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Genetic characterization by single nucleotide polymorphisms (SNPs) of Hungarian Grey and Maremmana cattle breeds

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Approximately 100 single nucleotide polymorphisms (SNPs) in genes candidate for meat traits were genotyped on individuals belonging to 4 different beef breeds. The Italian Maremmana and the Hungarian Grey breeds belong to the same podolic group of cattle, show a similar external conformation and recently underwent a similar demographic reduction. Marchigiana and Piemontese are two Italian meat breeds that went through different selection histories. Population genetic parameters such as allelic frequencies and heterozygosity values were assessed.

Genetic distances, calculated to evaluate the possibility of recent admixture between the populations, show that the similarity between Hungarian Grey and Maremmana cattle is mainly morphological, while they show genetically distinct features.

The assignment of individuals to breeds was inferred using Bayesian inference, confirming that the set of chosen SNPs is able to distinguish among populations.

A method for the identification of loci that were likely subject to selection was applied, suggesting that abnormal allelic frequencies at single loci could reflect similar selection or demographic history.

- Hungarian Grey
- Maremmana

same podolic group of cattle

similar external conformation

recently underwent a similar demographic reduction

Maremmana

- Existence of long horned cattle in Latium reported since Roman times (ancestors of the Maremmana?). Maremmana may be found to trace back to Grey Steppe cattle which entered Italy in large numbers during the 14th to 18th centuries.
- Herdbook registration started in 1935 (total breed population 274,000 head).
- During the 1930s and 40s exported to Hungary to improve the Hungarian Grey.
- Since 1945 head numbers have declined dramatically, due to land reform and mechanization, and by the mid 1960s extinction was predicted.
- Breed recovered in 1965-75 for its ability adapt to the environmental constraints of the hilly areas of the Maremma, reaching 60,000 head in 1975.
- In 1992 the total was estimated at 10,000, of which 4,000 females and 120 sires were herdbook registered.

Hungarian Grey

Theories on breed's origin

- imported by the Hungarian conquerors in the 9th century from the Podolic area
- came from the South, because there is an evidence of the presence of similar cattle in Egypt and Italy
- domestication of the wild cattle (Aurochs) in the Carpathian basin

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- Explicit reference to long-horned, '*magnus cornuotes boves Hungaricos*', first appears in a 16th century document. The breed became common by the 17-18th century.
- After World War II a radical decline followed, nearly reaching extinction in 1947-1967.
- During the late 1950's, some 1800 of the 2000-3000 cows were mated with sires of the Kostroma dairy breed.
- According to a 1962 central resolution only 200 purebred HG cows and 6 bulls were saved. Inbreeding was avoided by using a rotational mating scheme of originally inbred lines based on six local HG sires, two imports of the same breed and three Maremmana sires introduced during the early 1970's.
- After 7-9 generations, the initial lines became completely randomized.

Compared Morphology

- 1. Maremmana and HG have similar coat colour and not so different horn shape.
- 2. Maremmana cows are significantly bigger in every body measurements than Hungarian Grey.
- 3. The indexes of body proportions pointed out the significant differences of rump length/body length index. The rump length of Maremmana cows' is relatively bigger than Hungarian Greys.

(Maróti-Agóts et al 4th World Italian Beef Cattle Congress, Italy, April 29th - May 1st, 2005)

How much are Hungarian Grey and Maremmana related?

Controls

- Marchigiana
- Piemontese

Italian meat breeds subjected to different selection histories

SNPs genotyping

- Approximately 100 single nucleotide polymorphisms (SNPs) in genes candidate for meat traits (from Gemqual EU project) were genotyped on individuals belonging to the 4 breeds.

