

Hot off the Press features easy-to-read summaries of just a few of the interesting papers published in recent issues of our own journal, *Journal of Bryology*, and of other bryological and botanical journals that are available through the BBS reading circle (for details of the reading circle, please go to [www.britishbryologicalsociety.org.uk](http://www.britishbryologicalsociety.org.uk) and follow the link under 'Activities').

### When is a *Bryum* not a *Bryum*?

Holyoak, D. T. & Pedersen, N. (2007). Conflicting molecular and morphological evidence of evolution within the Bryaceae (Bryopsida) and its implications for generic taxonomy. *Journal of Bryology* 29, 111–124.

Traditionally, the taxonomy of all living things has been based more or less exclusively on visible characteristics. However, analysis of DNA sequence data has suggested that this traditional approach to taxonomy may not reflect the true relationships between species. Niklas Pedersen and colleagues have been analysing DNA data from one group of mosses in particular, the Bryaceae, and their studies have revealed that the current taxonomy of this group, based primarily on morphology, is misleading.

In their latest paper in *Journal of Bryology*, which forms part of a wider study of evolution within the family Bryaceae (see Pedersen *et al.*, 2007), they report the results of phylogenetic analyses on two particular groups of European Bryaceae – small tuber-bearing species of *Bryum* ('*Erythrocarpa*') and species with axillary bulbils (*Bryum dichotomum* group) – and show that the currently accepted relationships between many of these species are incorrect. This has implications for the genera in which a number of '*Bryum*' species are placed and the authors propose a new taxonomy for some species that more accurately reflects their phylogenetic relationships.

But what exactly is phylogenetic analysis? Put simply, phylogenetics is the study of the evolutionary history of organismal lineages as they change through time. Genetic variation is necessary for evolution to occur and this variation results from changes within the genetic make-up of a population. All organisms

possess a 'genome' made up of a set of discrete units called genes. Whenever a cell divides, a copy of its genome is made to be passed to the next generation. This process has to be accurate to avoid introducing errors (mutations), but the process is not 100% error-free and, inevitably, random mutations do occur. This means that each time a new generation is produced, there will be slight differences in the genome of the offspring from that of the parent. Over time, through subsequent generations, these mutations accumulate.

Plant cells contain three genomes – the main genome in the nucleus of the cell and two smaller genomes, one in the mitochondria (the internal batteries of a cell) and one in the chloroplasts (the organelles which carry out photosynthesis). It is known that in certain regions of the three genomes the rate at which mutations occur is fairly constant over time. Therefore, by analysing how the sequences of these regions from various species are related, one can build up a picture of how the species are related to each other – species whose sequences share a recent evolutionary history are most likely to be closely related; in contrast, species whose sequences split from each other in a distant past will only be distantly related.

In a project such as this, there is a vast amount of sequence data to analyse. The part of the study reported in the *J Bryol* paper looked at three separate regions of the chloroplast genome from 69 specimens. Consequently, the various possible permutations of the many accumulated mutations are very complex. The researchers used a series of computer programs to align all the sequences in order to analyse the evolutionary history among the species. The analyses placed species whose sequences share an evolutionary history into closely related groups and eventually the most reliable family tree for all the species included

in the study was generated, known as the most parsimonious phylogenetic tree.

The branching pattern, or topology, of the phylogenetic tree not only shows how species cluster together into groups of related species, known as clades, but the length of the branches also indicates the genetic distance between the species. A value for the statistical support of each branch, calculated using the wonderfully named 'bootstrap analysis', appears at the branching points, or nodes, in the tree. A study of the final tree then reveals how all the species in the study are most likely to be related. Very often, as in this case, a phylogenetic tree can reveal that traditional classifications of species based on morphology are inadequate and inaccurate.

There are a number of reasons why morphological approaches have led to inaccurate taxonomies. Two of these are highlighted in this study – convergent and divergent evolution. Despite how closely or distantly related species may be at the genetic level, the environment in which a species lives can have a great bearing on how it evolves. So, two species that are genetically distant from one another may have adapted over millennia to life in a particular environment in the same way. This means that their morphological characteristics may suggest that they are closely related when in fact they are not – this is known as convergent evolution. A classic example

is the development of wings in both birds and bats. Divergent evolution is the opposite of this, where two species that are very close genetically may appear to be very different if they have adapted to life in different environments, e.g. humans and monkeys.

