

## Characteristics of pigs raised in Poland in terms of frequency of glucosephosphate isomerase and phosphogluconate dehydrogenase

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A total of 2969 Polish Large White (PLW), Polish Landrace (PL), Hampshire (H), Duroc (D), Pietrain (P) and Line 990 gilts were considered. Two alleles – A and B – were found at the *GPI* and *PGD* loci. In most breeds, except PLW, frequency of the *GPI*<sup>A</sup> allele was lower than that of the *GPI*<sup>B</sup>. The lowest frequencies of the *GPI*<sup>A</sup> allele occurred in the P, H, and PL, and slightly higher in D and Line 990 pigs. Of all the breed groups analysed, D pigs showed the lowest frequency of the *PGD*<sup>A</sup> allele. In the other breeds, frequency of the *PGD*<sup>A</sup> allele was higher compared to the *PGD*<sup>B</sup> allele. Analysis of frequency of *GPI* genotypes shows that, among the PL, H, D, P and Line 990 breeds, per cent of animals with the *GPI*<sup>A/A</sup> was the smallest and that with the *GPI*<sup>B/B</sup> genotype the highest. Frequency of the *A/A* genotype at the *PGD* locus was high in PLW and H and the lowest in D pigs. Determination of the frequency of genotypes present at both loci at the same time showed that the *GPI*<sup>A/A</sup>/*PGD*<sup>B/B</sup> genotype hardly ever occurred in any of the breed groups studied.

**KEY WORDS:** gene polymorphism / genetic markers / *GPI* / *PGD* / pigs

Glucosephosphate isomerase (GPI) and phosphogluconate dehydrogenase (PGD) are erythrocyte enzymes. In terms of its biochemical function in the body, GPI is involved in glycolysis [Mayes 1995]. PGD is an enzyme of the pentose phosphate pathway [Matzke *et al.* 1985]. The polymorphism of these enzymes in pigs is coded by the genes of single loci localized on chromosome 6 [Yerle *et al.* 1990]. In most breeds of pigs, *GPI* and *PGD* polymorphism is controlled by two codominant alleles – A and B.

Exceptionally in a population of primitive pigs in east Bulgaria [Van de Weghe *et al.* 1988] the *GPI<sup>C</sup>* allele was found. Infrequent is also the *PGD<sup>C</sup>* allele, identified only in wild Japanese pigs [Kurosawa and Tanaka 1991] and in England in pigs of a synthetic line produced from multi-breed crossing [Archibald and McTeir 1988].

Within-breed and between-breed differences in allele frequencies in pigs have led to the use of *GPI* and *PGD* as markers in the analysis of genetic linkages [Andresen 1970]. *GPI* and *PGD*, as *loci* of the genes linked to the *locus* of the *RYR1* gene, were used to analyse the susceptibility and (or) resistance of pigs to stress [Doize *et al.* 1990, Blendl *et al.* 1991, Bigi *et al.* 1991]. Franceschi and Ollivier [1981], Kamyczek *et al.* [1996], and Van Zeveren *et al.* [1988] noticed high frequencies of the *GPI<sup>B</sup>* allele in breeds susceptible to stress, such as Pietrain and Belgian Landrace. Also the *PGD* gene played a major role in haplotyping the stress gene [Glodek *et al.* 1985, Russ *et al.* 1992].

In Poland, *GPI* and *PGD loci* have already been used to characterize pig breeds [Janik *et al.* 1998, Kamyczek and Kwaczyńska 1994, Koćwin-Podsiadła *et al.* 1992, Kurył *et al.* 1997a,b, 1991, Żurkowski *et al.* 1995]. Changes in the genetic structure of pigs resulting from selection work carried out in recent years, probably concern the genes under discussion.

The objective of this study was to identify *GPI* and *PGD* alleles by means of agarose gel electrophoresis and to evaluate the frequency of *GPI* and *PGD* alleles and genotypes in pigs raised in Poland.

### Material and methods

Pigs investigated in this study came from pedigree farms and were tested at the Slaughter Pig Testing Stations (SKURTCh) in Pawłowice and Mełno. A total of 2969 gilts were studied, of which 709 were Polish Large White (PLW), 1341 Polish Landrace (PL), 76 Hampshire (H), 141 Duroc (D), 167 Pietrain (P) and 535 Line 990.

