NON-PARAMETRIC MODELLING OF MULTIVARIATE GENETIC DISTANCES IN THE ANALYSIS OF SPATIAL POPULATION STRUCTURE AT FINE SCALE

*Bruno, C.[1], Macchiavelli, R.[2] y Balzarini M.[1]

[1]Biometry Unit, College of Agriculture. Universidad Nacional de Córdoba. Av. Valparaíso s/n. Ciudad Universitaria. CC 509 (5000). Córdoba. Argentina. [2]Department of Agronomy and Soils, University of Puerto Rico, P.O.Box 9030, Mayagüez, PR 00681-9030.

*Corresponding author: cebruno@agro.uncor.edu, TE: 54-351-4334116 ext 219

Species dispersal studies provide valuable information in biological research. Non-random dispersion patterns of individuals induce autocorrelation in the data. If population variance is estimated assuming independent data, such correlations could bias statistical inferences about genetic variability. Modelling spatial autocorrelation not only improves population parameter inferences, but also provides biological insight such as the extent of population structure. In population genetics, spatial autocorrelation has been analyzed via several univariate statistics and most of them are highly dependent on the sampling design. New geostatistical approaches (variogram-based analyses) can be used to overcome these problems. In this paper we propose a non-parametric variogram-based analysis of multivariate genetic distances between DNA samples that have been genotyped by means of multilocus-multiallele markers. The method allows inferring genetic structure in fine scale. Under the assumption of stationarity in the spatial process, an empirical variogram is expressed as a plot of the squared Euclidean genetic distances *vs*. spatial distances between pairs of samples. A non-parametric fit of the spatial trend is obtained by LOESS (Local Regression) smoothing. Then, the predicted LOESS values are explained by segmented regressions (SR) to obtain classical variogram parameters that explain the spatial structure. The autocorrelation analysis carried out by the LOESS/SR procedure was compared to the analysis via parametric variograms. We use multivariate and single-locus genetic distances calculated from a microsatellite data set for which autocorrelation was previously reported. The LOESS/SR method produced a good fit providing similar value of published autocorrelation for this data. The fit by LOESS/SR was simpler to obtain than the classical geostatistical analysis since initial parameter values are not required. The LOESS/SR method would facilitate spatial analysis in population genetic studies.