

Systematics of the *Sphagnum recurvum* Complex:

Morphological Variation, Hybridization and the Delineation of Intermediate
Taxa

by

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Thesis submitted in partial fulfillment of
the requirements for the degree of
Master of Science in the Department of
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ABSTRACT

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Abstract

The delineation of closely related plant species is difficult, as finding a discrete and distinct set of characters can be problematic in taxa that exhibit extreme morphological variability. Such difficulties arise in the genus *Sphagnum* because of its diversity and variability, as well as its propensity to hybridize. This study asks (1) do the five Norwegian morphospecies of the *Sphagnum recurvum* complex, a group of closely related and taxonomically controversial boreal species, correspond to genetically distinct entities? And (2) are morphologically intermediate plants a result of phenotypic plasticity or interspecific hybridization? Using “next generation” RADseq-based phylogenetic analyses, three highly distinct clades emerged, corresponding to *S. angustifolium*, *S. flexuosum*, and a clade containing *S. fallax*, *S. isoviitae* and *S. brevifolium*. This result suggests the boundaries of *S. fallax* should be expanded. The lack of genetic differentiation among the members of the *S. fallax* clade and the clear separation of the three clades was supported by DAPC multivariate clustering and a novel analysis comparing the lineages revealed by individual loci. These analyses also tested for genetic admixture within plant samples. However, there were no intermediate samples between the genetic clusters discerned from any of the analyses, and the phylogenetic tree demonstrates strong clade cohesion. This lack of genetic intermediates suggests that the morphological variation observed in these populations is likely to be due to intraspecific genetic variation or phenotypic plasticity. A revised key and diagnoses for Norwegian species in the *Sphagnum recurvum* complex is provided to facilitate identification by collectors.

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1. Introduction

Traditionally, systematics and taxonomy have relied solely on morphology to delineate and classify species. For organisms that exhibit high levels of morphological variation, these classical methods often fail to adequately represent species diversity because of morphologically cryptic speciation and phenotypic plasticity that can obscure the boundaries of phylogenetically meaningful units. A group that has caused particular controversy is the extremely variable peat mosses – *Sphagnum* L.

Sphagnum L. is one of the largest genera of bryophytes, containing some 200-400 species. *Sphagnum* has a disproportionate impact on global climate and biogeochemistry through the creation and maintenance of *Sphagnum*-dominated peatlands. Boreal peatlands currently act as carbon sinks because of low decomposition rates that are facilitated by plant tissue characters and habitat features (Rydin et al., 2013). *Sphagnum* includes six well-supported monophyletic groups, classified as subgenera (Shaw et al., 2010b: *Acutifolia*, *Sphagnum*, *Rigida*, *Subsecunda*, *Squarrosa* and *Cuspidata*). The Subgenus *Cuspidata* (Shaw et al., 2010b) includes the *S. recurvum* complex, which contains some of the most taxonomically difficult species of *Sphagnum* (Isoviita, 1966; Flatberg, 1992a; Stenøien et al., 1997). *Sphagnum angustifolium* (Russow) C. E. O. Jensen and *Sphagnum fallax* (Klinggr.) Klinggr are the two most common, widespread, and well-studied species in the *S. recurvum* complex. *Sphagnum fallax* is currently the focus of a genome sequencing initiative and, therefore, understanding its relationship to closely related species is important for future comparative studies. The *S. recurvum* complex contains closely related species that often occur in sympatry because of their similar habitat

preferences, with at least one documented case of gene flow between two putative species in the complex (Sastad et al., 1999).

Most *S. recurvum* complex species occur in northern hemisphere bogs and fens, and their impact on these ecosystems makes them important to peatland ecology and climate modeling. Therefore, confidence that morphological identifications reflect the phylogenetic relationships of species is important, as it allows for the accurate tracking of changes in regional habitat distribution and ecosystems.

Though the divergence of the Class Sphagnopsida took place approximately 380 million years ago and it is sister to almost all other mosses, the diversification of extant peat mosses is thought to have occurred during and subsequent to Miocene cooling (Newton et al., 2009; Shaw et al., 2010a). Thus, as species have diverged comparatively recently, reproductive barriers are likely to be porous (Lexer and Widmer, 2008). The high degree of plasticity and the small number of key morphological characters make delineation of species difficult; there is often discordance between species boundaries inferred from morphological versus molecular methods (Sastad, 1999; Shaw, 2001). In addition, *Sphagnum* divides the peatland landscape into small microniches, and competition can drive convergent evolution of traits adapted to these habits (Rydin et al., 2013). The issues underlying disagreements in species delineation may reflect rapid species divergence, morphologically cryptic speciation, phenotypic plasticity, hybridization, and allopolyploidization (Karlin et al., 2008; Shaw et al., 2008; Shaw et al., 2010a), or various combinations of these factors. Hybridization between species within subgenera of *Sphagnum* has been documented in the subgenera *Acutifolia*, *Sphagnum*, and *Cuspidata*, as well as between subgenera (Såstad et al., 2001; Cronberg and Natcheva, 2002; Karlin, 2014).

Interspecific hybridization can give rise to allopolyploid gametophytes and, potentially, new hybrid species (Såstad et al., 2001; Cronberg et al., 2002; Shaw et al., 2005; Karlin et al., 2010; Ricca and Shaw, 2010). However, there is disagreement about how significant the level of hybridization is, and how it contributes to taxonomic problems at the species level (Natcheva and Cronberg, 2004).

The first species described in the *S. recurvum* complex was *S. recurvum* P. Beauv, from South Carolina (Beauvois, 1805). Subsequent work on the complex was focused in Europe with several taxonomic descriptions in the late 1800s (Isoviita, 1966). *Sphagnum flexuosum* Dozy and Molkenboer was described in 1851, while *S. fallax* was described in 1880, *S. angustifolium* in 1891 and *S. balticum* (Russow) C. E. O. Jensen in 1890 (Isoviita, 1966). *Sphagnum brevifolium* (Lindb. ex Braithw.) Röhl was described in 1910, but the current description was amended by Flatberg (1992a). *Sphagnum balticum* was not considered part of the *S. recurvum* complex until recently, and its place in relation to the other members of the complex is still poorly resolved (Sastad et al., 1999a). Recently in Europe, *S. isoviitae* Flatberg was described as an additional member of the complex (Flatberg, 1992c). More recently, however, bryophyte taxonomists often group *S. brevifolium* and *S. isoviitae* under *S. fallax* (sensu Isoviita (1966), *Sphagnum recurvum* var. *mucronatum* (Russ.) Warnst. (sensu Daniels and Eddy (1985) or *S. recurvum* var. *brevifolium* (Braithw.) Warnst. (Crum, 1984). Taxonomic treatments of the *S. recurvum* complex has been inconsistent, largely depending upon whether taxonomists take a “lumping” or “splitting” approach to species delineation. One influential North American taxonomist of the early 20th century, A. L. Andrews, was a proponent of fewer species; in fact, Andrews recognized all of the morphological variation in this complex as a single polymorphic species, *S.*

recurvum (e.g., Andrews 1913). As a result, variation in the *S. recurvum* complex in North America was not further explored in the ensuing decades (Isoviita, 1966). Recent taxonomic treatments suggest that there is a greater degree of phenotypic variation, and therefore taxonomic ambiguity, on the North American continent than in northern Europe (Crum, 1984, Anderson, 1990).

Species in the *S. recurvum* complex species are widespread, with *S. angustifolium* having a reportedly Holarctic distribution. Several others are widespread around the northern hemisphere, across much of Asia, Europe, and North America. However, the status of taxa in North America requires further study. In addition to *S. recurvum* s. s., three species are considered exclusive to North America: *S. pacificum* Flatberg (Flatberg, 1989) from the Pacific Northwest, *S. rubroflexuosum* R. E. Andrus from Pennsylvania and Maryland (Andrus, 1988), and *S. splendens* Maass from Quebec (Maass, 1967). Little is known about the last two species as few collections have been made. Currently, taxonomists recognize between one and ten species in the *S. recurvum* complex, but these can be difficult to distinguish morphologically because of genetic and phenotypic variation (Daniels et al., 1985; Flatberg, 1992a; Crum, 1997; McQueen and Andrus, 2007).

Key characters for distinguishing species in the *S. recurvum* complex include spore color, branch leaf shape, leaf arrangement on branches (ranked, spiral, unranked), patterns of branches in the capitulum (clustered, curved, etc.), the arrangement and number of pores in the hyaline cells of branch leaves, the location and size of the chlorophyllous cells relative to the hyaline cells as seen in leaf cross sections, and stem leaf shapes (Daniels et al., 1985) (Table 1, Table S1). A major division in the complex is drawn between the brown spored species, including

S. angustifolium, *S. recurvum*, *S. flexuosum* and *S. rubroflexuosum*, and the yellow spored species, including *S. balticum*, *S. pacificum*, *S. fallax*, *S. isoviitae* and *S. brevifolium* (Maass, 1967; Andrus, 1988; Flatberg, 1989; Sastad et al., 1999a). Branch leaf cross sections vary within the group, as *S. flexuosum* has chlorophyllous cells that are widely exposed on the convex surface of the leaf, unlike the more enclosed triangular chlorophyllous cells of *S. fallax*, *S. isoviitae* and *S. brevifolium* (McQueen et al., 2007). Variation in stem leaf shape is a major defining feature differentiating species. *Sphagnum angustifolium* has small, equilaterally triangular leaves with obtuse tips. The larger leaves of *S. flexuosum* are more lingulate with similarly obtuse apices, while *S. balticum* has highly concave stem leaves of a similar but larger size. *Sphagnum angustifolium*, *S. flexuosum* and *S. balticum* have stem leaves that may all be erose at the apices. *Sphagnum fallax*, *S. isoviitae* and *S. brevifolium*, on the other hand, have mostly isosceles triangular-ovate leaves with varying acute apices. A summary of traits useful for distinguishing taxa in the *S. recurvum* complex is provided in Table 1 and Table S1.

Previous studies have documented a high degree of morphological variation due to environmental factors (Sastad, 1999) resulting in some discordance between morphological classifications and underlying genetic patterns. Szurdoki et al. (2014) found that approximately 8%-13% of their specimens identified by morphotype did not match groups based on microsatellite variation. They concluded that these conflicts are unlikely to be due to hybridization. Flatberg (1988) reported a population of gametophytes which appeared to share the characters of *S. angustifolium* and *S. pulchrum*, another member of the *S. recurvum* complex, and suggested hybridization may have been the cause of their intermediate morphology. Sastad

et al. (1999a) reported that *S. fallax* and *S. isoviitae* were genetically indistinguishable when living in sympatry.

Scandinavia is perhaps the most diverse region for species in the *S. recurvum* complex, where six of ten putative species occur (Flatberg, 2013). In addition, the boreal environment appears to lead to well defined and constant morphology compared to variability present in warmer, presumably less optimal southern climates. This makes Scandinavia an ideal study area to examine the genetic nature of the morphologically defined species, as they live in sympatry but remain characteristically distinct (Flatberg, personal communication).

The *S. fallax* genome will soon be available (Weston & Shaw, unpublished). This will facilitate study of the evolution, ecology, and phenotypic traits of this genus of important ecosystem engineers. Delineating *S. fallax* morphologically and genetically, and understanding its relationships to closely related species is thus of broad concern. We apply a next generation sequencing approach, RADseq (Davey and Blaxter, 2010), to probe the relationships between closely related morphological forms, and to examine the concordance of morphological and genetic patterns. Specifically, the goals are: 1) to test whether morphospecies recognized in *The Peat mosses of Norway* (Flatberg, 2013) correspond to monophyletic phylogenetic groups, and 2) to assess whether morphologically intermediate plants reflect a) phenotypic plasticity or b) interspecific hybridization.

Testing the two alternative hypotheses for morphological intermediacy of some plants was the primary goal of this study. By identifying individuals where the morphospecies appeared to conflict with the RADseq based phylogenetic analysis, we can assess whether the molecular data nevertheless suggests an unambiguous relationship with just one species. This may suggest

intraspecific genetic variation, phenotypic plasticity, or traces of hybridization as different RADSeq loci will indicate conflicting relationships to more than one species. These hypotheses were compared using multivariate clustering of samples based on the RADSeq data to assess genetic intermediacy, and also the use a novel approach that determines relationships based on analyses of individual loci to identify genetic (phylogenetic) admixture.

2. Materials and Methods

2.1 Taxon Sampling

Eighty-nine samples representing five morphospecies in the *S. recurvum* species complex were collected in August 2013 in Norway. Samples were collected from eleven sites in the regions of Sør- and Nord-Trøndelag, from 63°14'45.78"N to 64°39'50.58"N (Fig. 1). This included 24 *S. angustifolium* samples, 16 *S. flexuosum* samples, 23 *S. fallax* samples, 11 *S. brevifolium* samples and 15 *S. isoviitae* samples.

