

# **GENETIC STUDIES OF THE CASPIAN PONY**

by

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# **A new phenogroup in the horse D system of red cell alloantigens found in the Caspian Pony.**

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Summary. A new D blood group phenogroup consisting of the specificities adeo was observed in a stallion family of Caspian ponies from Iran. An additional six undescribed genetic variants were seen in a total of 82 Iranian horses. This result suggests extensive new genetic variation may be present in domestic horses from geographic regions that have not yet received scientific attention.

Keywords: alloantigens, blood typing, equine, erythrocyte, genetics, horse

The D blood group is among the most variable genetic systems of the horse. There are currently 17 internationally recognized specificities and 25 phenogroups (Bowling and Williams, 1991) assigned to the D red cell alloantigen system. Since the current nomenclature was established, most new variants have resulted from the discovery of new specificities that have split known phenogroups (e.g. Bowling, 1987) rather than new combinations of factors (e.g. Aguilar et al., 1987). Here we report a new combination of factors in a phenogroup found in the Caspian pony from Iran.

A total of 41 Caspian ponies from Iran were tested using hemagglutinating, alloimmune reagents. The D system reagents tested were a, b, c, d, e, f, g, h, k, m, n and o. Included within this sample was a stallion with an unusual combination of D system factors that did not conform to any described phenogroup. Seven offspring of this stallion also were typed along with the dams for six of the offspring. Absorption tests were run to confirm the types of all these individuals. The results are shown in Table 1. The stallion appears to have the phenogroups Ddfk/Dadeo. The new phenogroup Dadeo was passed on to five of the seven offspring of the stallion. We presume this phenogroup is actually Dadelo although we were unable to test for the D1 factor. Also, we were unable to test for Dq and Dr which frequently occur with the Dadl or Ddelo phenogroups (Bowling and Williams, 1991).

A total of eight D system phenogroups were found in this population of Caspian ponies. Included in this number was one individual that appeared to have the unusual phenogroup Ddlno (1 presumed) previously reported by Bowling and Williams (1991). No family data was available for this horse. The other variants present were Dbcm, Dcgm, Ddeo, Ddfk, Ddghm, and Ddk. An additional 53 Caspian ponies from England have been tested. With one possible exception this group did not have the Dadeo phenogroup. The exception was an individual that was positive for the factors Da, Dd, De and Do. However, this individual could have been Dad/Ddeo. The D system variants present in the English Caspians were Dad, Dbcm, Dcgm, Ddeo, Ddfk, Ddghm, and Ddk. The English population was derived from 20 ponies brought to England from Iran in the 1970s.

The observation of a new phenogroup within the equine D blood group system is not remarkable. However, this new D system variant was not the only new marker found in Iranian horses. We have tested 82 horses from Iran that are of breeds that are rare or unknown in the west. In addition to the Dadeo and Ddno, we observed six variants that, to our knowledge, represent new genetic variants for the horse. Two were in the A-1-B (alpha-1-beta glycoprotein) system, one was in Tf (transferrin) and three were in the Pi (protease inhibitor) system. Unfortunately, there was little or no family data to demonstrate Mendelian inheritance of these variants. The number of Asian and African horse breeds that have not been examined genetically means that there is likely to be considerably more genetic diversity in domestic horses than is now recognized.

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Table 1. Family data of Caspian ponies with the new D system phenogroup.

Sire phenotype	Dam phenotype	Offspring phenotype	Phenogroup inherited from sire	Phenogroup inherited from dam
Dadefko	Dcgm	Dacdegmo	Dadeo	Dcgm
	Dcdegmo	Ddefko	Ddfk	Ddeo
	Dbcdkm	Dadeko	Dadeo	Ddk
	Dbcdkm	Dbcdfk	Ddfk	Dbcm
	Dcdegmo	Dadeo	Dadeo	Ddeo
	Ddeo	Dadeo	Dadeo	Ddeo
	unknown	Dacedegmo	Dadeo	Dcgm

D system factors tested were a, b, c, d, e, f, g, h, k, m, n, o

# Genetic Studies of the Caspian Pony

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We have now blood typed 72 Caspian Ponies, 53 from England and 19 from Iran. We also have performed a detailed pedigree analysis of the English population. Here are the basic results of these analyses.

Genetic variability can be measured in two ways. First is the effective number of alleles (NE) which is a measure of gene diversity at the breed level. Average NE was 2.06 and 2.45 from the English and Iranian samples, respectively. The second measure is heterozygosity (H) which measures individual genetic variation. Mean H was 40.3% for the English sample and 41.8% for the Iranian sample. Both NE and H for the Iranian sample are near the average for domestic horse breeds. The values for the English herd are lower but not at a level that warrants concern. The lower variation of the English Caspians is probably a result of the small size of the founding population.

The genetic measures for the English Caspians are in agreement with the calculations of inbreeding levels. As would be expected, there is an overall positive inbreeding level for the breed, which would lead to reduced genetic variation, but the inbreeding is not high. In addition, there has been no increase in inbreeding level in the last six years, up to the 1990 foal crop.

