



Diversity of pea (*Pisum sativum*) accessions based on morphological data for sustainable field pea breeding in Argentina

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ABSTRACT. We characterized 13 accessions of dry peas of different origins from various growing regions in Argentina, based on three replications of 20 plants cultivated in 2009 and 2010 in a greenhouse, with the objective of selecting those with favorable characteristics for use in breeding programs. Significant differences were found for length and width of stipule and pod, length of the internodes and leaflets, plant height, total number of nodes, number of nodes at the first pod, number of days to flowering and to harvest, number of pods and seeds per pod, 100-seed weight and grain diameter, demonstrating a high degree of genetic variability. Phenotypic correlation analysis demonstrated that large pods produced more seeds per pod, but the seed weight decreased. Plants with smaller number of nodes in the first pod were more productive. Estimates of genotypic correlation coefficients indicated a strong inherent association among the different traits. Clustering methods grouped the accessions into five clusters. Cluster 5 included two accessions and showed the highest values for length and width of stipules (4.9 and 4.5 cm, respectively), length

of leaflets (7.43 cm) and days to flowering (122.6), while cluster 3, with one accession, and cluster 4, with two accessions, showed the highest values for number of seeds per pod (3.78 and 4.39), number of pods per plant (5.33 and 5.70), length of pods (5.54 and 5.72 cm), and width of pods (1.21 and 1.20 cm, respectively). We conclude that accessions in clusters 3 and 4 would be useful for crosses with other cultivars in pea breeding programs.

Key words: Genetic variability; Heritability; Principal component analysis; Cluster; Parental selection