used for morphological measurements and 55 were successfully sequenced. Between these two data sets there was a total of 35 samples with both morphological and molecular data and of these only 25 had reproductive characters. Because

of the lack of data present in this small set of 35 samples methods were employed to increase the number of samples and create a more robust data set. All samples from a single population with visible similarities and originating for the same geographic locations were placed into groups. If one of the members of these groups was included in the molecular data set then the remainder of the group was as well. This increased the data set from a mere 35 samples to 130 samples, which was then reduced to 63 after samples exhibiting no reproductive characters were removed. However this process also had the potential of placing *Fucus* samples in the wrong species groups leading to inaccuracies during clustering and discriminant analysis. The use of morphological characters for the separation of *Fucus* samples into species groups cannot be dismissed as the introduction of potential errors may have affected the outcomes of statistical analyses. Further sampling and statistical analysis is required to provide more statistical evidence for the importance of the 6 selected characters as potential informative characters for the delineation of *Fucus* species.

4.4 FUCUS NORTH AMERICAN BIOGEOGRAPHY

Pacific-Arctic-Atlantic biogeography, and the historical colonization routes of near shore fauna, has been the subject much debate and many studies (Coyer *et al.* 2006a, Lindstrom 2001, Serrão *et al.* 1999, Dunton 1992). The proposal of an Arctic algal paradox has been put forward (Dunton 1992). This 'paradox' indicates a low number of algal species with Pacific affinities compared to the Arctic near shore fauna. The biogeographic patterns and species distributions of *Fucus* reported in this thesis suggest *Fucus* biogeographic patterns that contradict this 'paradox'.

With a recent radiation, placed at 10 to 16 million years from Ascophyllum genus, *Fucus* is the most derived member of the Fucaceae (Hoarau *et al.* 2007). The phylogenetic analysis (Figure 11) of *Fucus* samples indicates the presence of 5 species, the Atlantic *F. vesiculosus* and *F. spiralis,* Adriatic endemic *F. virsoides,* the widely distributed *F. distichus,* and the well-supported *F. serratus* (Serrão *et al.* 1999). As the *F. virsoides* species is a special case as it represents a possible glacial refugial effect and is limited to a small region, its influence on the North American arctic biogeography need not be considered. Various hypotheses on the current biogeographic distribution and historical speciation of these five species have both re-enforced (Coyer *et al.* 2006a, Powell 1963) the presence of an extinct ancestral species giving rise to all extant *Fucus* species*;* As well as refuted this claim (Leclerc *et al.* 1998, Serrão *et al.* 1999). This thesis presents a modified scenario proposed by Coyer *et al.* (2006) as evidence of the historical influence of an ancestral *Fucus* species based on current biogeographic patterns.

The first theory proposed by Coyer *et al.* (2006) indicated a Pacific ancestor, which gave rise to two secondary pacific ancestors, one *F. spiralis* and the second *F. distichus.* These two secondary ancestors dispersed into the Arctic and Atlantic Oceans, which resulted in the establishment of the current clades of *F. spiralis, F. virsoides,* and *F. vesiculosus* (clade1 Figure 11) and *F. distichus* and *F. serratus.* The second theory presented by Coyer *et al.* (2006), suggested that the migration of a single ancestral *F. distichus/F. spiralis* species from the north Pacific to the north Atlantic which subsequently radiated into the two present lineages.

The historical dispersal patterns put forth by Coyer *et al.* (2006) are further supported by the Pacific endemic *Hesperophycus* genus (Serrão *et al.* 1999). As the closest common

ancestor to all *Fucus* species, this genus, with a single species *H. californicus,* is a Pacific endemic and as such the evolutionary movement of *Fucus* from this ancestral Pacific species to the waters of the Atlantic is established (Coyer *et al.* 2006a). Furthermore, *F. distichus* and *F. spiralis* are both monoecious which is a less evolved trait then single sexed plants like the more recent species *F. serratus* and *F. vesiculosus* which are both dioecious (Coyer *et al.* 2006a, Lindstrom 2001, Serrão *et al.* 1999). This further supports Coyer *et al.* (2006) theories that both *F. serratus* and *F. vesiculosus* are derived species from the respective *F. distichus* and *F. spiralis.* Also, the monoecious characteristics of *F. distichus* and *F. spiralis* enhances the dispersal ability of the species as only a single individual would be needed to establish a new colony (Coyer *et al.* 2006a). Although both of Coyer *et al.* (2006) historical *Fucus* movement theories are sound, Lindstrom (2006) indicates an opposing migration for *Fucus* where *F. distichus* originated in the North Atlantic and migrated to the north Pacific. This argument is also supported as the Arctic samples in clade 2B (Figure 10) that share more similarity with Atlantic Ocean samples then they do with Pacific Ocean samples, leading to what Dunton (1992) termed the 'arctic algal paradox'. Here I suggest third possibility (Figure 14) for the current northern Pacific-Arctic-Atlantic biogeography that will effectively address the 'arctic algal paradox', Pacific ancestor, and high molecular affinity of Atlantic *Fucus* to Arctic *Fucus*.

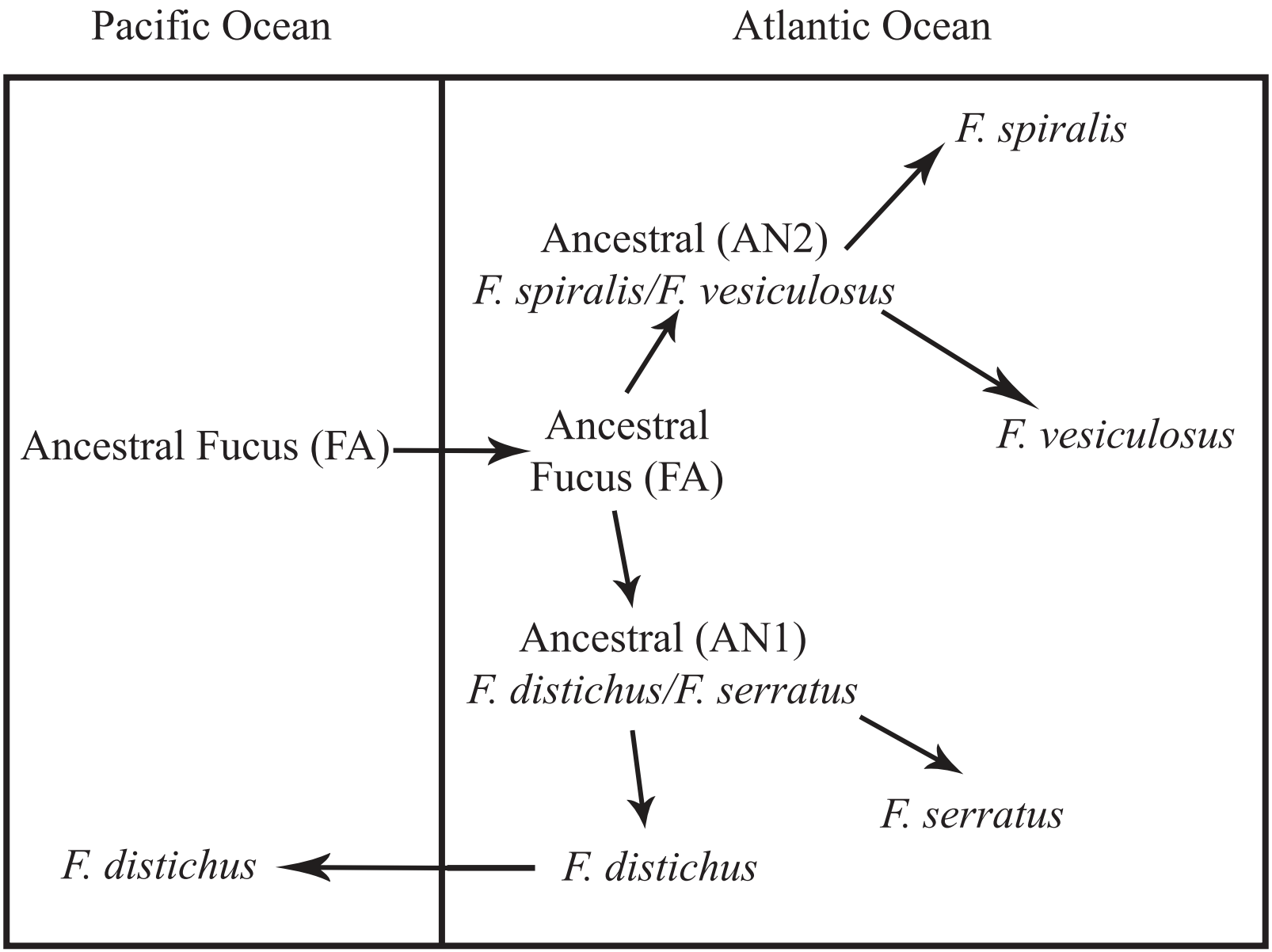
Initial migration of a single ancestral *Fucus* species from north Pacific to north Atlantic occurred during a period where the Bering Strait was open. This species then radiated into an ancestral *F. distichus* species. The ancestral *F. distichus* species then migrated back into the Pacific through the Arctic Ocean. The original ancestral *Fucus* species then radiated into *F. spiralis*. This established the presence of a more ancestral

Atlantic *F. distichus* species compared to Pacific *F. distichus.* The two lineages present in the Atlantic then radiated into the four species currently occupying the Atlantic Ocean. This historical *Fucus* movement and biogeographical hypothesis is established in both the literature and molecular phylogenetic analysis (Figure 10).

Phylogenetic analysis shows that all five members of *Fucus* emanate from a single direct ancestor (FA Figure 14) which is then divided into two distinct ancestral nodes resulting in two large *Fucus* clades, the first giving rise to the species *F. distichus* and *F. serratus* (AN1 Figure 14) and the second resulting in the species *F. virsoides, F. spiralis*, and *F. vesiculosus* (AN2 Figure 14). The *F. distichus* clade 2 (Figure 10) has a large geographic distribution (Canadian Arctic, Alaska, Europe, Norway, North American Pacific and Atlantic coasts).

This large distribution of *F. distichus* may be due, in part, to two possible influences. The first, factor contributing to this large distribution is the favourable North Atlantic Ocean cold-water habitat (Adey & Steneck 2001), which has resulted in a rapid expansion of *Fucus* to its current geographic range. The second possible factor contributing to the large north Atlantic distribution of *Fucus* is the early presence of the species in the Atlantic with a longer presence in the region to spread and colonize new habitats. We will assume that the first of these two statements is accurate as the survival and abundance of healthy *Fucus* populations has been well documented for at least 50 years (Coyer *et al.* 2006a, Lindstrom 2001, Lüning *et al.* c1990, Powell 1963, Rice & Chapman 1985). The second supports the biogeographic hypothesis of an early migration of an ancestral *Fucus* into the Atlantic region.

Figure 14. Proposed historical movement and speciation of the *Fucus* genus. Arrows indicate suspected movement of the species indicated. Abbreviations in parentheses indicate corresponding node on the maximum likelihood phylogenetic tree in Figure 20.


Pacific Ocean
Atlantic Ocean
F. spiralis
Ancestral (AN2)
F. spiralis/F. vesiculosus
F. vesiculosus
Ancestral Fucus (FA)
Ancestral
Fucus (FA)
Ancestral (AN1)
F. distichus/F. serratus
F. serratus
F. distichus
F. distichus

The subsequent radiation of this ancestral Atlantic *F. distichus* is supported through the phylogenetic analysis (Figure 10) where the *F. serratus* clade is sister to the extant *F. distichus.* Also, the slightly more recent establishment of this clade suggests that it may have been established just after the Atlantic *F. distichus.* The presence of Atlantic *F. serratus* and absence of a Pacific *F. serratus* further lends weight to this biogeographic hypothesis (Coyer *et al.* 2006a, Guiry & Guiry 2007, Serrão *et al.* 1999, Lüning *et al.* c1990, Graham & Wilcox 2000).

It was at this time that the reintroduction of *F. distichus*, a concept which has been supported (Lindstrom 2001), into the Arctic Ocean and then the Pacific Ocean occurred. It is probable that this re-introduction occurred during a period of glacial retreat, which allowed the flow of water from Atlantic Ocean, through the Arctic Ocean and into the Pacific as described by Marincovich and Gladenkov (1999) and Lindstrom (2001). This reintroduction can be seen on the maximum likelihood phylogenetic tree (Figure 10) as the more distal Arctic samples (NWT 1 [NT], Churchill 1 [MB], and Churchill 4 [MB]) and the more distant still Pacific samples (Port Angeles [WA], Buckleys Bay [BC], Whiffinspit Park [BC], Teahwitt 1 [WA], Porteau Park [BC], Botany Bay [BC], Ruby Beach [BC], Kalaloch Beach [BC], Parkville [BC], Teahwitt 2 [WA], and Sekui [WA]). During reintroduction into Pacific waters the secondary radiation of the Atlantic ancestral *Fucus* yielded the Atlantic ancestral *F. spiralis* species (Figure 10). Like *F. distichus* this ancestral species was most likely monoecious and gave rise to the two current species *F. spiralis* and *F. vesiculosus* (Figure 14)(Coyer *et al.* 2006a).

Arctic algal research has revealed that for many Arctic macroalgal species there is a distinctly Atlantic influence (Lindstrom 2001, Dunton 1992). The high number of

macroalgal species (Lindstrom 2001), and in particular *Fucus,* in the Atlantic compared to the Pacific may also be due to the inability for species to successfully migrate into the Pacific because of glaciations, ice barriers and ice scoring, the intermittent closing of the Bering land bridge, and direction of Arctic water flow. Lindstrom (2001) point out that a lack of Pacific speciation after Atlantic reintroduction is common across macroalgae, supporting my biogeographic model. The reintroduction of *F. distichus* supports this high Atlantic affinity present in Arctic *Fucus* samples and should remove the confusion surrounding a *Fucus* 'arctic algal paradox'.

5.0 CONCLUSION

The genus *Fucus* (Fucales, Heterokontophyta) is an abundant marine intertidal macroalgae with a wide distribution across northern hemisphere cold water shores (Seed & O'Connor 1981, Druehl 2000, Coyer *et al.* 2006, Lindstrom 2001, Lindstrom 2006). Despite considerable focus and research on morphology and ecology only a small number of molecular research studies have been conducted to discern the complex taxonomic issues residing within this genus (Lindstrom, 2001). The current taxonomic divisions for species within this genus have relied heavily on morphologically determined characteristics and geographical locations, however, additional studies employing the use of molecular tools to refute or support current taxonomy is essential (Fowler-Walker *et al.* 2006, Billard *et al.* 2005). This thesis has addressed several key features regarding the controversies surrounding taxonomic delineation as well as the biogeographic trends of the *Fucus* genus. This includes an analysis of the use of morphology to delineate species, the degree of influence of environmental factors on species morphology, examination of the current Pacific species complex as well as historical glacial influence on the biogeography of North American species.

The use of the morphological species concept to identify species within *Fucus* has been successfully utilized in previous studies (RICE *et al.* 1985, Wynne & Magne 1991, Silva 1953, Bergstrom *et al.* 2005). Results obtained in this thesis from morphological analyses (hierarchical clustering, discriminant analysis) support this conclusion. *Fucus* samples from 79 locations on Pacific and Atlantic shores were collected and 158 samples were measured based on 21 possible characters. The data set of 21 characters and 158 samples of *Fucus* (79 locations) were able to separate samples into groups based on several

selected criteria (geographic location, degree of exposure to open ocean, season of collection, phylogenetic molecular groupings).

However, not all morphological characters are useful in grouping *Fucus* species. Vesicle data had large variation across all geographic, seasonal, and molecular analyses. Due to the large variability across this wide range of samples the use of the vesicle characters is not recommended. Bäck (1993) reached a similar conclusion during an investigation of the species, *F. vesiculosus* suggesting that the use of similar morphological characters was only able to determine physical influences on species such as wave action and effective taxonomic separation based on these characters was unlikely. To add support to this conclusion, further study with a greater sample size across North American near shore coldwater environments is necessary.

The use of reproductive specimens and the remaining 17 measured characters were able to statistically separate all collected samples based on the remaining three grouping criteria of ocean of origin, seasonal collection and molecular phylogenetic groupings. This successful separation of samples was also reported by Rice and Chapman (1985) who were able to successfully separate over 1200 *Fucus* samples using many of the same characters used in this study. However, in an attempt to provide further support to current analyses, in particular the division of the molecularly defined *F. spiralis* and *F. vesiculosus,* in addition to the current 21character set, it is recommended to include several other characters used in the study by Rice and Chapman (1985). There are four notable and potentially informative characters absent in this thesis that may strengthen the morphological analyses. I therefore recommend the addition of these characters: the system of sexual reproduction (monoecious or diecious plants), diameter of oogonium, and width of conceptacle, and length of

conceptacle and number of oogonium per conceptacle (Coyer *et al.* 2006, Rice & Chapman 1985). The re-examination of current herbarium specimens based on these additional characters and addition of these characters in any future study is recommended.

The phylogenetic species concept, using molecular phylogenetics through amplification of the mitochondrial 23S ribosomal RNA gene-23S ribosomal RNA-tRNA-Val intergenic spacer region (23S mtDNA),, like the morphological analysis, was also informative. A total of 52 sequences were obtained from 48 locations across the North Pacific, Arctic, and North Atlantic shores of North America. Aligned sequences displayed variation in the form of large alignment insertion-deletion events, and a number of small nucleotide changes of both transversions and transitions. One large insertion deletion area of approximately 155 bp (nucleotide positions 179 to 334) and a smaller secondary insertion deletion event of 10 bp in length (nucleotide positions 555 to 565) clearly defined two major phylogenetic divisions. The presence of this large insertion deletion area contributed to the lack of support through bootstrap resampling due to the potentially increased number of absent sequences replacement and resampling. To address this problem future molecular analysis with the removal of these indel regions and substitution with a single weighted character should be conducted. If this analysis results in higher resampling support values the importance of the insertion deletion regions may not be as significant as is currently indicated. If this is the case then the resulting phylogenetic analysis may yield a phylogenetic tree with higher support values to refine our current understanding of the taxonomic structure of the *Fucus* genus.

