



## Determination of Genetic Distance Between East Anatolian Red, Brown Swiss, Holstein and Simmental Breeds of Cattle Using Polymorphic Systems

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### Abstract

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*Genetic distances were determined according to Nei, Cavalli-Sforza and Reynolds methods between the Brown Swiss (173), Simmental (80), Holstein (18) and East Anatolian Red (51) cattle breeds using milk protein ( $\alpha_s$ ) and blood protein types (Hb and Tf). The distribution of phenotypic frequencies in all the four breeds for all systems except  $\alpha_s$ -Cn was significant ( $P < 0.01$ ) using chi-square test. Phylogenetic trees based on the polymorphic systems of the populations obtained by three different methods of Nei, Cavalli-Sforza and Reynolds were found to be similar. According to the phylogenetic trees Brown Swiss and Simmental cattle breeds fall in one group and dairy (Holstein) and Native (East Anatolian Red) breeds in different groups.*

Keywords: Milk protein loci, transferrin, haemoglobin loci, phylogenetic tree.

### Introduction

Studies regarding conservation of genetic resources have been conducted in Turkey for the last ten years like in many countries in the World. Obviously, the genetic structure and the phylogene of a breed should be established first in order to conserve it. Support can be provided through conducting studies on blood groups, milk proteins and other biochemical systems. In addition

studies have also been carried out at molecular level (such as microsatellites and mtDNA) to determine the genetic structures of the population (Ceriotti *et al.*, 2003). In many studies, the polymorphic systems of alpha-casein ( $\alpha_s$ -Cn), beta-casein ( $\beta$ -Cn), kapa-casein (k-Cn), beta-lacto globulin ( $\beta$ -Lg), haemoglobin (Hb), transferrin (Tf) were investigated in protein and DNA levels (Rincon and Medrano, 2003; Ibeagha-Awemu *et al.*, 2004, Rincon *et al.*, 2006).

These polymorphic characteristics of cattle and other farm animals studied in both

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DNA and protein levels can be used especially for evolutionary and biodiversity analysis (Ceriotti *et al.*, 2003; Caroli *et al.*, 2004; Zaton-Dobrowolska *et al.*, 2006).

The aim of the present study was to determine the genetic diversity between some improved and native cattle breeds raised in Turkey utilizing the genetic variation structured by some polymorphic systems such as casein ( $\alpha_s$ -Cn,  $\beta$ -Cn, k-Cn), beta-lactoglobulin ( $\beta$ -Lg), transferrin (Tf) and haemoglobin (Hb) loci.

### **Materials and Methods**

Brown-Swiss, Holstein and Simmental improved cattle breeds raised at the Research and Experiment Farm of the College of Agriculture at Ataturk University and from the native Eastern Anatolian Red (EAR) breed raised at conservation sites as genetic resources at Eastern Anatolia Agricultural Research Institute were used in this study. 159, 87, 14 and 44 milk samples and 173, 80, 18 and 51 blood samples were collected from respective breeds. The four polymorphic structures present in milk ( $\alpha_s$ -Cn,  $\beta$ -Cn, k-Cn and  $\beta$ -Lg) and transferrin (Tf) and haemoglobin (Hb) present in blood were determined by using starch-gel electrophoresis (Aschaffenburg and Drewry, 1957; Dogrul, 1973).

The distinctions between  $\alpha_s$ -Cn,  $\beta$ -Cn, k-Cn,  $\beta$ -Lg, Hb and Tf phenotype and between the breeds were analyzed by means of chi-square test (Yildiz *et al.*, 1999). The pack software program PHYLIP 3.41 (Felsenstein 1993) was used to estimate the genetic distances between the four cattle breeds and to draw the dendograms. The phylogenetic tree was determined using independently each distance value obtained according to Nei, Cavalli-Sforza and Reynolds methods in accordance with Neighbour-joining Method (Saitou and Nei, 1987).

### **Result and Discussion**

The phenotype frequencies  $\beta$ -Cn, k-Cn,  $\beta$ -Lg, Hb and Tf except  $\alpha_s$ -Cn were found significant ( $P < 0.01$ ). Significant differences were also reported among the breeds with regards to phenotype frequencies of haemoglobin loci, transferring loci, and milk protein loci ( $\alpha_s$ -Cn,  $\beta$ -Cn, k-Cn and  $\beta$ -Lg) (Ceriotti *et al.*, 2004; Oner and Elmaci, 2006).

In order to develop conservation strategies for breeds, their genetic diversity must be determined. Despite the fact that their origins are the same, some genes that the breeds have and the frequencies of these genes may vary from breed to breed and even from population to population depending on such factors as natural selection, breeding strategies and genotype x environment interaction.

The distance between EAR and Brown Swiss was large as compared to the Simmental and Brown Swiss breeds according to Nei and Reynolds (Table 2). Whereas, according to Cavalli-Sforza the distance between EAR and Holstein breeds was larger than that of Simmental and Brown Swiss breeds (Table 2).