Genetic marker analysis also can be used to estimate genetic relatedness. The two Caspian populations were more like each other than they were like any other breed. Overall, the Caspian had greatest similarity with Arab breeds. There are suggestion that the Caspian genetic makeup could be ancestral to that of the other Arab type breeds. However, it is not possible to determine whether this is because the Caspians are in fact ancestral or because they have been interbred with other Arab breeds.

Finally, founder genetic contributions to the current population and the proportion of the remaining founder genome at risk of loss were estimated by pedigree analysis. In order to maximize the conservation of genetic variation in a closed population, such as the English Caspians, it is important to even up the genetic contribution of the founders. Six of the 20 founders account for 53.1% of the current genetic variation. The remaining 14 founders contribute from 6.7 to less than 1% to the genetic makeup of the current population. The founders with a disproportionately high contribution are Ostad, Ruba, Jehan Afrouz, Daria Nour, Mitra and Khorshid Kola in order of % contribution. The founders with the lowest contribution are Felfel, Pouran Dokht, Alamara, Toloche, Shirine and Fatemeh. Special effort should be made to increase the genetic contribution of these six founders in order to help preserve genetic variation within the breed. This means that offspring or descendants of these horses should be preferentially bred, especially compared to the six founders with the highest genetic contribution. In some cases, this may be difficult or undesirable.

# **Genetic variation and genetic conservation of a rare breed: The Caspian Pony**

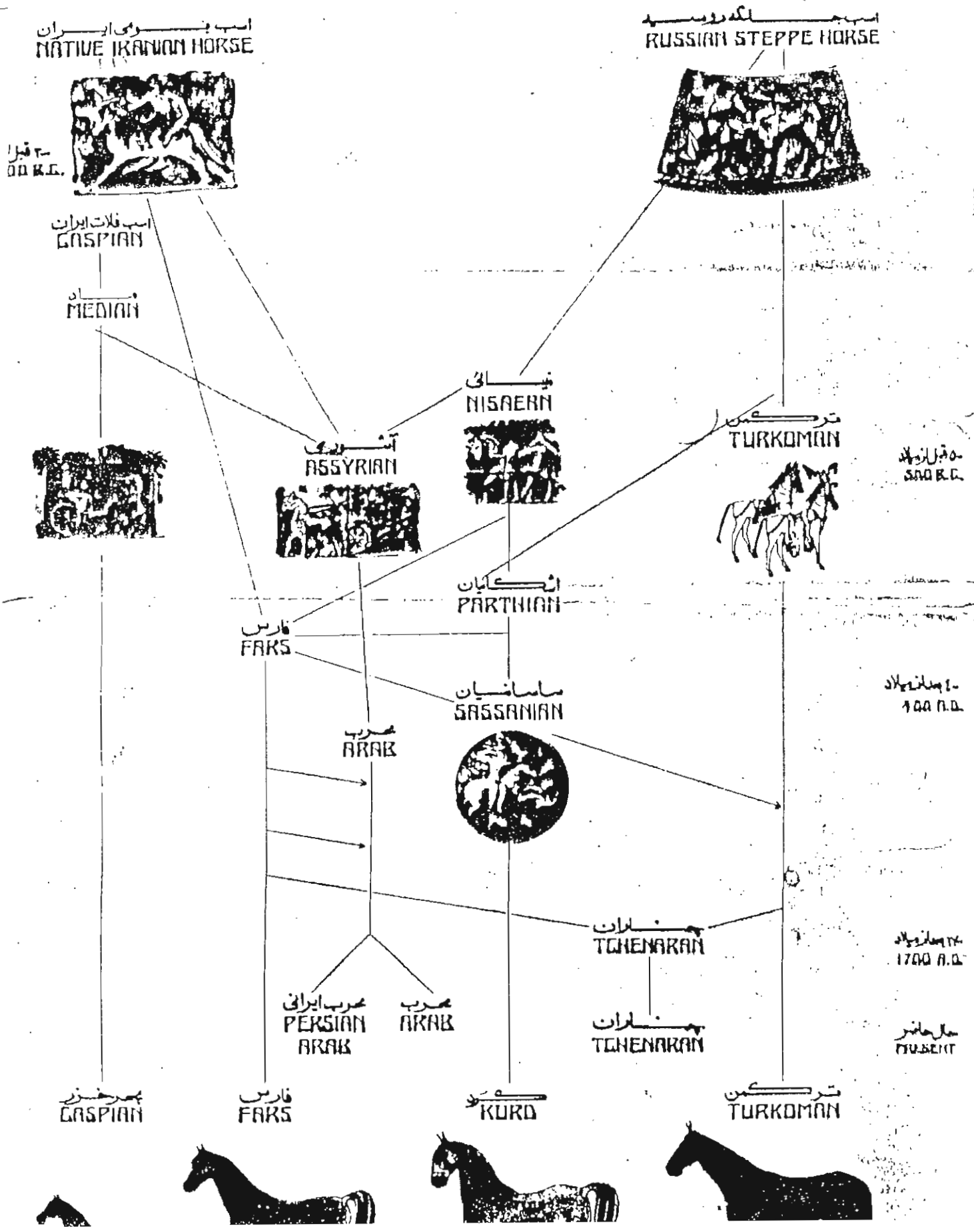
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The Caspian Pony is a breed of horse known from archeological evidence but unknown outside Iran before 1965. Between 1971 and 1978, 20 animals were exported to England to found a segment of the Caspian breed outside Iran. The small number of founders with little opportunity of new introductions leaves the Caspian breed at risk of loss of genetic variation and inbreeding. In this study we report analysis of genetic variation based upon seven blood group loci and 10 biochemical polymorphisms for 53 Caspian ponies from England and 19 from Iran. Measures of genetic variation were near the average for domestic breeds with the Iranian sample slightly more variable. Caspian ponies had highest genetic similarity with other Arab type breeds and the two samples were more like each other than like any other breed. Analysis of pedigrees of the English sample did not reveal significant inbreeding. However, gene drop simulation analysis did indicate possible long term problems. Several founders were poorly represented in the present day population and the risk of loss of the genetic contribution of many founders is high.