Plants were initially identified in the field by A. Garrett and K. I. Flatberg. The individual gametophyte sampled for genetic analysis was placed in a separate packet, and its morphological identity was confirmed microscopically by A. Garrett. Voucher specimens are archived in the Duke University herbarium (DUKE). Specimen information and voucher locations are provided in Table S2.

Five *S. balticum* individuals were sampled with the intent of providing the outgroup for this study; however, *S. balticum* was found to be non-monophyletic along the *S. fallax* and *S. angustifolium* branches, and due to the small number of samples, no conclusions could be made about the genetic relationship of *S. balticum* to species in the focal group. The *S. balticum* samples were excluded from the final analysis.

2.2 DNA isolation, amplification and sequencing

Genomic DNA was extracted from dried samples using tissue from the capitulum of the gametophyte, each with a mass of approximately 100mg. Extractions followed the CTAB protocol outlined in Shaw et al. (2003).

Genomic DNA was visualized using a 2% agarose gel to check for the success of extraction. DNA concentration was measured using a Qubit[®] 2.0 Fluorometer (Life Technologies), ensuring the sample DNA concentration was 20-100 ng/uL. Following the protocol described by Parchman et al. (2012), the restriction enzymes Mse1 and EcoR1 were added to the sample as part of a 3 uL master mix (Table S3) and digestion of 6 ul of the genomic DNA sample was accomplished over a period of eight hours at 37 °C. The sticky-ended restriction cut sites act as templates for the ligation of the oligonucleotide adaptors EcoR1 and Mse1, which are double stranded adaptor sequences containing Illumina adaptors, primer sequences, and a unique eight base pair barcode for the identification of read origin. Mse1 was added to the digested sample as part of a 1.4 uL master mix (Table S4), followed by the addition of 1uL of EcoR1. Ligation proceeded over a period of one hour at 23 °C. Using Illumina PCR primers (Illp1 and Illp2), amplification was carried out in two separate reactions per restriction-ligation product with a thermal cycler profile of 98°C for 30s; 30 cycles of: 98°C for 20s, 60°C for 30s, 72°C for 40s, followed by a final extension at 72°C for 10 min.; The two separate reactions were then combined (Table S5). Gel purification was done to select fragments of the desired size range by running the PCR product on a 2% agarose gel with a 100bp and 50 bp ladder, and the region of 300-400bp was extracted and purified using a gel purification kit. A Qubit[®] 2.0 Fluorometer was then used to measure the DNA concentration of the purified gel. Eighty-nine samples with a final concentration of 25-100

uL/ng of PCR amplification product were sequenced using an Illumina HiSeq 2000 at the Genome Sequencing Shared resource operated by the Duke Center for Genomic and Computational Biology (<https://oit.duke.edu/comp-print/research/>).

2.3 RAD-Seq

Once the raw RAD-Seq data had been generated, the software pipeline pyRAD (Eaton and Ree, 2013; Eaton, 2014) was used to discover SNPs. One mismatch in barcodes was allowed during data de-multiplexing, and the barcodes and restriction sites were trimmed from all sequences. A quality score of less than 20 for nucleotide base calls caused those bases to be replaced with N's, and sequences with more than four N's were discarded. pyRAD clusters sequences first by individual then sequences of a certain similarity are clustered into "stacks" using the program USEARCH (Edgar, 2010) and aligned using MUSCLE (Edgar, 2004). Sequences were clustered using a threshold of 80% sequence similarity. Using the aligned clusters, error rate and heterozygosity were estimated then used to make the consensus base calls. These consensus sequences were then clustered using 80% sequence similarity across individuals. This alignment was used to establish locus homology across individuals using USEARCH and MUSCLE, discarding any sequences that were heterozygous at more than three sites. Because all of the species have haploid gametophytes, heterozygosity within individuals was not permitted. Three samples from the 89 were discarded due to lack of coverage or extreme sequence variation suggesting contamination, leaving 86 for all subsequent analyses.

The result was three final datasets differing in the selection of loci for inclusion: i) all loci regardless of how many samples in which they were present, ii) only loci present in a minimum

of four samples, meaning that the loci with lowest coverage were excluded, and iii) only loci that were present in a minimum of 70 samples, meaning that all loci included in the final dataset had relatively complete coverage in all samples.

2.4 Phylogenetic analyses

RAxML v. 8.1.11 (Stamatakis, 2014) was used to estimate phylogenetic relationships among the sequences under maximum likelihood (ML). All trees are unrooted. The ML tree was estimated using random starting trees, the “-f a” rapid bootstrap analysis and best scoring ML tree search, and the GTRCAT nucleotide substitution model. The rapid hill-climbing search algorithm was used to estimate the best ML tree using 100 searches and 100 bootstrap replicates to determine support for branches. These analyses were carried out using the Duke Compute Cluster.

2.5 Clustering analysis

The R v. 3.0.3 package “adegenet” (Jombart, 2008) was used to assess patterns of genetic structure and admixture. The separation of genetic groups was evaluated using the 86 sample RAD-seq data set and a discriminant analysis of principal components (DAPC). DAPC was chosen over a principal component analysis (PCA) or a multidimensional scaling analysis because it can optimize variation between groups, while minimizing variation within groups. A DAPC analysis is a multivariate analysis that first uses a PCA to transform data into uncorrelated components, which are then analysed using a linear discriminant method. The clustering algorithm K-means uses the find.clusters function, which tests for the number of groups by maximizing variation between groups to identify the lowest Bayesian Information Criterion (BIC). This is then used to

ascertain the optimal number of groups. For this test, all principal components (PC) were retained. These clusters were then described using DAPC to calculate membership probabilities for each sample for each group. Fifty-five PCs were kept, and two linear discriminants as described by eigenvalues were also kept. We reasoned that if morphologically intermediate samples reflect hybridity and genetic admixture, these samples would also appear intermediate between genetic clusters resolved by the DAPC analysis.

2.6 Signal source estimation

For individuals with intermediate morphology, current or historical hybridization can be indicated through loci with conflicting phylogenetic histories. If varying phenotype is due to plasticity, all loci will exhibit a phylogenetic history that should match the phylogeny of the sample based on combined loci data.

After the initial phylogenetic analysis, the status of species cohesion was assessed with the expectation that individuals identified as the same species would “find each other” in the analysis. Individuals whose placement was inconsistent with morphologically-based taxonomy were further scrutinized on a locus-by-locus basis. PAUP* version 4a145 (Swofford, 2003; http://people.sc.fsu.edu/~dswofford/paup_test/) was used to generate a neighbor-joining tree and pairwise distance matrix using the HKY model of nucleotide substitution (Hasegawa, 1985); for each locus in which an individual of interest was present. Those individuals that had the shortest pairwise distance from the target sample were awarded the minimum evolution score of the neighbor-joining tree scaled by the number of individuals representing that locus. This is an approximation of the substitution rate, and uninformative loci in which most or all individuals

shared the shortest pairwise distance to the target (e.g., monomorphic loci) were downweighted. Scores for each non-target individual were summed across all loci, then scaled by the number of loci shared with the individual of interest. Finally, individuals were ranked according to score, with the expectation that the ranking of each individual should correspond to their relative position in the total evidence tree. A matrix of minimum evolution scores was then created and, using R R v. 3.0.3 package “gplot” (Warnes et al., 2009) function heatmap.2, a heatmap was generated that then had the concatenated ML tree mapped onto it. We used data set ii, which includes all loci represented in at least four samples, for these analyses.

3. Results

3.1 Morphological taxa assignment

The initial field identifications of most samples were supported by microscopic assessment – most of the samples where the taxon was reassigned were those growing in poor (few nutrients or little water) environments that made their macroscopic features difficult to distinguish. The majority of the samples with ambiguous characters were from poor habitats. Stem leaf characters for *S. angustifolium* were relatively unambiguous, mostly due to their short lengths and obtuse apices, except in habitats where they were somewhat more acute. Samples identified as *S. flexuosum* had the clearest character suite. Morphological characters used to distinguish *S. fallax*, *S. isoviitae* and *S. brevifolium* at the microscopic level were occasionally decoupled from the characters used for identification at the macroscopic level (mostly capitulum shape), leading to difficulties assigning them unambiguously to morphospecies. Additionally, stem leaf characters for these three taxa were widely variable and graded into each other.

3.2 Analysis of RADseq data

On average, 1,662,411 reads per sample were returned from the Illumina RAD sequencing. This overall value was reduced to an average of 41,406 locus-clusters with coverage greater than the required minimum of nine reads after filtering and clustering. This resulted in a mean coverage depth of 24.3. Approximately 36,845 loci per sample were found with consensus sequences returned for each cluster. The data set containing all loci present in all 86 sampled individuals (dataset i) contains 149,748 loci in total and 311,954 phylogenetically informative

sites. The data set, comprised of loci present in at least 70 samples, contained 8,693 loci and 34,449 phylogenetically informative sites. This constitutes 5.7% of the full dataset. The dataset used for primary analysis for the rest of this study (see below), created with the requirement of all loci being present in at least four samples, contained 113,723 loci and 309,064 phylogenetically informative sites (Table 2).

3.3 Phylogenetic analysis

The four-sample threshold dataset ii resolved three clear clades, each with 100% support from ML bootstrapping (Fig. 2). All samples identified as *S. angustifolium* and *S. flexuosum* were assigned to their own monophyletic groups that share a common ancestor. Because the tree is unrooted, it is not possible to assign sister group relationships.

The third clade contained all three of the yellow spore species in a single clade: *S. fallax*, *S. isoviitae* and *S. brevifolium*. Within this clade, no additional structure that corresponds to the three morphospecies was resolved (Fig. 2).

Maximum likelihood trees constructed using the minimum 70 sample threshold dataset and the four-sample threshold dataset resolved the identical three clades with 100% support. They differed only in that within the *S. fallax* and *S. flexuosum* clades, different samples were resolved as first-diverging (Figs. 1, S1). We therefore used the larger data set – which included all loci represented in at least four samples – for subsequent analyses to assess phenotypic plasticity versus possibility of hybridization to explain morphological intermediacy.

3.4 Cluster analysis

The lowest identified K-mean was a BIC value of $K = 3$; i.e., three genetic clusters were resolved (BIC = 735.65). All samples identified as *S. flexuosum* samples were included in Group 1, all *S. angustifolium* samples in Group 3, and all samples of *S. isoviitae*, *S. brevifolium* and *S. fallax* in Group 2 (Fig. 3).

There was considerable separation between the three clusters in the DAPC analysis along both discriminant factor axes (Fig. 4). The optimal number of PC's retained for the DAPC accounted for 80.5% of the overall variation, and the first discriminant factor accounted for 88.5% of the variation in the discriminant analysis. Group 2, which contains all *S. angustifolium* samples, and Group 3, which contains all *S. fallax*, *S. isoviitae*, and *S. brevifolium* samples, are relatively close on the second discriminant factor axis (Fig. 4). All samples that fall outside the main clusters on these two groups had low sequencing coverage.

3.5 Signal source estimation

Minimum evolution scores indicate that species cohesion is very strong – the highest scores for each sample were always assigned to the members of the clade resolved by the concatenated data (Fig. 5). Within a clade, close relatives did not consistently receive a higher score, however.

Some individuals had poor sequence coverage, and that was greatly reflected in their overall scores – these individuals are indicated by the consistently light colored rows and

columns in Fig. 5. Regardless of coverage, however, these samples still shared the best scores with members of the same major clade.

4. Discussion

The traditional method of delineating species is to present a hypothesis that outlines an exclusive set of discontinuous morphological traits (Wheeler, 2004). However, finding discrete and distinctive character sets can be difficult in taxa that exhibit extensive morphological variability. Such issues have plagued plant taxonomy in particular; as sessile organisms, plasticity is a necessary survival strategy for many plant taxa (Schlichting, 1986; Sultan, 1987).

Sphagnum has a very high dispersal capacity because of its small spores, and many species have large multi-continent ranges. This, along with the fact that many closely related *Sphagnum* species are distinguished by quantitative morphological differences, exacerbates problems related to understanding species limits. *Sphagnum* has demonstrated extensive phenotypic plasticity in lab cultivation and in field observation (Stenøien et al., 1997). Hybridization is also a source of morphological variation, either because polyploid plants may have greater potential for plasticity (Comai, 2005), or due to a mingling of their parents diagnostic characters (Arnold, 1992). Rieseberg et al. (1993a) found that intermediate character states are not the most common outcome of hybridization, but it is still a source of melding and mixing of parental traits. Hybridization is widespread in vascular plants (Rieseberg and Wendel, 1993b; Ellstrand et al., 1996), but has not historically been considered a major feature in bryology, and as such has only been examined as an explanation for taxonomic problems with the more recent availability of molecular tools (Wyatt et al., 1992; Cronberg, 1996; Shaw, 1998; Wyatt and Odrzykoski, 1998). *Sphagnum* has a number of key characters that are useful in diagnosing species (Table 1) but distinguishing character states is often challenging and character variability may overlap between species. Such morphological ambiguity is reflected in the controversial nature of *Sphagnum* taxonomy.

