
Genomics of niche evolution: tracking the emergence of plant parasitism and mycoheterotrophy

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Abstract

Plants are characterized by photosynthetic nutrition; however, several plant species have lost or reduced their photosynthetic activity, and obtain nutrients and energy through direct connections to host plants or via fungi. Parasitism has appeared independently at least twelve times within plants, whereas mycoheterotrophy did so over 40 times. Currently, complete plastomes of non-photosynthetic plants have been sequenced only for some lineages, including just one or a few species per clade; a total of 25 parasitic or mycoheterotrophic species have been studied to date. This knowledge gap hampers disentangling selective pressures related to this trophic niche shift. Here, we quantify how genetic changes on coding regions of the plastome are correlated with the transition from autotrophy to heterotrophy with an unprecedented dataset with 155 parasitic and mycoheterotrophic species that include obligate and facultative species belonging to eight lineages, together with close autotrophic relatives. Specifically, we sequenced and assembled *de novo* the plastid genome of these species using a shotgun approach on genomic DNA, performed phylogenomic analyses, tested for relaxation or intensification of selective pressures in parasitic and mycoheterotrophic lineages compared to autotrophic relative, and assessed the relationship between time since heterotrophy and plastome degradation. This study thus constitutes a significant advance on our understanding of the macroevolutionary context of the emergence of parasitic lifestyles.

Keywords: niche evolution, parasitism, plastome, mycoheterotrophy, selective pressure, trophic shift

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