A core set of bean genotypes established from phenotyping of a Snap Bean Panel

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Introduction

Snap beans, also known 'green beans', are a group of common bean cultivars (*Phaseolus vulgaris* L.) whose immature pods are edible. The objective of this work was to investigate the pod phenotypic diversity in snap bean accessions collected from European gene banks, working collections and seed companies (Snap Bean Panel, SBP) in order to establish a core set (Core-SBP) including the maximum phenotypic diversity and minimum redundancy.

Material and Methods

A total of 311 snap bean lines were obtained in greenhouse by self-crossing of individual plants (SBP). The SBP was evaluated at Villaviciosa, Spain *(43°2901N, 5°2611W; elevation 6.5 m*) in greenhouse (2018) and field (2019 and 2020) using a randomized design with a plot per line and 10 plants per plot. Ten pods per line in each trial were digitally phenotyped using Tomato Analyzer software[1]. Number of seeds per pod and 25 seed-weight were also recorded as well as pod color and mains seed coat color.

A HCPC (Hierarchical Clustering on Principal Components) analysis was carried out to identify the main clusters from the quantitative pod dimension traits. Statistical analyses were carried out using the mean phenotypic data and performed with the packages FactoMineR and FactoExtra in R platform[2, 3].

To establish a subset of lines (Core-SBP) that represents most of the phenotypic diversity gathered in the SBP, a hierarchical method was followed[4]. The lines were grouped considering the results provide by HCPC and, into each group, the lines were classified according to pod color and main seed coat color.
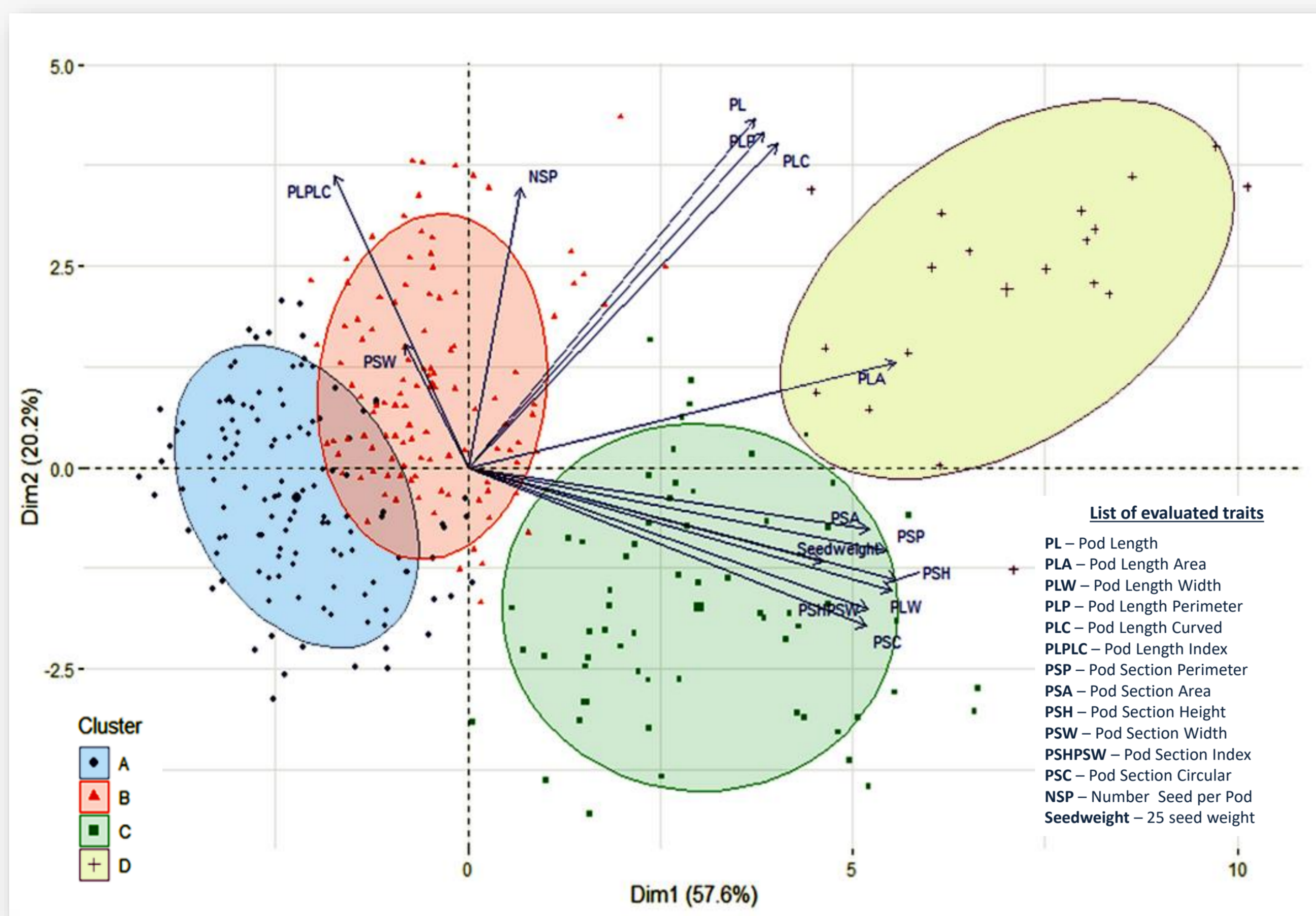

Figure 1. Biplot showing the distribution of the 311 snap bean lines considering the two main estimated dimensions revealed by Principal Components Analysis.

Results: phenotypic variation

The SBP showed a wide phenotypic variation for all pod traits and redundant lines. HCPC analysis using the 14 pod quantitative traits revealed two dimensions explaining 78 % of the variation, and four main clusters *(see Figure 1)* with significant differences among them for shape and size were established.

The SBP also showed wide variation for color with green (212 lines), yellow (80), purple (7), green mottled (17), and yellow mottled (1) pod colors. More than half the lines had a seed coat color (170) including cream (37), brown and dark brown (66), red (4), purple (10), and black (53).

Results: establishment of Core-SBP

Considering the four groups provide by HCPC analysis, the five pod colors and, the nine main seed coat colors, a total of 54 phenotypic classes were identified in the SBP. Cluster C was the most diverse with 17 classes followed by cluster A (15 classes), cluster B (13), and cluster D (9). The largest class has short green pods and white seed (73 lines included in cluster A) followed by the class with medium-length green pods and white seeds (23 lines included in cluster B) and a class with medium-length green pods and black seeds (20 lines included in cluster B). Finally, one line per phenotypic class was randomly selected to establish the Core-SBP *(see Figure 2).*

Figure 2. Pod phenotype of the 54 snap bean lines selected to represent the pod diversity included in the Snap Bean Panel.

Conclusions

- Using the phenotypic variation, a set of 54 lines (Core-SBP) was selected to represent the pod phenotypic diversity included in the Snap Bean Panel.

- Additional phenotyping and genotyping of the SBP can lead to validate or change the composition of that Core-SBP.

References:
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