In this study, the authors have shown that the morphologically similar *Bryum rubens* and *Bryum subapiculatum* are actually only distantly related and they were placed in different clades in the phylogenetic tree. *Bryum rubens* was found to be closer to *Bryum capillare*, whereas *Bryum subapiculatum* was closer to *Bryum alpinum*. On the other hand, rapid morphological changes have occurred within some clades, notably of *Plagiobryum zieri* from within the genus *Ptychostomum*. To reflect the true relationships between the species highlighted by this study, the authors have proposed that a number of species need to be reclassified.

And so in conclusion – *Ptychostomum capillare*, *Imbribryum alpinum*, *Ptychostomum zieri*, etc. – what does all this mean to the average field bryologist? Well, apart from possibly having to learn a suite of new names, it will not make the identification of these species in the field or at home under the microscope any more difficult than it already is (and, unfortunately, no easier either!). The morphological characters that are currently used to separate these species will still be valid – there will be no need to resort to a spot of DIY DNA sequencing and bootstrap analysis just yet. However, the proposed changes to the generic organization of these species will provide a more accurate reflection of the true evolutionary relationships between members of this fascinating group of mosses.

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#### REFERENCE

Pedersen, N., Holyoak, D.T. & Newton, A.E. (2007). Systematics and morphological evolution within the moss family Bryaceae: a comparison between parsimony and Bayesian methods for reconstruction of ancestral character states. *Molecular Phylogenetics and Evolution* 43, 891–907.

< *Bryum (Imbribryum) alpinum*. Graham Motley



## Please don't wipe your feet

Jägerbrand, A.K. (2007). A new method for assessing dispersal and colonization of bryophytes. *Journal of Bryology* 29, 133–134.

Understanding how any species disperses and colonizes new areas is of fundamental importance to ecologists. Traditional methods to measure these processes in bryophytes are necessarily destructive, often involving the clearing of areas of ground, rock or tree branches and observing the pattern of recolonization over long periods of time. Such experiments can take several decades in more extreme cold environments.

However, Annika Jägerbrand from the University of Göteborg, Sweden, has discovered that a method originally developed for studying higher plant seed dispersal can be extended to bryophyte studies. The unlikely saviour of many a colony of bryophytes that might otherwise disappear in the interest of science is a plastic doormat made from a material called FinnTurf™. Twenty such mats have been trialled in a 6-year study in the species-poor moss heathlands of the Thingvellir National Park in Iceland.

In 1998, small pieces (20x30 cm) of doormat were nailed to the ground in an area dominated by *Racomitrium lanuginosum*. In summer 2004, Dr Jägerbrand returned to the site to collect the mats. Although 8 of them had disappeared, 12 were retrieved and taken back to the laboratory for analysis. Over the time period of the study, a thin layer of dust had settled on the mats, providing a layer in which small fragments of bryophytes had started to grow.

Disappointingly, the only species recorded on the mats was *R. lanuginosum*, a species known for its ability to colonize new areas and substrates of different textures. Some of the mats had been completely covered by this species. However, the study did show that these plastic mats may provide a cheap and easy, non-destructive method for studying dispersal, colonization and species succession. The only drawback noted by the researchers was that the mats would not be suitable for studying dispersal of sexual or vegetative units below 0.3 mm in size.