Blood samples were collected into tubes containing a preservative. *GPI* and *PGD* erythrocyte enzymes were genotyped following the method of Gahne and Juneja [1985]. The result in the form of bands appeared after 15 min for *GPI* and within 45 min of gel staining for *PGD*. The result was read out directly from bands obtained in gel.

Statistical analysis was made of the frequency of alleles and *GPI* and *PGD* genotypes in different breed groups. Significance of differences was estimated between the observed and predicted distribution of genotypes using the chi-square test.

### Results and discussion

The results obtained showed that in pigs raised in Poland, two alleles – A and B – occur at the *GPI* and *PGD loci*. As can be seen in Table 1, which presents the frequency of *GPI* alleles, in the overwhelming majority of breeds the *GPI<sup>A</sup>* allele was less frequent than the *GPI<sup>B</sup>* allele. An exception appeared in the PLW gilts, in which both

*GPI* alleles occurred with the same frequency. Table 1 gives also the frequency of *PGD* alleles. The most significant difference in allele frequency was observed in D pigs which were characterized by the lowest frequency of the *PGD<sup>A</sup>* allele being simultaneously the only breed in which the *PGD<sup>A</sup>* was less frequent than *PGD<sup>B</sup>* allele.

**Table 1.** Frequency of *GPI* and *PGD* alleles in the breeds analysed

Breed	<i>GPI</i> locus		<i>PGD</i> locus	
	allele		allele	
	<i>A</i>	<i>B</i>	<i>A</i>	<i>B</i>
PLW	0.511	0.489	0.733	0.267
PL	0.181	0.819	0.558	0.442
Hampshire	0.145	0.855	0.849	0.151
Duroc	0.280	0.720	0.277	0.723
Pietrain	0.141	0.859	0.632	0.368
Line 990	0.269	0.731	0.621	0.379

Analysis of frequency of *GPI* genotypes in PL, H, D, P and Line 990 pigs (Tab. 2) showed the lowest frequency of the *AA* and the highest frequency of the *BB* genotype. In PLW pigs, the proportions of homozygous animals were similar. Table 2, which gives also the frequency of genotypes at the *PGD* locus, shows high frequencies of the *PGD<sup>AA</sup>* homozygotes in the PLW and H, and the lowest in D pigs. Calculations proved that the frequencies observed of genotypes within the *GPI* and *PGD* loci did not differ significantly from those predicted (Tab. 2). This means that the pigs were in genetic equilibrium.

Table 3, which presents the frequency of genotypes at both loci, shows that in all the breed groups analysed except for H and P, the maximum number of nine potential genotypes was found.

Determining the frequency of alleles in genetic systems provides a basis for identifying genetic variation in pig breeds. Genetic structure is strongly affected by animal selection that improves performance traits in different breeds and populations. Change in the frequency of alleles that control performance traits and of alleles of genes linked to them is related to a change in the level of quantitative traits.

Genetic structure of pigs in terms of *GPI* and *PGD* draw attention due to their mutual linkage and the fact that they belong to the halothane linkage group [Andresen and Jensen 1977]. For this reason, many studies analysed the polymorphism of *GPI* and *PGD* genes concurrently.

Based on the present study it is concluded that the lowest frequency of the *A* allele at the *GPI* gene locus is characteristic of the H and P breeds, while the highest - of the PLW pigs. These conclusions are in agreement with the results reported by Van Zaveren *et al.* [1990], Russ *et al.* [1992], Widar *et al.* [1975], Kamyczek and Kwaczyńska

Table 2. Frequency of the *GPI* and *PGD* genotypes

Breed	<i>GPI</i> locus genotypes				<i>PGD</i> locus genotypes			
	<i>AA</i>	<i>AB</i>	<i>BB</i>	chi-square	<i>AA</i>	<i>AB</i>	<i>BB</i>	chi-square
<b>PLW</b>								
no. of animals	184	357	168		380	280	49	
observed	0.239	0.504	0.237	0.0484	0.536	0.395	0.069	0.0692
predicted	0.260	0.500	0.240		0.537	0.391	0.071	
<b>PL</b>								
no. of animals	42	402	897		416	665	260	
observed	0.031	0.300	0.669	0.1379	0.310	0.496	0.194	0.0392
predicted	0.033	0.296	0.671		0.311	0.493	0.195	
<b>Hampshire</b>								
no. of animals	3	16	57		56	17	3	
observed	0.039	0.211	0.750	0.1264	0.737	0.224	0.039	0.0942
predicted	0.021	0.248	0.731		0.721	0.256	0.023	
<b>Duroc</b>								
no. of animals	15	49	77		16	46	79	
observed	0.106	0.348	0.546	2.6495	0.114	0.326	0.560	4.8361
predicted	0.078	0.400	0.518		0.076	0.401	0.523	
<b>Pietrain</b>								
no. of animals	4	39	124		67	77	23	
observed	0.024	0.233	0.743	0.0198	0.401	0.461	0.138	0.5698
predicted	0.020	0.242	0.734		0.399	0.466	0.135	
<b>Line 990</b>								
no. of animals	37	214	284		207	250	78	
observed	0.069	0.400	0.531	0.1489	0.387	0.467	0.146	0.0334
predicted	0.072	0.393	0.534		0.386	0.471	0.143	