Under the current taxonomic structure, *Fucus* has six species inhabiting North American near shore environments (*F. gardneri, F. evanescens, F. distichus, F. serratus, F.*

spiralis, and *F. vesiculosus*) (Serrão *et al.* 1999). Numerous research studies, based on shared habitat, (Lindstrom 2006), morphologically similarity (Rice & Chapman 1985) and close genetic relationship as determined through phylogenetic analysis of mitochondrial DNA (Coyer *et al.* 2006), have suggested reducing this number to four North American species (*F. distichus, F. serratus, F. spiralis,* and *F. vesiculosus*). Results of this study agree with this assessment based on the inability of morphological characters to effectively separate *F. distichus, F. evanescens* and *F. gardneri* from samples collected on the Pacific coast. Also, phyogenetic analysis of the mtDNA lends further support to this conclusion.

As such there appears to be four distinct *Fucus* species in North American near shore waters and in agreement with our molecular analysis and previous studies results of this study suggests that the three *Fucus* inhabiting the North Pacific intertidal (*F. gardneri, F. evanescens,* and *F. distichus*) should be considered to be part of the first described species *F. distichus by* Linnaeus, C. (1753). Analysis results of this thesis maintain the taxonomic separation of Atlantic *F. serratus, F. spiralis,* and *F. vesiculosus* based on phylogenetic results.

Among the four North American species, results of the 23S mtDNA maximum likelihood phylogenetic analysis indicated patterns of biogeography within only one of the four species, *F. distichus.* These patterns indicated lineages of Arctic, Pacific and Atlantic samples. With a more basal Atlantic groupings and more distal Arctic and Pacific clades there are clear biogeogrpahic patterns among sampled *Fucus.* This grouping of distinct geographical regions in the *F. distichus* species across North American support the previous study results of Serrão *et al.* (1999) and Coyer *et al.* (2006). Furthermore, as indicated by previous studies, there are close relationships between *Fucus* from the Atlantic with those

from the Arctic. This relationship is closer then the relationship between Pacific and Arctic *Fucus* (Lindstrom 2001, Dunton 1992).

Past phylogenetic studies of the Fucaceae have highlighted the difficulty in resolving *Fucus* species using the molecular nrITS region (Serrão *et al.* 1999). As such, the more variable mitochondrial spacer region was chosen as the molecular region for phylogenetic analysis. In a study utilizing the same molecular region with various samples from North America and Europe, Coyer *et al.* (2006) put forward a hypothesis for the origins of the genus *Fucus* and method of trans Arctic dispersal. Results of this thesis agree with the conclusions of Coyer *et al.* (2006), but suggest a third alternative not considered in the study.

This third alternative is supported by historical glaciations and land mass movements, as well as current species distributions and molecular data the movement of an ancestral *Fucus* species from its origins in the Pacific to Atlantic and then returning to the Pacific approximately 12 million years later. The most recent opening of the Bering Strait as early as 17 million years ago allowed the flow of North Pacific water and species access into the North Atlantic Ocean (Sher 1999). The subsequent glaciations of the region terminated this access from 5.4 mya to approximately 18,000 years ago (Gladenkov *et al.* 2002). The last glacial maximum approximately 18000 years before present then receded reopening this Arctic connection (Van Oppen, M. J. H. *et al.* 1995). The age of the genus *Fucus* is hypothesized to be between 10 and 17 mya (Hoarau *et al.* 2007) and this supports these historical movements and is further supported by molecular phylogenetic data in this thesis. The endemic presence of the ancestral species *H. californicus* in the Pacific and the phylogenetic grouping of the Arctic samples with Atlantic samples supports these movement hypotheses.

Future research to support these conclusions should consist of the continued sampling of *Fucus* in the Arctic region to supplement the current data set. In addition, further collections of samples during alternate seasons and including mature plants from the current collection locations would aid in removing bias during the morphological analyses. The measurement of present collections using the five suggested reproductive characters (system of sexual reproduction, diameter of oogonium, width of conceptacle, length of conceptacle, and number of eggs per oogonium) and use of all previously reported characters should be employed for all future collections. Finally, future molecular work is recommended to support taxonomic divisions based on current molecular phylogenetics and reinforce current biogeographic trends. The selective amplification of the ITS region for the identification of sample groups at genus level is necessary to verify samples as *Fucus* as this region has more sequence data available for use in comparison. Also, the continued amplification of samples using the variable 23S mtDNA region is necessary to increase the overall sequenced data set and reinforce species divisions and biogeographic trends. With an increased sample size, particularly in northern arctic regions, the discovery of biogeographic influences, such as glacial refugia, can help us understand past *Fucus* transarctic migrations.

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Appendix A

Date Collected	Collected By	Collection Location	GPS - N	GPS - W	Sample Identification
12-Aug-98	R Sheath and K Müller	Beechy Island NWT Canada	74.70	-91.81	NWT SW2
12-Aug-98	R Sheath and K Müller	Devon Island NWT Canada	74.67	-91.70	NWT SW3
12-Aug-98	R Sheath and K Müller	Resolute Town NWT Canada	74.68	-94.90	NWT SW4
12-Aug-98	R Sheath and K Müller	West end of Assistance Bay southside of Cornwallis NWT Canada	74.65	-94.36	NWT SW1
27-Aug-98	K Müller	Roberts Creek, British Columbia Canada	49.42	-123.64	Fucus Small
27-Aug-98	K Müller	Roberts Creek, British Columbia Canada	49.42	-123.64	Fucus Large
12-Aug-01	W Adey (Smithsonian)	Massacre Island, off Port Mouton Nova Scotia Canada	43.93	-64.82	F. distichus
9-Jun-02	K Müller	Bay Bulls Newfoundland Canada	47.31	-52.81	NF2
9-Jun-02	K Müller	Clarenville Newfoundland Canada	48.16	-53.96	NF1
9-Jun-02	K Müller	Trespassey Newfoundland Canada	46.73	-53.37	NF6
9-Jun-02	K Müller	Witless Bay Newfoundland Canada	47.28	-52.83	NF3
10-Jun-02	K Müller	Middle Cove Newfoundland Canada	47.65	-52.70	NF9
10-Jun-02	K Müller	Bauline Newfoundland Canada	47.72	-52.83	NF11
10-Jun-02	K Müller	Bear Cove Newfoundland Canada	48.54	-58.56	NF5
10-Jun-02	K Müller	Brigus Newfoundland Canada	47.54	-53.19	NF15
10-Jun-02	K Müller	Ferryland Newfoundland Canada	47.03	-52.89	NF4
10-Jun-02	K Müller	Harbour Grace Newfoundland Canada	47.70	-53.21	NF17
10-Jun-02	K Müller	Spaniards Bay Newfoundland Canada	47.61	-53.28	NF16
1-Jul-04	W Adey (Smithsonian)	Myra Island Skerry, Blind Bay Nova Scotia Canada	44.51	-63.84	F. distichus
27-Jul-04	W Adey (Smithsonian)	Georges Ledge, Tor Bay Nova Scotia Canada	45.20	-61.39	F. distichus
5-Aug-04	W Adey (Smithsonian)	Battery Point Breakwater, Lunenburg Nova Scotia Canada	44.36	-64.30	F. distichus
16-Aug-04	W Adey (Smithsonian)	Harts Point, Shelburne Nova Scotia Canada	43.73	-65.34	F. distichus
18-Aug-04	W Adey (Smithsonian)	Western Way, Shelburne Nova Scotia Canada	43.76	-65.32	F. distichus
28-Aug-04	W Adey (Smithsonian)	Long Point, Cranberry Island Maine USA	44.26	-68.27	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
2-Aug-05	W Adey (Smithsonian)	Fishing Point, St Anthony Newfoundland Canada	51.36	-55.56	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
5-Aug-05	W Adey (Smithsonian)	Cape Onion Newfoundland Canada	51.61	-55.62	F. distichus
2-Jun-06	M Lynch and K Müller	Brigus Newfoundland Canada	47.54	-53.20	Fucus 1
2-Jun-06	M Lynch and K Müller	Hants Harbour Newfoundland Canada	48.02	-53.27	Fucus 1
2-Jun-06	M Lynch and K Müller	Hants Harbour Newfoundland Canada	48.02	-53.27	Fucus 1
2-Jun-06	M Lynch and K Müller	Hearts Desire Newfoundland Canada	47.81	-53.44	Fucus 1
2-Jun-06	M Lynch and K Müller	Hearts Desire Newfoundland Canada	47.81	-53.44	Fucus 2
2-Jun-06	M Lynch and K Müller	Hearts Desire Newfoundland Canada	47.81	-53.44	Fucus 3
2-Jun-06	M Lynch and K Müller	Holyrood Newfoundland Canada	47.39	-53.13	Fucus 1
2-Jun-06	M Lynch and K Müller	Holyrood Newfoundland Canada	47.39	-53.13	Fucus 1
2-Jun-06	M Lynch and K Müller	Holyrood Newfoundland Canada	47.39	-53.13	Fucus 1
2-Jun-06	M Lynch and K Müller	Perry Cove Newfoundland Canada	49.73	-55.98	Fucus 1A
2-Jun-06	M Lynch and K Müller	Perry Cove Newfoundland Canada	49.73	-55.98	Fucus 1B
2-Jun-06	M Lynch and K Müller	Perry Cove Newfoundland Canada	49.73	-55.98	Fucus 1C
2-Jun-06	M Lynch and K Müller	Perry Cove Newfoundland Canada	49.73	-55.98	Fucus 2A
2-Jun-06	M Lynch and K Müller	Whiteway Newfoundland Canada	47.69	-53.49	Fucus 1
2-Jun-06	M Lynch and K Müller	Whiteway Newfoundland Canada	47.69	-53.49	Fucus 2A
2-Jun-06	M Lynch and K Müller	Whiteway Newfoundland Canada	47.69	-53.49	Fucus 2B
2-Jun-06	M Lynch and K Müller	Whiteway Newfoundland Canada	47.69	-53.49	Fucus 2C
2-Jun-06	M Lynch and K Müller	Whiteway Newfoundland Canada	47.69	-53.49	Fucus 3
3-Jun-06	M Lynch and K Müller	Argentia Newfoundland Canada	47.29	-53.99	Fucus 1A
3-Jun-06	M Lynch and K Müller	Argentia Newfoundland Canada	47.29	-53.99	Fucus 1B
3-Jun-06	M Lynch and K Müller	Foxtrap Newfoundland Canada	47.52	-52.99	Fucus 1
3-Jun-06	M Lynch and K Müller	Foxtrap Newfoundland Canada	47.52	-52.99	Fucus 1
3-Jun-06	M Lynch and K Müller	Foxtrap Newfoundland Canada	47.52	-52.99	Fucus 1
3-Jun-06	M Lynch and K Müller	Goose Berry Cove Newfoundland Canada	48.03	-53.64	Fucus 1
3-Jun-06	M Lynch and K Müller	Goose Berry Cove Newfoundland Canada	48.03	-53.64	Fucus 1
3-Jun-06	M Lynch and K Müller	Goose Berry Cove Newfoundland Canada	48.03	-53.64	Fucus 1

Appendix A

Date Collected	Collected By	Collection Location	GPS - N	GPS - W	Sample Identification
3-Jun-06	M Lynch and K Müller	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93	Fucus 1A
3-Jun-06	M Lynch and K Müller	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93	Fucus 1B
3-Jun-06	M Lynch and K Müller	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93	Fucus 1C
3-Jun-06	M Lynch and K Müller	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93	Fucus 2A
3-Jun-06	M Lynch and K Müller	Rocky Beach Along Highway 100 Newfoundland Canada	47.27	-53.93	Fucus 2B
4-Jun-06	M Lynch and K Müller	Bauline Newfoundland Canada	47.72	-52.83	Fucus 1A
4-Jun-06	M Lynch and K Müller	Bauline Newfoundland Canada	47.72	-52.83	Fucus 1B
4-Jun-06	M Lynch and K Müller	Bauline Newfoundland Canada	47.72	-52.83	Fucus 1
4-Jun-06	M Lynch and K Müller	Bauline Newfoundland Canada	47.72	-52.83	Fucus 2
4-Jun-06	M Lynch and K Müller	Bauline Newfoundland Canada	47.72	-52.83	Fucus 2
4-Jun-06	M Lynch and K Müller	Flatrock Newfoundland Canada	47.71	-52.71	Fucus 1
4-Jun-06	M Lynch and K Müller	Flatrock Newfoundland Canada	47.71	-52.71	Fucus 1
4-Jun-06	M Lynch and K Müller	Flatrock Newfoundland Canada	47.71	-52.71	Fucus 1
4-Jun-06	M Lynch and K Müller	Middle Cove Newfoundland Canada	47.65	-52.70	Fucus 1A
4-Jun-06	M Lynch and K Müller	Middle Cove Newfoundland Canada	47.65	-52.70	Fucus 2A
4-Jun-06	M Lynch and K Müller	Middle Cove Newfoundland Canada	47.65	-52.70	Fucus 2B
4-Jun-06	M Lynch and K Müller	Portugal Cove Newfoundland Canada	47.63	-52.86	Fucus 1A
4-Jun-06	M Lynch and K Müller	Portugal Cove Newfoundland Canada	47.63	-52.86	Fucus 1B
19-Jul-06	K M Müller and B Brace	Singing Sands PEI Canada	46.38	-62.11	Fucus 1
26-Jul-06	T F Dawson	Halifax Nova Scotia Canada	44.65	-63.58	Fucus 1 (NS1)
26-Jul-06	T F Dawson	Peggy's Cove Nova Scotia Canada	44.49	-63.92	Fucus 2A
26-Jul-06	T F Dawson	Peggy's Cove Nova Scotia Canada	44.49	-63.92	Fucus 2B
26-Jul-06	T F Dawson	Peggy's Cove Nova Scotia Canada	44.49	-63.92	Fucus 3A
26-Jul-06	T F Dawson	Peggy's Cove Nova Scotia Canada	44.49	-63.92	Fucus 1
26-Jul-06	T F Dawson	Peggy's Cove Nova Scotia Canada	44.49	-63.92	Fucus 3A
2-Aug-06	K M Müller and B Brace	Arches Provincial Park Newfoundland Canada	50.16	-57.62	Fucus 1
2-Aug-06	K M Müller and B Brace	Arches Provincial Park Newfoundland Canada	50.16	-57.62	Fucus 2
2-Aug-06	K M Müller and B Brace	Arches Provincial Park Newfoundland Canada	50.16	-57.62	Fucus 3
2-Aug-06	K M Müller and B Brace	L'anseaut Meadows Newfoundland Canada	49.00	-58.06	Fucus 1
2-Aug-06	K M Müller and B Brace	L'anseaut Meadows Newfoundland Canada	49.00	-58.06	Fucus 2A
2-Aug-06	K M Müller and B Brace	L'anseaut Meadows Newfoundland Canada	49.00	-58.06	Fucus 2B
2-Aug-06	K M Müller and B Brace	L'anseaut Meadows Newfoundland Canada	49.00	-58.06	Fucus 2C
2-Aug-06	K M Müller and B Brace	Nameless Cove Newoundland Canada	48.62	-53.01	Fucus 1A
2-Aug-06	K M Müller and B Brace	Nameless Cove Newoundland Canada	48.62	-53.01	Fucus 1B
2-Aug-06	K M Müller and B Brace	Nameless Cove Newoundland Canada	48.62	-53.01	Fucus 2
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1A
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1B
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1C
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1D
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1E
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1F
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1G
30-Nov-06	M Lynch and R Young	Brant Rock Massachusetts USA (Along Rocky Shore)	42.09	-70.65	Fucus 1H
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1A
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1B
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1C
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1D
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1E
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1F
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1G
30-Nov-06	M Lynch and R Young	Hampton Beach New Hampshire	42.90	-70.81	Fucus 1H
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1A
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1B
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1C
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1D
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1E
30-Nov-06	M Lynch and R Young	Stonington Connecticut USA	41.33	-71.91	Fucus 1F
30-Nov-06	M Lynch and R Young	Horseneck Beach Massachusetts	41.51	-71.06	Fucus 1A
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1A
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1B
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1C
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1D
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1E
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1F

Appendix A

Date Collected	Collected By	Collection Location	GPS - N	GPS - W	Sample Identification
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1G
1-Dec-06	M Lynch and R Young	Fortune Rocks Maine USA	43.43	-70.38	Fucus 1H
1-Dec-06	M Lynch and R Young	Goose Rocks Beach Maine USA	43.40	-70.41	Fucus 1A
1-Dec-06	M Lynch and R Young	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22	Fucus 1A
1-Dec-06	M Lynch and R Young	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22	Fucus 1B
1-Dec-06	M Lynch and R Young	Kettle Creek/Cape Elizabeth Maine USA	43.56	-70.22	Fucus 1C
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1A
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1B
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1C
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1D
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1E
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 1F
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 2A
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3A
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3B
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3C
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3D
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3E
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3F
1-Dec-06	M Lynch and R Young	Pemaquid Point Maine USA	43.84	-69.51	Fucus 3G
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1A
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1B
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1C
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1D
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1E
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1F
1-Dec-06	M Lynch and R Young	Rockland Maine USA	44.10	-69.11	Fucus 1G
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1A
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1B
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1C
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1D
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1E
1-Dec-06	M Lynch and R Young	York Point Maine USA (In park near Lighthouse)	43.17	-70.59	Fucus 1F
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1A
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1B
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1C
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1D
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1E
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1F
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1G
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1H
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1I
2-Dec-06	M Lynch and R Young	Cutler Naval Base Maine USA	44.67	-67.25	Fucus 1J
2-Dec-06	M Lynch and R Young	On the road to Corea Maine USA	44.41	-68.01	Fucus 1A
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1A
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1B
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1C
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1D
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1E
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1F
2-Dec-06	M Lynch and R Young	Just Past Jonesport Maine USA	44.56	-67.57	Fucus 1G
2-Dec-06	M Lynch and R Young	Lubec Maine USA (under boarder crossing)	44.67	-66.98	Fucus 1A
2-Dec-06	M Lynch and R Young	Lubec Maine USA (under boarder crossing)	44.67	-66.98	Fucus 1B
2-Dec-06	M Lynch and R Young	Lubec Maine USA (under boarder crossing)	44.67	-66.98	Fucus 1C
2-Dec-06	M Lynch and R Young	Lubec Maine USA (under boarder crossing)	44.67	-66.98	Fucus 1D
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1A
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1B
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1C
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1D
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1E
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1F
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1G
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1H
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1I