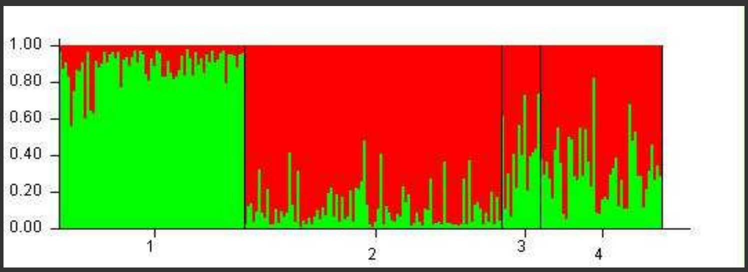
Nei 83 genetic distances

OTU	HG	MM	MR	PD
HG	0.000	0.036	0.029	0.031
MM	0.036	0.000	0.033	0.033
MR	0.029	0.033	0.000	0.031
PD	0.031	0.033	0.031	0.000

Structure output
(Pritchard 2000)
K=2

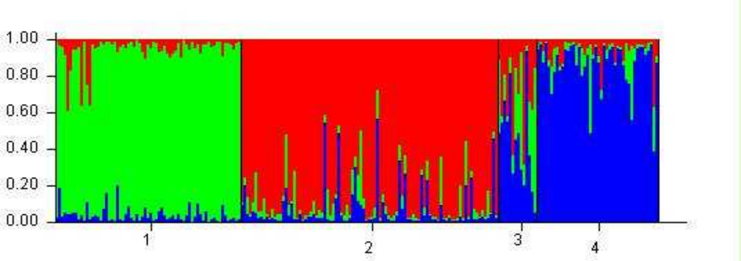
100000 burning in
200000 MCMC

admixture model



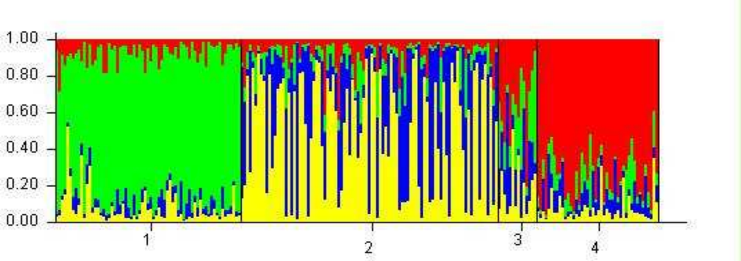
Hungarian grey	1	Marchigiana	3
Maremmana	2	Piemontese	4

K=3



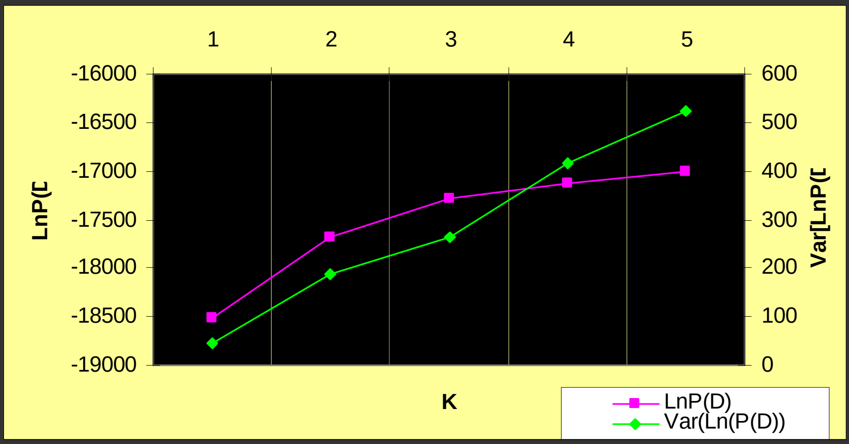
Hungarian grey	1	Marchigiana	3
Maremmana	2	Piemontese	4

