Genetic Diversity in Canadian Common Bean Varieties Since 1930

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Introduction

Genetic improvement of common bean (*Phaseolus vulgaris* L.) in Canada has a history of more than 120 years.

Early breeding efforts, which started soon after the establishment of the Central Experimental Farm in Ottawa in 1886, included testing of dry and garden bean introductions.

Long-term dry bean production data (Stats Canada, 2008) suggests that average dry bean yield in Canada has increased by 63% from 1.1 $t\ ha^{-1}$ during 1910s and 1920s (20 year average) to 1.8 $t\ ha^{-1}$ in 1990s and 2000s (18 year average).

Over the years, the genetic diversity in the natural gene pools of *P. vulgaris*, introduction from other national and international bean breeding programs, along with variation derived through hybridization and recombination, as well as occasional inter-specific hybridizations have been the main sources of genetic variation employed by the Canadian bean breeders.

The coefficient of parentage, also referred to as coefficient of co-ancestry or kinship, is one of the tools used to study genetic diversity among genotypes.

First used by Malecot (1948), the coefficient of parentage (f_{ij}) is computed based on the pedigree data and estimates the probability that, at a single locus, a random allele from the i^{th} individual and a random allele from the j^{th} individual are identical by descent (Bernardo 2002).

Objectives

To develop a database of Canadian common bean pedigree information, containing the available lineage of the Canadian bean varieties, and their ancestors.

To assess the genetic diversity among common bean varieties released in Canada since 1930.

Materials and methods

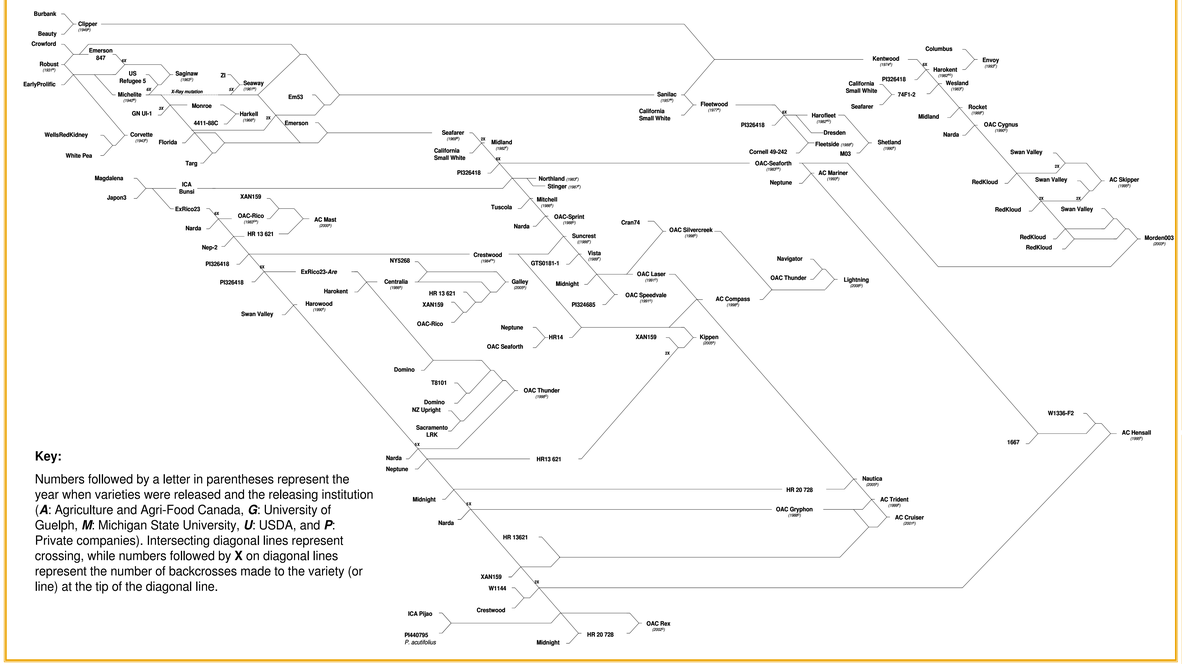
A pedigree database of the dry bean varieties of different Canadian market classes (navy, black, great northern, pinto, pink, small red, dark red kidney, light red kidney, and cranberry) released in Canada from 1931 to 2008 were developed.

The coefficient of parentage was estimated for all possible pairwise combinations of varieties, parental and (or) ancestral genotypes using the software 'KIN' (Tinker and Mather 1993).

Cluster analysis (PROC CLUSTER in SAS) was employed to study the genetic diversity of contemporary common bean varieties released in Canada. Dendrograms were generated separately for varieties of Mesoamerican, Durango and Nueva Granada races.

A RAPD fingerprinting dataset (S Mack, T Michaels, and KP Pauls; unpublished) including a sub-set of 28 bean genotypes with 150 RAPD fragments (400-3000 bp) were used to compare the results of pedigree- and RAPD-based diversity analyses.

Ancestry of Navy Bean Varieties Registered in Canada Since 1930



Key:

Numbers followed by a letter in parentheses represent the year when varieties were released and the releasing institution (***A***: Agriculture and Agri-Food Canada, ***G***: University of Guelph, ***M***: Michigan State University, ***U***: USDA, and ***P***: Private companies). Intersecting diagonal lines represent crossing, while numbers followed by **X** on diagonal lines represent the number of backcrosses made to the variety (or line) at the tip of the diagonal line.

