

CAN POPULATION GENETIC STRUCTURE BE PREDICTED FROM LIFE HISTORY TRAITS?

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Population genetic structure is a feature of paramount importance in evolutionary biology. Earlier comparative studies have shown that genetic structure depends on species ecological attributes and life history traits, but species relatedness had not been accounted for. Here we reevaluate the relationships between genetic structure and species traits in seed plants. Each species was characterized by a set of life history and ecological features as well as by its geographic range size, its heterozygote deficit (F_{IS}) and its genetic structure (G_{ST}) at nuclear and organelle markers, to distinguish between pollen- and seed-mediated gene flow. We use both a conventional regression approach and a method that controls for phylogenetic relationships among taxa. Many relations between ecological traits and G_{ST} observed in conventional analyses vanish when using phylogenetically independent contrasts. Once covariation among traits is taken into account, genetic structure is shown to be related with only on a few synthetic traits such as mating system for nuclear markers and seed dispersability or geographic range size for organelle markers. These results suggest that the relationships between genetic structure and life history traits cannot be easily generalised as they are strongly context-dependent.