Galin Gospodinov

Taxonomic and genetic investigation on sect. *Ricciella* genus *Riccia* in Europe with emphasis on *R. fluitans and R. rhenana*

Abstract

Taxonomy provides a systematic framework for classifying living organisms, which is continuously evolving to accommodate the diversity and dynamics of life. The species, as the fundamental unit of taxonomic classification, has historically been defined based on morphological characters, ecological traits, and geographic distribution. In the pregenetic era, researchers collected specimens, documented their morphology, ecology, and distribution, and published detailed descriptions. Once published and compliant with the rules of the relevant International Code of Nomenclature, a species was formally recognized. However, the scientific community could reject a proposed species, or multiple species epithets might emerge for the same organism across different regions, reflecting the dynamic and iterative nature of taxonomy. Advances in genetic research have significantly enhanced taxonomic science, enabling more precise species delineation and fostering ongoing refinements to classification systems. In a simpler way, taxonomy today is a systematic framework that integrates morphological and genetic traits to classify living organisms. With the species rank being the backbone to the entire taxonomic science, the processes of speciation and their understanding have the fundamental role of moving taxonomy forward. Hybridization is a key mechanism of speciation, producing hybrids through sexual reproduction between individuals of different species. The genetic structure of a hybrid varies depending on the parental species, resulting in either homoploid hybridization, where the hybrid retains the same chromosome number as its parents, or polyploid hybridization, where the hybrid inherits the combined chromosome sets of both parents, forming a polyploid. Polyploidy can also arise through mechanisms other than hybridization, such as somatic doubling, apospory, or apogamy. Polyploids are classified as autopolyploids when chromosome duplication occurs within a single species, or allopolyploids when resulting from interspecific hybridization. These processes are particularly relevant to the speciation of sect. *Ricciella* genus *Riccia*, where genetic diversity and morphological simplicity drive taxonomic complexity.

The main focus of this work is the genetic relationship between *R. fluitans* and *R. rhenana*. In order this relationship to be revealed, the entire section Ricciella is taken into account. Major works dealing with the genus are analyzed and essential taxonomic clarification are made. Important biological aspects are discussed and a new species-specific characteristics identified. Genome sizes, chromosome counts, isozyme data, and barcodes are generated and analyzed. The results obtained during my work strongly support the hybrid origin of *R. rhenana* and by this its taxonomic position as a separate species, and not as a cytotype of *R. fluitans*. I also prove the already existing hypothesis of *R. fluitans* being a complex of closely related cryptic species. Based on the obtained preliminary results, section *Ricciella* does not form a monophyletic clade, within subgenus *Ricciella*. The current species composition of the section is here not supported. A possible section rearrangement could be as follows: sect. *Ricciella* comprised by the aquatic species *R. fluitans, R. rhenana*, *R. stricta*, *R. stenophylla* and the cryptic species belonging to them, including the different hybrids, withing the R. rhenana complex. A separate section should be established for the *R. canaliculata* group, including also *R. perennis, R. duplex* and the potential other hybrid species. Whether *R. huebeneriana* and *R. multifida* should be included together within the Canaliculata group at this points is still unclear. At the current stage of knowledge on the genus, definite taxonomic rearrangements cannot be made. The data and interpretations on section *Ricciella* presented herein will be used as foundation for further investigation.