The area sampled for this study, western Norway, could be considered an ideal habitat for *Sphagnum* – moist, boreal and moderate summer temperatures. There, *Sphagnum* exhibits fewer morphological aberrations, and morphotypes remain more distinct from each other than among individuals growing in less “optimal” regions. It is, therefore, an ideal location to explore the genotypic nature of the putative species and the validity of species erected on morphological grounds.

Of the samples used in this study, most were indeed morphologically distinct, and any initial difficulties could be resolved with microscopic examination. Samples assigned to *S. fallax*, *S. brevifolium* and *S. isoviitae* (henceforth called the *S. fallax* clade) were more difficult to distinguish from each other because of overlapping morphology in the three species, but each syndrome could be identified with reasonable confidence. Using characters such as relative acuteness of stem leaves was comparatively subjective relative to the more distinctive stem leaves of *S. angustifolium* and *S. flexuosum*. During the course of this study, the set of characters used to identify *S. fallax* clade samples was eventually reduced to prevent confusion caused by among-character conflicts – by focusing on a small number of traits, names could be assigned to samples which would otherwise be ambiguous. The range of morphology present within the *S. fallax* clade is extreme.

This study indicates that *S. fallax*, *S. flexuosum* and *S. angustifolium* are genetically distinct taxa, thus agreeing with the results of studies using isozymes/RAPDs (Sastad et al., 1999a) and microsatellites (Szurdoki et al., 2014). The current study clarifies relationships among these taxa, providing better resolution including long branches with well supported clades. The DAPC analyses indicate no genetic overlap among clusters. This greater resolution is likely due, in part, to the extensive dataset used, with 113,723 loci and 309,064 phylogenetically informative sites.

Three distinct clades emerge, with extremely deep splits between the clades compared to within clade differentiation. The long branches are also well supported using bootstraps, regardless of whether a highly inclusive or the more limited dataset is used. Within the clades, there is very little branch support - the only well supported relationships are those between sample pairs. None of the relationships resolved in the phylogenetic analyses correspond to geographic proximity of the sampling sites.

There is no evidence of hybridization or gene flow between the clades. The phylogenetic tree revealed little ambiguity, and the possible outliers at the base of those clades are not outliers in the signal source estimation test, demonstrating strong cohesion with the rest of their clade. The DAPC, designed to maximize between-group variations, revealed very distinct clusters with no membership ambiguity. Gene flow is one of the possible explanations for the overlapping morphology among some plants in the *S. recurvum* complex, along with plasticity. However, in this study, there were neither a) a large number of samples with difficult morphologies, nor b) any samples whose placement was ambiguous in the phylogenetic analyses. This result was contrary to our prediction: a clade of recently diverged species that live in close proximity reproducing via motile sperm in wet environments, would appear to be a good candidate for interspecific gene flow. Many allopolyploid or homoploid hybrid *Sphagnum* species have been identified (Sastad et al., 1999b; Sastad et al., 2000; S astad et al., 2001; Shaw et al., 2005; Flatberg et al., 2006; Ricca et al., 2010) but hybridization does not appear to be prominent in this group.

Interspecific gene flow may occur in less optimal or isolated regions such as eastern North America or southern Europe. Szurdoki et al. (2014) provided evidence for a small amount of genetic admixture using microsatellites with samples from southern Europe, a geographically and ecologically

marginal region for *Sphagnum*. North America also has a number of endemic and systematically unexamined species not represented in this study, including *S. recurvum*, *S. pacificum*, *S. rubroflexuosum*, and *S. splendens*. For a complete study, the five “species” included in this study, plus the other circumboreal species, *S. balticum*, and the North American endemics, should be sampled globally to assess whether habitat or geographic region affect inferences about species delineation and relationship.

The lack of resolution among the morphospecies *S. fallax*, *S. brevifolium* and *S. isoviitae* is clear. They are intermixed in a very well supported clade. This concurs with the results of Sastad et al. (1999a), though the total lack of structure and intermixture of species within the clade is even more evident here. The DAPC analysis fails to demonstrate any significant genetic differences among the taxa in the *S. fallax* clade as well, where only the three phylogenetic clades form tight and distinct groups (i.e., *S. angustifolium*, *S. flexuosum*, *S. fallax*). The only samples not clustered tightly in the DAPC are those samples with poor sequence coverage. The distance between the *S. angustifolium* and *S. fallax* groups along the second axis is closer than that of either species with the *S. flexuosum*, which is noteworthy as *S. flexuosum* and *S. angustifolium* share a spore color. Conversely, the minimum evolution scores between members of the *S. angustifolium* and *S. flexuosum* clade indicate they are close, though *S. angustifolium* still appears to be closer to *S. fallax* than is *S. flexuosum*. No conclusion can be made about sister groups relationships based on this study, but the question of whether spore color indicates monophyletic groups within the broader *S. recurvum* complex deserves further investigation.

Among the binomials, *S. fallax*, *S. isoviitae*, and *S. brevifolium*, *S. fallax* (Klinggr.) Klinggr has priority as the first species described. The recommendation as a result of this study is that the boundaries of *S. fallax* should be expanded to include *S. isoviitae* and *S. brevifolium*, thus also expanding the range of morphotypes encompassed by this polymorphic species. With the upcoming *S. fallax*

genome, investigation into the notably wide range of phenotypes in *S. fallax* should be pursued, possibly by investigating the linkage between genotypic and phenotypic variation, and habitat.

5. Taxonomic Treatment

We provide the key below to facilitate identification of the *Sphagnum* species examined in this study. We also provide a brief diagnosis for each species and photographs to illustrate two of the most important traits for distinguishing them: stem leaf shape and capitulum morphology.

5.1 Key to Norwegian species of the *S. recurvum* complex

1. Stem leaves <0.8 mm long, equilaterally triangular with length from base to tip approximately the same as width at leaf base. Stem leaves with a rounded apex, often broadly obtuse, sometimes erose or weakly acute. Capitulum with primarily straight branches; branches end with squared-off apices..... *S. angustifolium*

1. Stem leaves >0.8 mm, longer from apex to tip than width of leaf at the base. Capitulum with recurved branches; branches end with acute points..... **2**

2. Stem leaves lingulate-triangular to lingulate, with an obtuse and often eroded apex. Capitulum with an outer ring of recurved branches; branches ending with broadly pointed tip..... *S. flexuosum*

2. Stem leaves ovate triangular to lingulate triangular, with an acute to apiculate apex. Capitulum with primarily recurved branches; branches ending with broadly or narrowly acute *S. fallax*

5.1.1 *Sphagnum angustifolium* (Russow) C. E. O. Jensen

Stem leaf shape and size, <0.8 mm long and equilateral triangular, is relatively consistent, as is the rounded obtuse apex, though the degree of apical erosion is variable. Fig. 6a represents an “ideal” leaf, while Figs. 6b-f illustrate examples of commonly encountered variations. The branch fascicle provides an additional character – the spreading branches are sometimes as little as half the length of pendant branches. However, other species growing in dry habitats can sometimes also exhibit this trait. The branch leaf cross section has ovate-triangular chlorophyllous cells widely exposed on the convex surface and weakly enclosed on the concave surface *Sphagnum angustifolium* typically has a distinctive capitulum – weakly to strongly convex, with straight branches ending in blunt tips; the apical bud is not visible. The blunt branch tips may not be evident in actively growing plants. Inner capitulum branches have a distinctive form – basal leaves are tightly appressed while more apical leaves spread, creating a Vshape. Fig. 6g represents an “ideal” *S. angustifolium* capitulum. *Sphagnum angustifolium* is notable in the *S. recurvum* complex, and in *Sphagnum* as a whole, as being capable of growing in a wide variety of habitats. It is the only member of the *S. recurvum* complex commonly found growing in drier areas like hummocks, raised above the peatland water table, or in woodlands. The convex shape of the capitulum also varies with distance from the water table and sun exposure – shadier sites can produce flat topped *S. angustifolium*. Its habitat affinity and morphology seem to vary by region (e.g., the extremely convex and hummock-living *S. angustifolium* of Alaska, USA), suggesting there may be a genetic component to its variability.

5.1.2 *Sphagnum flexuosum* Dozy and Molkenboer

Stem leaf shape is long compared to other taxa in the *S. recurvum* complex, and it is more lingulate than triangular. The stem leaf apex is always blunt and typically with a wide erose section (Figs. 7a, b, c, e). Fig. 7a represents an ideal leaf. Fig. 7f is an example of a leaf with fibrils in the cells in the upper half of the leaves, an occasional occurrence in *S. flexuosum*, more so than in other members of the complex. The *S. flexuosum* capitulum characteristically has a tight central ball of short, straight, and mostly vertical branches around a hidden apical bud (Figs. 7g-i). The middle ring of capitulum branches is recurved, with a mildly recurved to straight ring of outer branches. In the field, the capitulum of *S. flexuosum* is often distinguishable by color; the ball of branches at the center of the capitulum usually has a gradient of color from yellow/green near the stem to pink/brown at the branch tips (Fig. 7g).

Overall, the plants is typically pale green or yellow, though darker morphotypes (Fig. 7i) are not unusual. The wide chlorophyllous cells as viewed in transverse section of the branch leaves provide a distinctive microscopic character, though not always consistent. Branch leaf cross section has triangular chlorophyllous cells as widely exposed on the convex surface as the hyaline cells are exposed on the concave. *Sphagnum flexuosum* is less common than *S. fallax* or *S. angustifolium*, and is often found growing as individual stems mixed into mats of other Sphagna in topographically intermediate areas and in lawns.

5.1.3 *Sphagnum fallax* (Klinggr.) Klinggr.

Sphagnum fallax stem leaf shape is relatively variable. Stem leaves can vary from triangular to ovate-triangular or lingulate-triangular. The most distinctive character is the acute to apiculate stem leaf apices (Fig. 8). However, even this is variable, as many individuals have notched or less acute leaf apices

(Figs. 8). The capitulum in *S. fallax* usually has mildly recurved branches around the sometimes visible apical bud, with more or less recurved outer rings of branches (Fig. 8). Plant color can vary from green to yellow, orange/brown and dark brown, and plant size is also highly variable (Figs. 8). Branch leaf cross sections have triangular to narrowly triangular chlorophyllous cells exposed on the convex surface and enclosed on the concave. *Sphagnum fallax* has fairly wide habitat tolerance, though more limited to wet locations than *S. angustifolium*. Many characters vary greatly with habitat or population, such as color, level of leaf acuteness, how ranked the branch leaves are, “tidiness” of the capitulum branches, etc., making it difficult to specify a character syndrome beyond stem leaf shape.

7. Figures

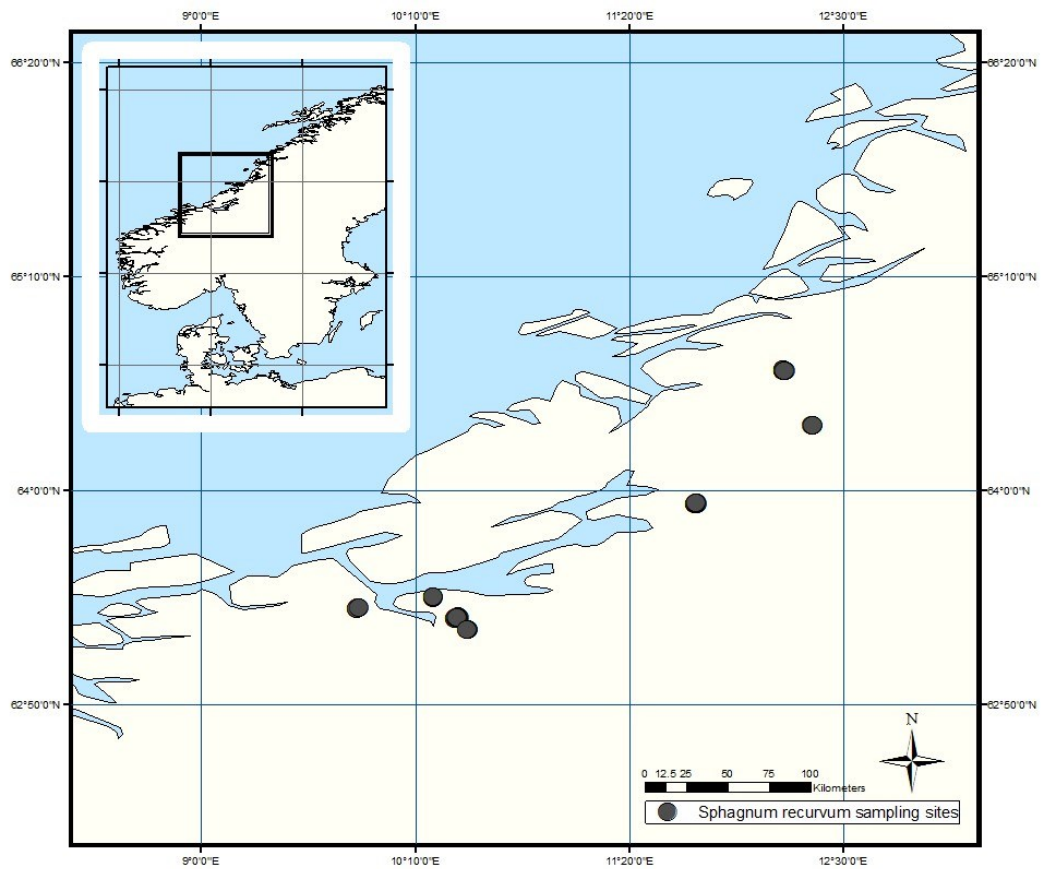


Figure 1: Map of sample locations in Norway – the inset map of Norway provides context for the closer view of the Trøndelag region. The green points indicate collection sites.

