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SUBTYPE DETERMINATION OF PHOSPHOGLUCOMUTASE (PGM) AND GROUP - SPECIFIC COMPONENT (Gc) BY ISOELECTRIC FOCUSING AMONG SOME IRANIAN POPULATIONS

S.Y. Seyedna [1] , PhD

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Abstract

A total of 781 serum and 827 red cell samples from four populations of Iran (Kashan , Ardestan , Astara and Ardabil) were sub-typed by isoelectric focusing for group-specific component and red cell enzyme Phosphoglucomutase, locus one , respectively. Heterogeneity test revealed no significant differences among the populations studied regarding both PGM1 and Gc systems.

Introduction

Phosphoglucomutase (PGM) is an important enzyme in carbohydrate metabolism since it catalyzes the interconversion of glucose 1 - phosphate and glucose 6 - phosphate in the presence of catalytic amounts of the cofactor glucose 1 , 6 - diphosphate.

Investigations of phosphoglucomutase locus one (PGM1) phenotypes by isoelectric focusing have shown four common alleles at this locus (2,3,11,16,20). Various reports (3,4,24) have shown that thses alleles are determined by one locus with Mendelian inheritance.

The Group - Specific componenet (Gc) polymorphism previously detected by starch gel electrophoresis (4,10,15,18) was characterized by two common alleles Gc^1 and Gc^2 in all human populations. Later on , isoelectric focusing technique (5,6) revealed different electrophoretic patterns. These patterns can be explained by the existence of three autosomal codominant Gc^{1F}, Gc^{1S} and Gc^2 genes controling the synthesis of the protein bands revealed by electrophoretic mobilities. When the first data on gene frequencies became

1- Department of Biology , Faculty of Sciences , University of Shahid Beheshti , Tehran , Iran.

available , the allele Gc^2 turned out to have low frequencies in area of high aridity.

This finding was explained when the function of the Gc proteins was discovered (7). They are carrier proteins of vitamin D.

A more recent survey suggests a relationship between sunshine and the Gc polymorphism , in the aboriginal habitats of the world populations , high frequencies of Gc^2 were found in most of the populations who had been living for a long time in areas with low sunlight intensity. This geographical distribution suggests a selective advantage due to a more efficient transport of vitamin D , especially if the supply is limited (12).

Materials and methods

To study phosphoglucomutase locus 1 and group - specific componet systems, blood samples were collected from four Iranian populations located in north and central parts of the country. Blood was drawn into syringes, transferred to vials and transported at the earliest possible time at wet ice temperature, to Manchester, England, for analysis. Serum and red cells were separated, haemolysates prepared and stored at -20 °C until tested. 827 red cell haemolysates were tested for PGM1 sub - types. Acid starch gel electrophoresis was performed (14). Isozymes were visualized by the staining technique(19). 781 serum samples were sub - typed for group specific component (6).

Results and discussion

The populations studied and their observed and expected numbers of PGM_1 , and Gc phenotypes and their gene frequencies are given in tables 1 and 2 respectively. X^2 was not significant and showed lack of deviaton from Hardy - Weinberg equilibrium in either systems in all the populations studied. Test of heterogeneity among the population studied for both PGM_1 and Gc systems showed lack of heterogeneity ($X^2 = 18.3$ for PGM_1 and $X^2 = 24.4$ for Gc) , indicating that populations do not differ significantly for subtypes studies.

The highest gene frequency for Gc^{1S} was observed in Kashan and the lowest in Ardabil populations , for Gc^{1F} the highest value occured in Ardestan

and the lowest in Ardabil. The highest value for Gc^2 was observed in Ardabil and the lowest in Kashan.

In PGM_1 system , the highest gene frequency for PGM_1^{1+} occured in Astara and the lowest in Ardabil , for PGM_1^{1-} the highest occured in Ardabil and the lowest in Astara.

For PGM_1^{2+} , the highest was in Ardabil and the lowest in Astara. For PGM_1^{2-} the highest was in Kashan and the lowest in Astara.

With regard to PGM_1^{1+} allele values , around 60-70% , found in the present investigation , showed affinity to Europeans frequencies. Frequencies of PGM_1^{1+} is low and close to previous report from Iranian Zoroastrians (14) and the combined frequency of the PGM_1^{1+} and PGM_1^{1-} alleles ranging from 0.747 to 0.764 is very similar to that of migrant Parsis and Iranis studied in India (21,22) , and is within the range for the Iranian populations reported previously (8,17).