Appendix A

Date Collected	Collected By	Collection Location	GPS - N	GPS - W	Sample Identification
2-Dec-06	M Lynch and R Young	Millbridge Maine USA	44.54	-67.88	Fucus 1J
2-Dec-06	M Lynch and R Young	Sealys Bay New Brunswick Canada	45.08	-66.65	Fucus 1A
2-Dec-06	M Lynch and R Young	Sealys Bay New Brunswick Canada	45.08	-66.65	Fucus 1B
29-Mar-07	R Sheath and K Müller	Pt. Lona California USA	32.67	-117.25	Unknown Brown
28-Jun-07	M Lynch and R Young	Seal Rock Orgeon USA	44.49	-124.08	Fucus 1
28-Jun-07	M Lynch and R Young	Seal Rock Orgeon USA	44.49	-124.08	Fucus 2
28-Jun-07	M Lynch and R Young	Seal Rock Orgeon USA	44.49	-124.08	Unknown Brown
29-Jun-07	M Lynch and R Young	Kalaloch Beach Washington USA	47.64	-124.39	Fucus 1
29-Jun-07	M Lynch and R Young	Port Angeles Washington USA	48.12	-123.43	Fucus 1
29-Jun-07	M Lynch and R Young	Ruby Beach Washington USA	47.64	-124.39	Fucus 1
29-Jun-07	M Lynch and R Young	Sekui Washington USA	48.26	-124.28	Fucus 1
29-Jun-07	M Lynch and R Young	Teahwhit Washington USA	47.91	-124.64	Fucus 1
29-Jun-07	M Lynch and R Young	Teahwhit Washington USA	47.91	-124.64	Fucus 2
29-Jun-07	M Lynch and R Young	Teahwhit Washington USA	47.91	-124.64	Unknown Brown
30-Jun-07	M Lynch and R Young	Botany Bay British Columbia Canada	48.53	-124.45	Fucus 1
30-Jun-07	M Lynch and R Young	Botany Bay British Columbia Canada	48.53	-124.45	Fucus 2
30-Jun-07	M Lynch and R Young	Botany Bay British Columbia Canada	48.53	-124.45	Fucus 3
30-Jun-07	M Lynch and R Young	Near Jordan River Hwy 14 Vancouver Island B.C. Canada	48.42	-124.05	Fucus 1
30-Jun-07	M Lynch and R Young	Parker Bay British Columbia Canada	48.36	-123.54	Fucus 1
30-Jun-07	M Lynch and R Young	Whiffin Spit Park British Columbia Canada	48.36	-123.73	Fucus 1
1-Jul-07	M Lynch and R Young	Bukley's Bay British Columbia Canada	49.53	-124.85	Fucus 1
1-Jul-07	M Lynch and R Young	Campbell River British Columbia Canada	40.03	-125.24	Fucus 1
1-Jul-07	M Lynch and R Young	Kitty Coleman Provincial Park B.C. Canada	49.79	-125.00	Fucus 1
2-Jul-07	M Lynch and R Young	Cordoba Bay B.C. Canada	48.52	-123.37	Fucus 1
2-Jul-07	M Lynch and R Young	Kin Beach Cowichen B.C Canada	48.93	-123.72	Fucus 1
2-Jul-07	M Lynch and R Young	Lantzville British Columbia Canada	49.25	-124.07	Fucus 1
2-Jul-07	M Lynch and R Young	Parksville British Columbia Canada	49.32	-124.26	Fucus 1
3-Jul-07	M Lynch and R Young	Dunderave Park West Vancouver B.C. Canada	49.33	-123.18	Fucus 1
3-Jul-07	M Lynch and R Young	Dunderave Park West Vancouver B.C. Canada	49.33	-123.18	Fucus 1
3-Jul-07	M Lynch and R Young	Porteau Provincial Park B.C. Canada	49.55	-123.24	Fucus 1
17-Jul-07	J Witt	Churchill Manitoba Canada	58.77	-94.13	Fucus 1
17-Jul-07	J Witt	Churchill Manitoba Canada	58.77	-94.13	Fucus 2
17-Jul-07	J Witt	Churchill Manitoba Canada	58.77	-94.13	Fucus 3
17-Jul-07	J Witt	Churchill Manitoba Canada	58.77	-94.13	Fucus 4

Appendix B

Name$	ML	SUMVWINT	GEOG	EXPOSE	PLTLG	PLTWD	STPMULT	STPNUM	STPLG	STPWD	SERNUM	FRNDNUM	FRNDWD	FRNDLG	FRNDDISTWD	BRCHDIST	BRCHNUM	BRCHLOW	BRCHUP	RECYN	RECNUM	RECWD	RECLG	VESYN	VESPRD	VESDISTBT2	VESDISTBTPRS	VESNUM	VESLG	VESWD	FRNDLCK
Arches Provincial Park 1	0	1	2	1	17.60	27.70	1	1	2.20	0.20	0	49	0.62	15.74	0.52	1.72	33	11	22	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Arches Provincial Park 2	0	1	2	1	11.00	16.00	0	2	1.15	0.25	0	24	1.64	9.66	0.46	1.80	31	17	14	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Arches Provincial Park 3	0	1	2	1	19.00	20.70	1	1	4.70	0.20	0	33	1.32	17.24	0.52	2.38	28	6	22	1	5	0.70	0.86	0	0	0.00	0.00	0	0	0	0
Argentia 1A	0	1	2	1	6.30	10.30	1	1	1.40	0.20	0	38	0.40	5.86	0.36	2.52	31	9	22	1	5	0.32	0.32	0	0	0.00	0.00	0	0	0	0
Argentia 1B	0	1	2	1	28.90	23.10	1	1	7.70	0.30	0	59	0.76	25.06	0.50	2.18	44	9	35	1	61	0.72	1.66	0	0	0.00	0.00	0	0	0	0
Bauline 1A	1	1	2	1	15.30	16.50	1	1	4.50	0.30	0	17	0.40	12.64	0.70	1.78	14	6	8	1	4	0.60	2.90	0	0	0.00	0.00	0	0	0	0
Bauline 1B	1	1	2	1	18.30	22.50	1	1	3.40	0.50	0	34	0.62	16.44	0.70	3.20	29	8	21	1	7	0.72	3.26	0	0	0.00	0.00	0	0	0	0
Bauline 2A	1	1	2	1	9.00	6.90	1	1	2.60	0.30	0	11	0.90	8.34	0.40	0.45	7	1	6	0	0	0.00	0.00	1	1	0.00	0.17	6	0.5	0.4	0
Bauline 2B	1	1	2	1	11.70	16.30	1	1	1.80	0.20	0	34	0.88	12.13	0.50	0.54	26	3	23	1	8	0.78	1.04	1	1	0.00	0.25	10	0.5	0.4	0
Bauline 2C	1	1	2	1	13.70	12.50	1	1	3.40	0.40	0	15	0.86	11.72	0.56	0.40	10	5	5	1	9	1.10	1.48	1	1	0.00	0.20	2	0.65	0.4	0
Botany Bay 1	2	1	1	2	5.80	9.00	0	3	0.43	0.10	0	76	0.30	4.56	0.14	0.84	81	47	34	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Botany Bay 2	2	1	1	2	3.60	5.20	0	7	0.20	0.10	0	51	0.26	2.72	0.16	0.90	61	21	40	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Botany Bay 3	2	1	1	2	10.90	7.30	1	1	3.80	0.20	0	14	0.90	9.50	0.50	2.46	14	1	13	1	4	0.85	1.30	0	0	0.00	0.00	0	0	0	0
Brant Point 1A	1	2	2	2	19.00	9.30	1	1	8.00	0.90	0	16	0.68	18.00	0.28	2.34	15	1	14	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Brant Point 1C	1	2	2	2	15.00	7.20	1	1	4.20	0.20	0	10	1.04	14.85	0.44	3.22	7	2	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Brant Point 1D	1	2	2	2	21.80	15.00	1	1	6.60	0.40	0	56	0.68	20.34	0.28	3.48	49	12	37	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Brant Point 1F	1	2	2	2	17.00	3.00	1	1	7.00	1.50	0	5	1.50	16.50	0.64	0.83	5	2	3	0	0	0.00	0.00	1	0	0.00	0.00	1	0.5	0.5	0
Brant Point 1G	1	2	2	2	30.10	17.50	1	1	6.30	0.30	0	77	0.54	24.78	0.20	3.84	93	51	42	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Brant Point 1H	1	2	2	2	26.20	15.30	1	1	0.10	0.30	0	43	0.86	23.76	0.30	5.66	45	15	30	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Brigus (M&L Collection)	1	1	2	1	21.20	21.20	1	1	6.10	0.40	0	125	0.66	20.15	0.54	2.48	87	5	82	1	97	0.54	0.92	1	0	0.10	0.00	7	0.6	0.5	0
Campbell River 1	0	1	1	1	13.20	16.30	1	1	2.80	0.30	0	16	1.32	12.62	0.66	3.44	18	8	10	1	5	0.50	1.20	0	0	0.00	0.00	0	0	0	0
Cutler Naval Base 1A	1	2	2	2	5.40	1.90	1	1	3.20	0.50	0	2	0.50	5.30	0.60	0.00	1	0	1	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1B	1	2	2	2	11.30	6.70	1	1	2.80	0.40	0	7	0.94	8.62	0.26	2.63	6	3	3	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	0
Cutler Naval Base 1C	1	2	2	2	10.90	5.00	1	1	5.00	3.00	0	7	1.00	9.53	0.42	2.68	6	2	4	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1D	1	2	2	2	11.30	7.00	1	1	7.00	5.00	0	8	1.24	10.00	0.40	1.92	8	3	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1E	1	2	2	2	15.70	8.90	1	1	8.90	7.00	0	19	0.94	13.58	0.22	1.90	16	1	15	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1F	1	2	2	2	16.60	18.70	1	1	0.10	0.80	0	56	1.22	14.64	0.38	3.50	21	12	9	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1G	1	2	2	2	6.50	5.40	0	2	2.35	0.60	0	11	0.60	5.24	0.50	1.08	10	3	7	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1H	1	2	2	2	9.50	5.00	1	1	4.40	0.10	0	5	1.10	8.30	0.50	2.08	6	2	4	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1I	1	2	2	2	14.60	11.70	1	1	5.30	0.10	0	2	1.22	12.76	0.26	2.40	22	3	19	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Cutler Naval Base 1J	1	2	2	2	11.70	6.70	1	1	5.50	0.10	0	9	0.98	10.30	0.38	2.66	10	2	8	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Dundrave Park 1	0	1	1	1	8.50	8.50	1	1	1.00	0.20	0	12	1.30	8.14	0.32	2.24	11	1	10	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Dundrave Park 2	0	1	1	1	8.80	10.00	1	1	1.30	0.20	0	13	0.88	8.06	0.54	2.06	12	4	8	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Flat Rock 1A	0	1	2	2	13.00	14.90	1	1	14.90	1.50	0	11	0.78	11.30	0.56	2.86	10	5	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Flat Rock 1B	0	1	2	2	13.40	14.30	1	1	14.30	2.10	0	26	0.42	10.52	0.33	1.30	30	24	6	1	23	0.64	3.30	0	0	0.00	0.00	0	0	0	0
Flat Rock 1C	0	1	2	2	10.20	13.40	0	3	2.27	0.27	0	14	0.86	8.20	0.48	2.50	13	10	3	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Fortune Rocks 1A	1	2	2	2	29.20	22.50	0	2	5.95	0.35	0	57	0.56	26.68	0.26	4.84	51	8	43	1	5	0.32	1.04	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1B	1	2	2	2	19.40	13.20	1	1	3.00	0.30	0	35	0.48	17.36	0.46	3.08	30	9	21	1	6	0.23	0.48	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1D	1	2	2	2	32.40	10.90	1	1	7.20	0.40	0	49	0.48	28.00	0.36	2.52	61	18	43	1	6	0.34	1.50	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1E	1	2	2	2	27.90	11.40	0	4	6.25	0.33	0	33	0.38	23.88	0.32	4.22	47	15	32	1	7	0.18	0.60	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1F	1	2	2	2	24.90	29.20	0	2	3.45	0.30	0	329	0.42	21.46	0.32	1.88	413	55	358	1	69	0.44	0.74	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1G	1	2	2	2	30.00	11.40	1	1	6.40	0.40	0	41	0.50	24.74	0.34	2.86	34	7	27	1	13	0.32	0.88	0	0	0.00	0.00	0	0	0	0
Fortune Rocks 1H	1	2	2	2	33.80	24.60	0	7	6.54	0.32	0	128	0.46	28.40	0.36	4.56	146	37	109	1	28	0.42	1.12	0	0	0.00	0.00	0	0	0	0
Foxtrap A	1	1	2	1	10.40	15.50	1	1	1.10	0.10	0	27	0.68	9.72	0.58	1.98	19	2	17	1	6	0.46	0.70	0	0	0.00	0.00	0	0	0	0
Foxtrap B	1	1	2	1	10.50	16.60	0	2	1.15	0.10	0	15	0.96	9.40	0.52	2.54	11	5	6	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1