Table 1: Summary of morphological characters used for identification of the species in the *Sphagnum recurvum* complex used in this study.
 Compiled from: (Isoviita, 1966; Crum, 1984; Daniels et al., 1985; Flatberg, 1992c; Flatberg, 1992a; Laine et al., 2009)

	Spore color	Plant color	Capitulum shape	Branch number and arrangement	Leaves on spreading branches
<i>Sphagnum angustifolium</i>	Brown	Green with some orange	Branches straight throughout, squared/blunt appearance at tips. Overall shape is very pompom.	Two short spreading branches, 2 long pendant.	Non-ranked in most environments. Little recurve observed when growing in dry environments, more recurved in wet.
<i>Sphagnum flexuosum</i>	Brown	Green, usually some mix of color yellow/orange shades in the inner branches	Outer and inner branches distinct - tight, concentrically arranged branch cluster in center, a small bumpy ball. Furthest ring of inner ball has a twist in the branches.	Two spreading branches, 2 slightly longer pendant.	Non-ranked in all cases, more spirally arranged. Undulate when dry, mildly recurved.
<i>Sphagnum fallax</i>	Yellow	Green/white, some pink/brown, or a dark reddish-brown.	Inner branches are slightly curving to straight. Outer branches are laterally curved. Stellate, often star-shaped in inner branches as well, very orderly.	Pendant and spreading branches the same length. Fascicles of 4-5 branches.	Non-ranked to indistinctly 5 ranked, dry leaves distinctly recurved.
<i>Sphagnum brevifolium</i>	Yellow	Green to yellow brown	Visible apical bud, more distinctly stellate than <i>S. fallax</i> . Curved inner branches, straight outer. Branches acutely pointed.	Pendant and spreading branches the same length. Fascicles of 4-5 branches.	Indistinctly to distinctly 5 ranked, dry leaves only occasionally recurved.
<i>Sphagnum isoviitae</i>	Yellow	Yellow/brown to very brown	Fairly distinct apical bud, indistinctly stellate overall shape. Most branches curved and acute.	Pendant branches usually slightly shorter than spreading branches. Fascicles of 4-5 branches.	Often distinctly 5 ranked, dry leaves only occasionally recurved.

Table 1 ...continued

	Branch leaf shape	Branch leaf cells	Leaf cross section	Stem leaf size	Stem leaf shape
<i>Sphagnum angustifolium</i>	Narrow ovate-lanceolate, involute near apex	Resorption gap in convex apical angle, 2-3 small pores along cell wall. Concave side with apical gap and 4-10 small pores depending whether cell is near apex or base.	Chlorophyllous cells ovate-triangular, widely expose on convex surface, only just enclosed on the concave.	Small, less than 0.8mm long and approximately the same width as length.	Equilaterally triangular. The tip is rounded obtuse and usually eroded.
<i>Sphagnum flexuosum</i>	Ovate-lanceolate, to broadly ovate-lanceolate.	Chlorophyllous cells as wide or wider than hyaline cells. Rarely pores (only 1-3), just an apical resorption gap on the convex side is common.	Chlorophyllous cells triangular, as exposed as hyaline cells on convex surface, exposed on the concave.	mid-size, 0.7-1.3mm long, rarely more than 0.9mm wide.	Lingulate to triangular-lingulate. The apex is obtuse and often eroded.
<i>Sphagnum fallax</i>	Ovate-lanceolate, often with an ovate base connected to an acute terminal point.	Few pores, one apical pore on convex side, wall thinning's in cell angles.	Chlorophyllous cells narrowly triangular, exposed on convex surface, slightly exposed or enclosed the concave	0.8-1.0mm long and wide.	Ovate triangulate with wide base, slightly lingulate. Apex apiculate, acute to obtuse. Distantly placed.
<i>Sphagnum brevifolium</i>	Ovate-lanceolate, sometimes ovate then involute above.	Few pores, one apical pore on convex side, wall thinning's in cell angles.	Chlorophyllous cells broadly to narrowly triangular, exposed on convex surface, enclosed the concave	0.9-1.1mm long. 0.8-0.9mm wide.	Ovate triangulate with broad base, slightly lingulate. Apex apiculate, acute to obtuse. Tightly spaced.
<i>Sphagnum isoviitae</i>	Ovate-lanceolate, tapering evenly to point.	Some pores, one apical pore on convex side, wall thinning's in cell angles.	Chlorophyllous cells ovate to ovate-triangular, exposed on convex surface, enclosed the concave.	0.8-0.9mm long and wide.	Ovate triangulate with broad base, slightly lingulate. Apex acutely apiculate. Distantly placed.

Table 2: RADseq results from filtering and clustering for 86 samples from the *Sphagnum recurvum* complex.

Taxon	Reads per sample	Reads after clustering at 80% with coverage greater than the minimum 9	Mean coverage depth greater than set min of 9	Loci per sample with consensus sequences for clusters	Final average number of loci with all loci present	Final average number of loci with 4 sample presence requirement	Final average number of loci with 70 sample presence requirement
<i>S. angustifolium</i>	1662080	40702.3	23.4	36054.8	32505	29624	7645
<i>S. brevifolium</i>	1545755	38316.1	23.9	33921.1	31181	30682	7709
<i>S. fallax</i>	1612725	39691.9	25.4	35356.6	33988	33408	8220
<i>S. flexuosum</i>	1675071	43008.1	23.5	38379.9	35127	33862	8029
<i>S. isoviitae</i>	1798723	45256.9	25.0	40458.4	37219	36523	8196

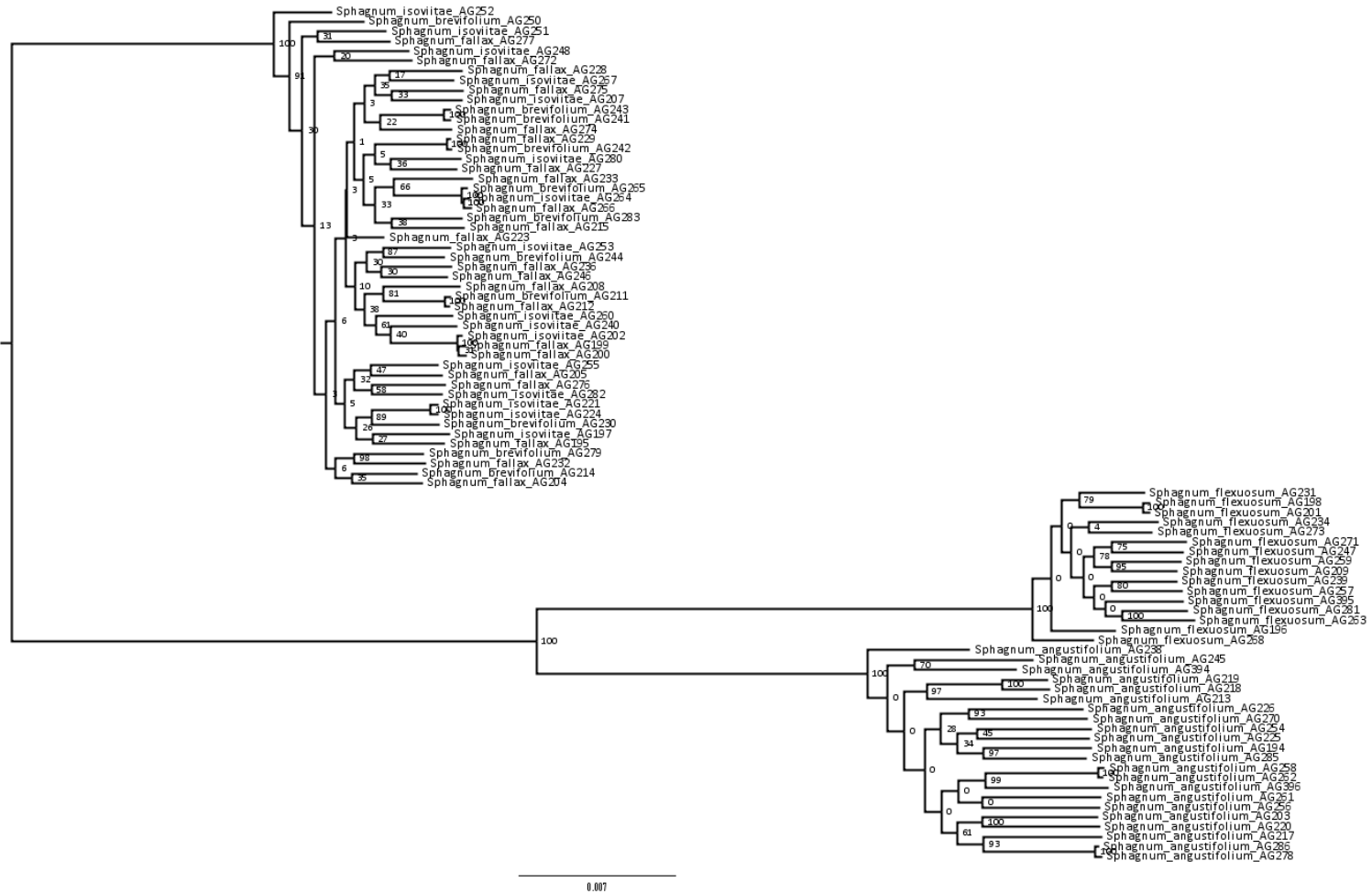


Figure 2: Maximum likelihood reconstruction of the phylogenetic relationships among 86 Norwegian samples of five putative *Sphagnum* species within the *S. recurvum* complex. The data used for this analysis are the 4-sample minimum threshold RADseq dataset. Numbers on nodes are bootstrap percentages and the scale is substitutions per site.

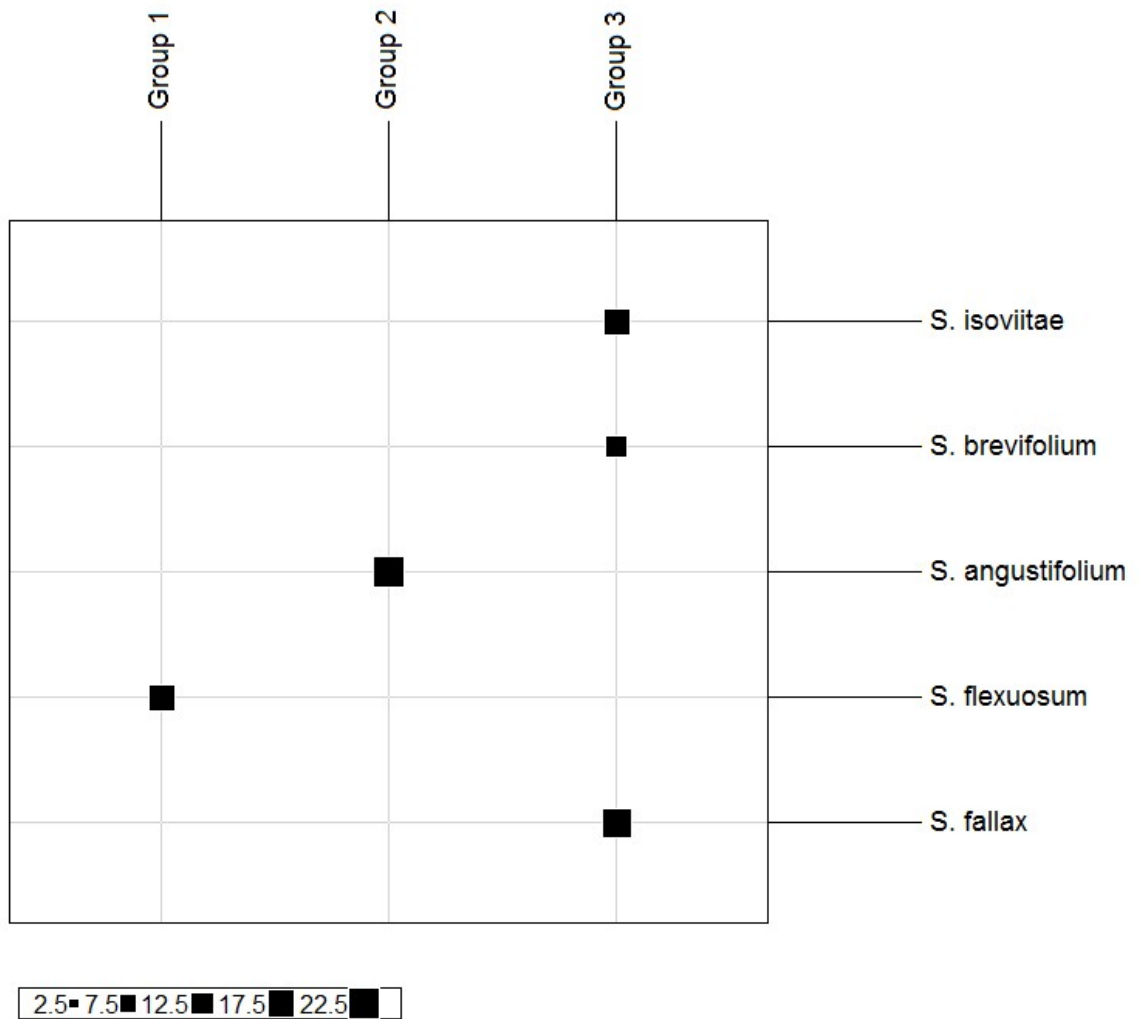


Figure 3: Groups 1, 2 and 3 are the K clusters identified by the find.clusters function of 'adeget'. Group membership, indicated by black box at grid junction, is correlated with morphospecies of the 86 *S. recurvum* samples, with box size representing the numbers of samples in each category.