[1994], and Oishi *et al.* [1979], who also found that the frequency of the *GPI<sup>A</sup>* allele was lower than that of the *GPI<sup>B</sup>* allele in almost all pig breeds under study. One exception was a population of LW pigs investigated by Renard *et al.* [1988], in which higher frequencies of the *GPI<sup>A</sup>* allele were determined (0.53). These results were close to our results obtained in the present study for the same breed. In another population of LW in Poland, Kurył *et al.* [1997b] found a lower frequency of the *GPI<sup>A</sup>* allele (0.39).

Our own results (Tab. 1) and those from the literature show that in the majority of pig breeds, the *PGD<sup>A</sup>* allele is more frequent than the *PGD<sup>B</sup>*. This has never been observed in Durocs, neither in the present, nor in any other population [Oishi *et al.* 1979, Gahne and Juneja 1985, Bigi *et al.* 1991, Kamyczek and Kwaczyńska 1994]. Lower frequencies of *PGD<sup>B</sup>* allele were determined in several populations of the Landrace breed [Agergaard *et al.* 1977, Hojny *et al.* 1988, Van Zeveren *et al.* 1990, Kamyczek and Kwaczyńska 1994] and in Złotnicka Spotted breed [Kurył *et al.*, 1997b].

**Table 3.** Frequency of *GPI-PGD* loci genotypes in the analyzed pig breeds

Genotype <i>GPI-PGD</i>		Breed						total
		PLW	PL	Hampshire	Duroc	Pietrain	Large 990	
AA-AA	n	88	20	3	4	4	12	133
	frequency	0.124	0.015	0.040	0.043	0.024	0.022	0.045
AA-AE	n	84	13	0	7	7	17	123
	frequency	0.121	0.010	0.000	0.050	0.050	0.032	0.041
AA-BE	n	10	9	0	2	0	8	29
	frequency	0.014	0.004	0.000	0.014	0.000	0.013	0.010
AE-AA	n	208	104	7	3	18	48	408
	frequency	0.294	0.077	0.092	0.021	0.108	0.127	0.137
AE-AE	n	131	214	8	17	19	107	494
	frequency	0.185	0.140	0.105	0.120	0.114	0.200	0.147
AE-BE	n	18	84	1	29	2	39	173
	frequency	0.025	0.043	0.013	0.204	0.012	0.073	0.058
BE-AA	n	84	292	44	7	45	127	601
	frequency	0.118	0.218	0.405	0.050	0.249	0.238	0.202
BE-AE	n	43	438	9	22	58	124	714
	frequency	0.089	0.327	0.119	0.154	0.347	0.233	0.242
BE-BE	n	21	147	2	48	2	31	290
	frequency	0.030	0.124	0.024	0.340	0.124	0.058	0.098
Total	n	709	1341	74	141	147	535	2949
	frequency	1.000	1.000	1.000	1.000	1.000	1.000	1.000

n - number of animals.

High frequencies of the *GPI<sup>B</sup>* alleles in PL, H and P pigs affected the high frequencies of *GPI<sup>B/B</sup>* genotypes in these breeds (Tab. 2). Similar results to those obtained in PL pigs were reported by Hsiu-Luan *et al.* [1998] and Andersen *et al.* [1981]. However, even higher values were found in the populations of Italian Landrace [Bigi *et al.* 1991], German Landrace [Glodek *et al.* 1985, Kubek and Dinklage 1971, Macke *et al.* 1985], and French Landrace pigs [Renard *et al.* 1988]. Reinecke and Kalm [1988] did not find any animals of the *GPI<sup>A/A</sup>* genotype in Belgian Landrace pigs, while the *GPI<sup>B/B</sup>* genotype occurred in 93.6% of the animals. Frequency of *GPI<sup>B/B</sup>* genotype (90.4%) higher than in present study was found also in Pietrain pigs in Germany by Reinecke and Kalm [1988].