K=4

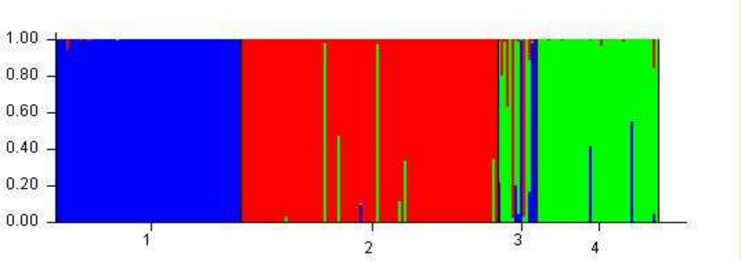


Hungarian grey	1	Marchigiana	3
Maremmana	2	Piemontese	4

Ln likelihood and Variance among repeated runs

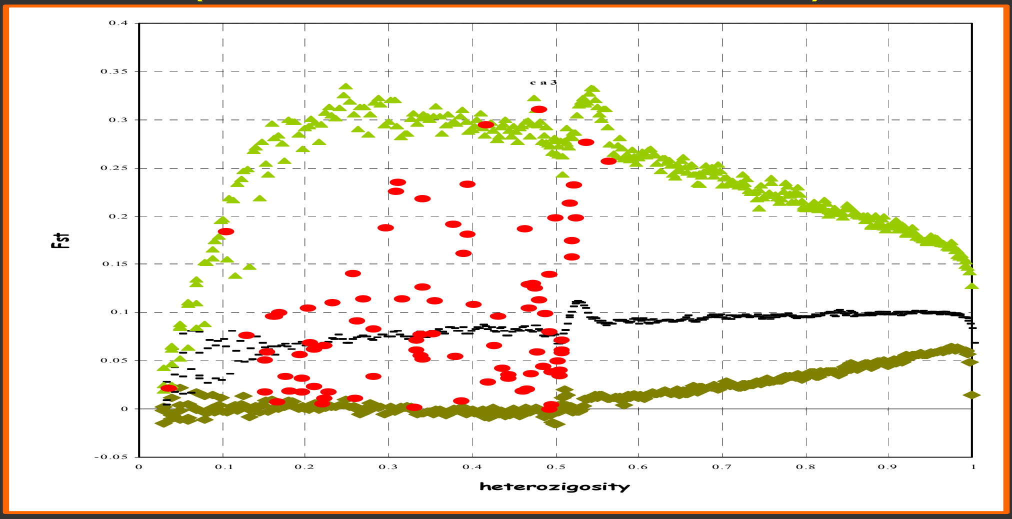


K=3 no admixture



Fdist results

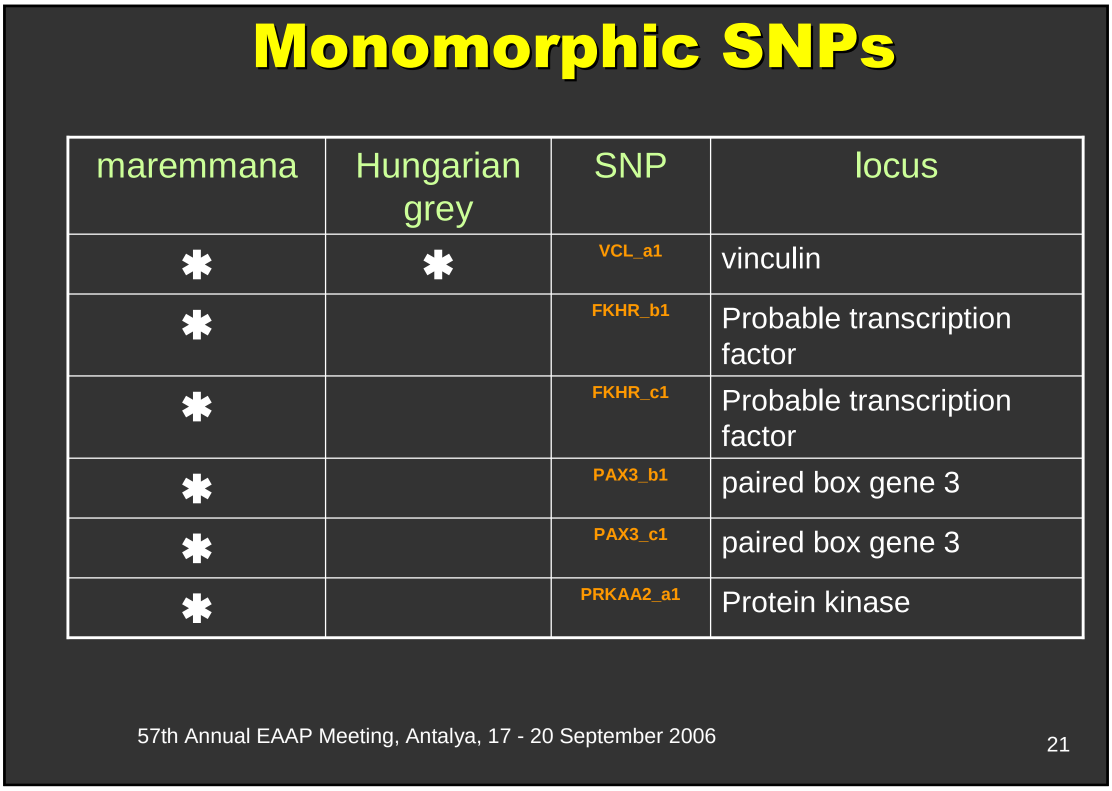
(Beaumont and Nichols 1996)



