Multiple analyses from multiple loci support three major liverwine lineages
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Introduction.
One of the major factors influencing the ability of phylogenetic data to answer this question is appropriate tissue-sampling (Solis & Solis 2004). Many studies on land plant phylogeny have been clouded by the fact that the sampling of liverworts is typically based on the sporophyte, resulting in a biased and incomplete representation of the evolutionary history of these plants. In addition, the sporophyte typically shows a large number of autapomorphies, which can make it difficult to determine the true phylogenetic relationships within the group. To overcome these issues, it is necessary to sample multiple loci and multiple tissues when studying the evolutionary relationships of liverworts.

Materials and methods. Tissue sampling.
The molecular dataset consists of 25 genera of hepatics (18 non-leafy and 7 leafy liverworts) and 6 species of vascular plants and one algae used to polarize the analyses. DNA extraction, amplification, and sequencing. The molecular dataset includes loci from three different plant lineages: DNA, 18S rDNA, and chloroplast sequences. The 18S rDNA data were obtained from the model of DNA evolution with the best fit to the data for the model DNA matrix, and for each locus individually. Maximum likelihood (ML) analysis was conducted in PAUP* 4.0b10 (Swofford 2002), using the Neighbor Joining algorithm. The 18S rDNA data were performed using the General Time Reversible model of nucleotide substitution, plus a gamma distribution of rate variation among sites, and invariant sites. Bootstrap support was calculated using 100 replicates, with ‘fast’ stepwise addition. MrBayes 3.0 (Huelsenbeck & Ronquist 2002) was used to perform multiple analyses from multiple loci. The maximum likelihood analysis was performed using the General Time Reversible model of nucleotide substitution, plus a gamma distribution of rate variation among sites, and invariant sites. Bootstrap support was calculated using 100 replicates, with ‘fast’ stepwise addition. MrBayes 3.0 (Huelsenbeck & Ronquist 2002) was used to

Results.
The number of liverworts is well-supported by all analyses, but the three major clades within the liverworts are strongly supported by all analyses, in agreement with previous publications, allowing the recognition of three major lineages: Haplomitroopsida Stotler & Crand.-Stotl., Marchantiopsida Stotler & Crand.-Stotl., and Haematomitopsida Stotler & Crand.-Stotl.

Morphology.
Multiple analyses from multiple loci support three major liverwine lineages. For the liverworts, there is strong support for the recognition of three major lineages: Haplomitroopsida Stotler & Crand.-Stotl., Marchantiopsida Stotler & Crand.-Stotl., and Haematomitopsida Stotler & Crand.-Stotl.

Summary.
Nucleotide sequence data from six nuclear, chloroplast and mitochondrial genes were obtained from 23 species of liverworts, representing 12 families and 25 genera. The results of this study support the recognition of three major lineages: Haplomitroopsida Stotler & Crand.-Stotl., Marchantiopsida Stotler & Crand.-Stotl., and Haematomitopsida Stotler & Crand.-Stotl., the three major lineages recognized in previous studies. The results also support the recognition of three major lineages: Haplomitroopsida Stotler & Crand.-Stotl., Marchantiopsida Stotler & Crand.-Stotl., and Haematomitopsida Stotler & Crand.-Stotl., the three major lineages recognized in previous studies. These results provide strong support for the recognition of these three major lineages, which are supported by all analyses and are in agreement with previous publications.