The phylogenetic trees were found to be similar for all three different methods, whereas, the Brown Swiss and Simmental breeds constituted the close cluster and the EAR breed remained far away from this cluster. It was also observed that two groups are formed Brown Swiss and Simmental (multi purposed breeds) forms the first group and Eastern Anatolian Red second group. EAR native cattle breed was the most distant breed as compared to other breeds due to the fact that it is a native breed that neighbors to Near East which is known as the first center of domestication. The extent of this distance is caused by the allele composition determined to be peculiar to the EAR breed and this explains the significance of the conservation of this breed as a genetic resource.

Table 1  
Distribution of phenotypic frequencies of milk and blood protein types according to the breeds and loci

System	Phenotype	Brown Swiss		Holstein		Simmental		EAR		$\chi^2$ value
$\alpha_s$ -Cn	BB	108	110.9	69	60.7	7	9.8	28	30.7	7.386 ns
	BC	51	48.1	18	26.3	7	4.2	16	13.3	
$\beta$ -Cn	AA	87	110.9	76	60.7	11	9.8	38	30.7	39.422**
	AB	66	42.4	8	23.2	2	3.7	5	11.7	
	BB	6	5.7	3	3.1	1	0.5	1	1.6	
k-Cn	AA	26	31.9	14	15.7	3	1.6	16	9.8	35.873**
	AB	54	53.6	22	26.4	1	2.6	22	16.4	
	AC	1	1.6	2	0.8	0	0.1	0	0.5	
	BB	58	49.3	24	24.3	3	2.4	6	15.1	
	BC	2	5.4	8	2.7	0	0.3	0	1.7	
	CC	3	2.2	1	1.1	0	0.1	0	0.7	
$\beta$ -Lg	AA	28	19.5	6	10.3	1	1.7	2	5.4	28.931**
	AB	84	75.5	40	39.9	8	6.7	11	20.9	
	BB	47	63.9	38	33.8	5	5.6	31	17.7	
Tf	AA	26	22.1	12	10.1	1	2.3	2	6.5	274.630**
	DD	75	55.5	13	25.3	10	5.8	5	16.4	
	EE	0	3.2	5	1.5	0	0.3	1	1.0	
	AD	62	49.6	20	22.6	3	5.2	7	14.6	
	DE	7	13.5	15	6.2	1	1.4	2	4.0	
	AE	3	10.8	14	4.9	3	1.1	0	3.2	
	AB	0	1.1	0	0.5	0	0.1	2	0.3	
	AF	0	3.2	0	1.5	0	0.3	6	1.0	
	AH	0	1.1	0	0.5	0	0.1	2	0.3	
	BF	0	1.6	0	0.7	0	0.2	3	0.5	
	BD	0	0.5	0	0.2	0	0.1	1	0.2	
	DF	0	5.9	0	2.7	0	0.6	11	1.7	
	FH	0	2.2	0	1.0	0	0.2	4	0.6	
	FF	0	1.6	0	0.7	0	0.2	3	0.5	
	HH	0	1.1	0	0.5	0	0.1	2	0.3	
Hb	AA	139	153.1	80	70.8	18	15.9	48	45.1	25.633**
	AB	34	19.9	0	9.2	0	2.1	3	5.9	

\*\* :  $p < 0.01$ ; ns: non-significant.

Table 2  
Genetic distances of cattle breeds

Methods	Breeds	Brown Swiss	Holstein	Simmental
Nei	Holstein	0.030636		
	Simmental	0.014390	0.030078	
	EAR	0.071961	0.047622	0.045379
Cavalli-Sforza	Holstein	0.061867		
	Simmental	0.035555	0.053749	
	EAR	0.139919	0.151649	0.117064
Reynolds	Holstein	0.054386		
	Simmental	0.025211	0.055835	
	EAR	0.112192	0.086145	0.078971

It may be concluded that the distinction between the breed groups was made correctly, easily and inexpensively by means of the polymorphic systems investigated with the phylogenetic analysis.

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यू. दोग्रु, एम. ओज्देमीर, एम. आई. सोयसल, एम. टोपल। बहुरूपता पद्धति से गोवंश के पूर्वी एनाटोली लाल, ब्राउन स्वीस, होल्सटीन और साइमेटल नस्लों में आनुवंशिक दूरी ज्ञात करना।

दुग्ध प्रोटीन (अल्फा) और रुधिर प्रोटीन (एचवी और टीएफ) के उपयोग से नेई, कावाल्ली-स्फोर्जा और रेनाल्ड की विधियों से ब्राउन स्वीस (173) साइमेटल (80), होल्सटीन (18) और पूर्वी लाल एनाटोली (51) नस्लों में आनुवंशिक दूरी ज्ञात की गयी। काई स्ववायर टेस्ट से अल्फा 1-सी एन के अतिरिक्त सभी पद्धति से सभी चार नस्लों में समलक्षणी बारंबारता वितरण सार्थक था। तीन भिन्न विधियों, नेई, कावाल्ली-स्फोर्जा और रेनाल्ड से प्राप्त जनसंख्या की बहुरूपता पद्धति पर आधारित जाति वंशवृक्ष समान पाया गया। जाति वंशवृक्ष के अनुसार ब्राउन स्वीस और साइमेटल नस्लों एक वर्ग में तथा दुधारु होल्सटीन और स्थानीय (पूर्वी लाल एनेटोली) नस्लों भिन्न वर्ग में थीं।