200000 features

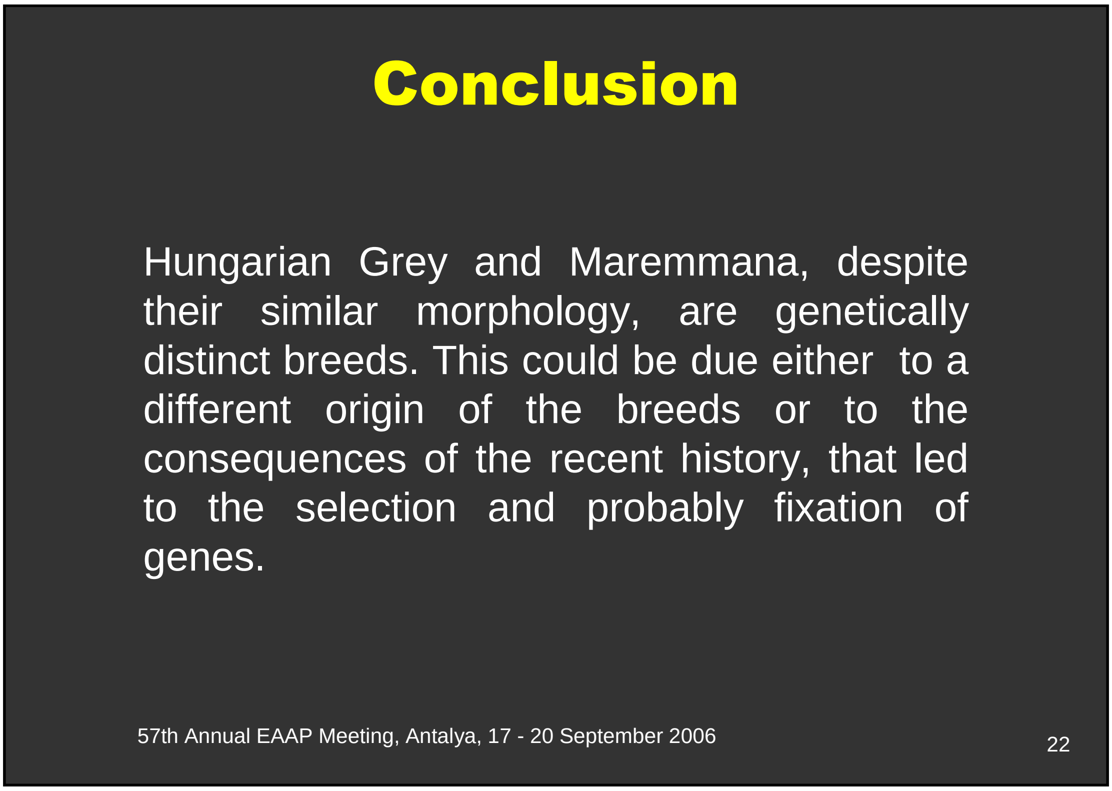
Outliers (P<0.05)

CA3_c1_191C	carbonic anhydrase, muscle-specific
CKM_a1_336C	creatine kinase,
LPL_c1_287C	lipoprotein lipase
LUM_a1_94ctRI	lumican
NRAP_b1_320T	nebulin-related anchoring protein, sarcomeric
PCSK1_a1_93ctRI	proprotein convertase
PGAM2_a1_272C	phosphoglycerate mutase



Monomorphic SNPs

maremmana	Hungarian grey	SNP	locus
✱	✱	VCL_a1	vinculin
✱		FKHR_b1	Probable transcription factor
✱		FKHR_c1	Probable transcription factor
✱		PAX3_b1	paired box gene 3
✱		PAX3_c1	paired box gene 3
✱		PRKAA2_a1	Protein kinase



Conclusion

Hungarian Grey and Maremmana, despite their similar morphology, are genetically distinct breeds. This could be due either to a different origin of the breeds or to the consequences of the recent history, that led to the selection and probably fixation of genes.