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Pollinator shifts and geographic range evolution in the origin of *Aeschynanthus acuminatus* (Gesneriaceae)

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How do plants evolve under a geographic mosaic of pollinators? The Grant-Stebbins model predicts that a plant species encountering different pollinators across its range may undergo local adaptation and, subsequently, ecological speciation. We test this hypothesis in the SE Asian genus *Aeschynanthus*, whose 160 species mostly overlap with their putative pollinators, nectar-specialist sunbirds. A conspicuous exception is *A. acuminatus*, a species widespread across mainland East Asia that also occurs in Taiwan, beyond the range of sunbirds. Previous studies of *A. acuminatus* in Taiwan have shown it to be exclusively pollinated by a group of uncommon avian pollinators, generalist passerines. However, comparable data are lacking in mainland Asia, where both sunbirds and generalist passerines are available. In this study, we integrate population genetics with pollination studies to investigate the roles of pollinator shifts and range expansion in the origin of *A. acuminatus*. Genome-wide SNPs acquired by restriction-site associated DNA (RAD) sequencing revealed a mainland origin, preceding range expansion to Taiwan. Pollinator observations at 14 populations of *A. acuminatus* across its range showed varied visitation by both sunbirds and generalist passerines on mainland Asia. The origin of *A. acuminatus* was thus likely coincident with a shift from ancestral sunbird pollination to a more generalized pollination system, possibly driven by selection for reproductive assurance in an unpredictable pollinator climate. This ecological shift then allowed *A. acuminatus* to expand its range beyond that of sunbirds. Our research sheds light on how the evolution of pollination systems can influence the origin and range dynamics of species.

Keywords: Pollinator shift; Ornithophily; Generalization; RADseq; Range expansion