Appendix B

Name$	ML	SUMVWINT	GEOG	EXPOSE	PLTLG	PLTWD	STPMULT	STPNUM	STPLG	STPWD	SERNUM	FRNDNUM	FRNDWD	FRNDLG	FRNDDISTWD	BRCHDIST	BRCHNUM	BRCHLOW	BRCHUP	RECYN	RECNUM	RECWD	RECLG	VESYN	VESPRD	VESDISTBT2	VESDISTBTPRS	VESNUM	VESLG	VESWD	FRNDLCK
Foxtrap C	1	1	2	1	12.40	14.10	0	2	3.60	0.35	0	9	1.06	10.96	0.46	3.60	8	3	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Goose Berry's Cove A	1	1	2	1	11.60	12.80	0	2	1.75	0.15	0	53	0.28	8.24	0.50	2.12	30	8	22	1	32	0.38	0.52	0	0	0.00	0.00	0	0	0	0
Goose Berry's Cove B	1	1	2	1	10.50	14.90	0	2	2.20	0.20	0	35	0.22	8.46	0.40	1.64	29	11	18	1	20	0.28	0.28	0	0	0.00	0.00	0	0	0	0
Goose Berry's Cove C	1	1	2	1	13.60	15.10	1	1	2.10	0.30	0	38	0.22	10.24	0.45	6.06	32	8	24	1	29	0.34	0.50	0	0	0.00	0.00	0	0	0	0
Halifax 1	0	1	2	2	16.50	25.70	1	1	2.50	0.20	0	91	0.66	15.48	0.64	2.02	67	35	32	1	73	0.74	1.13	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1A	1	2	2	2	7.70	9.20	0	15	1.32	0.10	0	79	0.40	6.32	0.24	1.40	83	44	39	1	11	0.36	0.56	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1B	1	2	2	2	7.40	2.50	1	1	1.90	0.30	0	9	0.52	6.24	0.20	1.78	10	2	8	1	3	0.33	0.50	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1C	1	2	2	2	5.10	2.90	0	4	1.16	0.34	0	8	0.44	3.38	0.30	1.80	8	5	3	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Hampton Beach 1D	1	2	2	2	6.40	2.00	0	2	1.90	0.10	0	7	0.36	4.64	0.26	1.53	8	3	5	1	3	0.30	0.50	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1E	1	2	2	2	5.30	3.50	0	2	1.80	0.20	0	9	0.50	4.38	0.27	0.90	7	2	5	1	5	0.32	0.70	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1F	1	2	2	2	9.10	9.90	0	5	2.48	0.40	0	28	0.50	7.30	0.28	2.04	20	10	10	1	11	0.34	0.83	0	0	0.00	0.00	0	0	0	0
Hampton Beach 1H	1	2	2	2	7.30	10.80	0	12	1.88	0.40	0	33	0.46	5.38	0.35	1.47	22	10	12	1	6	0.32	0.85	0	0	0.00	0.00	0	0	0	0
Hants Harbour 1A	1	1	2	1	8.50	11.70	0	2	1.40	0.25	0	17	1.04	7.56	0.46	2.16	15	8	7	0	0	0.00	0.00	1	0	0.28	0.00	29	0.5	0.4	0
Hants Harbour 1B	1	1	2	1	7.50	6.30	1	1	2.50	0.20	0	6	0.88	7.10	0.42	2.20	5	1	4	0	0	0.00	0.00	0	0	0.00	0.25	0	0	0	1
Hearts Desire 1	2	1	2	1	29.00	22.40	1	1	9.20	0.30	0	21	0.68	25.08	0.00	2.70	19	7	12	1	21	0.90	7.42	0	0	0.00	0.25	0	0	0	0
Hearts Desire 2	2	1	2	1	17.00	19.80	1	1	3.70	0.50	0	22	0.76	14.68	0.38	2.54	21	4	17	1	6	0.62	4.46	0	0	0.00	0.00	0	0	0	0
Holyrood A	1	1	2	1	8.50	9.00	1	1	1.60	0.10	0	18	0.32	7.64	0.00	1.64	10	5	5	1	18	0.38	0.48	0	0	0.00	0.00	0	0	0	0
Holyrood B	1	1	2	1	10.70	11.50	1	1	1.00	0.40	0	13	0.85	9.53	1.35	2.66	9	1	8	1	9	0.78	0.82	0	0	0.00	0.00	0	0	0	0
Holyrood C	1	1	2	1	10.50	11.80	1	1	1.30	0.15	0	18	0.50	9.67	0.00	1.40	14	4	10	1	11	0.52	0.76	0	0	0.00	0.00	0	0	0	0
Jones Port 1A	1	2	2	2	18.40	10.70	1	1	1.20	0.20	0	58	0.48	17.14	0.40	1.96	57	17	40	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Jones Port 1B	1	2	2	2	20.10	9.90	1	1	3.20	0.30	0	44	0.42	17.94	0.44	2.42	42	8	34	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Jones Port 1C	1	2	2	2	28.00	14.40	0	3	2.63	0.20	0	71	0.30	25.40	0.34	2.94	133	45	88	1	1	0.40	0.50	0	0	0.00	0.00	0	0	0	0
Jones Port 1E	1	2	2	2	17.60	11.20	1	1	3.70	0.20	0	38	0.54	13.90	0.28	2.06	41	8	33	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Jones Port 1F	1	2	2	2	13.10	7.70	1	1	3.70	0.20	0	28	0.40	11.96	0.32	2.02	20	5	15	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Jones Port 1G	1	2	2	2	20.60	13.20	1	1	2.50	0.20	0	61	0.48	17.16	0.34	1.82	41	17	24	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Jordan River Vancouver	0	1	1	1	5.80	6.10	1	1	0.20	0.20	0	9	0.72	4.54	0.38	2.78	11	5	6	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Kalaloch Beach 1	2	1	1	2	5.90	6.70	1	1	0.10	0.20	0	47	0.22	4.78	0.16	0.80	51	28	23	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Kettle Creek 1A	1	2	2	2	19.10	15.70	0	10	3.46	0.20	0	93	0.62	15.44	0.38	2.04	107	49	58	1	4	0.35	0.70	0	0	0.00	0.00	0	0	0	0
Kettle Creek 1B	1	2	2	2	44.90	9.80	1	1	2.20	0.20	0	41	0.50	41.80	0.36	4.30	53	17	36	1	3	0.20	0.87	0	0	0.00	0.00	0	0	0	0
Kettle Creek 1C	1	2	2	2	28.00	13.70	0	2	2.55	0.15	0	108	0.52	24.12	0.22	2.44	131	41	90	1	13	0.16	0.50	1	0	0.00	0.00	4	0.5	0.5	0
Kin Beach 1	0	1	1	1	15.20	10.30	1	1	10.30	0.90	0	13	0.68	12.30	0.24	2.96	14	13	1	1	1	0.70	2.90	0	0	0.00	0.00	0	0	0	0
Kitty Coleman 1	0	1	1	1	10.40	11.50	1	1	1.70	0.30	0	13	1.02	8.68	0.56	3.10	14	4	10	1	6	0.54	1.24	0	0	0.00	0.00	0	0	0	0
Lanseaux Meadows 1	0	1	2	1	16.20	14.60	0	4	1.80	0.28	0	121	0.90	13.66	0.34	2.46	85	38	47	1	16	0.50	0.62	0	0	0.00	0.00	0	0	0	0
Lanseaux Meadows 2A	0	1	2	1	9.60	15.00	1	1	0.90	0.10	0	21	0.30	7.88	0.88	1.66	17	11	6	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Lanseaux Meadows 2B	0	1	2	1	10.70	19.90	1	1	0.10	0.20	0	23	0.74	9.74	0.92	2.30	23	6	17	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Lanseaux Meadows 2C	0	1	2	1	27.70	29.80	1	1	6.40	0.20	0	69	0.84	22.68	0.34	2.80	61	17	44	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Lantzville 1	0	1	1	1	8.20	7.60	1	1	7.60	1.50	0	9	0.98	7.92	0.38	2.18	9	3	6	1	5	0.44	0.94	0	0	0.00	0.00	0	0	0	0
Lebec 1A	1	2	2	1	20.10	22.00	0	9	1.04	0.10	0	323	0.66	14.32	0.28	2.58	173	76	97	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Lubec 1C	1	2	2	1	13.00	11.90	0	2	3.10	0.35	0	33	0.96	11.30	0.60	3.10	24	6	18	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Lubec 1D	1	2	2	1	20.10	15.90	1	1	7.50	0.40	0	18	0.96	19.20	0.48	2.98	19	3	16	0	0	0.00	0.00	1	0	0.00	0.00	11	0.6	0.3	0
Middle Cove 1A	2	1	2	1	14.40	22.90	1	1	1.80	0.30	0	13	0.88	13.68	0.74	2.66	11	6	5	1	4	1.40	2.48	0	0	0.00	0.00	0	0	0	0
Middle Cove 2A	2	1	2	1	14.70	22.80	1	1	2.30	0.40	0	14	2.10	12.90	1.44	2.82	6	5	1	1	3	1.17	2.70	0	0	0.00	0.00	0	0	0	0
Middle Cove 2B	2	1	2	1	18.20	18.70	1	1	2.50	0.20	0	20	2.34	15.42	0.68	2.82	17	8	9	1	11	0.88	2.40	0	0	0.00	0.00	0	0	0	0
Millbridge 1A	1	2	2	2	7.80	3.30	1	1	1.10	0.10	0	6	0.74	7.68	0.35	1.12	7	1	6	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1B	1	2	2	2	7.90	2.40	1	1	1.00	0.10	0	3	0.53	5.80	0.37	2.10	3	1	2	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1

Appendix B

Name$	ML	SUMVWINT	GEOG	EXPOSE	PLTLG	PLTWD	STPMULT	STPNUM	STPLG	STPWD	SERNUM	FRNDNUM	FRNDWD	FRNDLG	FRNDDISTWD	BRCHDIST	BRCHNUM	BRCHLOW	BRCHUP	RECYN	RECNUM	RECWD	RECLG	VESYN	VESPRD	VESDISTBT2	VESDISTBTPRS	VESNUM	VESLG	VESWD	FRNDLCK
Millbridge 1C	1	2	2	2	7.60	2.90	1	1	1.90	0.10	0	4	0.45	7.55	0.45	2.00	3	1	2	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1D	1	2	2	2	6.40	2.20	1	1	0.10	0.10	0	10	0.45	3.26	0.53	1.60	8	6	2	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1E	1	2	2	2	7.00	2.90	1	1	0.10	0.10	0	4	0.73	5.65	0.40	2.65	3	1	2	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1F	1	2	2	2	14.20	9.50	1	1	2.90	0.10	0	19	0.62	13.84	0.38	2.04	15	2	13	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1G	1	2	2	2	7.60	4.90	1	1	0.10	0.10	0	14	0.76	7.66	0.42	1.32	12	5	7	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1H	1	2	2	2	7.60	4.00	0	2	0.45	0.10	0	7	0.63	6.52	0.37	1.60	7	4	3	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1I	1	2	2	2	9.20	5.70	0	2	2.25	0.10	0	24	0.80	8.16	0.46	1.38	13	8	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Millbridge 1J	1	2	2	2	7.90	6.00	0	4	2.58	1.20	0	28	0.84	7.44	0.48	1.74	26	18	8	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Nameless Cove 1A	2	1	2	2	9.40	11.30	1	1	0.40	0.10	0	183	0.36	6.50	0.14	1.22	202	56	146	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Nameless Cove 1B	2	1	2	2	8.60	12.60	1	1	0.40	0.10	0	111	0.42	6.22	0.18	1.02	173	74	99	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Nameless Cove 2	2	1	2	2	12.00	17.70	1	1	1.70	0.30	0	35	1.28	11.88	0.48	3.42	26	5	21	0	0	0.00	0.00	0	0	0.00	0.00	3	0.5	0.4	1
Parker Beach 1	0	1	1	1	10.30	11.10	1	1	0.80	0.30	0	14	0.40	7.22	0.47	1.22	15	12	3	1	10	0.72	2.50	0	0	0.00	0.00	0	0	0	0
Peggy's Cove 2A	0	1	2	2	10.70	9.20	0	16	1.98	0.18	0	109	0.44	9.26	0.38	1.02	87	24	63	1	69	0.36	0.46	0	0	0.00	0.00	0	0	0	0
Peggy's Cove 2B	0	1	2	2	22.70	26.10	0	6	6.50	0.18	0	161	1.34	16.62	0.70	3.78	176	131	45	1	7	0.90	0.98	1	1	0.60	0.12	39	1	0.9	0
Peggy's Cove 3B	0	1	2	2	18.50	29.80	1	1	3.60	0.30	0	77	0.76	16.92	0.62	2.42	65	11	54	1	52	0.78	0.94	0	0	0.00	0.00	0	0	0	0
Pemaquid Pt 1A	1	2	2	2	19.70	26.20	1	1	1.90	0.20	0	93	0.76	17.24	0.40	3.20	83	16	67	1	32	0.32	0.38	1	0	0.00	0.00	3	0.65	0.5	0
Pemaquid Pt 1B	1	2	2	2	26.70	21.70	1	1	2.80	0.30	0	57	0.74	23.48	0.36	1.12	55	8	47	1	17	0.26	0.38	1	0	0.00	0.00	1	0.7	0.5	0
Pemaquid Pt 1D	1	2	2	2	21.40	18.80	1	1	0.30	0.30	0	93	0.74	20.16	0.36	2.46	106	34	72	1	16	0.42	0.56	1	1	0.00	0.27	6	0.8	0.5	0
Pemaquid Pt 1F	1	2	2	2	19.00	9.00	1	1	9.00	0.30	0	21	0.54	17.54	0.22	2.34	18	2	16	1	5	0.25	1.50	0	0	0.00	0.00	0	0	0	0
Pemaquid Pt 3A	1	2	2	2	9.20	3.10	1	1	0.10	0.20	0	18	0.43	5.82	0.46	1.28	13	9	4	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3B	1	2	2	2	7.80	3.10	1	1	0.10	0.10	0	18	0.43	6.30	0.38	0.78	15	10	5	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3C	1	2	2	2	8.00	3.10	1	1	1.20	0.20	0	17	0.43	7.28	0.34	1.56	13	2	11	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3D	1	2	2	2	6.00	3.00	0	6	1.40	0.10	0	17	0.48	3.72	0.50	1.38	11	9	2	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3E	1	2	2	2	7.10	5.50	0	3	1.50	0.23	0	15	0.56	6.64	0.44	1.86	12	4	8	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3F	1	2	2	2	8.40	5.10	0	3	1.40	0.13	0	21	0.44	5.98	0.40	1.46	24	14	10	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Pemaquid Pt 3G	1	2	2	2	8.30	2.70	0	4	2.23	0.15	0	20	0.38	6.60	0.38	2.70	19	8	11	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Perry's Cove 1A	1	1	2	2	19.50	7.60	1	1	4.40	0.20	0	33	0.68	15.94	0.42	2.64	24	3	21	1	21	0.48	0.64	1	1	0.00	0.17	5	0.4	0.6	0
Perry's Cove 1B	1	1	2	2	15.20	16.20	1	1	3.20	0.20	0	19	0.62	13.44	0.40	3.04	15	3	12	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Perry's Cove 1C	1	1	2	2	15.30	4.50	1	1	4.90	0.20	0	34	0.58	13.00	0.30	1.98	31	4	27	1	17	0.28	0.36	1	1	0.40	0.10	13	0.4	0.5	0
Perry's Cove 2A	1	1	2	2	6.90	10.60	1	1	0.20	0.50	0	30	0.36	6.62	0.34	1.54	19	11	8	1	5	0.48	0.98	0	0	0.00	0.00	0	0	0	0
Porteau Park BC 1	2	1	1	1	10.40	11.40	1	1	11.40	2.40	0	33	1.00	8.98	0.34	1.44	26	7	19	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Portugal Cove A	2	1	2	1	15.50	16.10	1	1	0.20	0.20	0	23	0.90	11.84	0.32	2.72	24	6	18	1	17	0.70	1.18	0	0	0.00	0.00	0	0	0	0
Portugal Cove B	2	1	2	1	13.10	10.50	1	1	1.30	0.10	0	15	0.40	11.86	0.18	1.88	9	3	6	1	8	0.42	0.88	0	0	0.00	0.00	0	0	0	0
Rockland 1C	1	2	2	2	19.50	22.20	1	1	0.80	0.20	0	113	0.70	17.24	0.30	2.34	107	27	80	1	11	0.74	1.28	0	0	0.00	0.00	0	0	0	0
Rockland 1D	1	2	2	2	24.70	10.20	1	1	0.10	0.20	0	31	0.98	23.04	0.56	2.68	25	4	21	1	5	0.64	1.42	1	0	0.00	0.00	3	0.6	0.7	0
Rockland 1E	1	2	2	2	19.80	8.20	1	1	5.20	0.20	0	16	1.12	18.48	0.42	2.08	17	5	12	1	1	0.80	1.50	0	0	0.00	0.00	0	0	0	0
Rockland 1F	1	2	2	2	19.50	9.70	1	1	5.50	0.20	0	18	0.80	17.62	0.42	1.78	15	1	14	1	3	0.33	0.60	1	1	0.00	0.20	2	0.6	0.5	0
Rockland 1G	1	2	2	2	18.10	11.50	1	1	3.60	0.40	0	37	0.62	17.45	0.48	1.66	35	5	30	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Rocky Beach Highway 100 1A	1	1	2	1	14.90	15.60	1	1	2.20	0.20	0	87	0.36	12.72	0.14	1.08	67	28	39	1	53	0.30	0.56	0	0	0.00	0.00	0	0	0	0
Rocky Beach Highway 100 1B	1	1	2	1	6.30	8.60	1	1	0.40	0.10	0	12	0.30	5.68	0.38	2.02	11	3	8	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Rocky Beach Highway 100 1C	1	1	2	1	8.20	10.00	1	1	1.00	0.10	0	35	0.36	7.58	0.38	2.02	31	19	12	1	6	0.28	0.30	0	0	0.00	0.00	0	0	0	0
Rocky Beach Highway 100 2A	1	1	2	1	13.70	16.90	1	1	3.90	0.30	0	22	0.54	12.96	0.36	1.68	26	5	21	1	10	0.50	0.94	0	0	0.00	0.00	0	0	0	0
Rocky Beach Highway 100 2B	1	1	2	1	18.70	22.60	1	1	3.70	0.40	0	22	0.84	17.92	0.44	3.58	16	2	14	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Ruby Beach	2	1	1	2	3.30	4.90	1	1	0.10	0.10	0	38	0.28	2.82	0.20	0.84	31	16	15	1	2	0.55	0.70	0	0	0.00	0.00	0	0	0	0
Seal Rock 1	0	1	1	2	5.40	6.80	0	2	0.95	0.25	0	37	0.22	4.56	0.12	1.04	21	13	8	1	33	0.20	0.74	0	0	0.00	0.00	0	0	0	0

Appendix B

Name$	ML	SUMVWINT	GEOG	EXPOSE	PLTLG	PLTWD	STPMULT	STPNUM	STPLG	STPWD	SERNUM	FRNDNUM	FRNDWD	FRNDLG	FRNDDISTWD	BRCHDIST	BRCHNUM	BRCHLOW	BRCHUP	RECYN	RECNUM	RECWD	RECLG	VESYN	VESPRD	VESDISTBT2	VESDISTBTPRS	VESNUM	VESLG	VESWD	FRNDLCK
Sealy's Cove 1A	1	2	2	1	41.20	28.90	1	1	8.00	0.40	0	127	0.66	38.70	0.56	2.92	131	16	115	1	41	0.52	0.80	1	1	0.78	0.26	83	0.9	0.5	0
Sealy's Cove 1B	1	2	2	1	41.50	29.20	0	2	4.25	0.35	0	171	1.16	37.66	0.72	4.56	147	39	108	1	19	0.38	0.64	1	1	0.56	0.34	149	0.9	0.7	0
Sekui 1	2	1	1	1	10.50	9.30	1	1	1.40	0.50	0	18	0.88	9.30	0.44	2.20	12	4	8	1	8	0.88	0.96	0	0	0.00	0.00	0	0	0	0
Singing Sands	0	1	2	1	23.00	34.50	1	1	2.50	1.00	13	55	2.64	23.64	0.70	3.64	51	7	30	1	13	0.40	1.06	0	0	0.00	0.00	0	0	0	1
Stonington 1B	1	2	2	1	27.10	8.90	1	1	2.60	0.20	0	53	0.54	24.46	0.56	1.84	77	27	50	1	5	0.40	0.72	0	0	0.00	0.00	0	0	0	0
Stonington 1C	1	2	2	1	15.20	10.00	1	1	3.90	0.10	0	31	0.42	14.06	0.32	2.34	39	5	34	1	20	0.30	0.40	0	0	0.00	0.00	0	0	0	0
Stonington 1D	1	2	2	1	27.00	8.50	1	1	5.70	0.20	0	29	0.64	22.18	0.40	2.58	31	5	26	1	3	0.53	1.37	0	0	0.00	0.00	0	0	0	0
Stonington 1E	1	2	2	1	18.70	15.40	1	1	1.40	0.20	0	65	0.62	17.28	0.22	2.96	77	15	62	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Stonington 1F	1	2	2	1	32.00	17.30	0	6	0.68	0.10	0	97	0.62	19.02	0.42	2.08	147	101	46	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Teahwitt 1	2	1	1	2	13.40	10.60	1	1	2.10	0.20	0	17	0.38	11.00	0.28	2.22	19	6	13	0	0	0.00	0.00	0	0	0.00	0.00	0	0	0	1
Whiffin Spit Park 1	2	1	1	1	0.00	0.00	0	5	3.13	0.27	0	17	1.42	9.60	0.70	2.76	15	8	7	0	0	0.00	0.00	1	0	0.00	0.00	2	7.6	2.7	0
Whiteway 1	0	1	2	1	18.60	20.10	1	1	2.20	0.30	0	344	0.30	16.22	0.20	1.76	225	22	203	1	38	0.44	0.58	0	0	0.00	0.00	0	0	0	0
Whiteway 2A	0	1	2	1	7.40	9.50	1	1	1.30	0.20	0	38	0.40	6.52	0.00	1.60	19	2	17	1	35	0.28	0.78	0	0	0.00	0.00	0	0	0	0
Whiteway 2B	0	1	2	1	6.50	7.00	1	1	1.80	0.80	0	21	0.42	6.00	0.00	1.58	15	4	11	1	22	0.40	0.60	0	0	0.00	0.00	0	0	0	0
Whiteway 2C	0	1	2	1	11.80	14.00	1	1	2.90	0.30	0	77	0.46	10.50	0.00	1.66	47	9	38	1	69	0.44	0.68	0	0	0.00	0.00	0	0	0	0
Whiteway 3	0	1	2	1	17.20	24.90	1	1	1.00	0.30	0	71	0.50	15.86	0.36	2.08	57	28	29	1	47	0.82	4.86	0	0	0.00	0.00	0	0	0	0
York Point 1B	1	2	2	2	13.60	7.80	1	1	1.90	0.20	0	14	0.53	12.22	0.34	2.18	13	4	9	1	1	0.40	0.70	0	0	0.00	0.00	0	0	0	0
York Point 1C	1	2	2	2	16.00	9.00	1	1	1.00	0.20	0	10	0.43	13.68	0.22	3.94	17	4	13	1	2	0.25	0.55	0	0	0.00	0.00	0	0	0	0
York Point 1D	1	2	2	2	17.20	10.50	1	1	0.60	0.20	0	9	0.38	16.98	0.32	1.88	9	5	4	1	2	0.20	0.70	0	0	0.00	0.00	0	0	0	0
York Point 1E	1	2	2	2	19.90	17.60	1	1	0.90	0.20	0	40	0.42	15.20	0.38	1.58	28	14	14	1	11	0.32	0.42	0	0	0.00	0.00	0	0	0	0
York Point 1F	1	2	2	2	17.20	11.70	1	1	0.10	0.40	0	32	0.48	14.70	0.44	3.00	26	13	13	1	3	0.28	0.47	0	0	0.00	0.00	0	0	0	0