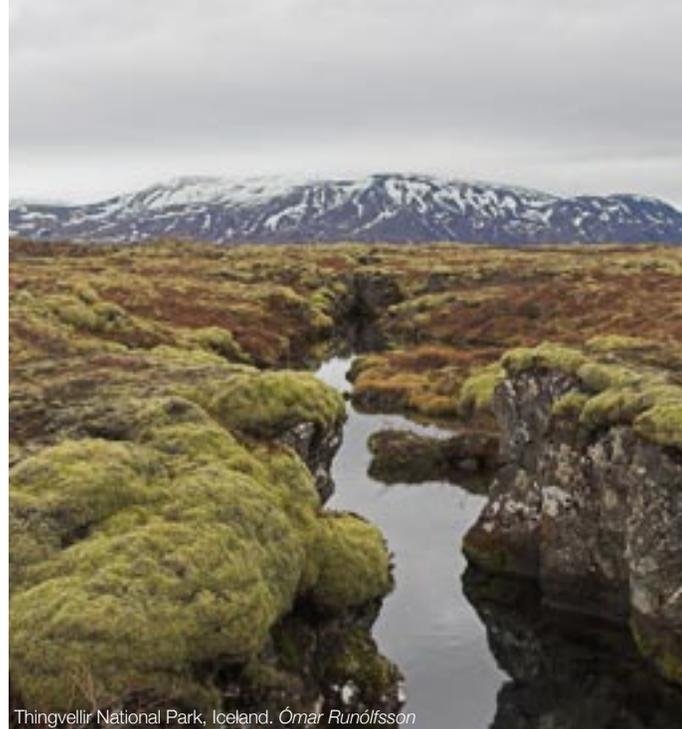
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## Global distribution patterns in pleurocarpous mosses

Hedenäs, L. (2007). Global diversity patterns among pleurocarpous mosses. *Bryologist* 110, 319–331.

Some controversy has existed concerning the relative levels of bryophyte species diversity in tropical and temperate areas. In a recent paper in the *Bryologist* Lars Hedenäs describes diversity patterns in the pleurocarpous mosses on a global scale. He extracted

checklists from the literature for countries, states and large floristic provinces so as to obtain information from all continents with habitats suitable for bryophytes. In practice he collected useable checklists for 78 areas covering all continents except Antarctica. To see if any patterns were present, the data were analysed using Nonmetric Multidimensional Scaling (NMDS) software, which uses a series of statistical techniques to detect similarities amongst sets of data. NMDS was conducted on a simple correlation matrix with two different indices of similarity, used frequently



Thingvellir National Park, Iceland. Ómar Runólfsson

in comparisons of plant distribution between different areas. The results of NMDS were broadly similar regardless of the matrix used.

The author found that distribution patterns revealed seven distinct regions: Boreal; Cool-temperate Asia; Sino-Japanese; Holarctic; Tropical Asia, Australia and Oceania; Sub-Saharan Africa; and Neotropics.

The findings also show that the pleurocarp floras of Boreal areas are very similar to each other. With the exception of Cool-temperate Asia, which shows a similar narrow diversity pattern to the Boreal region. All of the other areas show greater intraregional differentiation than the Boreal. In addition, differentiation

between regions outside the Boreal, or between these regions and the Boreal, is considerably greater than within the Boreal itself. The data also supports the view that each of the tropical land masses has its own distinctive bryophyte flora.

The study concludes that by far the most floristic diversity in the pleurocarpous mosses comes from the tropics. Although there has been no similar study for the acrocarps or hepatics, Hedenäs believes that the results would be broadly similar and calls for these diversity patterns to inform future research priorities in a global context.

Martin Godfrey

## Bygone bryologists

### Samuel Brewer (ca 1669–1743) – an update

Further to a previous article about Brewer (*Field Bryology* 88, 9–11), I have become aware of the existence of an oil painting that depicts a Samuel Brewer who may be the same man. The painting measures 27x34 inches (ca 675x850 mm), with the words 'Samuel Brewer, armiger' in the top right corner. The Royal College of Arms has no record of a coat of arms registered for a Wiltshire family named Brewer, but the word *armiger* at that period was merely a Latinization of 'esquire', and had not yet acquired its later heraldic meaning.

Two authorities have independently dated the painting to ca 1700, which is consistent with the man portrayed being Brewer the botanist, for he is clearly a young man in his prime. The styles of dress, hair, etc., also indicate that the sitter is contemporary with Brewer the botanist. The National Portrait Gallery has a portrait of a Samuel Brewer (1724–1796) who was an independent minister in Stepney, London, but he was of a later era.

I thank David Hawkins, Morlin Ellis, Jim Lawley, David Moore-Gwyn and P.L. Dickinson for their interest in and comments about the painting and sitter.

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