

Bioinformatic Approaches in Population Genetics and Phylogenetic Studies

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Abstract : Biologists with a special field of population genetics and phylogeny have different research tasks such as populations' genetic variability and divergence, species relatedness, the evolution of genetic and morphological characters, and identification of DNA SNPs with adaptive potential. To tackle these problems and reach a concise conclusion, they must use the proper and efficient statistical and bioinformatic methods as well as suitable genetic and morphological characteristics. In recent years application of different bioinformatic and statistical methods, which are based on various well-documented assumptions, are the proper analytical tools in the hands of researchers. The species delineation is usually carried out with the use of different clustering methods like K-means clustering based on proper distance measures according to the studied features of organisms. A well-defined species are assumed to be separated from the other taxa by molecular barcodes. The species relationships are studied by using molecular markers, which are analyzed by different analytical methods like multidimensional scaling (MDS) and principal coordinate analysis (PCoA). The species population structuring and genetic divergence are usually investigated by PCoA and PCA methods and a network diagram. These are based on bootstrapping of data. The Association of different genes and DNA sequences to ecological and geographical variables is determined by LFMM (Latent factor mixed model) and redundancy analysis (RDA), which are based on Bayesian and distance methods. Molecular and morphological differentiating characters in the studied species may be identified by linear discriminant analysis (DA) and discriminant analysis of principal components (DAPC). We shall illustrate these methods and related conclusions by giving examples from different edible and medicinal plant species.

Keywords : GWAS analysis, K-Means clustering, LFMM, multidimensional scaling, redundancy analysis

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