FLOW CYTOMETRY IN LICHENOLOGY: IS THE GENOME SIZE CONNECTED WITH ECOLOGY AND FUNCTIONAL TRAITS?

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General knowledge about fungal as well as algal genome size in lichens is extremely poor. Flow cytometry is quite a simple tool for such measurements, routinely used in vascular plants and animal tissues analyses. However, this method has several limitations in lichenology. For example, fungal genomes are very small (ø 37 Mbp in Ascomycota) and lichen thalli usually contain algal or additional fungal partners. We developed and apply a method for a measurement of lichen genome size. Our pilot study on European lichens includes first results on genome sizes of fungal partners, which spans from 22.2 Mbp to 133.4 Mbp. Additionally, we correlated fungal genome sizes with several ecological (substrate preferences) and phenotypical traits (ascospore volume, thallus and reproductive type) and life-history strategy (r or K-strategists). For example, we found that genome size correlates with ascospores volume and r-strategist have smaller genome size than K-strategist. Possible applications of flow cytometry in lichenology (e.g. in taxonomy, polyploids evolution) will be briefly discussed.