Observations about risks of genetic erosion and drift during multiplication and regeneration of germplasm, using wild common bean as model.

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Introduction

Conservation of genetic variability and integrity of seed accessions is one of the major duties of genebanks. This is particularly relevant for wild forms the interest of which often lies in their higher genetic diversity as compared to cultivated forms that might have suffered founder effects during domestication (Debouck 1999). Seed multiplication and regeneration might result in losses of genetic diversity or erosion if not enough individuals from the original sample are allowed to contribute their genes to the next generations (Roos 1984). Drift and shift can occur in case individuals contribute differently to the genetic makeup of the next generations (Breese 1989). Using wild *Phaseolus vulgaris* L. as a crop model, we were interested in testing practical multiplication procedures to limit genetic erosion and drift.

Materials and Methods

In order to quickly promote drift a single population of wild common bean (G21244, or DGD-1956, from Peru, Cajamarca, San Pablo, 78°50'W, 7°11'S, 2,020 masl) was planted in three contrasting environments in Colombia. These were A (Palmira, 1,000 masl, 24°C, 1,000 mm rainfall, bimodal distribution), B (Popayán, 1,750 masl, 17°C, 2,100 mm rainfall rather unimodal), and C (Popayán, 1,750 masl, 17°C, no rainfall because of a complete plastic roof cover but hand watering to maintain plants without water stress). Seventy-nine original plantlets were established and four root cuttings were obtained from each. One cutting was planted in each environment for yield evaluation, and the last cutting was used for metabolism enzyme assays. Three systems (diaphorase DIA, isocitrate dehydrogenase IDH, and peroxidase PRX) were tested through starch electrophoresis (after Wendel & Weeden 1989). Observed alleles were named after the nomenclature proposed by Koenig & Gepts (1989). Original frequencies were obtained from the fourth cutting, while calculated frequencies were estimated from computing observed genotypes with their respective seed production in each environment.

Results and Discussion

Different allelic frequencies were observed for the three allozymes (Table 1). Original frequencies partly reflect frequencies at the collection site, and some alleles seem often to occur at quite low frequencies. Calculated frequencies indicate how these frequencies would evolve given observed seed productions over one generation: frequencies are likely to change instead of remaining constant and rare alleles are likely to disappear.

Table 1. Original and calculated frequencies for alleles found in the three enzyme systems.

Enzyme	Allele	Original frequency	Calculated frequency in environment A	Calculated frequency in environment B	Calculated frequency in environment C
DIA1	95	0.405	0.730	0.401	0.282
	100	0.595	0.270	0.599	0.718
IDH	98	0.013	0	0.021	0.019
	100	0.987	1	0.979	0.981
PRX	98	0.937	1	0.986	0.957
	100	0.063	0	0.014	0.043

Variance analysis shows significant differences in average seed production among the three environments. Seed production in environment C is higher as compared to environments A and B,

and differences among individuals are lesser (Figure 1). The number of individuals producing no seed is reduced in environment C as compared to environments A and B. In environment A the accession indeed did not adapt and chance to survive over several years is nil, while chances to produce offspring are slightly better in environment B. While environments B and C have the same altitude and average temperature, they differ completely in the rainfall regime. In the latter, in view of a conservation target of a minimum of 2,000 seeds (Anonymous 1994), at least fifty individuals would contribute to that target; two individuals in environment C produce more than 1,800 seed each.

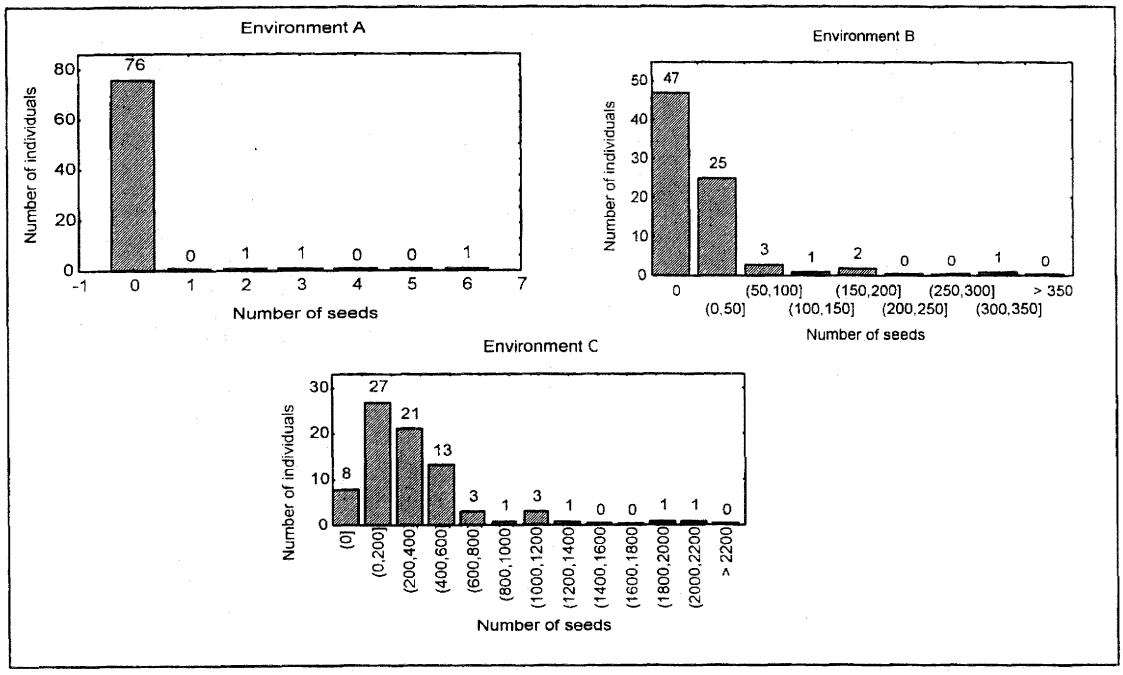

Figure 1. Histograms of individual seed production in the three environments.

One can tentatively conclude that i) germplasm should be multiplied in a site the ecological conditions (namely altitude) of which are close to the original ones, ii) the sample used for regeneration should be the largest possible (at least 70 reproducing plants), and iii) the same number of seeds should be harvested on each reproducing plant with due consideration to the final number of seeds to be stored.

References

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