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Resolution of phylogenetic patterns within the angiosperm order Asparagales

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The angiosperm order Asparagales, is an economically important monocot order that includes onions (*Allium*), asparagus (*Asparagus*), and agaves (*Agave*). The core Asparagales includes ten families that form a monophyletic group (*Agapanthaceae*, *Agavaceae*, *Alliaceae*, *Amaryllidaceae*, *Aphyllantaceae*, *Asparagaceae*, *Hyacinthaceae*, *Laxmaniaceae*, *Ruscaceae*, and *Themidaceae*). Phylogenetic studies based on four chloroplast gene regions leave numerous relationships among these families unresolved or inadequately supported. In addition, questions remain about the origin, patterns of morphological divergence, geographic diversification, and ecological radiation of this group. Our primary goal is to resolve indistinct relationships among Asparagales families by adding data based on DNA sequence variation of an additional chloroplast region. To date, we have screened six chloroplast gene regions across fifteen taxa representing seven core Asparagales families and outgroups, *Iridaceae* and *Xanthorrhoeaceae* to identify informative phylogenetic variation. A one kilobase region of the large ribosomal subunit protein (rpL14-rpL 36) shows variation between closely related families and we are now expanding our taxonomic sampling within each family. We will conduct independent phylogenetic analyses of this region and combine our new data with existing data from previous studies and from a low-copy nuclear gene (PHYC). This combined phylogeny will potentially provide the additional data needed to resolve the evolutionary relationships among families and help interpret patterns of morphological diversification among Asparagales lineages.