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Why Africa matters: evolution of Old World *Salvia* (Lamiaceae) in Africa FREE

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Abstract

Background and Aims

Salvia is the largest genus in Lamiaceae and it has recently been found to be non-monophyletic. Molecular data on Old World *Salvia* are largely lacking. In this study, we present data concerning *Salvia* in Africa. The focus is on the colonization of the continent, character evolution and the switch of pollination systems in the genus.

Methods

Maximum likelihood and Bayesian inference were used for phylogenetic reconstruction. Analyses were based on two nuclear markers [internal transcribed spacer (ITS) and external transcribed spacer (ETS)] and one plastid marker (*rpl32-trnL*). Sequence data were generated for 41 of the 62 African taxa (66 %). Mesquite was used to reconstruct ancestral character states for distribution, life form, calyx shape, stamen type and pollination syndrome.

Key Results

Salvia in Africa is non-monophyletic. Each of the five major regions in Africa, except Madagascar, was colonized at least twice, and floristic links between North African, south-west Asian and European species are strongly supported. The large radiation in Sub-Saharan Africa (23 species) can be traced back to dispersal from North Africa via East Africa to the Cape Region. Adaptation to bird pollination in southern Africa and Madagascar reflects parallel evolution.

Conclusions

The phenotypic diversity in African *Salvia* is associated with repeated introductions to the continent. Many important evolutionary processes, such as colonization, adaptation, parallelism and character transformation, are reflected in this comparatively small group. The data presented in this study can help to understand the evolution of *Salvia sensu lato* and other large genera.

Keywords: *Salvia*, Lamiaceae, Canary Islands, character evolution, ITS, ETS, Madagascar, ornithophily, pollination, *rpl32-trnL*, Sub-Saharan Africa

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