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CHLOROPLAST, MITOCHONDRIAL AND NUCLEAR DIVERSITY IN PLANT POPULATIONS: A COMPARATIVE ANALYSIS

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Plants offer excellent models to investigate how gene flow shapes the organization of genetic diversity. Their three genomes can have different modes of transmission and hence experience varying levels of gene flow. We have compiled studies of genetic structure based on chloroplast DNA (cpDNA), mitochondrial DNA (mtDNA) and nuclear markers in seed plants. Based on a data set of 183 species belonging to 103 genera and 52 families, we show that the precision of estimates of genetic differentiation (G_{ST}) used to infer gene flow is mostly constrained by the sampling of populations. Mode of inheritance appears to have a major effect on G_{ST}. Maternally inherited genomes experience considerably more subdivision (median value of 0.67) than paternally or biparentally inherited genomes (~0.10). G_{ST} at cpDNA and mtDNA markers covary narrowly when both genomes are maternally inherited, whereas G_{ST} at paternally and biparentally inherited markers also covary positively but more loosely and G_{ST} at maternally inherited markers are largely independent of values based on nuclear markers. A model-based gross estimate suggests that, at the rangewide scale, historical levels of pollen flow are generally at least an order of magnitude larger than levels of seed flow (median of the pollen-to-seed migration ratio: 17) and that pollen and seed gene flow vary independently across species. Finally, we show that measures of subdivision that take into account the degree of similarity between haplotypes (N_{ST} or R_{ST}) make better use of the information inherent in haplotype data than standard measures based on allele frequencies only. The use of these estimators emphasizes the high level of geographical structure found in most plant species when using maternally inherited markers, in stark contrast with biparentally inherited nuclear markers. This finding has attracted much interest, giving birth to a new discipline, plant phylogeography, and leading to the development of many important practical applications, such as traceability and ecocertification of forest products and the identification of plant populations for conservation. Some examples are provided.