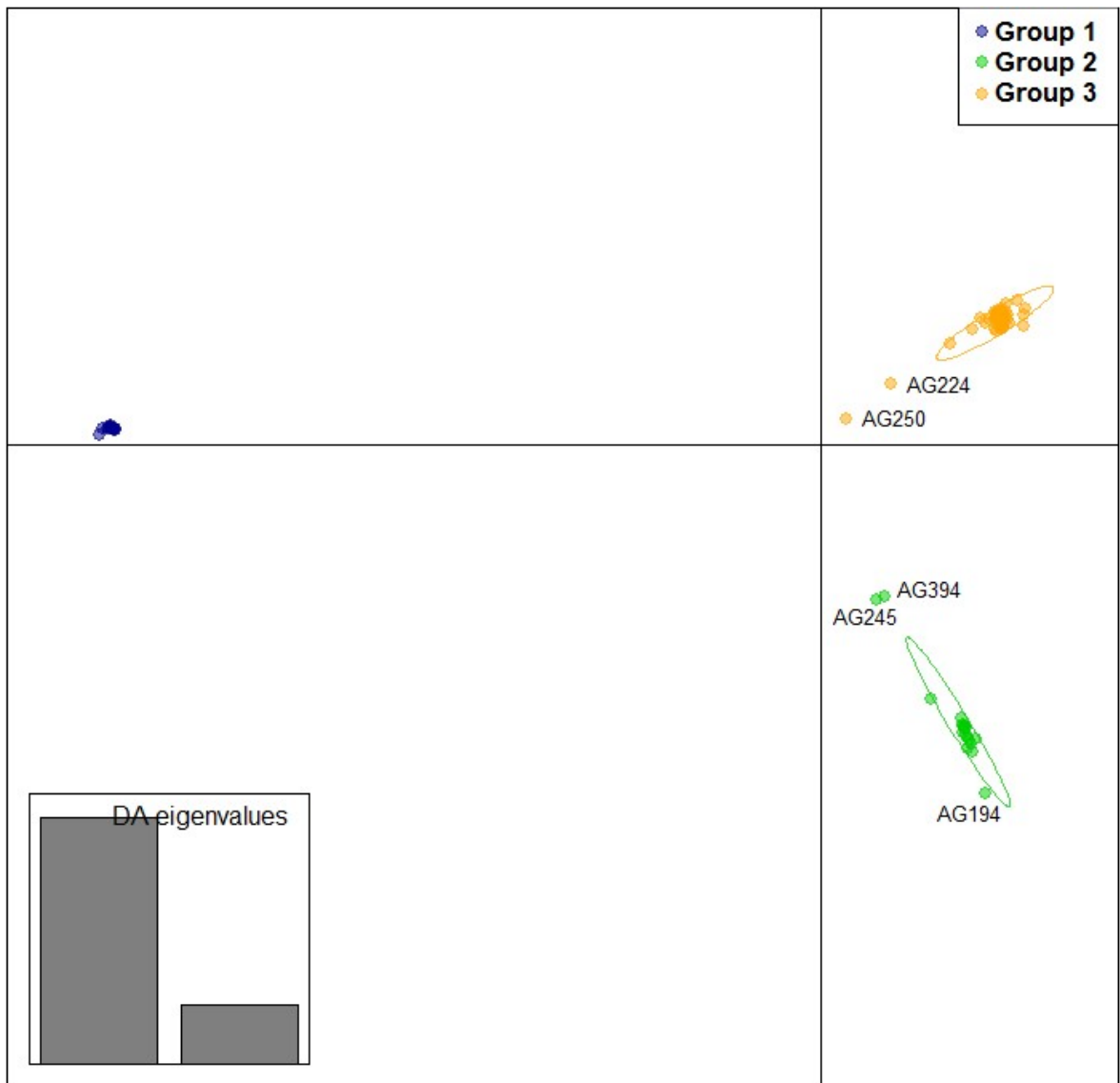


Figure 4: DAPC scatter plot using genotype clusters of $K = 3$. Each point represents an individual genotype, with each color depicting a different cluster. Group 1 (blue) contains all *S. flexuosum* samples, Group 2 (green) contains all *S. angustifolium* samples and Group 3 (orange) contains all *S. fallax*, *S. isoviitae* and *S. brevifolium* samples. The names for clusters are based on the species in each cluster. The Eigenvalue plot represents the amount of genetic variation explained by each discriminant factor.

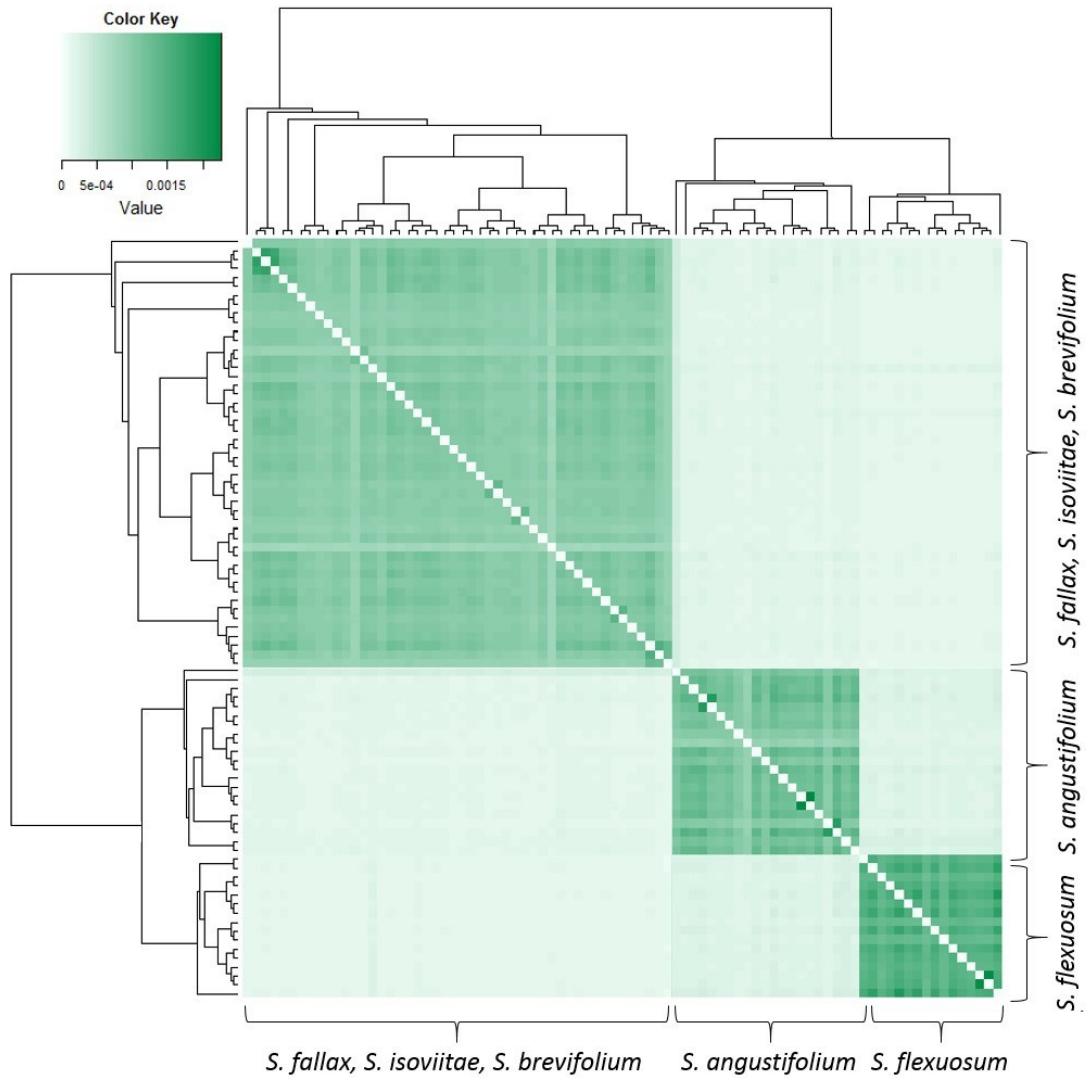


Figure 5: Heatmap of minimum evolution scores by sample, correlated with position of each sample in the four-sample threshold ML phylogenetic tree based on concatenated data. Identical trees are mirrored to facilitate comparison between individuals. Each row and column corresponds to the taxa located on branch tips. Each of the three major clades is indicated by brackets on the opposite axis. Darker green represents high minimum evolution scores while lighter green represents low minimum evolution scores.

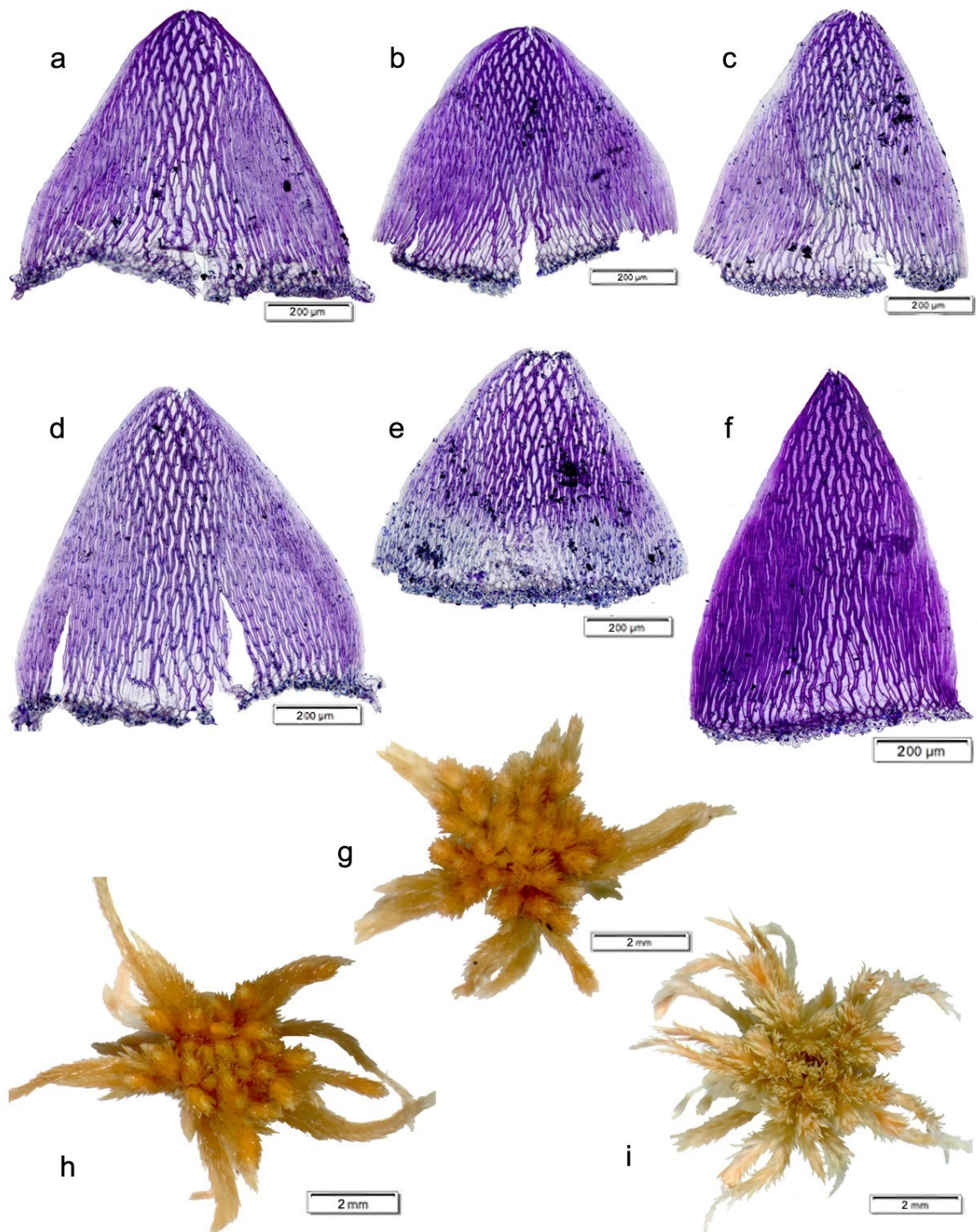


Figure 6: Morphology of *Sphagnum angustifolium*. (a – f) Stem leaves (DNA sample numbers: AG203, AG226, AG245, AG261, AG86, AG396) (g – i) Capitula (AG203, AG226 - dry, AG396).