Regarding Gc system , Gc^{1F} allele frequency in the present study is much lower than that in Iraq and Israel (13) , and well fits to the European range of 12 - 20%. This is true for Gc^{1S} frequency too.

The sum of the allele frequencies of Gc^{1S} and Gc^{1F} in the populalions studied is from 0.673 (Ardabil) to 0.808 (Kashan) , which is close to the previous reports (1,14,23).

Nei,s genetic distance estimated for PGM1 subtypes (Table 3) showed Astara population to have less similarity to other populations followed by Ardabil.

The same values for Gc subtypes showed less similarity of Ardabil population with others , followed by Astara. Hence Ardabil and Astara populations are well separated from other two populations with regared to PGM1 and Gc subtypes (Table 4).

The results indicate the necessity of further investigations on other populations of Iran in order to reach a sound conclusion , however present study well indicates differences among the populations.

High frequencies of Gc^2 , seems to exist among populations of Ardabil and Astara , where the sunlight intensity in contrast with the areas of Ardestan and Kashan is low (12). In conclusion the different geographical distribution of Gc^2 in the present study may be an association between Gc gene

frequencies and diet , incident ultraviolet - a function of cloud cover latitude and altitude - or , possibly skin color. We emphasise that in the absence of specific supportive evidence of a biochemical or physiological nature , any environmental correlation with Gc phenotype can at least be only suggestive , and further studies of large samples from different populations of Iran will certainly be profitable.

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Table 1- Observed and expected numbers of PGM1 and Gc subtypes in four Iranian populations.

System/ Phenotype	Populations							
	Kashan		Ardestan		Astara		Ardabil	
	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.	Obs.	Exp.
PGM1								
1 + 1	89	82.6	104	100.1	84	81	122	115.7
1 + 1 -	19	19.6	20	21.7	15	9.5	26	29.7
1 - 1 -	2	1.2	3	1.2	1	0.7	5	2.0
1 + 2 +	32	39.3	43	48.1	29	36.3	53	60.8
1 - 2 +	2	4.6	4	5.2	6	3.3	8	7.8
1 + 2 -	15	19.5	24	22.3	19	16.7	27	26.0
1 - 2 -	4	2.3	2	2.4	0	1.5	1	3.3
2 + 2 +	9	4.7	11	5.8	7	4.1	10	8.0
2 + 2 -	6	4.6	7	5.4	3	3.8	11	6.8
2 - 2 -	2	1.2	0	1.2	1	0.9	1	1.5
Total	180		218		165		264	
Gc								
1S - 1S	79	79.3	67	66.5	64	62.4	72	69.4
1S - 1F	37	37.3	39	39.2	27	27.1	30	33.6
1F - 1F	5	4.4	6	5.7	3	2.9	5	4.0
2 - 1S	47	46.5	55	55.6	48	51.1	82	83.6
2 - 1F	10	10.9	16	16.34	11	11.1	22	20.2
2 - 2	7	6.8	12	11.6	12	10.4	25	25.2
Total	185		195		165		236	

Table 2- Gene frequenceis of PGM1 and Gc systems in four Iranian populations.

System/ Phenotype	Populations			
	Kashan	Ardestan	Astara	Ardabil
PGM_1				
PGM_1^{1+}	0.6775	0.6775	0.70	0.662
PGM_1^{1-}	0.0805	0.0735	0.0641	0.085
PGM_1^{2+}	0.161	0.163	0.157	0.174
PGM_1^{2-}	0.0980	0.0755	0.0725	0.0744
Gc				
Gc^{1S}	0.6540	0.5840	0.6115	0.5425
Gc^{1F}	0.1540	0.1720	0.1335	0.1310
Gc^{2}	0.1920	0.2440	0.2515	0.3265

Table 3- NEI'S genetic distance for PGM subtypes

	Kashan	Ardestan	Astara	Ardebil
Kashan	0.0000000			
Ardestan	0.0001211	0.0000000		
Astara	0.1531892	0.1599088	0.0000000	
Ardebil	0.0004464	0.0004403	0.1455595	0.0000000

Table 4 - NEI'S genetic distance for Gc subtypes

	Kashan	Ardestan	Astara	Ardebil
Kashan	0.0000000			
Ardestan	0.0032187	0.0000000		
Astara	0.0076603	0.0032831	0.0000000	
Ardebil	0.0271980	0.0142900	0.0062587	0.0000000

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