

SUPPLEMENTARY MATERIALS

Genetic position of Hungarian Grey among European cattle and identification of breed-specific markers.

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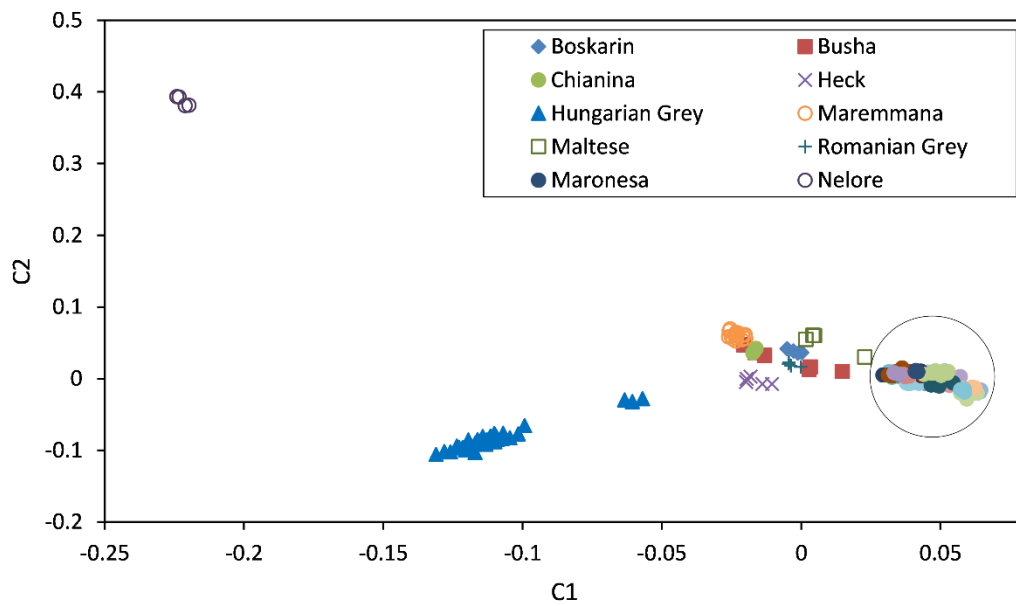
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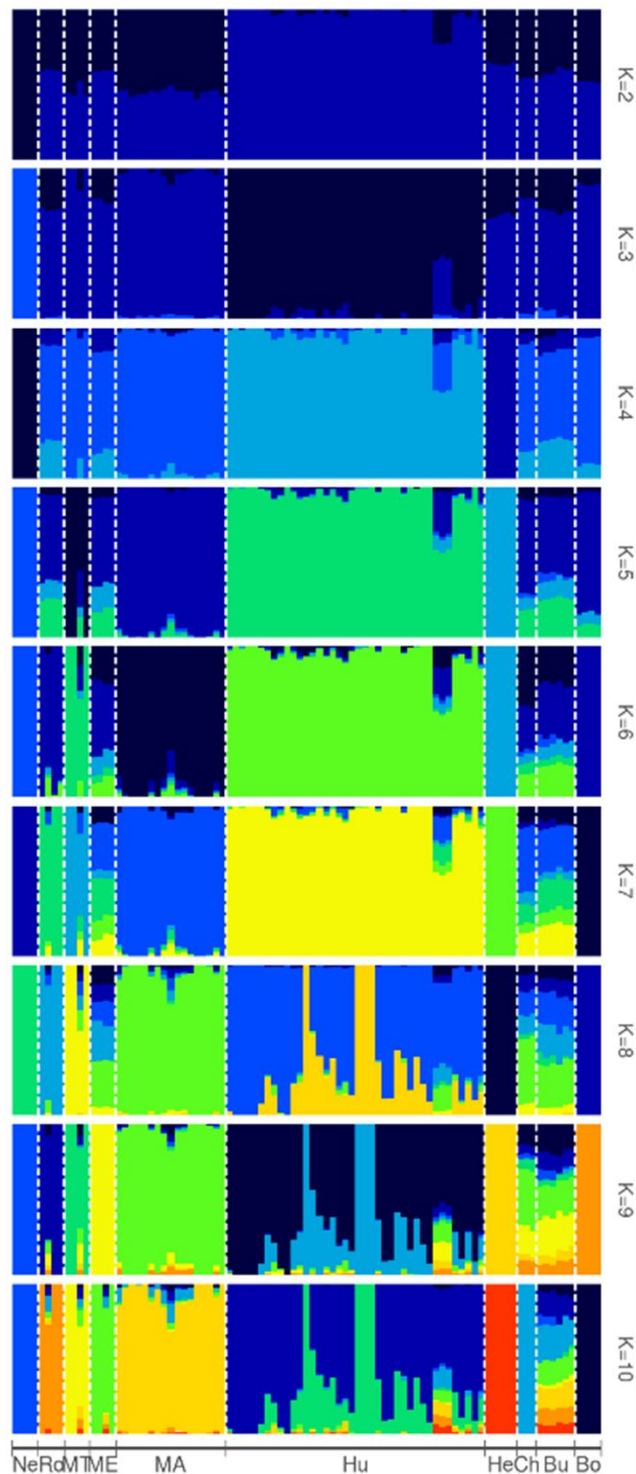
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Supplementary Figure S1 Multidimensional scaling plot of Hungarian Grey and European cattle populations. Nelore was selected as an outgroup. Encircled breeds are from Upadhyay *et al.* (2017) including Fleckvieh and Holstein-Friesian sampled in Hungary. The following codes are used: C1=1st component (eigenvalue=7.681); C2=2nd component (eigenvalue=2.797)

Hungarian Grey	0	0.086	0.118	0.187	0.148	0.146	0.067	0.105	0.134	0.299
Maremmana	0.086	0	0.111	0.182	0.131	0.157	0.062	0.086	0.137	0.308
Maronesa	0.118	0.111	0	0.245	0.195	0.201	0.084	0.144	0.191	0.426
Maltese	0.187	0.182	0.245	0	0.291	0.295	0.172	0.235	0.288	0.492
Boskarin	0.148	0.131	0.195	0.291	0	0.250	0.125	0.185	0.238	0.455
Heck	0.146	0.157	0.201	0.295	0.250	0	0.139	0.204	0.241	0.446
Busha	0.067	0.062	0.084	0.172	0.125	0.139	0	0.071	0.116	0.321
Chianina	0.105	0.086	0.144	0.235	0.185	0.204	0.071	0	0.192	0.415
Romianian Grey	0.134	0.137	0.191	0.288	0.238	0.241	0.116	0.192	0	0.447
Nelore	0.299	0.308	0.426	0.492	0.455	0.446	0.321	0.415	0.447	0
	Hungarian Grey	Maremmana	Maronesa	Maltese	Boskarin	Heck	Busha	Chianina	Romianian Grey	Nelore

Supplementary Figure S2 Graphical representation of pairwise coefficients of genetic differentiation (F_{ST}) values of Hungarian Grey cattle and the presented cattle breeds.



Supplementary Figure S3 Admixture analysis of Hungarian Grey and selected cattle populations for a range of K-values ($K = 2-10$). Each individual is represented by a single column divided into K colored segments, where K is the number of assumed clusters. Populations are separated by dashed lines. The following codes are used: Ne = Nelore; RO = Romanian Grey; MT = Maltese; ME = Maronese; MA = Maremmiana; Hu = Hungarian Grey; He = Heck; Ch = Chianina; Bu = Busha; Bo = Boskarin