Appendix B

Name$	STPLGM1	STPLGM2	STPLGM3	STPLGM4	STPLGM5	STPWDM1	STPWDM2	STPWDM3	STPWDM4	STPWDM5	FRNDWDM1	FRNDWDM2	FRNDWDM3	FRNDWDM4	FRNDWDM5	FRNDLGM1	FRNDLGM2	FRNDLGM3	FRNDLGM4	FRNDLGM5	FRNDDISTWDM1	FRNDDISTWDM2	FRNDDISTWDM3	FRNDDISTWDM4	FRNDDISTWDM5	BRCHDISTM1	BRCHDISTM2
Arches Provincial Park 1	2.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.40	0.80	0.60	0.70	17.60	17.30	15.80	14.20	13.80	0.70	0.60	0.30	0.30	0.70	3.30	0.90
Arches Provincial Park 2	0.40	1.90	N/A	N/A	N/A	0.30	0.20	N/A	N/A	N/A	1.60	1.70	1.70	1.60	1.60	11.00	9.10	9.30	10.30	8.60	0.50	0.50	0.40	0.40	0.50	1.80	2.70
Arches Provincial Park 3	4.70	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	2.00	1.40	0.80	1.30	1.10	19.00	18.50	15.20	16.50	17.00	0.40	0.40	0.30	0.50	1.00	1.50	4.80
Argentia 1A	1.40	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.50	0.30	0.30	0.40	6.30	5.50	6.50	6.50	4.50	0.50	0.40	0.30	0.20	0.40	1.20	3.20
Argentia 1B	7.70	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	1.00	0.90	0.80	0.50	0.60	28.90	22.70	25.20	23.50	25.00	0.50	0.50	0.40	0.40	0.70	0.90	2.20
Bauline 1A	4.50	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.30	0.40	0.50	0.30	0.50	15.30	14.00	12.20	10.70	11.00	0.50	0.70	0.80	0.80	0.70	0.40	1.00
Bauline 1B	3.40	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	0.50	0.70	0.50	0.80	0.60	18.30	17.00	16.00	15.20	15.70	0.70	0.80	0.70	0.60	0.70	2.70	3.00
Bauline 2A	2.60	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.90	0.60	1.00	1.10	N/A	9.00	8.70	8.80	8.10	7.10	0.50	0.40	0.50	0.30	0.30	0.80	0.40
Bauline 2B	1.80	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.00	0.70	1.00	0.80	0.90	11.70	12.00	13.80	11.00	1N/A	0.60	0.40	0.50	0.50	0.50	0.90	0.30
Bauline 2C	3.40	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.80	1.00	0.90	1.00	0.60	13.70	11.00	11.50	13.40	9.00	0.90	0.50	0.60	0.50	0.30	0.30	0.50
Botany Bay 1	0.30	0.30	0.70	N/A	N/A	0.10	0.10	0.10	N/A	N/A	0.30	0.30	0.20	0.30	0.40	5.80	5.40	5.60	3.90	2.10	0.10	0.10	0.20	0.20	0.10	1.30	0.99
Botany Bay 2	0.20	0.20	0.20	0.20	0.20	0.10	0.10	0.10	0.10	0.10	0.30	0.30	0.20	0.20	0.30	3.60	2.80	2.50	2.30	2.40	0.10	0.20	0.20	0.10	0.20	0.60	1.40
Botany Bay 3	3.80	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.10	0.60	1.00	0.80	1.00	10.90	9.70	8.30	9.40	9.20	0.50	0.60	0.40	0.50	0.50	2.90	3.60
Brant Point 1A	8.00	N/A	N/A	N/A	N/A	0.90	N/A	N/A	N/A	N/A	0.50	0.60	0.60	0.70	1.00	19.00	17.00	17.50	17.70	18.80	0.50	0.20	0.20	0.20	0.30	2.00	2.00
Brant Point 1C	4.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.00	1.30	1.10	0.80	1.00	15.00	14.80	14.80	14.80	N/A	0.50	0.40	0.50	0.40	0.40	2.70	2.70
Brant Point 1D	6.60	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.60	0.50	0.50	0.80	1.00	21.80	21.40	21.20	19.30	18.00	0.20	0.30	0.30	0.30	0.30	4.50	1.90
Brant Point 1F	7.00	N/A	N/A	N/A	N/A	1.50	N/A	N/A	N/A	N/A	1.50	1.50	N/A	N/A	N/A	17.00	16.00	16.50	N/A	N/A	0.80	0.60	0.50	0.70	0.60	0.50	1.50
Brant Point 1G	6.30	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.50	0.50	0.60	0.60	0.50	30.10	16.50	26.90	23.80	26.60	0.20	0.20	0.10	0.20	0.30	4.10	7.00
Brant Point 1H	0.10	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	1.00	0.70	0.70	1.10	0.80	26.20	18.20	25.30	26.70	22.40	0.10	0.20	0.30	0.40	0.50	8.20	2.70
Brigus (M&L Collection)	6.10	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.80	0.60	0.70	0.70	0.50	21.20	19.00	19.90	20.50	2N/A	0.50	0.60	0.70	0.50	0.40	4.80	1.00
Campbell River 1	2.80	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	1.50	1.00	1.30	1.00	1.80	13.20	12.00	12.40	12.50	13.00	0.60	0.90	0.80	0.60	0.40	3.30	3.70
Cutler Naval Base 1A	3.20	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	5.40	5.20	N/A	N/A	N/A	0.60	0.60	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1B	2.80	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.60	0.80	1.20	1.10	1.00	11.30	9.60	10.20	5.40	6.60	0.40	0.20	0.30	0.30	0.10	1.80	2.20
Cutler Naval Base 1C	5.00	N/A	N/A	N/A	N/A	3.00	N/A	N/A	N/A	N/A	0.80	0.70	1.20	1.30	1.00	10.90	1N/A	7.00	10.60	9.60	0.40	0.40	0.40	0.40	0.50	2.00	2.40
Cutler Naval Base 1D	7.00	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	1.30	1.10	1.30	1.20	1.30	11.30	9.30	11.00	8.50	9.90	0.40	0.50	0.30	0.40	0.40	0.70	0.60
Cutler Naval Base 1E	8.90	N/A	N/A	N/A	N/A	0.70	N/A	N/A	N/A	N/A	0.90	0.90	1.10	1.00	0.80	15.70	12.70	15.20	12.00	12.30	0.20	0.20	0.10	0.20	0.40	1.10	1.40
Cutler Naval Base 1F	0.10	N/A	N/A	N/A	N/A	0.80	N/A	N/A	N/A	N/A	1.80	1.10	1.50	0.70	1.00	16.60	16.60	15.50	15.00	9.50	0.40	0.30	0.50	0.50	0.20	2.50	2.50
Cutler Naval Base 1G	2.10	2.60	N/A	N/A	N/A	0.70	0.50	N/A	N/A	N/A	0.70	0.70	0.60	0.50	0.50	6.50	5.50	4.30	4.70	5.20	0.50	0.40	0.60	0.50	0.50	1.30	1.10
Cutler Naval Base 1H	4.40	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	1.40	1.20	0.70	N/A	N/A	9.50	8.20	7.20	N/A	N/A	0.40	0.50	0.70	0.50	0.40	3.50	2.30
Cutler Naval Base 1I	5.30	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	1.60	1.30	1.50	0.80	0.90	14.60	13.50	14.30	10.90	10.50	0.20	0.30	0.50	0.10	0.20	4.60	3.00
Cutler Naval Base 1J	5.50	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	1.30	1.10	0.80	0.70	N/A	11.70	10.70	9.30	9.50	N/A	0.30	0.40	0.50	0.30	0.40	3.40	1.20
Dundrave Park 1	1.00	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.40	1.20	1.40	1.20	1.30	8.50	8.20	8.40	7.60	8.00	0.40	0.20	0.30	0.20	0.50	2.50	2.70
Dundrave Park 2	1.30	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.10	0.80	0.70	1.00	0.80	8.80	7.40	8.50	8.40	7.20	0.60	0.50	0.40	0.30	0.90	2.10	3.00
Flat Rock 1A	14.90	N/A	N/A	N/A	N/A	1.50	N/A	N/A	N/A	N/A	0.70	0.50	0.90	0.80	1.00	13.00	11.40	9.00	12.80	10.30	0.30	0.90	0.40	0.50	0.70	3.80	2.20
Flat Rock 1B	14.30	N/A	N/A	N/A	N/A	2.10	N/A	N/A	N/A	N/A	0.50	0.30	0.30	0.60	0.40	13.40	9.80	13.10	10.40	5.90	0.50	0.20	0.20	0.40	N/A	0.90	1.30
Flat Rock 1C	2.90	1.80	2.10	N/A	N/A	0.30	0.30	0.20	N/A	N/A	0.70	0.70	0.90	1.00	1.00	10.20	9.00	5.90	6.00	9.90	0.50	0.70	0.50	0.30	0.40	1.90	2.50
Fortune Rocks 1A	5.50	6.40	N/A	N/A	N/A	0.40	0.30	N/A	N/A	N/A	0.60	0.60	0.50	0.50	0.60	29.20	29.00	25.50	26.70	23.00	0.20	0.20	0.30	0.30	0.30	6.00	5.00
Fortune Rocks 1B	3.00	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.50	0.50	0.50	0.40	0.50	19.40	12.80	17.10	19.50	18.00	0.30	0.40	0.60	0.60	0.40	3.00	2.00
Fortune Rocks 1D	7.20	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.50	0.50	0.50	0.40	0.50	32.40	20.50	29.60	29.40	28.10	0.40	0.40	0.40	0.30	0.30	2.60	3.10
Fortune Rocks 1E	6.20	6.90	6.00	5.90	N/A	0.40	0.30	0.30	0.30	N/A	0.40	0.40	0.50	0.30	0.30	27.90	24.60	20.90	24.20	21.80	0.30	0.40	0.40	0.30	0.20	5.90	3.20
Fortune Rocks 1F	3.80	3.10	N/A	N/A	N/A	0.30	0.30	N/A	N/A	N/A	0.50	0.30	0.40	0.40	0.50	24.90	20.80	22.50	22.70	16.40	0.20	0.30	0.40	0.30	0.40	1.50	1.80
Fortune Rocks 1G	6.40	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.60	0.40	0.30	0.90	0.30	30.00	14.40	24.50	29.80	25.00	0.40	0.60	0.30	0.20	0.20	1.40	7.90
Fortune Rocks 1H	7.90	5.50	7.00	6.50	5.80	0.30	0.30	0.40	0.30	0.30	0.50	0.50	0.40	0.50	0.40	33.80	29.20	28.00	25.60	25.40	0.50	0.40	0.30	0.30	0.30	4.50	7.50
Foxtrap A	1.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.80	0.60	0.70	0.70	0.60	10.40	10.40	9.50	9.90	8.40	0.80	0.50	0.60	0.60	0.40	2.40	1.50
Foxtrap B	1.30	1.00	N/A	N/A	N/A	0.10	0.10	N/A	N/A	N/A	1.30	1.10	1.10	0.70	0.60	10.50	9.50	8.50	7.80	10.70	0.60	0.50	0.40	0.70	0.40	1.20	3.50