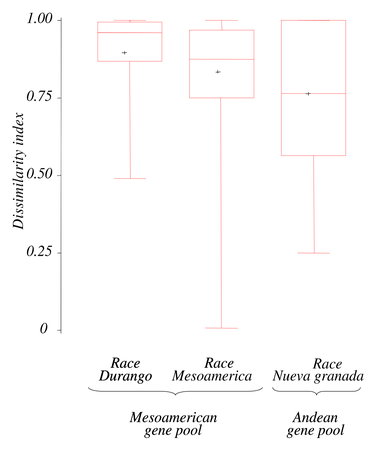


Figure 1. Frequency distribution of dissimilarity index values between pair-wise combinations of varieties of different evolutionary race- and gene pool-origins. Boxes represent the inter-quartile range. The whiskers represent the range. The solid line across the box indicates the median, while + indicates the average.

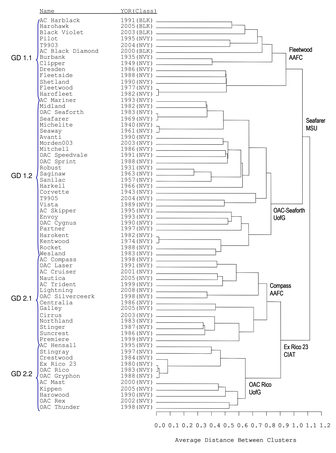


Figure 2. Dendrogram resulting from cluster analysis of varieties of **race Mesoamerica origin** (Navy and black market classes; NVY and BLK, respectively). Varieties on the branches of the dendrogram are the representative varieties with the highest value of average coefficient of parentage. GD1.1 to GD2.2 represent 4 genetic diversity groups.

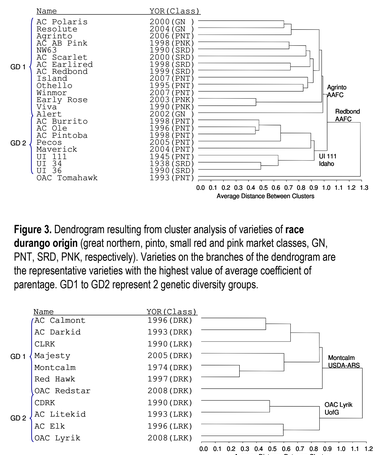


Figure 3. Dendrogram resulting from cluster analysis of varieties of **race durango origin** (great northern, pinto, small red and pink market classes, GN, PNT, SRD, PNK, respectively). Varieties on the branches of the dendrogram are the representative varieties with the highest value of average coefficient of parentage. GD1 to GD2 represent 2 genetic diversity groups.

Figure 4. Dendrogram resulting from cluster analysis of varieties of **race Nueva granada origin** (dark and light red kidney market classes, DRK and LRK, respectively). Varieties on the branches of the dendrogram are the representative varieties with the highest value of average coefficient of parentage. GD1 to GD2 represent 2 genetic diversity groups.

Table 1. Average coefficient of parentage for inter-market class pair-wise combinations, representing the frequency of inter-market class introgressions since 1930 in Canadian beans.

Market Class	Mesoamerican gene pool						Andean gene pool		
	Race Mesoamerica		Race Durango				Race Nueva Granada		
	Navy	Black	Pinto	GN	Pink	SR	LRK	DRK	CRN
Navy		2.0	1.3	2.1	0.9	0.8	0.1	0.1	0.0
Black			0.2	4.5	0.1	0.0	0.2	0.0	0.0
Pinto				1.2	1.4	4.1	0.1	0.1	0.0
Great Northern					0.3	0.2	1.3	0.0	0.0
Pink						5.1	0.0	0.1	0.0
Small Red							0.0	0.1	0.0
Light Red Kidney								7.3	0.0
Dark Red Kidney									0.0

Summary of results

Narrow genetic diversity of Canadian bean varieties of Andean-origin (dark and light red kidney and cranberry market classes) is notable.

The genetic diversity within bean varieties of race mesoamerica origin (navy and black market classes) can be divided into two major genetic diversity groups identified by the navy varieties Ex Rico 23 and Seafarer. These two diversity groups can further be divided into 4 sub-groups, identified by OAC Rico, AC Compass, OAC Seaforth and Fleetwood.

Two major diversity groups were identified in Canadian beans of race Durango, identified by varieties Agrinto and UI111, while varieties of Nueva granada-origin were divided into two groups identified by varieties Montcalm and OAC Lyrick.

The highest levels of inter-market class introgressions were observed within bean varieties of race durango, while occasional inter-market class introgressions existed for varieties of other evolutionary race origins.

The pedigree- and RAPD-based dendrograms were somewhat similar suggesting that pedigree information will continue to be useful to inexpensively identify diverse parents in the bean breeding programs.

References

Bernardo, R. 2002. Breeding for quantitative traits in plants. Stemma Press, Woodbury, MN. Malecote G. 1948. Masson et Cie., Paris. Tinker NA and DE Mather. 1993. The Journal of Heredity 84:238.

Acknowledgment

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