Supplementary Materials

Genetic diversity among wild and cultivated germplasm of the perennial pasture grass *Phalaris aquatica*, using DArTseq SNP marker analysis

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Supplementary Table S1. Analysis of molecular variance (AMOVA) of the 9 populations of *Phalaris aquatica* identified by structure analysis of the 94 wild and cultivated accessions/cultivars.

Source of variation	Degrees	Sum of	Variance	Percentage of	P-value†
	of	squares	component	total variance	
	freedom				
Among populations	8	0.1777	7.10	29.01	<0.001
Within populations	85	0.2529	32.31	70.99	< 0.003
Total	93	0.4306	39.41	100	

 \dagger on the basis of 1023 permutations across the full data set and signifies the probability of obtaining by chance a higher or equal value of observed F_{ST} value (0.29).

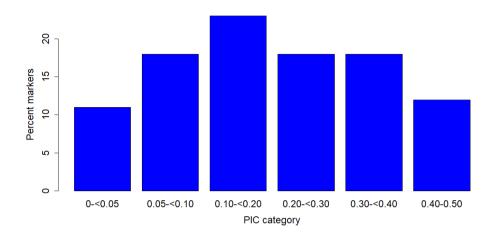


Fig. S1. Distribution of PIC values of SNP markers.

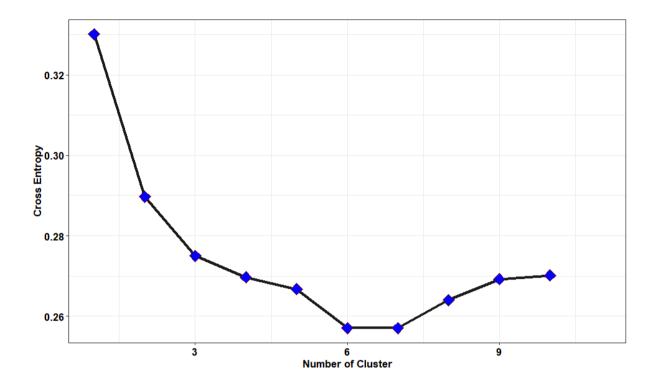


Fig. S2. Values of the cross-entropy criterion for sNMF runs for wild accessions. The crossentropy criterion curve exhibited a monotonic decrease and plateaued at K = 6 possible populations. The minimum cross-entropy value (0.2570) denotes the possible number of clusters in a population.

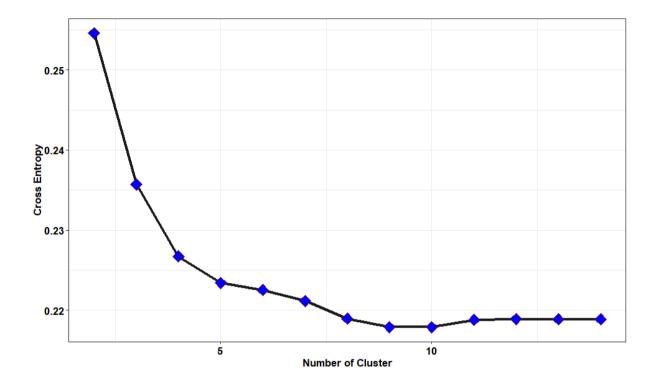


Fig. S3. Values of the cross-entropy criterion for sNMF runs for wild and cultivated accessions. The cross-entropy criterion curve exhibited a monotonic decrease and plateaued at K = 9 possible populations. The minimum cross-entropy value (0.2179) denotes the possible number of clusters in a population.

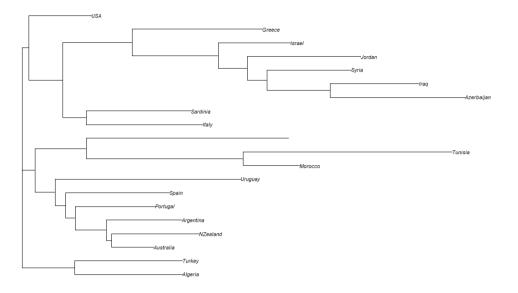


Fig. S4. Dendrogram of relations between countries based on the pairwise genetic distance matrix of F_{ST} values.