

How to identify edible-pod pea varieties in a germplasm collection

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In breeding of multi-purpose crops, such as peas (*Pisum sativum*), there is always a concern about which are the best quantitative descriptors to characterize germplasm for each one of their uses and to apply in multi-trait selection in breeding programs (3, 7). The characterization of the genetic material has to be mostly based upon high heritable traits in order to know the variability within the collection. Only those characters that show consistent genetic versus environmental basis should be taken into account, because those markedly influenced by the environment are unreliable and uneven from one place to another. As many metrical characters (that are important from an agricultural point of view but has not been yet genetically analyzed) either have low stability in different environments or their genetic basis are low, they are not able to be used for breeding programs until they were better known. Instead, reproductive characters less affected by environmental factors and interactions must be considered (2). They are useful along with the habitual quantitative ones when the material is intended for a breeding program.

The objective of this paper is to assess the role of some quantitative traits with consistent genetic basis to identify varieties of pea that own edible pod characters usable in a breeding program. Since these edible-pod peas are becoming important in many countries as food, and they can be grown as winter alternative to snap bean, the development of a protocol for an early identification of such sources of germplasm from large pea collections is highly relevant.

To meet this objective, the genetic parameter C , called constancy by Ron and Ordas (5) and repeatability by Sanchez et al. (6) was estimated on the accessions of pea from the germplasm collection maintained at the Mision Biologica de Galicia (Pontevedra, Spain) (4). This parameter was first estimated by Goodman and Paterniani (2) as the ratio genotypic versus non genotypic variances ($\Phi^2g / \Phi^2g + \Phi^2e$, where Φ^2g is the genotypic variance and Φ^2e is the environmental one) as an useful parameter to choose traits for taxonomical classification of maize germplasm.

The values of C were reported by Amurrio et al. (Legumes Breeding Group) (1) from the study of 105 accessions from Spain and Portugal grown in field trials carried out in two different environments in the NW of Spain in two years (1991 and 1992). The genetic parameter C , as based upon variance components, depends on allelic frequencies so it is not an universal value. Nevertheless it must be considered that the variances in this case were estimated over a wide range of accessions so the trend showed for their values must be seriously regarded as a general one that could be an useful orientation when studying other germplasm sources.

Values for C over 0.5 indicate half proportion of genotypic versus environmental variance while values over 1.0 show that genotypic variance exceed the value of

environmental one. The estimates obtained in the studied germplasm regarding relevant traits for edible-pod varieties appear in table 1.

Table 1. Values of C for some quantitative traits in pea (1).

Trait	C
Pod length (cm)	1.43
Pod width (cm)	1.22
Index length/width	0.70
Number of ovules/pod	0.66
Pod fresh weight (g)	1.06
Pod dry weight (g)	0.74

In germplasm characterization a large number of accessions are usually evaluated so it is not possible to use as descriptors quantitative traits which demand a lot of time and resources to be measured. Nevertheless, when evaluation of germplasm is focused in breeding, the number of varieties to be studied is more reduced since many of the accessions maintained in a germplasm collection have no agronomic value by themselves. In these conditions, it could be possible to make the evaluation according to quantitative traits. The chosen ones should have previously shown a consistent genetic basis displaying medium-high values for C in the traits of particular interest.

As a conclusion, the traits listed in table 1 could be used as genetic-based descriptors for the identification of edible-pod pea varieties based upon the evaluation data from large germplasm collections as a preliminary step in breeding programs before further evaluations.

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