Appendix B

Name$	STPLGM1	STPLGM2	STPLGM3	STPLGM4	STPLGM5	STPWDM1	STPWDM2	STPWDM3	STPWDM4	STPWDM5	FRNDWDM1	FRNDWDM2	FRNDWDM3	FRNDWDM4	FRNDWDM5	FRNDLGM1	FRNDLGM2	FRNDLGM3	FRNDLGM4	FRNDLGM5	FRNDDISTWDM1	FRNDDISTWDM2	FRNDDISTWDM3	FRNDDISTWDM4	FRNDDISTWDM5	BRCHDISTM1	BRCHDISTM2
Foxtrap C	3.90	3.30	N/A	N/A	N/A	0.30	0.40	N/A	N/A	N/A	1.00	1.10	1.30	1.00	0.90	12.40	11.00	12.00	11.00	8.40	0.40	0.40	0.50	0.50	0.50	4.00	4.00
Goose Berry's Cove A	1.60	1.90	N/A	N/A	N/A	0.20	0.10	N/A	N/A	N/A	0.20	0.20	0.30	0.30	0.40	11.60	9.00	7.70	6.80	6.10	0.50	0.50	N/A	N/A	N/A	1.60	1.70
Goose Berry's Cove B	2.20	2.20	N/A	N/A	N/A	0.20	0.20	N/A	N/A	N/A	0.30	0.20	0.20	0.20	0.20	10.50	7.80	6.20	8.00	9.80	0.60	0.40	0.30	0.40	0.30	1.00	2.70
Goose Berry's Cove C	2.10	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.30	0.20	0.20	0.20	0.20	13.60	6.70	9.60	10.20	11.10	0.40	0.50	N/A	N/A	N/A	3.00	1.00
Halifax 1	2.50	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.70	0.50	0.90	0.60	16.50	14.40	16.40	15.70	14.40	0.90	0.70	0.50	0.60	0.50	2.00	2.00
Hampton Beach 1A	1.40	1.40	1.60	1.00	1.20	0.10	0.10	0.10	0.10	0.10	0.40	0.40	0.30	0.50	0.40	7.70	6.40	5.20	6.20	6.10	0.10	0.20	0.20	0.30	0.40	1.40	2.20
Hampton Beach 1B	1.90	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.60	0.60	0.50	0.40	0.50	7.40	5.80	6.70	4.30	7.00	0.30	0.20	0.20	0.10	0.20	1.90	1.60
Hampton Beach 1C	2.00	1.40	0.80	0.70	0.90	0.40	0.40	0.40	0.30	0.20	0.50	0.60	0.40	0.30	0.40	5.10	2.90	2.60	2.10	4.20	0.20	0.20	0.40	0.30	0.40	1.20	2.30
Hampton Beach 1D	2.20	1.60	N/A	N/A	N/A	0.10	0.10	N/A	N/A	N/A	0.40	0.40	0.30	0.30	0.40	6.40	3.40	5.40	5.40	2.60	0.20	0.30	0.20	0.30	0.30	0.50	1.60
Hampton Beach 1E	2.00	1.60	N/A	N/A	N/A	0.10	0.30	N/A	N/A	N/A	0.40	0.50	0.60	N/A	N/A	5.30	4.20	5.00	3.00	4.40	0.30	0.20	0.30	N/A	N/A	0.30	0.70
Hampton Beach 1F	2.60	2.40	3.10	3.00	1.30	0.40	0.30	0.40	0.50	0.40	0.40	0.50	0.50	0.70	0.40	9.10	7.10	7.50	7.80	5.00	0.50	0.20	0.20	0.30	0.20	2.20	1.20
Hampton Beach 1H	2.00	2.40	1.40	1.90	1.70	0.40	0.30	0.40	0.50	0.40	0.40	0.60	0.50	0.30	0.50	7.30	4.30	5.80	4.00	5.50	0.30	0.30	0.50	0.30	N/A	1.10	1.90
Hants Harbour 1A	1.30	1.50	N/A	N/A	N/A	0.30	0.20	N/A	N/A	N/A	1.00	1.10	0.80	1.20	1.10	8.50	8.60	7.90	6.80	6.00	0.50	0.30	0.40	0.40	0.70	2.20	2.50
Hants Harbour 1B	2.50	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.00	0.50	0.80	1.00	1.10	7.50	6.10	7.40	7.30	7.20	0.50	0.50	0.40	0.40	0.30	2.60	2.30
Hearts Desire 1	9.20	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.60	0.70	0.90	0.70	0.50	29.00	23.20	22.70	27.00	23.50	N/A	N/A	N/A	N/A	N/A	2.80	2.60
Hearts Desire 2	3.70	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	0.90	0.90	0.60	0.50	0.90	17.00	16.30	14.50	12.80	12.80	0.30	0.30	0.40	0.50	0.40	1.80	1.70
Holyrood A	1.60	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.20	0.30	0.40	0.40	0.30	8.50	8.70	7.10	7.20	6.70	N/A	N/A	N/A	N/A	N/A	1.50	1.70
Holyrood B	1.00	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	1.20	1.00	0.80	0.60	0.65	10.70	10.50	1N/A	9.40	7.50	1.50	1.20	N/A	N/A	N/A	2.00	2.50
Holyrood C	1.30	N/A	N/A	N/A	N/A	0.15	N/A	N/A	N/A	N/A	0.50	0.40	0.60	0.50	0.50	10.50	10.30	8.20	1N/A	1N/A	N/A	N/A	N/A	N/A	N/A	1.50	1.30
Jones Port 1A	1.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.50	0.40	0.60	0.40	18.40	15.90	15.50	18.30	17.60	0.50	0.50	0.40	0.30	0.30	4.20	0.80
Jones Port 1B	3.20	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.50	0.50	0.40	0.40	0.30	20.10	15.90	17.00	18.00	18.70	0.30	0.30	0.40	0.70	0.50	2.00	2.40
Jones Port 1C	2.00	3.40	2.50	N/A	N/A	0.20	0.20	0.20	N/A	N/A	0.40	0.40	0.30	0.20	0.20	28.00	24.20	24.30	25.00	25.50	0.30	0.30	0.50	0.30	0.30	3.60	2.90
Jones Port 1E	3.70	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.70	0.50	0.70	0.50	0.30	17.60	14.10	7.80	16.20	13.80	0.30	0.30	0.20	0.30	0.30	1.70	1.30
Jones Port 1F	3.70	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.30	0.50	0.40	0.30	13.10	12.10	11.10	11.50	12.00	0.30	0.40	0.30	0.40	0.20	2.00	3.70
Jones Port 1G	2.50	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.40	0.30	0.60	0.50	0.60	20.60	12.30	17.20	15.20	20.50	0.30	0.30	0.40	0.40	0.30	1.50	0.60
Jordan River Vancouver	0.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	0.60	0.90	0.50	0.80	5.80	5.20	5.40	4.40	1.90	0.30	0.40	0.30	0.40	0.50	3.20	3.70
Kalaloch Beach 1	0.10	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.30	0.30	0.10	0.20	0.20	5.90	4.20	5.20	4.60	4.00	0.20	0.20	0.20	0.10	0.10	0.50	0.30
Kettle Creek 1A	2.50	3.60	4.70	4.00	2.50	0.20	0.20	0.20	0.20	0.20	0.80	0.80	0.40	0.70	0.40	19.10	18.40	16.00	12.00	11.70	0.50	0.50	0.40	0.30	0.20	1.50	0.70
Kettle Creek 1B	2.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.50	0.70	0.40	0.40	44.90	42,5	43.00	42.70	36.60	0.50	0.40	0.30	0.30	0.30	2.60	5.80
Kettle Creek 1C	2.70	2.40	N/A	N/A	N/A	0.10	0.20	N/A	N/A	N/A	0.90	0.50	0.50	0.40	0.30	28.00	24.40	23.80	20.70	23.70	0.30	0.20	0.20	0.30	0.10	2.80	1.40
Kin Beach 1	10.30	N/A	N/A	N/A	N/A	0.90	N/A	N/A	N/A	N/A	0.60	0.70	0.60	0.90	0.60	15.20	12.20	14.70	6.30	13.10	0.30	0.10	0.20	0.20	0.40	2.00	4.00
Kitty Coleman 1	1.70	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	1.70	0.90	0.80	0.80	0.90	10.40	8.00	7.80	7.00	10.20	0.70	0.60	0.50	0.50	0.50	3.40	2.60
Lanseaux Meadows 1	0.90	0.60	1.80	3.90	N/A	0.50	0.30	0.20	0.10	N/A	0.80	0.70	1.00	1.00	1.00	16.20	11.50	14.00	11.00	15.60	0.30	0.30	0.40	0.50	0.20	3.00	1.90
Lanseaux Meadows 2A	0.90	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.30	0.30	0.30	0.40	0.20	9.60	8.20	8.70	7.00	5.90	0.70	0.80	1.20	1.00	0.70	2.00	1.50
Lanseaux Meadows 2B	0.10	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.90	0.90	0.40	1.00	10.70	11.00	9.50	7.70	9.80	1.50	1.00	0.90	0.60	0.60	2.00	2.60
Lanseaux Meadows 2C	6.40	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	1.00	1.00	0.80	0.80	0.60	27.70	16.30	25.30	25.30	18.80	0.30	0.30	0.40	0.40	0.30	3.00	3.10
Lantzville 1	7.60	N/A	N/A	N/A	N/A	1.50	N/A	N/A	N/A	N/A	0.90	0.90	1.00	1.10	1.00	8.20	7.90	8.00	7.50	8.00	0.40	0.20	0.60	0.40	0.30	1.60	2.70
Lebec 1A	1.40	1.00	0.40	0.90	1.50	0.10	0.10	0.10	0.10	0.10	0.70	0.70	0.70	0.50	0.70	20.10	12.70	11.80	13.10	13.90	0.30	0.30	0.20	0.30	0.30	2.40	3.40
Lubec 1C	2.70	3.50	N/A	N/A	N/A	0.40	0.30	N/A	N/A	N/A	1.00	1.00	1.00	1.00	0.80	13.00	10.10	11.60	9.30	12.50	0.80	0.70	0.50	0.50	0.50	4.10	2.30
Lubec 1D	7.50	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	1.00	1.00	1.10	0.90	0.80	20.10	19.40	19.30	18.00	2N/A	0.40	0.60	0.50	0.40	0.50	1.90	2.90
Middle Cove 1A	1.80	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.80	0.70	0.60	0.40	1.90	14.40	13.70	12.90	13.90	13.50	0.60	0.50	1.10	0.80	0.70	1.80	2.40
Middle Cove 2A	2.30	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	2.20	2.00	2.30	1.90	2.10	14.70	11.90	10.20	14.50	13.20	1.40	1.30	1.50	1.10	1.90	3.00	2.70
Middle Cove 2B	2.50	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	2.90	2.20	2.40	2.50	1.70	18.20	15.20	17.00	14.20	12.50	0.80	0.50	0.60	0.90	0.60	2.40	2.70
Millbridge 1A	1.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.70	1.00	0.90	0.40	0.70	7.80	7.50	7.60	7.90	7.60	0.40	0.40	0.35	0.30	0.30	1.00	1.20
Millbridge 1B	1.00	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.70	0.80	0.10	N/A	N/A	7.90	7.70	1.80	N/A	N/A	0.60	0.40	0.10	N/A	N/A	1.20	3.00

Appendix B

Name$	STPLGM1	STPLGM2	STPLGM3	STPLGM4	STPLGM5	STPWDM1	STPWDM2	STPWDM3	STPWDM4	STPWDM5	FRNDWDM1	FRNDWDM2	FRNDWDM3	FRNDWDM4	FRNDWDM5	FRNDLGM1	FRNDLGM2	FRNDLGM3	FRNDLGM4	FRNDLGM5	FRNDDISTWDM1	FRNDDISTWDM2	FRNDDISTWDM3	FRNDDISTWDM4	FRNDDISTWDM5	BRCHDISTM1	BRCHDISTM2
Millbridge 1C	1.90	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.50	0.40	N/A	N/A	N/A	7.60	7.50	N/A	N/A	N/A	0.40	0.50	N/A	N/A	N/A	2.30	1.70
Millbridge 1D	0.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.50	0.80	0.30	0.20	N/A	6.40	5.80	1.30	2.00	0.80	0.40	0.90	0.30	N/A	N/A	1.00	2.80
Millbridge 1E	0.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.90	1.00	0.30	N/A	N/A	7.00	6.80	6.70	2.10	N/A	0.40	0.50	0.40	0.30	N/A	3.80	1.50
Millbridge 1F	2.90	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.50	0.60	0.70	0.60	0.70	14.20	14.50	13.50	13.50	13.50	0.50	0.50	0.30	0.30	0.30	1.20	2.50
Millbridge 1G	0.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.60	0.90	0.60	1.00	0.70	7.60	7.70	7.50	8.00	7.50	0.50	0.60	0.40	0.40	0.20	1.50	1.30
Millbridge 1H	0.50	0.40	N/A	N/A	N/A	0.10	0.10	N/A	N/A	N/A	0.90	0.90	0.10	N/A	N/A	7.60	7.70	7.80	7.70	1.80	0.40	0.40	0.30	N/A	N/A	1.20	1.10
Millbridge 1I	2.50	2.00	N/A	N/A	N/A	0.10	0.10	N/A	N/A	N/A	0.90	1.00	0.90	0.80	0.40	9.20	9.30	9.10	4.10	9.10	0.40	0.40	0.50	0.50	0.50	0.50	1.10
Millbridge 1J	0.80	3.10	3.00	3.40	N/A	0.10	0.30	4.00	0.40	N/A	1.00	1.00	1.20	0.70	0.30	7.90	7.60	7.80	7.80	6.10	0.50	0.40	0.60	0.60	0.30	1.70	1.50
Nameless Cove 1A	0.40	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.30	0.30	0.30	0.40	0.50	9.40	5.70	5.90	6.30	5.20	0.20	0.20	0.10	0.10	0.10	1.00	1.20
Nameless Cove 1B	0.40	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.50	0.50	0.40	0.30	0.40	8.60	6.80	8.00	3.80	3.90	0.20	0.20	0.10	0.10	0.30	1.00	1.00
Nameless Cove 2	1.70	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	1.20	1.30	1.30	1.40	1.20	12.00	11.70	11.80	11.90	12.00	0.60	0.70	0.50	0.30	0.30	3.80	4.50
Parker Beach 1	0.80	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.40	0.60	0.40	0.40	0.20	10.30	6.10	7.90	6.30	5.50	0.60	0.40	0.40	N/A	N/A	1.40	0.70
Peggy's Cove 2A	2.00	2.00	2.20	1.80	1.90	0.20	0.20	0.20	0.10	0.20	0.30	0.40	0.40	0.50	0.60	10.70	9.10	9.80	7.80	8.90	0.40	0.40	0.40	0.40	0.30	0.80	0.80
Peggy's Cove 2B	10.40	6.50	4.00	8.00	3.60	0.20	0.20	0.20	0.20	0.10	1.50	1.20	1.20	1.40	1.40	22.70	15.80	10.40	13.20	21.00	0.80	0.90	0.60	0.70	0.50	1.60	3.40
Peggy's Cove 3B	3.60	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.80	0.90	0.80	0.50	0.80	18.50	14.00	16.70	18.60	16.80	0.70	0.70	0.60	0.60	0.50	2.70	2.20
Pemaquid Pt 1A	1.90	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.70	0.70	0.80	1.10	0.50	19.70	15.70	16.20	18.40	16.20	0.50	0.30	0.50	0.30	0.40	3.80	2.10
Pemaquid Pt 1B	2.80	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.80	0.70	1.00	0.60	0.60	26.70	21.90	16.20	25.90	26.70	0.30	0.30	0.40	0.50	0.30	1.80	1.00
Pemaquid Pt 1D	0.30	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.60	0.60	0.70	1.00	0.80	21.40	18.80	20.90	20.80	18.90	0.30	0.20	0.40	0.50	0.40	2.20	4.10
Pemaquid Pt 1F	9.00	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.50	0.50	0.60	0.70	0.40	19.00	15.00	16.00	18.50	19.20	0.10	0.10	0.20	0.40	0.30	3.00	3.00
Pemaquid Pt 3A	0.10	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.40	0.30	N/A	N/A	9.20	7.90	6.50	2.90	2.60	0.40	0.40	0.60	0.50	0.40	0.50	1.00
Pemaquid Pt 3B	0.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.60	0.50	0.40	0.20	N/A	7.80	5.80	6.50	7.90	3.50	0.30	0.40	0.40	0.30	0.50	1.70	0.70
Pemaquid Pt 3C	1.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.30	0.50	0.30	N/A	8.00	6.80	7.00	6.90	7.70	0.30	0.30	0.30	0.40	0.40	1.70	1.50
Pemaquid Pt 3D	1.40	1.90	1.70	0.80	1.20	0.10	0.10	0.10	0.10	0.10	0.50	0.70	0.40	0.40	0.40	6.00	5.90	2.50	2.60	1.60	0.30	0.70	0.70	0.60	0.20	1.00	1.20
Pemaquid Pt 3E	1.10	0.80	2.60	N/A	N/A	0.20	0.40	0.10	N/A	N/A	0.80	0.50	0.60	0.40	0.50	7.10	6.70	7.10	6.30	6.00	0.40	0.40	0.50	0.50	0.40	1.20	2.40
Pemaquid Pt 3F	1.20	1.40	1.60	N/A	N/A	0.10	0.10	0.20	N/A	N/A	0.50	0.60	0.30	0.40	0.40	8.40	6.20	4.00	4.10	7.20	0.30	0.40	0.40	0.40	0.50	1.30	2.10
Pemaquid Pt 3G	1.60	2.10	3.00	2.20	N/A	0.20	0.20	0.10	0.10	N/A	0.40	0.50	0.40	0.30	0.30	8.30	7.80	3.80	7.20	5.90	0.40	0.40	0.30	0.30	0.50	4.00	2.30
Perry's Cove 1A	4.40	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.60	0.80	0.70	0.70	19.50	13.40	13.70	18.00	15.10	0.40	0.30	0.30	0.50	0.60	3.60	4.10
Perry's Cove 1B	3.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.50	0.80	0.60	0.70	15.20	13.40	9.90	14.60	14.10	0.30	0.30	0.70	0.40	0.30	2.60	3.40
Perry's Cove 1C	4.90	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	0.50	0.50	0.60	0.50	15.30	10.90	11.20	13.40	14.20	0.30	0.20	0.40	0.30	0.30	2.70	2.10
Perry's Cove 2A	0.20	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	0.40	0.40	0.10	0.50	0.40	6.90	6.50	6.50	6.20	7.00	0.50	0.30	0.30	0.30	0.30	0.80	1.40
Porteau Park BC 1	11.40	N/A	N/A	N/A	N/A	2.40	N/A	N/A	N/A	N/A	1.20	1.00	1.00	1.10	0.70	10.40	9.90	10.40	8.40	5.80	0.40	0.50	0.20	0.30	0.30	1.10	2.00
Portugal Cove A	0.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	0.90	0.70	0.70	1.40	15.50	9.10	10.50	11.80	12.30	0.20	0.50	0.30	0.40	0.20	2.10	3.40
Portugal Cove B	1.30	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.40	0.40	0.40	0.30	0.50	13.10	13.00	10.50	10.30	12.40	0.20	0.10	0.20	0.20	N/A	1.10	1.30
Rockland 1C	0.80	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.90	0.90	0.50	0.70	0.50	19.50	17.90	15.60	16.40	16.80	0.30	0.30	0.20	0.30	0.40	1.60	3.20
Rockland 1D	0.10	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	1.20	0.90	1.40	0.60	24.70	24.20	24.20	21.40	20.70	0.50	0.70	0.70	0.60	0.30	3.50	2.80
Rockland 1E	5.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	0.90	1.40	1.10	1.40	19.80	17.00	18.40	17.70	19.50	0.30	0.30	0.60	0.60	0.30	2.40	2.90
Rockland 1F	5.50	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.80	1.10	0.80	0.80	19.50	16.80	17.20	15.70	18.90	0.30	0.40	0.50	0.40	0.50	2.00	2.50
Rockland 1G	3.60	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.50	0.80	0.60	0.70	0.50	18.10	1N/A	17.00	16.80	17.90	0.50	0.60	0.80	0.30	0.20	1.40	2.20
Rocky Beach Highway 100 1A	2.20	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.30	0.30	0.40	0.40	0.40	14.90	12.50	9.20	14.60	12.40	0.20	0.20	0.10	0.10	0.10	0.70	0.80
Rocky Beach Highway 100 1B	0.40	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.40	0.30	0.30	0.20	0.30	6.30	5.50	5.90	5.00	5.70	0.30	0.30	0.40	0.40	0.50	0.30	2.20
Rocky Beach Highway 100 1C	1.00	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.40	0.40	0.30	0.30	0.40	8.20	8.20	8.20	7.50	5.80	0.30	0.30	0.40	0.50	0.40	1.00	3.70
Rocky Beach Highway 100 2A	3.90	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.60	0.40	0.70	0.50	0.50	13.70	12.90	12.40	12.60	13.20	0.40	0.40	0.30	0.30	0.40	3.00	1.00
Rocky Beach Highway 100 2B	3.70	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.70	0.80	0.70	1.00	1.00	18.70	18.30	18.10	17.10	17.40	0.40	0.30	0.40	0.40	0.70	4.90	5.30
Ruby Beach	0.10	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.30	0.30	0.30	0.30	0.20	3.30	3.30	3.00	2.90	1.60	0.20	0.20	0.20	0.20	0.20	0.90	1.10
Seal Rock 1	1.00	0.90	N/A	N/A	N/A	0.20	0.30	N/A	N/A	N/A	0.20	0.20	0.30	0.20	0.20	5.40	3.60	4.40	5.00	4.40	0.10	0.10	0.10	0.20	0.10	1.10	1.10