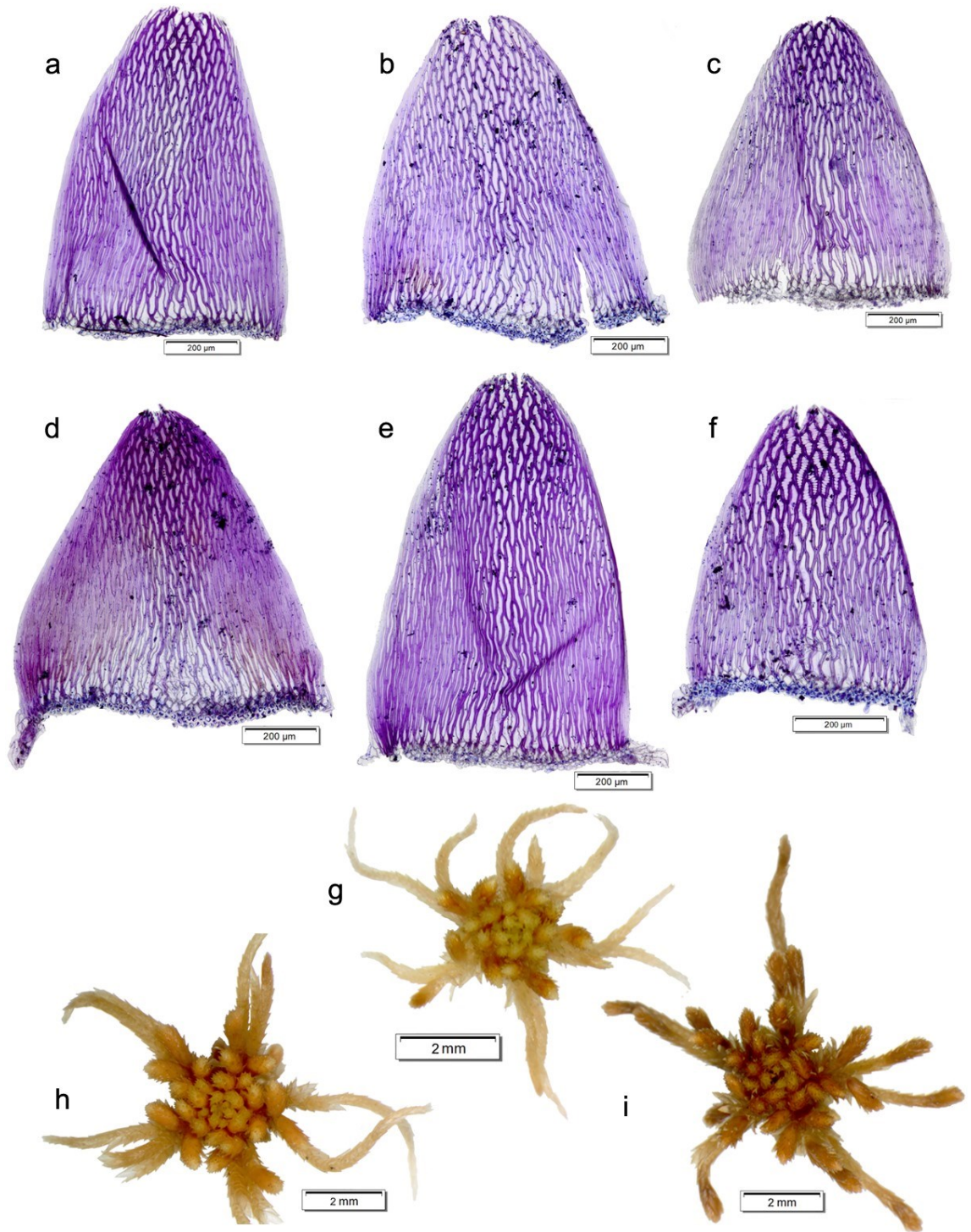


Figure 7: Morphology of *Sphagnum flexuosum*. (a – f) Stem leaves (DNA sample numbers: AG209, AG231, AG234, AG268, AG71, AG395) (g – i) Capitula (AG234, AG268, AG271).

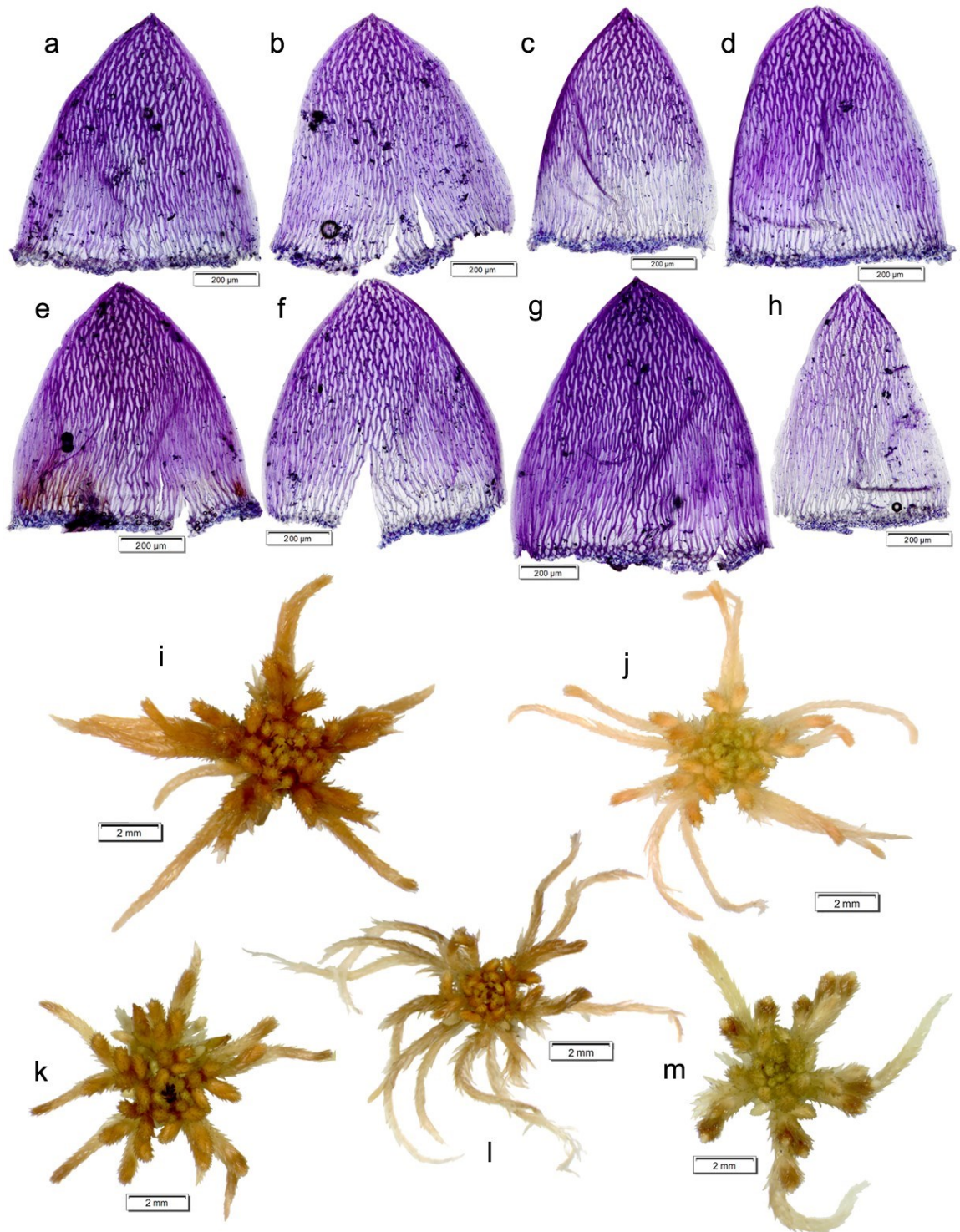


Figure 8: Morphology of *Sphagnum fallax*. (a – h) Stem leaves (DNA sample numbers: AG211, AG215, AG219, AG230, AG41, AG252, AG272, AG279) (i – m) Capitula (AG211, AG215, AG219, AG229, AG272).

Supplementary Information

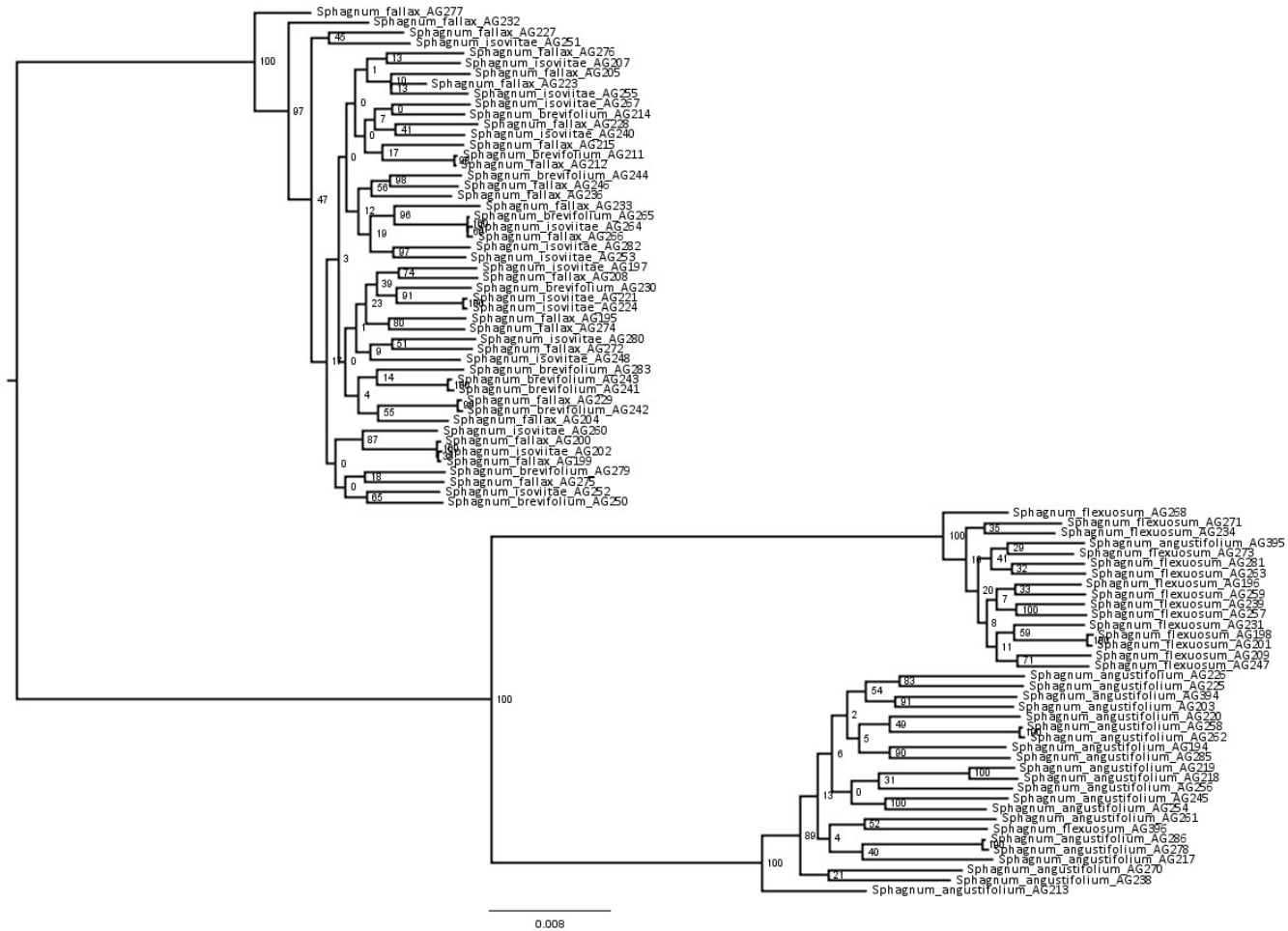


Figure S1: Maximum likelihood reconstruction of the phylogenetic relationships among 86 Norwegian samples of five putative *Sphagnum* species within the *S. recurvum* complex. The data used for this analysis are the 70 sample minimum threshold dataset RADseq dataset. The numbers on nodes are bootstrap percentages and the scale is substitution per site.