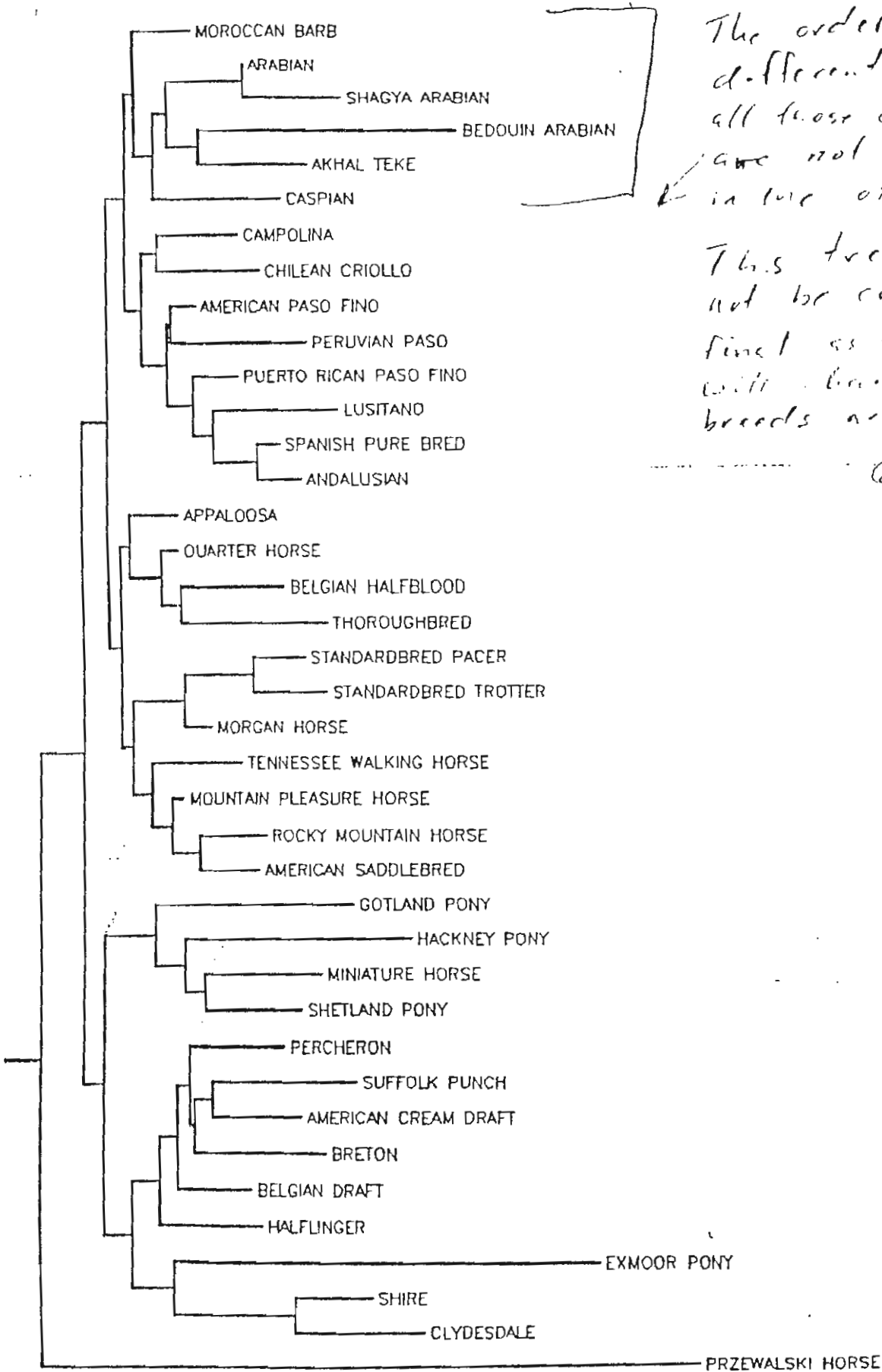
# تکامل اسب ایرانیان

## DEVELOPMENT OF THE PERSIAN HORSE





⊙ = your samples



The order is different because all those other breeds are not considered in the other tree

This tree should not be considered final as things will change as more breeds are added.

Corr