Appendix B

Name$	STPLGM1	STPLGM2	STPLGM3	STPLGM4	STPLGM5	STPWDM1	STPWDM2	STPWDM3	STPWDM4	STPWDM5	FRNDWDM1	FRNDWDM2	FRNDWDM3	FRNDWDM4	FRNDWDM5	FRNDLGM1	FRNDLGM2	FRNDLGM3	FRNDLGM4	FRNDLGM5	FRNDDISTWDM1	FRNDDISTWDM2	FRNDDISTWDM3	FRNDDISTWDM4	FRNDDISTWDM5	BRCHDISTM1	BRCHDISTM2
Sealy's Cove 1A	8.00	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.60	0.90	0.60	0.50	0.70	41.20	39.00	39.50	34.40	39.40	0.70	0.50	0.60	0.60	0.40	2.60	2.10
Sealy's Cove 1B	5.60	2.90	N/A	N/A	N/A	0.40	0.30	N/A	N/A	N/A	0.70	1.90	1.30	1.00	0.90	41.50	34.20	38.60	39.30	34.70	0.60	0.50	0.90	0.70	0.90	3.60	5.90
Sekui 1	1.40	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	1.00	0.60	0.80	1.10	0.90	10.50	9.30	8.50	9.70	8.50	0.40	0.40	0.40	0.50	0.50	1.70	1.20
Singing Sands	2.50	N/A	N/A	N/A	N/A	1.00	N/A	N/A	N/A	N/A	2.80	3.20	2.00	2.10	3.10	23.00	24.40	24.10	22.10	24.60	0.60	0.70	0.50	0.80	0.90	2.20	4.50
Stonington 1B	2.60	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.50	0.70	0.40	0.60	27.10	22.40	22.70	22.90	27.20	0.90	0.40	0.30	0.50	0.70	1.20	0.90
Stonington 1C	3.90	N/A	N/A	N/A	N/A	0.10	N/A	N/A	N/A	N/A	0.40	0.40	0.30	0.50	0.50	15.20	14.70	14.30	13.70	12.40	0.30	0.30	0.40	0.40	0.20	3.40	3.40
Stonington 1D	5.70	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.80	0.80	0.70	0.60	0.30	27.00	20.90	21.50	23.20	18.30	0.30	0.40	0.50	0.40	0.40	2.50	2.00
Stonington 1E	1.40	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.70	0.70	0.80	0.50	0.40	18.70	18.50	18.30	17.20	13.70	0.20	0.20	0.30	0.20	0.20	1.40	4.90
Stonington 1F	0.80	0.40	1.30	0.40	0.50	0.10	0.10	0.10	0.10	0.10	0.60	0.60	0.70	0.60	0.60	32.00	16.50	16.60	17.80	12.20	0.20	0.30	0.40	0.70	0.50	2.00	1.50
Teahwitt 1	2.10	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.50	0.30	0.20	0.30	13.40	9.10	11.60	9.90	1N/A	0.10	0.20	0.30	0.40	0.40	2.30	2.90
Whiffin Spit Park 1	1.50	4.00	3.90	N/A	N/A	0.20	0.50	0.10	N/A	N/A	1.40	1.40	1.60	1.50	1.20	0.00	12.00	12.10	12.50	11.40	0.50	0.60	0.50	0.70	1.20	4.90	2.10
Whiteway 1	2.20	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.40	0.30	0.30	0.30	0.20	18.60	17.00	17.00	16.00	12.50	0.20	0.20	0.10	0.30	0.20	0.60	3.00
Whiteway 2A	1.30	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.40	0.50	0.50	0.30	0.30	7.40	6.00	6.40	5.70	7.10	N/A	N/A	N/A	N/A	N/A	2.30	1.40
Whiteway 2B	1.80	N/A	N/A	N/A	N/A	0.80	N/A	N/A	N/A	N/A	0.50	0.50	0.30	0.40	0.40	6.50	6.30	6.10	6.10	5.00	N/A	N/A	N/A	N/A	N/A	2.50	1.00
Whiteway 2C	2.90	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.50	0.50	0.40	0.40	0.50	11.80	11.00	9.50	9.50	10.70	N/A	N/A	N/A	N/A	N/A	2.50	1.70
Whiteway 3	1.00	N/A	N/A	N/A	N/A	0.30	N/A	N/A	N/A	N/A	0.30	0.60	0.40	0.60	0.60	17.20	16.50	15.20	15.00	15.40	0.30	0.40	0.40	0.40	0.30	2.10	2.30
York Point 1B	1.90	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.50	0.60	0.40	0.60	N/A	13.60	13.60	12.60	11.60	9.70	0.40	0.30	0.40	0.30	0.30	2.80	2.00
York Point 1C	1.00	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.30	0.50	0.50	N/A	N/A	16.00	16.30	5.50	15.60	15.00	0.30	0.20	0.10	0.20	0.30	5.80	5.60
York Point 1D	0.60	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.40	0.40	0.30	0.40	N/A	17.20	17.10	17.00	17.00	16.60	0.30	0.30	0.40	0.30	0.30	1.10	2.30
York Point 1E	0.90	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A	0.60	0.30	0.40	0.40	0.40	19.90	14.50	14.80	13.90	12.90	0.30	0.40	0.30	0.50	0.40	1.90	1.10
York Point 1F	0.10	N/A	N/A	N/A	N/A	0.40	N/A	N/A	N/A	N/A	0.30	0.60	0.50	0.50	0.50	17.20	12.20	14.20	13.90	16.00	0.40	0.60	0.50	0.40	0.30	2.40	2.70

Appendix B

Name$	BRCHDISTM3	BRCHDISTM4	BRCHDISTM5	RECWDM1	RECWDM2	RECWDM3	RECWDM4	RECWDM5	RECLGM1	RECLGM2	RECLGM3	RECLGM4	RECLGM5	VESDISTBT2M1	VESDISTBT2M2	VESDISTBT2M3	VESDISTBT2M4	VESDISTBT2M5	VESDISTBTPRSM1	VESDISTBTPRSM2	VESDISTBTPRSM3	VESDISTBTPRSM4	VESDISTBTPRSM5
Arches Provincial Park 1	0.60	1.70	2.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Arches Provincial Park 2	1.80	1.30	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Arches Provincial Park 3	1.60	2.90	1.10	0.60	0.40	1.10	0.90	0.50	1.30	0.70	1.00	0.90	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Argentia 1A	3.50	1.10	3.60	0.50	0.40	0.30	0.20	0.20	0.40	0.50	0.30	0.20	0.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Argentia 1B	0.70	4.40	2.70	0.80	0.80	0.60	1.10	0.30	1.50	2.00	1.40	2.40	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Bauline 1A	2.50	2.30	2.70	0.60	0.50	1.00	0.30	N/A	0.30	4.10	3.70	3.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Bauline 1B	2.30	5.50	2.50	0.50	0.60	1.00	1.10	0.40	0.60	0.70	5.30	4.70	5.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Bauline 2A	0.30	0.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.20	0.10	0.20	N/A	N/A
Bauline 2B	0.40	0.50	0.60	0.90	0.80	0.70	0.70	0.80	1.10	1.20	1.10	0.80	1.00	N/A	N/A	N/A	N/A	N/A	0.40	0.20	0.20	0.20	N/A
Bauline 2C	0.50	0.30	0.40	1.20	0.90	1.20	1.20	1.00	1.50	1.70	1.70	1.60	0.90	N/A	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A
Botany Bay 1	0.30	0.80	0.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Botany Bay 2	1.10	0.60	0.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Botany Bay 3	2.50	1.60	1.70	1.20	0.90	0.80	0.50	N/A	1.50	1.60	1.00	1.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1A	2.20	2.90	2.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1C	3.20	4.70	2.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1D	4.00	3.00	4.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1F	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1G	3.10	2.90	2.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brant Point 1H	4.50	2.20	10.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Brigus (M&L Collection)	3.10	1.00	2.50	0.50	0.60	0.50	0.60	0.50	0.80	0.70	1.00	1.10	1.00	0.10	0.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Campbell River 1	3.80	3.60	2.80	0.50	0.40	0.30	0.50	0.80	0.80	0.80	1.00	2.40	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1B	2.00	4.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1C	2.20	4.50	2.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1D	1.60	2.80	3.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1E	1.20	2.00	3.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1F	2.80	3.20	6.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1G	1.40	0.70	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1H	1.50	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1I	1.70	1.20	1.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Cutler Naval Base 1J	3.40	2.50	2.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Dundrave Park 1	2.00	2.10	1.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Dundrave Park 2	1.80	2.00	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Flat Rock 1A	2.40	2.50	3.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Flat Rock 1B	1.20	2.00	1.10	1.00	0.70	0.60	0.40	0.50	3.40	3.40	2.50	2.90	4.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Flat Rock 1C	1.50	3.60	3.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1A	5.50	4.20	3.50	0.40	0.30	0.20	0.20	0.50	1.20	0.80	1.20	1.00	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1B	2.40	3.80	4.20	0.20	0.25	0.20	0.20	0.30	0.30	0.40	0.50	0.60	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1D	3.10	1.60	2.20	0.40	0.40	0.30	0.20	0.40	1.80	1.70	0.70	2.00	1.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1E	3.50	3.90	4.60	0.30	0.30	0.10	0.10	0.10	0.30	0.40	0.70	0.70	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1F	2.20	2.00	1.90	0.40	0.40	0.60	0.50	0.30	0.60	0.50	0.90	1.00	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1G	2.10	1.00	1.90	0.30	0.20	0.40	0.40	0.30	1.20	0.80	0.40	1.10	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Fortune Rocks 1H	1.00	3.90	5.90	0.40	0.50	0.30	0.50	0.40	1.50	0.60	0.60	1.20	1.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Foxtrap A	2.90	0.70	2.40	0.70	0.30	0.50	0.40	0.40	0.70	0.70	0.70	0.70	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Foxtrap B	3.00	1.80	3.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Appendix B

Name$	BRCHDISTM3	BRCHDISTM4	BRCHDISTM5	RECWDM1	RECWDM2	RECWDM3	RECWDM4	RECWDM5	RECLGM1	RECLGM2	RECLGM3	RECLGM4	RECLGM5	VESDISTBT2M1	VESDISTBT2M2	VESDISTBT2M3	VESDISTBT2M4	VESDISTBT2M5	VESDISTBTPRSM1	VESDISTBTPRSM2	VESDISTBTPRSM3	VESDISTBTPRSM4	VESDISTBTPRSM5
Foxtrap C	4.00	3.50	2.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Goose Berry's Cove A	3.40	1.80	2.10	0.50	0.40	0.30	0.40	0.30	0.70	0.40	0.60	0.40	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Goose Berry's Cove B	2.60	0.80	1.10	0.30	0.30	0.20	0.30	N/A	0.30	0.40	0.20	0.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Goose Berry's Cove C	23.00	0.70	2.60	0.40	0.30	0.30	0.30	0.40	0.40	0.40	0.70	0.60	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Halifax 1	2.50	1.60	2.00	0.90	0.60	0.90	0.90	0.40	1.50	1.50	0.13	1.10	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1A	1.50	0.60	1.30	0.40	0.40	0.30	0.30	0.40	0.70	0.40	0.50	0.70	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1B	2.00	1.10	2.30	0.30	0.30	0.30	0.40	N/A	0.50	0.50	0.40	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1C	1.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1D	2.40	1.60	N/A	0.40	0.20	0.30	N/A	N/A	0.50	0.60	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1E	1.70	N/A	N/A	0.30	0.20	0.40	0.40	0.30	1.10	0.90	0.60	0.40	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1F	2.50	1.90	2.40	0.50	0.20	0.30	0.30	0.40	1.90	0.40	0.60	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hampton Beach 1H	1.40	N/A	N/A	0.30	0.40	0.30	0.30	0.30	1.20	0.90	1.00	0.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Hants Harbour 1A	2.30	2.00	1.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.50	0.40	0.20	0.20	0.10	N/A	N/A	N/A	N/A	N/A
Hants Harbour 1B	2.50	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.20	0.30	N/A	N/A	N/A
Hearts Desire 1	3.50	2.90	1.70	1.30	1.10	0.60	0.70	0.80	9.10	9.90	6.40	6.60	5.10	N/A	N/A	N/A	N/A	N/A	0.20	0.30	N/A	N/A	N/A
Hearts Desire 2	2.80	3.40	3.00	0.70	0.50	0.50	0.50	0.90	3.50	2.60	6.90	3.90	5.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Holyrood A	1.80	1.70	1.50	0.40	0.40	0.20	0.60	0.30	0.50	0.40	0.40	0.50	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Holyrood B	3.70	3.10	2.00	1.00	0.70	0.80	0.80	0.60	1.10	0.70	1.00	0.70	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Holyrood C	2.00	1.20	1.00	0.80	0.60	0.40	0.30	0.50	0.70	0.90	1.00	0.60	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1A	1.10	1.80	1.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1B	3.00	3.30	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1C	4.20	1.40	2.60	0.40	N/A	N/A	N/A	N/A	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1E	2.90	2.00	2.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1F	1.60	1.90	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jones Port 1G	3.20	0.70	3.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Jordan River Vancouver	2.40	3.20	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kalaloch Beach 1	1.40	0.70	1.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kettle Creek 1A	2.70	2.50	2.80	0.50	0.40	0.30	0.20	N/A	0.50	0.70	0.90	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kettle Creek 1B	6.60	4.60	1.90	0.20	0.20	0.20	N/A	N/A	0.80	0.80	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kettle Creek 1C	0.80	4.70	2.50	0.20	0.20	0.10	0.10	0.20	0.80	0.50	0.40	0.40	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kin Beach 1	3.40	2.40	3.00	0.70	N/A	N/A	N/A	N/A	2.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Kitty Coleman 1	4.30	2.60	2.60	0.60	0.30	0.50	0.50	0.80	0.70	1.50	1.50	1.10	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lanseaux Meadows 1	4.00	1.00	2.40	0.50	0.60	0.40	0.50	0.50	0.60	0.60	0.70	0.60	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lanseaux Meadows 2A	1.50	1.10	2.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lanseaux Meadows 2B	3.30	2.00	1.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lanseaux Meadows 2C	3.10	2.50	2.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lantzville 1	2.00	2.00	2.60	0.50	0.30	0.40	0.60	0.40	0.70	0.90	0.40	0.60	2.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lebec 1A	2.50	2.40	2.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lubec 1C	3.10	3.00	3.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lubec 1D	4.00	4.10	2.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Middle Cove 1A	3.60	3.20	2.30	1.60	1.30	1.40	1.30	N/A	3.90	2.80	1.00	2.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Middle Cove 2A	2.20	3.10	3.10	1.00	1.50	1.00	N/A	N/A	2.20	3.40	2.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Middle Cove 2B	1.70	4.40	2.90	1.10	0.90	0.80	0.70	0.90	1.40	2.00	3.10	3.10	2.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1A	1.70	0.70	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1B	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