Table S1: Summary of the major morphological characters used for identification of the species in the *Sphagnum recurvum* complex not addressed in this study. Compiled from: (Isoviita, 1966; Maass, 1967; Daniels et al., 1985; Flatberg, 1989; Flatberg, 1992c, b; Flatberg, 1994; Sastad, 1999; Sastad et al., 1999a; Laine et al., 2009).

	Spore color	Plant color	Capitulum shape	Branch number and arrangement	Leaves on spreading branches
<i>Sphagnum rubroflexuosum</i>	Unknown	Green/yellow with some pink coloration in the red/purple spectrum.	Outer and inner branches distinct - tight cluster in center, a small bumpy ball, usually with a color shift from bottom to tip with a reddish tinge.	Two spreading branches, 2 slightly longer pendant.	Non-ranked in all cases, more spirally arranged. Undulate when dry, mildly recurved.
<i>Sphagnum pacificum</i>	Pale yellow	Green to yellow green/yellow brown	Rounded capitulum, indistinctly 5-radiate to non-radiate. Terminal bud inconspicuous, branches straight or slightly curved.	2 spreading and 2-3 pendant, which are usually thinner and maybe be slightly shorter or longer than spreading branches.	Usually unranked, distinctly recurved when dry.
<i>Sphagnum balticum</i>	Yellow	Yellow/orange to brown	Apical bud not differentiated, 5-radiate and unranked. Mid-inner branches acute and laterally twisted.	2 spreading, 1(-2) pendant branches. Capitulum side branches are not paired.	Often ranked, little to no undulation, often secund when dry.
<i>Sphagnum recurvum</i>	Brown	Bright green/yellow green, rarely tending brownish	Strongly 5-radiate, could be flattened in shade or rounded in open habitats.	Two spreading, two pendant branches.	Spirally arranged, distinctly recurved.

Table S1 ... continued.

	Branch leaf shape	Branch leaf cells	Leaf cross section	Stem leaf size	Stem leaf shape
<i>Sphagnum rubroflexuosum</i>	Ovate-lanceolate, to broadly ovate-lanceolate.	Chlorophyllous cells as wide or wider than hyaline cells. 3-10 pores per cell on the convex surface. Chlorophyllous cells are fully enclosed.	Chlorophyllous cells triangular, as widely exposed as hyaline cells on convex surface, and enclosed on the concave.	mid-size, 0.7-1.3mm long, rarely more than 0.9mm wide.	Lingulate to triangular-lingulate. Apex blunt but may be slightly pointed. Crowded to the stem and fibrillose - may even have hyaline cell pores.
<i>Sphagnum pacificum</i>	Ovate-lanceolate, with involute and slightly subsecund points.	One pore at apical end on the convex side and a few pseudopores in cell angles. On the concave side, 5-10 small pseudopores/wall thinning.	Chlorophyllous cells small and ovate to ovate-triangular, exposed on convex surface, tightly enclosed on the concave.	1.0-1.1mm long.	Triangular to lingulate triangular, apex acute to apiculate. Very rarely septate.
<i>Sphagnum balticum</i>	Ovate to ovate-lanceolate, usually concave when wet.	Strong border of 2-3 linear cells. Pores on the concave surface can be few or numerous, usually small. On the convex side, 5-12 pores along the margins is common.	Chlorophyllous cells triangular, widely expose on convex surface, slightly exposed to enclosed on the concave.	0.9-1.2mm, long, slightly less wide, not appressed to stem (spreading).	Lingulate-triangular, highly concave, tip appears acute because of it but is actually rounded obtuse. Fibrillose hyaline cells on as much as 50% of the leaf.
<i>Sphagnum recurvum</i>	Narrowly to strongly ovate-lanceolate.	Single apical pore on convex surface, 3-7 moderately small pores in cell ends and angles on concave surface.	Chlorophyllous cells triangular, widely expose on convex surface, enclosed on the concave.	Greater than 0.8mm long.	Lingulate to triangular-lingulate, with straight to very slightly curved sides. Apex abruptly rounded with strong erose to fimbriate tip. May have fibrils in the upper half of the leaf.

Table S2: Voucher table of all specimens used in this study.

Sample ID	DNA number	Herbarium Catalogue Number	Field Collection Number	Taxon Name	Collection date	Country	State	County/Municipality	Locality
Sphagnum_angustifolium_AG194	AG194	AG0266	A152	<i>Sphagnum angustifolium</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG195	AG195	AG0268	A154	<i>Sphagnum fallax</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_flexuosum_AG196	AG196	AG0272	A158	<i>Sphagnum flexuosum</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_isoviitae_AG197	AG197	AG0273	A159	<i>Sphagnum isoviitae</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_flexuosum_AG198	AG198	AG0275	A161	<i>Sphagnum flexuosum</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG199	AG199	AG0278	A164	<i>Sphagnum angustifolium</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG200	AG200	AG0279	A165	<i>Sphagnum fallax</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_flexuosum_AG201	AG201	AG0280	A166	<i>Sphagnum flexuosum</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_isoviitae_AG202	AG202	AG0281	A167	<i>Sphagnum isoviitae</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_angustifolium_AG203	AG203	AG0282	A168	<i>Sphagnum angustifolium</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG204	AG204	AG0284	A170	<i>Sphagnum isoviitae</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG205	AG205	AG0285	A171	<i>Sphagnum fallax</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_isoviitae_AG207	AG207	AG0289	A175	<i>Sphagnum fallax</i>	12/08/2013	Norway	Sør-Trøndelag	Trondheim	Gråkallen
Sphagnum_fallax_AG208	AG208	AG0291	A177	<i>Sphagnum isoviitae</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1

Sphagnum_flexuosum_AG209	AG209	AG0292	A178	<i>Sphagnum flexuosum</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_brevifolium_AG211	AG211	AG0294	A180	<i>Sphagnum isoviitae</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_fallax_AG212	AG212	AG0296	A182	<i>Sphagnum fallax</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_angustifolium_AG213	AG213	AG0298	A184	<i>Sphagnum angustifolium</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_brevifolium_AG214	AG214	AG0300	A186	<i>Sphagnum fallax</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_fallax_AG215	AG215	AG0302	A188	<i>Sphagnum isoviitae</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_angustifolium_AG217	AG217	AG0306	A192	<i>Sphagnum angustifolium</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 4
Sphagnum_angustifolium_AG218	AG218	AG0307	A193	<i>Sphagnum angustifolium</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 5
Sphagnum_angustifolium_AG219	AG219	AG0308	A194	<i>Sphagnum fallax</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 6
Sphagnum_angustifolium_AG220	AG220	AG0311	A197	<i>Sphagnum angustifolium</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla, mountain-side by parking lot
Sphagnum_isoviitae_AG221	AG221	AG0312	A198	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel
Sphagnum_isoviitae_AG224	AG224	AG0315	A201	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel

Sphagnum_angustifolium_AG225	AG225	AG0319	A205	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel
Sphagnum_angustifolium_AG226	AG226	AG0322	A208	<i>Sphagnum angustifolium</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel
Sphagnum_fallax_AG227	AG227	AG0323	A209	<i>Sphagnum fallax</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel
Sphagnum_fallax_AG228	AG228	AG0324	A210	<i>Sphagnum fallax</i>	14/08/2013	Norway	Sør-Trøndelag	Trondheim	Skjøla. Vasstjell Chapel
Sphagnum_fallax_AG229	AG229	AG0325	A211	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Tømmerdalsmyran mire
Sphagnum_brevifolium_AG230	AG230	AG0326	A212	<i>Sphagnum fallax</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Tømmerdalsmyran mire
Sphagnum_flexuosum_AG231	AG231	AG0328	A214	<i>Sphagnum flexuosum</i>	14/08/2013	Norway	Sør-Trøndelag	Melhus	Eundørshaūgen
Sphagnum_fallax_AG232	AG232	AG0329	A215	<i>Sphagnum fallax c.f.</i>	14/08/2013	Norway	Sør-Trøndelag	Melhus	Eundørshaūgen
Sphagnum_fallax_AG233	AG233	AG0332	A218	<i>Sphagnum brevifolium</i>	14/08/2013	Norway	Sør-Trøndelag	Melhus	Eundørshaūgen
Sphagnum_flexuosum_AG234	AG234	AG0333	A219	<i>Sphagnum flexuosum</i>	14/08/2013	Norway	Sør-Trøndelag	Melhus	Eundørshaūgen
Sphagnum_fallax_AG236	AG236	AG0338	A224	<i>Sphagnum balticum c.f.</i>	14/08/2013	Norway	Sør-Trøndelag	Melhus	Eundørshaūgen
Sphagnum_angustifolium_AG238	AG238	AG0340	A226	<i>Sphagnum angustifolium</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen
Sphagnum_flexuosum_AG239	AG239	AG0341	A227	<i>Sphagnum flexuosum</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen
Sphagnum_isoviitae_AG240	AG240	AG0342	A228	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen
Sphagnum_brevifolium_AG241	AG241	AG0346	A232	<i>Sphagnum brevifolium</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen
Sphagnum_brevifolium_AG242	AG242	AG0347	A233	<i>Sphagnum fallax</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen
Sphagnum_brevifolium_AG243	AG243	AG0348	A234	<i>Sphagnum isoviitae</i>	14/08/2013	Norway	Sør-Trøndelag	Klæbū	Damtønnbekken W Stream fen

Sphagnum_brevifolium_AG244	AG244	AG0350	A236	<i>Sphagnum flexuosum</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_angustifolium_AG245	AG245	AG0352	A238	<i>Sphagnum angustifolium</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_fallax_AG246	AG246	AG0353	A239	<i>Sphagnum fallax</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_flexuosum_AG247	AG247	AG0355	A241	<i>Sphagnum flexuosum</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_isoviitae_AG248	AG248	AG0356	A242	<i>Sphagnum fallax</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_brevifolium_AG250	AG250	AG0363	A249	<i>Sphagnum brevifolium c.f.</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_isoviitae_AG251	AG251	AG0364	A250	<i>Sphagnum isoviitae</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_isoviitae_AG252	AG252	AG0365	A251	<i>Sphagnum isoviitae</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_isoviitae_AG253	AG253	AG0366	A252	<i>Sphagnum isoviitae</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_angustifolium_AG254	AG254	AG0368	A254	<i>Sphagnum angustifolium</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_isoviitae_AG255	AG255	AG0369	A254	<i>Sphagnum fallax</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_angustifolium_AG256	AG256	AG0372	A257	<i>Sphagnum angustifolium</i>	15/08/2013	Norway	Nord-Trøndelag	Steinkjer	Henning-Vatnet
Sphagnum_flexuosum_AG257	AG257	AG0373	A258	<i>Sphagnum flexuosum</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_angustifolium_AG258	AG258	AG0374	A259	<i>Sphagnum angustifolium</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_flexuosum_AG259	AG259	AG0375	A260	<i>Sphagnum fallax</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_isoviitae_AG260	AG260	AG0376	A261	<i>Sphagnum isoviitae</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia

Sphagnum_angustifolium_AG261	AG261	AG0377	A262	<i>Sphagnum something weird</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_angustifolium_AG262	AG262	AG0378	A263	<i>Sphagnum something weird</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_flexuosum_AG263	AG263	AG0379	A264	<i>Sphagnum flexuosum</i>	15/08/2013	Norway	Nord-Trøndelag	Grong	Heia
Sphagnum_isoviitae_AG264	AG264	AG0382	A267	<i>Sphagnum brevifolium c.f.</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_brevifolium_AG265	AG265	AG0386	A271	<i>Sphagnum isoviitae</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG266	AG266	AG0387	A272	<i>Sphagnum isoviitae</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_isoviitae_AG267	AG267	AG0388	A273	<i>Sphagnum fallax</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_flexuosum_AG268	AG268	AG0389	A274	<i>Sphagnum flexuosum</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_angustifolium_AG270	AG270	AG0394	A279	<i>Sphagnum angustifolium</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_flexuosum_AG271	AG271	AG0395	A280	<i>Sphagnum flexuosum</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG272	AG272	AG0396	A281	<i>Sphagnum brevifolium c.f.</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake

