

GENE FLOW AMONG WILD *Phaseolus lunatus* L. POPULATIONS IN THE CENTRAL VALLEY OF COSTA RICA

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The Central Valley of Costa Rica is considered as a region of diversity for the wild *Phaseolus lunatus* form. Lima bean is a self-compatible annual or short-living perennial species with a mixed mating system. Despite small population sizes (66% of populations with fewer than 30 individuals), frequent bottlenecks, a low allogamy rate ($t < 10\%$), major alleles at several loci, and restricted genetic neighborhood area ($NA = 56 \text{ m}^2$), isozyme studies revealed very few heterozygous individuals ($H_o = 0.013$) and significant polymorphism within population ($GST = 0.575$). Using microsatellites markers, few heterozygous individuals ($H_o = 0.012$) and high intrapopulation polymorphism ($GST = 0.303$) were also found (Baudoin et al., 2000). This significant intrapopulation diversity could be due in part to the existence of gene flow. According to Slatkin (1981, 1985a), gene flow encompasses several mechanisms of gene exchange among populations, including movement of gametes, zygotes, individuals or groups of individuals from one place to another, and extinction and recolonization of entire populations.

To assess gene flow, 9 populations from Heredia were scored with 10 pairs of microsatellites primers isolated from *Phaseolus vulgaris* L. by the Centro Internacional de Agricultura Tropical (CIAT). Two models were applied : i) Wright's island model (1951). The mean rate of migration (Nm) was calculated by analysing ten microsatellites loci using the Crow and Aoki (1984) formula. ii) Slatkin's private alleles model (1985b) and the corrected estimate of Nm by Slatkin and Barton's method (1989). The estimation of gene flow was made using the Genepop software (Raymond, Rousset, 1995). An average of the genetic differentiation coefficients was calculated by the SpaGeDI software according to classes of distance between pairs of wild populations (Hardy, Vekemans, 2002).

Estimation of gene flow

The fixation index (F_{ST}) was 0.346, and average inbreeding coefficient within populations was high ($F_{IS} = 0.916$). The number of migrants per population and per generation from Wright's method was 0.47. By the method of Slatkin using private alleles, Nm was estimated at 0.099 for $n = 10$, 0.075 for $n = 25$, and 0.060 for $n = 50$. The mean number of individuals per population was 33 and the mean frequency of the private alleles was 0.35. The corrected number of migrants per population and per generation was 0.06. Nm is underestimated with Slatkin's method when the seed number per population is heterogeneous (Slatkin, 1985b).

1000 900 800 700 600 500 400 300 200 100 01,00,50,0DistanceFst

Figure 1. Linear relation between geographic distance (in m) and genetic coefficient differentiation (F_{ST}).

Spatial structure of genes and isolation by distance

For distances ranging between 0 and 997 m, a linear relation ($P = 0.000$) between genetic coefficient differentiation and geographic distance was obtained (Fig. 1). Geographic distance explained 18% of the divergence among populations. A linear relation between gene flow and geographic distance ($P = 0.005$) was also noticed for this range of distances. Beyond 1000 m, however, no relation between genetic coefficient differentiation of gene flow and geographic distance was observed.

Assuming no selection of populations and an equilibrium between genetic drift and gene flow, genetic differentiation coefficient between populations is inversely related to gene flow between populations ($Nm = (1-F_{ST})/(4F_{ST})$; Slatkin, Barton, 1989). The genetic differentiation coefficient decreased from 0.64 to 0.43 while Nm increased from 0.14 to 0.33 comparing distance classes "227-997m" and "0-226 m". Such genetic differentiation coefficients characterize populations with very significant divergence and weak to moderate gene flow (Wright, 1978).

Conclusion and prospects

The island model and isolation by distance models were employed to measure indirectly the cumulative effects of gene flow. Wright's method is adequate for situation where equilibrium between genetic drift and gene flow has been reached in a large number of populations, which are constant in size and never go extinct (Whitlock, Mc Cauley, 1999). Slatkin and Barton (1989) compared indirect methods for estimating average level of gene flow and showed that F_{ST} and rare alleles methods yield comparable estimates under a wide variety of conditions and found that F_{ST} is likely to be more useful under realistic conditions. With enzymes (previous work) and microsatellites (this study), low to moderate levels of gene flow (0.06 to 0.47) were noticed in wild Lima bean populations in the Central Valley of Costa Rica. Both enzymes and microsatellites markers showed that very great divergence (Wright, 1978) occurs among populations. This is probably due to restricted gene flow, with genetic drift therefore playing a major role in the genetic structure of Lima bean populations in the study area.

References

- Baudoin JP., Maquet A., Rocha O. (2000). Final report, Phase II, IPGRI.
- Crow JF., Aoki K. (1984). Proc. Natl. Acad. Sci. USA 81: 6073-6077.
- Hanski IA., Gilpin ME. (1997). Academic Press, New York, USA.
- Hardy O., Vekemans X. (2002). Molecular Ecology Notes 2 : 618-620.
- Raymond M., Rousset F. (1995). J. Hered. 86 :248-249.
- Slatkin M. (1981). Genetics 99: 323-335.
- Slatkin M. (1985a). Annu. Rev. Ecol. Syst. 16: 393-430.
- Slatkin M. (1985b). Evolution 39: 53-65.
- Slatkin M., Barton NH. (1989). Evolution 43: 1349-1368.

Whitlock MC., McCauley DE. (1999). *Heredity* 82: 117-125.

Wright S.(1951). *Ann. Eugen.* 15: 325-354.

Wright S.(1978). Chicago, USA. University of Chicago Press.

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