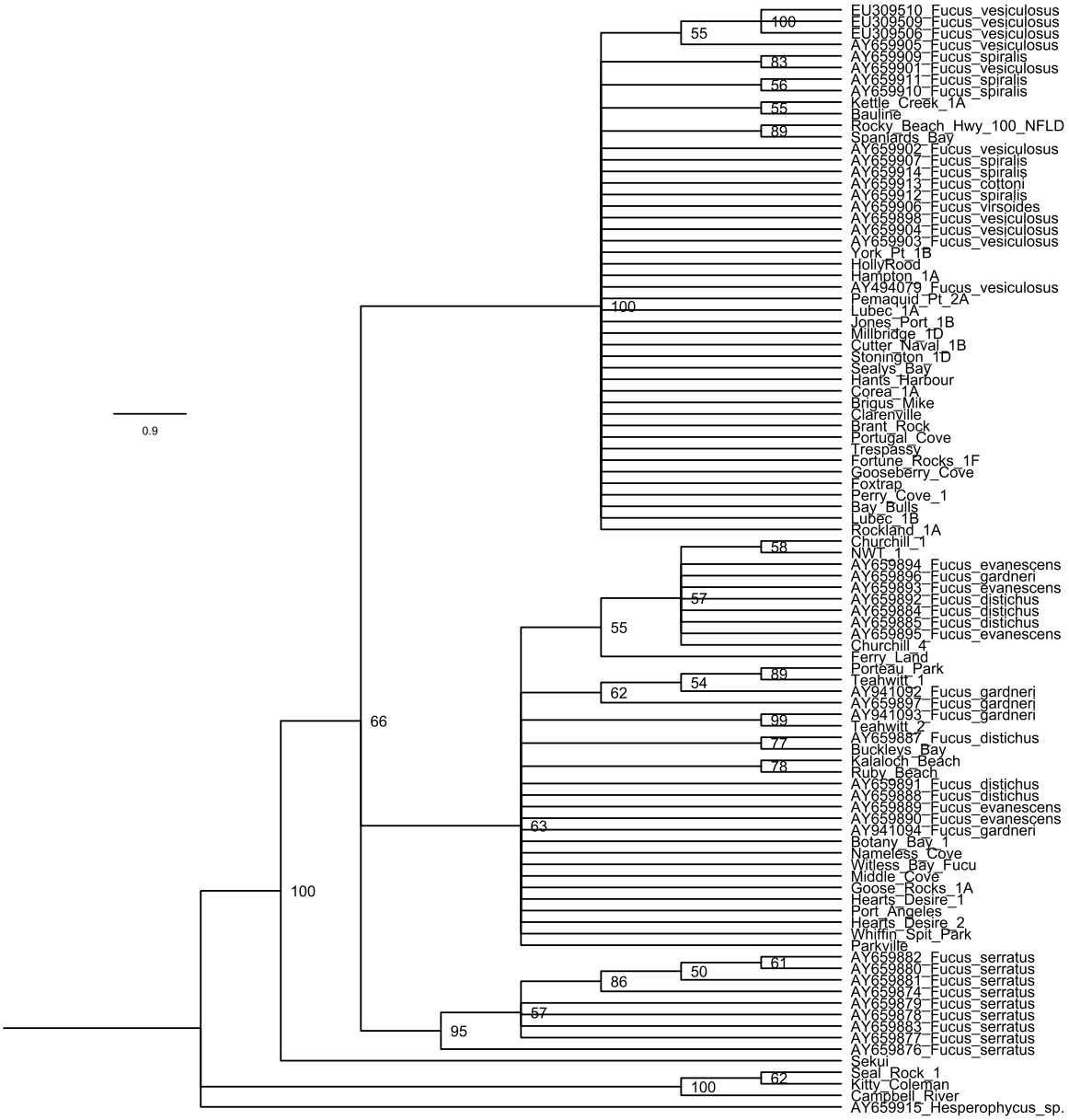
Appendix B

Name$	BRCHDISTM3	BRCHDISTM4	BRCHDISTM5	RECWDM1	RECWDM2	RECWDM3	RECWDM4	RECWDM5	RECLGM1	RECLGM2	RECLGM3	RECLGM4	RECLGM5	VESDISTBT2M1	VESDISTBT2M2	VESDISTBT2M3	VESDISTBT2M4	VESDISTBT2M5	VESDISTBTPRSM1	VESDISTBTPRSM2	VESDISTBTPRSM3	VESDISTBTPRSM4	VESDISTBTPRSM5
Millbridge 1C	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1D	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1E	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1F	2.20	3.00	1.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1G	1.00	1.50	1.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1H	1.60	2.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1I	1.50	2.60	1.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Millbridge 1J	1.80	1.70	2.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Nameless Cove 1A	1.30	1.30	1.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Nameless Cove 1B	0.90	1.10	1.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Nameless Cove 2	4.00	2.80	2.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Parker Beach 1	1.40	1.20	1.40	0.90	1.00	0.50	0.40	0.80	3.40	3.20	1.10	2.40	2.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Peggy's Cove 2A	0.60	1.40	1.50	0.40	0.40	0.50	0.30	0.20	0.60	0.50	0.30	0.50	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Peggy's Cove 2B	3.70	5.20	5.00	1.00	1.00	0.90	0.90	0.70	1.20	1.00	1.00	0.80	0.90	0.60	0.90	0.50	0.50	0.50	0.10	0.10	0.10	0.20	0.10
Peggy's Cove 3B	2.10	1.50	3.60	0.70	0.90	0.80	0.90	0.60	1.00	1.00	0.90	0.90	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 1A	3.60	2.00	4.50	0.40	0.40	0.30	0.30	0.20	0.50	0.50	0.30	0.40	0.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 1B	1.00	0.50	1.30	0.20	0.20	0.40	0.30	0.20	0.50	0.40	0.30	0.50	0.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 1D	1.90	1.40	2.70	0.50	0.50	0.40	0.30	0.40	0.70	0.60	0.60	0.50	0.40	N/A	N/A	N/A	N/A	N/A	0.20	0.30	0.30	N/A	N/A
Pemaquid Pt 1F	2.50	2.20	1.00	0.30	0.30	0.20	0.20	0.25	1.80	1.50	1.40	1.30	1.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3A	1.30	1.30	2.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3B	0.90	0.40	0.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3C	1.30	1.50	1.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3D	1.60	2.00	1.10	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3E	2.20	1.80	1.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3F	1.30	0.70	1.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Pemaquid Pt 3G	1.30	2.60	3.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Perry's Cove 1A	2.20	2.40	0.90	0.70	0.60	0.40	0.40	0.30	0.90	0.60	0.70	0.60	0.40	N/A	N/A	N/A	N/A	N/A	0.20	0.10	0.20	N/A	N/A
Perry's Cove 1B	3.20	3.60	2.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Perry's Cove 1C	2.50	2.20	0.40	0.20	0.30	0.30	0.20	0.40	0.50	0.30	0.30	0.30	0.40	0.40	N/A	N/A	N/A	N/A	0.10	0.10	0.10	0.10	0.10
Perry's Cove 2A	1.60	2.80	1.10	0.60	0.30	0.60	0.40	0.50	1.00	0.70	1.00	1.00	1.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Porteau Park BC 1	1.00	1.60	1.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Portugal Cove A	1.10	4.30	2.70	0.70	0.70	1.00	0.40	0.70	1.40	1.30	1.00	1.00	1.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Portugal Cove B	3.80	2.30	0.90	0.50	0.50	0.50	0.20	0.40	1.00	1.10	1.10	0.70	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rockland 1C	2.00	2.90	2.00	1.40	0.50	0.60	0.70	0.50	0.90	1.40	1.70	1.80	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rockland 1D	2.70	1.80	2.60	0.70	0.60	0.40	0.90	0.60	2.40	1.00	1.50	0.80	1.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rockland 1E	2.00	2.10	1.00	0.80	N/A	N/A	N/A	N/A	1.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rockland 1F	0.80	2.90	0.70	0.40	0.30	0.30	N/A	N/A	0.70	0.60	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.20	N/A	N/A	N/A	N/A
Rockland 1G	1.60	2.10	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rocky Beach Highway 100 1A	1.00	0.70	2.20	0.40	0.40	0.30	0.20	0.20	0.70	0.50	0.60	0.50	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rocky Beach Highway 100 1B	3.10	3.20	1.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rocky Beach Highway 100 1C	1.00	3.20	1.20	0.30	0.20	0.20	0.40	0.30	0.30	0.20	0.40	0.30	0.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rocky Beach Highway 100 2A	1.20	1.60	1.60	0.50	0.60	0.60	0.40	0.40	0.90	0.80	1.10	1.00	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Rocky Beach Highway 100 2B	2.30	3.10	2.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Ruby Beach	0.80	0.70	0.70	0.40	0.70	N/A	N/A	N/A	0.70	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Seal Rock 1	1.40	0.80	0.80	0.20	0.20	0.20	0.20	0.20	0.50	0.50	1.00	1.00	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

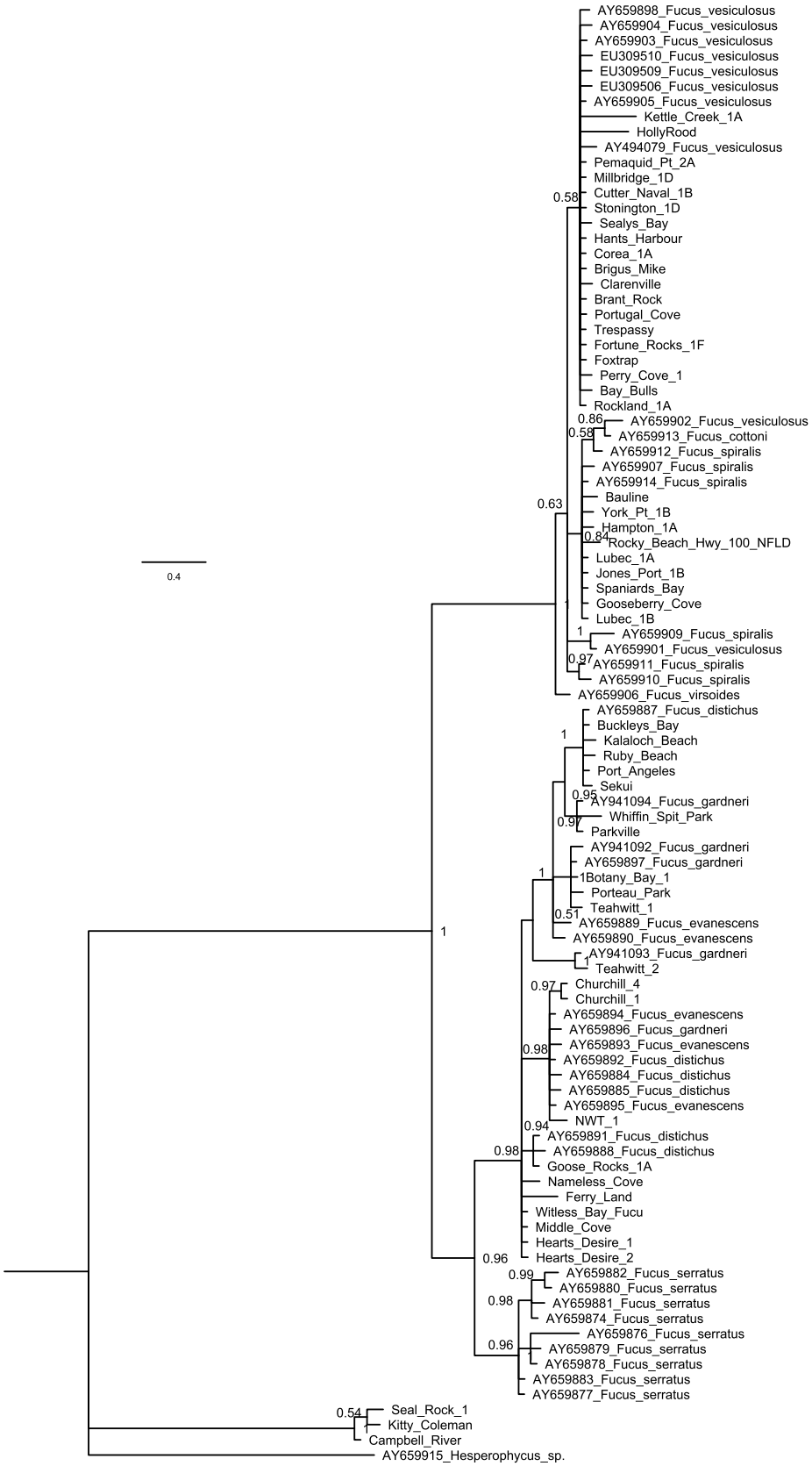
Appendix B

Name$	BRCHDISTM3	BRCHDISTM4	BRCHDISTM5	RECWDM1	RECWDM2	RECWDM3	RECWDM4	RECWDM5	RECLGM1	RECLGM2	RECLGM3	RECLGM4	RECLGM5	VESDISTBT2M1	VESDISTBT2M2	VESDISTBT2M3	VESDISTBT2M4	VESDISTBT2M5	VESDISTBTPRSM1	VESDISTBTPRSM2	VESDISTBTPRSM3	VESDISTBTPRSM4	VESDISTBTPRSM5
Sealy's Cove 1A	6.40	1.80	1.70	0.50	0.40	0.40	0.60	0.70	1.10	1.00	0.50	0.70	0.70	0.80	0.80	0.90	0.70	0.70	0.20	0.20	0.40	0.30	0.20
Sealy's Cove 1B	5.10	3.30	4.90	0.40	0.40	0.30	0.50	0.30	0.70	0.70	0.90	0.40	0.50	0.60	0.30	0.20	0.90	0.80	0.30	0.30	0.20	0.50	0.40
Sekui 1	2.30	2.80	3.00	0.60	0.80	0.90	0.60	1.50	0.60	0.90	0.80	0.90	1.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Singing Sands	3.60	4.50	3.40	0.50	0.60	0.40	0.30	0.20	0.90	1.50	1.00	1.20	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Stonington 1B	2.00	2.90	2.20	0.50	0.40	0.40	0.40	0.30	0.80	0.80	0.70	0.70	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Stonington 1C	1.60	1.30	2.00	0.30	0.30	0.20	0.40	0.30	0.70	0.50	0.20	0.30	0.30	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Stonington 1D	4.10	2.40	1.90	0.70	0.40	0.50	N/A	N/A	1.40	1.50	1.20	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Stonington 1E	1.60	3.90	3.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Stonington 1F	2.70	2.40	1.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Teahwitt 1	1.70	3.30	0.90	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiffin Spit Park 1	2.20	1.60	3.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiteway 1	1.00	1.80	2.40	0.40	0.40	0.50	0.30	0.60	0.50	0.50	0.80	0.60	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiteway 2A	2.00	1.00	1.30	0.30	0.40	0.20	0.30	0.20	0.50	0.50	1.10	1.10	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiteway 2B	2.00	1.40	1.00	0.70	0.50	0.30	0.20	0.30	0.70	0.50	0.60	0.60	0.60	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiteway 2C	1.00	1.60	1.50	0.40	0.40	0.60	0.40	0.40	0.70	0.70	0.50	0.50	1.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Whiteway 3	2.00	2.60	1.40	0.90	0.80	0.70	0.70	1.00	7.00	5.50	4.60	3.40	3.80	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
York Point 1B	3.60	1.10	1.40	0.40	N/A	N/A	N/A	N/A	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
York Point 1C	4.30	2.70	1.30	0.30	0.20	N/A	N/A	N/A	0.40	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
York Point 1D	1.40	2.70	N/A	0.20	N/A	N/A	N/A	N/A	0.70	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
York Point 1E	0.40	1.50	3.00	0.40	0.40	0.30	0.30	0.20	0.60	0.40	0.30	0.40	0.40	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
York Point 1F	5.70	2.50	1.70	0.30	0.30	0.30	0.20	N/A	0.50	0.40	0.50	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Appendix C


0.9
EU309510_Fucus_vesiculosus
EU309509_Fucus_vesiculosus
EU309506_Fucus_vesiculosus
AY659905_Fucus_vesiculosus
AY659909_Fucus_spiralis
AY659901_Fucus_vesiculosus
AY659911_Fucus_spiralis
AY659910_Fucus_spiralis
Kettle_Creek_1A
Bauline
Rocky_Beach_Hwy_100_NFLD
Spaniards_Bay
AY659902_Fucus_vesiculosus
AY659907_Fucus_spiralis
AY659914_Fucus_spiralis
AY659913_Fucus_cottoni
AY659912_Fucus_spiralis
AY659906_Fucus_virsoides
AY659898_Fucus_vesiculosus
AY659904_Fucus_vesiculosus
AY659903_Fucus_vesiculosus
York_Pt_1B
HollyRood
Hampton_1A
AY494079_Fucus_vesiculosus
Pemaquid_Pt_2A
Lubec_1A
Jones_Port_1B
Millbridge_1D
Cutler_Naval_1B
Stonington_1D
Sealys_Bay
Hants_Harbour
Corea_1A
Brigus_Mike
Clarenville
Brant_Rock
Portugal_Cove
Trespassy
Fortune_Rocks_1F
Gooseberry_Cove
Foxtrap
Perry_Cove_1
Bay_Bulls
Lubec_1B
Rockland_1A
Churchill_1
NWT_1
AY659894_Fucus_evanescens
AY659896_Fucus_gardneri
AY659893_Fucus_evanescens
AY659892_Fucus_distichus
AY659884_Fucus_distichus
AY659885_Fucus_distichus
AY659895_Fucus_evanescens
Churchill_4
Ferry_Land
Porteau_Park
Teahwitt_1
AY941092_Fucus_gardneri
AY659897_Fucus_gardneri
AY941093_Fucus_gardneri
Teahwitt_2
AY659887_Fucus_distichus
Buckleys_Bay
Kalaloch_Beach
Ruby_Beach
AY659891_Fucus_distichus
AY659888_Fucus_distichus
AY659889_Fucus_evanescens
AY659890_Fucus_evanescens
AY941094_Fucus_gardneri
Botany_Bay_1
Nameless_Cove
Witless_Bay_Fucu
Middle_Cove
Goose_Rocks_1A
Hearts_Desire_1
Port_Angeles_1
Hearts_Desire_2
Whiffin_Spit_Park
Parkville
AY659882_Fucus_serratus
AY659880_Fucus_serratus
AY659881_Fucus_serratus
AY659874_Fucus_serratus
AY659879_Fucus_serratus
AY659878_Fucus_serratus
AY659883_Fucus_serratus
AY659877_Fucus_serratus
AY659876_Fucus_serratus
Sekui
Seal_Rock_1
Kitty_Coleman
Campbell_River
AY659915_Hesperophycus_sp.
100
55
83
56
55
89
100
58
57
55
89
54
62
66
99
77
78
63
100
61
50
86
57
95
62
100

Appendix D


AY659898_Fucus_vesiculosus
AY659904_Fucus_vesiculosus
AY659903_Fucus_vesiculosus
EU309510_Fucus_vesiculosus
EU309509_Fucus_vesiculosus
EU309506_Fucus_vesiculosus
AY659905_Fucus_vesiculosus
Kettle_Creek_1A
HollyRood
AY494079_Fucus_vesiculosus
Pemaquid_Pt_2A
Millbridge_1D
Cutter_Naval_1B
Stonington_1D
Sealys_Bay
Hants_Harbour
Corea_1A
Brigus_Mike
Clarenville
Brant_Rock
Portugal_Cove
Trespassy
Fortune_Rocks_1F
Foxtrap
Perry_Cove_1
Bay_Bulls
Rockland_1A
AY659902_Fucus_vesiculosus
AY659913_Fucus_cottoni
AY659912_Fucus_spiralis
AY659907_Fucus_spiralis
AY659914_Fucus_spiralis
Bauline
York_Pt_1B
Hampton_1A
Rocky_Beach_Hwy_100_NFLD
Lubec_1A
Jones_Port_1B
Spaniards_Bay
Gooseberry_Cove
Lubec_1B
AY659909_Fucus_spiralis
AY659901_Fucus_vesiculosus
AY659911_Fucus_spiralis
AY659910_Fucus_spiralis
AY659906_Fucus_virsoides
AY659887_Fucus_distichus
Buckleys_Bay
Kalaloch_Beach
Ruby_Beach
Port_Angeles
Sekui
AY941094_Fucus_gardneri
Whiffin_Spit_Park
Parkville
AY941092_Fucus_gardneri
AY659897_Fucus_gardneri
Botany_Bay_1
Porteau_Park
Teahwitt_1
AY659889_Fucus_evanescens
AY659890_Fucus_evanescens
AY941093_Fucus_gardneri
Teahwitt_2
Churchill_4
Churchill_1
AY659894_Fucus_evanescens
AY659896_Fucus_gardneri
AY659893_Fucus_evanescens
AY659892_Fucus_distichus
AY659884_Fucus_distichus
AY659885_Fucus_distichus
AY659895_Fucus_evanescens
NWT_1
AY659891_Fucus_distichus
AY659888_Fucus_distichus
Goose_Rocks_1A
Nameless_Cove
Ferry_Land
Witless_Bay_Fucu
Middle_Cove
Hearts_Desire_1
Hearts_Desire_2
AY659882_Fucus_serratus
AY659880_Fucus_serratus
AY659881_Fucus_serratus
AY659874_Fucus_serratus
AY659876_Fucus_serratus
AY659879_Fucus_serratus
AY659878_Fucus_serratus
AY659883_Fucus_serratus
AY659877_Fucus_serratus
Seal_Rock_1
Kitty_Coleman
Campbell_River
AY659915_Hesperophycus_sp.
0.4