Supplementary files - Captions

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Table S7 AMOVA's pairwise φST values and corresponding P-values between Croatian common bean morphogenetic groups based on SNP marker data

Figures

Figure S1 The choice of the most likely number of clusters (K) inferred from SSR marker data of 174 Croatian common bean accessions: ln P(X| K) values for each of the 30 independent runs for each K using a model-based clustering method of Pritchard et al. (2000) and ΔK values for each K based on the second-order rate of change of the likelihood function with respect to K described by Evanno et al. (2005)

Figure S2 The choice of the most likely number of clusters (K) inferred from SNP marker data of 174 Croatian common bean accessions: ln P(X| K) values for each of the 30 independent runs for each K using a model-based clustering method of Pritchard et al. (2000) and ΔK values for each K based on the second-order rate of change of the likelihood function with respect to K described by Evanno et al. (2005)