Sphagnum_flexuosum_AG273	AG273	AG0397	A282	<i>Sphagnum flexuosum</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG274	AG274	AG0398	A283	<i>Sphagnum isoviitae</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG275	AG275	AG0399	A284	<i>Sphagnum brevifolium c.f.</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG276	AG276	AG0400	A285	<i>Sphagnum isoviitae</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_fallax_AG277	AG277	AG0401	A286	<i>Sphagnum angustifolium</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_angustifolium_AG278	AG278	AG0402	A287	<i>Sphagnum angustifolium</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_brevifolium_AG279	AG279	AG0404	A289	<i>Sphagnum brevifolium</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_isoviitae_AG280	AG280	AG0405	A290	<i>Sphagnum brevifolium c.f.</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_flexuosum_AG281	AG281	AG0406	A291	<i>Sphagnum flexuosum</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_isoviitae_AG282	AG282	AG0407	A292	<i>Sphagnum brevifolium c.f.</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_brevifolium_AG283	AG283	AG0408	A293	<i>Sphagnum brevifolium</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_angustifolium_AG285	AG285	AG0413	A298	<i>Sphagnum angustifolium</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran
Sphagnum_angustifolium_AG286	AG286	AG0415	A300	<i>Sphagnum angustifolium</i>	17/08/2013	Norway	Sor-Trøndelag	Klæbū	Måisjømyran

Sphagnum_angustifolium_AG394	AG394	AG0299	A185	<i>Sphagnum angustifolium</i>	13/08/2013	Norway	Sør-Trøndelag	Orkdal	Husdalen, mires around lake Husdalen 1
Sphagnum_flexuosum_AG395	AG395	AG0393	A278	<i>Sphagnum angustifolium</i>	16/08/2013	Norway	Nord-Trøndelag	Høylandet	Grestjonra lake and Latmyrbukta lake
Sphagnum_angustifolium_AG396	AG396	AG0391	A276	<i>Sphagnum flexuosum</i>	16/08/2013	Norway	Sør-Trøndelag	Klæbū	Grestjonra lake and Latmyrbukta lake

Table S2 ... con't.

Sample ID	GPS	Habitat	Collector	Determined by	Notes
Sphagnum_angustifolium_AG194	63*25.140 N 10*15.776 E	Mixed lawn under sedge, 6m from pond edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	Mixed with <i>S.</i> <i>riperium</i> and <i>S.</i> <i>fallax</i> , very pompom
Sphagnum_fallax_AG195	63*25.150 N 10*15.773 E	Mixed lawn under sedge, 6m from pond edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG196	63*25.328 N 10*15.944 E	Mixed mat 1m from stream with <i>S. lingergii</i>	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG197	63*25.323 N 10*15.950 E	Edge of Stream, a bit mixed with <i>S. linbergii</i>	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG198	63*25.344 N 10*15.955 E	Patch in very mixed hummock 30cm from stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG199	63*25.344 N 10*15.955 E	Patch in very mixed hummock 30cm from stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG200	63*25.341 N 10*15.959 E	Hummock with sedge, beside rivulet	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG201	63*25.341 N 10*15.959 E	Hummock with sedge, beside rivulet	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG202	63*25.341 N 10*15.959 E	Hummock with sedge, beside rivulet	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG203	63*25.340 N 10*15.901 E	Drier hummock back from stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG204	63*25.360 N 10*16.042 E	Near edge of fen/forest, mat quite wet	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG205	63*25.368 N 10*16.033 E	Mat on slope	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG207	63*25.317 N 10*15.820 E	mound up from trickle, some <i>S. balticum</i> mixed in	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	

Sphagnum_fallax_AG208	63*21.719 N 9*51.387 E	in slight hummock, out of water	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG209	63*21.719 N 9*51.387 E	mixed with Subgenus Sphagnum	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG211	63*21.736 N 9*51.473 E	Right at edge of water (across from 179)	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG212	63*21.736 N 9*51.473 E	under carex shade, on same hummock	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG213	63*21.777 N 9*51.192 E	Slope under heather at edge of fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG214	63*21.807 N 9*51.542 E	Slope down into/at edge of mire	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	Odd looking
Sphagnum_fallax_AG215	63*21.828 N 9*51.531 E	in water beside stream with carex	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG217	63*21.512 N 9*51.010 E	ombiotrophic sloping bog, wet shrub-ish	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG218	63*21.480 N 9*51.066 E	on sloping fen hill, under vaccinium	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG219	63*21.470 N 9*51.098 E	at base of hummock with heather	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG220	63*18.961 N 10*24.153 E	Open clearing with grass in damp spruce forest	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG221	63*18.546 N 10*24.332 E	edge of stream by path, with polytrichum	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG224	63*18.558 N 10*24.326 E	mixed stand of <i>S. fallax</i> , <i>S. isoviitae</i> , <i>S. angustifolium</i> and <i>S. russowii</i> in moist hollow between trickle stream and path	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	Some *Very* transitional between <i>S.</i> <i>isoviitae</i> and <i>S.</i> <i>fallax</i>
Sphagnum_angustifolium_AG225	63*18.550 N 10*24.167 E	Very rich base of small hummock with <i>S. contorum</i>	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	

Sphagnum_angustifolium_AG226	63*18.492 N 10*24.170 E	steep slope with heather, polytrichum and S. fallax	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG227	63*18.493 N 10*24.171 E	steep slope with heather, polytrichum and S. fallax	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG228	63*18.478 N 10*24.150 E	Very poor slope at mountain top with S. angustifolium and S. balticum	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG229	63*18.471 N 10*24.113 E	Near vertical bank down from open mire, under shrub with S. russowii and Polytrichum	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG230	63*18.472 N 10*24.095 E	Open fen under heather with S. russowii and A213	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG231	63*18.350 N 10*23.267 E	in wet puddle with S. balticum on sloping intermediate fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG232	63*18.340 N 10*23.257 E	Spoing wet under Andromeda	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG233	63*18.258 N 10*23.046 E	Edge of stream flowing through rich fen with S. linbergii	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG234	63*18.258 N 10*23.047 E	Edge of stream flowing through rich fen with S. linbergii, down from A218	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_fallax_AG236	63*18.305 N 10*23.047 E	Mound at edge of flowing stream/edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG238	63*18.538 N 10*23.411 E	Hummock near/at downhill seep in intermediate fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG239	63*18.538 N 10*23.411 E	Hummock near/at downhill seep in intermediate fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG240	63*18.538 N 10*23.411 E	Hummock near/at downhill seep in intermediate fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG241	63*18.680 N 10*23.703 E	low mat mixed with S. papillosum, S. balticum, S. angustifolium, S. fallax	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	Odd looking S. brevifolium
Sphagnum_brevifolium_AG242	63*18.680 N 10*23.703 E	Same hummock as A232	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG243	63*18.680 N 10*23.703 E	Just a hummock down from A233 with no S. brevifolium	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	

Sphagnum_brevifolium_AG244	63*55.851 N 11*41.531 E	loose hummock under sedge cover 2m from stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG245	63*55.859 N 11*41.521 E	in hummock mat around birch esker	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG246	63*55.881 N 11*41.528 E	Under heavy sedge/grass cover at stream edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG247	63*55.921 N 11*41.520 E	mat/base of hummock under some bog birch/sedge/saxifage	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG248	63*55.921 N 11*41.520 E	mat/base of (different) hummock under some bog birch/sedge/saxifage	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_brevifolium_AG250	63*55.926 N 11*42.085 E	Bottom of ditch without open flower but clear seep	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG251	63*55.955 N 11*42.206 E	Lawn under sedge in minerotropic fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG252	63*55.955 N 11*42.206 E	Lawn with sedge 1m from stream. <i>S. papillosum</i> and <i>S. flexuosum</i> too	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG253	63*56.106 N 11*42.259 E	mat 20cm up from pool edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG254	63*56.102 N 11*41.946 E	Hummock with andromeda and <i>S. russowii</i> at fen margin	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG255	63*56.075 N 11*41.800 E	Very edge of a tiny rush filled stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG256	63*55.988 N 11*41.795 E	Very side of dry hummock (very small) with heather	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG257	64*21.390 N 12*19.935 E	Mat at edge of salix/birch margin	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG258	64*21.390 N 12*19.935 E	Mat at edge of salix/birch margin	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG259	64*21.390 N 12*19.935 E	Mat at edge of salix/birch margin	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG260	64*21.401 N 12*19.938 E	middle of dryish mat with saxifrage	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG261	64*21.405 N 12*19.931 E	On low hummock under birch & sedge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg

Sphagnum_angustifolium_AG262	64*21.402 N 12*19.957 E	mixed with <i>S. flexuosum</i> *A264) on mat	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG263	64*21.402 N 12*19.957 E	mixed with <i>S. weird isoviitae</i> *A263) on mat	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG264	64*39.858 N 12*10.482 E	edge of pool <i>S. pulcrum</i> , <i>S. trondelagicum</i> , <i>S. papillosum</i>	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_brevifolium_AG265	64*39.849 N 12*10.518 E	at edge of pool up and down 15cm hummock with <i>S. pulcrum</i> and <i>S. majus</i>	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG266	64*39.843 N 12*10.522 E	edge into sedge. 6m from water, 50cm from A273-5	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_isoviitae_AG267	64*39.843 N 12*10.522 E	Sedge-y 10cm hummock with <i>S. isoviitae</i> around. A274-4 beside.	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG268	64*39.843 N 12*10.522 E	Mixed with <i>S. fallax</i> and <i>S. isoviitae</i> at base of hummock and lawn	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG270	64*39.461 N 12*11.044 E	Slope down into mire, dry-ish	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG271	64*39.298 N 12*10.513 E	by rivulet in sloping intermediate fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG272	64*39.296 N 12*10.510 E	mat 70cm from rivulet edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_flexuosum_AG273	64*39.296 N 12*10.510 E	mat 70cm from rivulet edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG274	64*39.278 N 12*10.567 E	mat 1m from rivulet, some dry	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG275	64*39.314 N 12*10.668 E	Massively mixed species mat in sloping fen by puddle	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG276	64*39.314 N 12*10.668 E	Massively mixed species mat in sloping fen by puddle	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_fallax_AG277	64*39.314 N 12*10.668 E	Massively mixed species mat in sloping fen by puddle	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_angustifolium_AG278	63*14.815 N 10*26.989 E	lawn and hummock in birch lag	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg
Sphagnum_brevifolium_AG279	63*14.763 N 10*27.384 E	slight rise out of seep in intermediate poor fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg

Sphagnum_isoviitae_AG280	63*14.763 N 10*27.384 E	slight rise out of seep in intermediate poor fen	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_flexuosum_AG281	63*14.757 N 10*27.358 E	10cm rise at edge of pool under vaccinicum	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_isoviitae_AG282	63*14.757 N 10*27.358 E	10cm rise at edge of pool under vaccinicum, same hummock	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_brevifolium_AG283	63*14.739 N 10*27.395 E	in bed of flood stream with sedge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG285	63*14.814 N 10*27.055 E	sloping edge of rich fen down to stream	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG286	63*14.819 N 10*26.991 E	very edge of S. angustifolium mat into puddle, under salix shade	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG394	63*21.789 N 9*51.515 E	Extremely mixed carpet near edge	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	MIXED
Sphagnum_flexuosum_AG395	64*39.462 N 12*11.043 E	sloping mat at seep in/near lag	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	
Sphagnum_angustifolium_AG396	64*39.456 N 12*10.992 E	in shate at stream with sedge, almost lag	Arielle Garrett	Arielle Garrett & Dr. Kjell Ivar Flatberg	

Table S3: Restriction digest master mix – Reagents and volumes needed for 3uL to be prepared per sample.

Reagent	Volume per one sample (1x) (uL)
10x T4 Buffer	1.15
1M NaCl	0.60
1 mg/mL BSA	0.60
Water	0.25
Mse1	0.12
EcoR1	0.28

Table S4: Restriction-Ligation master mix – Reagents and volumes needed for 1.4uL to be prepared per sample.

Reagent	Volume per one sample (1x) (uL)
T4 DNA ligase	0.1675
10x T4 Buffer	0.1
1M NaCl	0.05
1 mg/mL BSA	0.05
Water	0.072
Mse1 adaptor	1

Table S5: PCR amplification reactions – Reagents and volumes needed for a 20uL reaction.

Reagent	Volume per 20uL reaction (uL)
Water	9.67
5x Iproof buffer	4.0
dNTP (10mM)	0.4
MgCl ₂ (50mM)	0.4
Pre-mixed PCR primers, 5 uM	1.33
Iproof taq	0.2
DMSO	0.15
R/L product	4.0

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