Checking the status of infraspecific taxa within *Galactia jussiaeana* (Fabaceae) using Berg's correlation-pleiades hypothesis

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Abstract

Berg's correlation-pleiades hypothesis proposes that phenotypic variation between plant vegetative and reproductive traits is decoupled (i.e. varies independently) due to different selective pressures: pollinators in reproductive traits and environment in vegetative traits. We used this hypothesis to check if the intraspecific leaf variation in *Galactia jussiaeana* is accompanied by an equal variation in floral traits. If so, we might be facing a process of divergence between the two lineages, since differences in floral morphology could restrict gene flow due to a mismatch with pollinators. Our results showed that there was no correlation between the variation in vegetative and reproductive traits in *G. jussiaeana* var. *angustifolia*, demonstrating that both are genetically uncoupled and respond to different selective pressures. There were also no significant differences in reproductive structures between the alternative and the typical variety. For these reasons, we propose the synonymization of *G. jussiaeana* var. *angustifolia* under *G. jussiaeana*.

Key words: alpha taxonomy, floral traits, variety, subspecies, Leguminosae, taxonomic theory

Introduction

Species are the basic units for biogeographic, ecological, evolutionary, and conservation studies; thus, methods for delimiting species are necessary to achieve greater rigor and objectivity in scientific research. Some attempts to delimit species have achieved relative success, such as the use of small sequences of mitochondrial DNA for animals (DNA Barcode; Hebert *et al.* 2004). There is not yet a sequence working as a DNA barcode for all plant lineages, although several candidates have been tested (Cowan *et al.* 2006; Hollingsworth *et al.* 2009; CBOL 2009). Despite efforts to discover these DNA barcode sequences, morphology is still the main source of characters for description and recognition of plant species; hence, the discovery of methods to employ in morphological taxonomy must be objective and robust.

Some authors point out that taxonomy is a hypothesis-driven science (Henderson 2005), so an explicit methodology to test hypotheses should be applied. Currently, the method most used to test differences among groups of individuals is multivariate analysis (e.g. cluster analysis, PCA, MANOVA; Henderson 2006; Pedersen 2010). These tests quantify the amount of trait similarities and differences for clustering or splitting the individuals into two or more species. Yet, it remains unclear how much, or what kind, of difference is enough to recognize two groups of individuals as different taxa.

According to de Queiroz (2005), species are metapopulation lineages (or segments of) evolving separately. These lineages are joined together by gene flow in organisms with sexual reproduction (Templeton