In the available literature no data were found to allow comparing the results obtained for H pigs to the Hampshire populations raised in other countries.

The results obtained from the studies of PLW pigs indicate that the breed is characterized by the most similar frequencies of the *GPI<sup>A/A</sup>* and *GPI<sup>B/B</sup>* genotypes. In the studies of different populations, the respective values were 22.2% and 18.5% in PLW [Kuryl *et al.* 1996], 20.7% and 34.1% in Italian Large White [Bigi *et al.* 1991], 31.6% and 25.0% in French Large White [Renard *et al.* 1988] and 25.9% and 23.7% in PLW pigs investigated in this study.

For Duroc pigs, results obtained in the present study were similar to those obtained by Hsiu-Luan *et al.* [1998] and Bigi *et al.* [1991].

For Line 990 pigs investigated during a similar period by Janik *et al.* [1998], the results were similar to those presented herein.

Data on the frequency of *PGD* genotypes (Tab. 2) indicate, except for the D breed, the low frequencies of the *PGD<sup>B/B</sup>* genotype in the pigs studied. The same proportions were observed in other D populations. The high frequencies of the *PGD<sup>B/B</sup>* genotype in D pigs were observed also by Bigi *et al.* [1991] and Hsiu-Luan *et al.* [1998]. Comparable results for the frequency of genotypes at the *PGD* locus were also demonstrated in Large White [Bigi *et al.* 1991, Kurył *et al.* 1996, Renard *et al.* 1988], Pietrain [Reinecke and Kalm 1988], and Line 990 [Janik *et al.* 1998] pigs. Different frequencies were determined especially in Landrace populations in Germany [Glodek *et al.* 1985], Taiwan [Hsiu-Luan *et al.* 1998], Italy [Bigi *et al.* 1991], France [Renard *et al.* 1988] and Belgium [Reinecke and Kalm 1988].

The present study on the frequency of individual alleles at the *GPI* and *PGD* loci included also the analysis of frequencies of genotypes that account for both these loci simultaneously (Tab. 3). The results obtained could only be related to the observations made in Taiwan by Hsiu-Luan *et al.* [1998]. While studying Landrace, Large White, Duroc and Berkshire pigs, they observed the presence of all ten possible genotypes in the former three breeds, and no *GPI<sup>A/B</sup>-PGD<sup>B/B</sup>* genotype in the Berkshire breed. In the present study, in H and P pigs no animals with the *GPI<sup>A/A</sup>-PGD<sup>A/B</sup>* and *GPI<sup>A/A</sup>-PGD<sup>B/B</sup>* genotypes were found. Besides, there was higher proportion of animals found with the *GPI<sup>B/B</sup>-PGD<sup>A/A</sup>* genotype in H (frequency 0.605), and with the *GPI<sup>B/B</sup>-PGD<sup>A/B</sup>* genotype in P (frequency 0.347) pigs. Among pigs raised in Taiwan, the highest frequencies of the *GPI<sup>B/B</sup>-PGD<sup>A/A</sup>* genotype were found in the Landrace breed (0.409). Furthermore, in Landrace pigs the *GPI<sup>B/B</sup>-PGD<sup>A/B</sup>* genotype was relatively frequent (0.275), while the least frequent was *GPI<sup>A/A</sup>-PGD<sup>A/A</sup>* genotype (0.003). In the present study, there were high frequencies of both these genotypes found also in Polish Landrace pigs. In case of Durocs, studies by Hsiu-Luan *et al.* [1998] as well as results presented in this study showed that the highest proportion was shared by animals with the *GPI<sup>B/B</sup>-PGD<sup>B/B</sup>* (0.388 and 0.340, respectively) and *GPI<sup>A/B</sup>-PGD<sup>B/B</sup>* genotypes (0.353 and 0.206, respectively). Comparison of genotype frequencies among the breeds clearly shows the lowest per cent of animals with the *GPI<sup>A/A</sup>-PGD<sup>B/B</sup>* genotype. Low frequency of the *PGD<sup>B/B</sup>* genotype in PLW, PL, H, P and Line 990 pigs is the reason for low frequency of the *GPI<sup>B/B</sup>-PGD<sup>B/B</sup>*, *GPI<sup>A/B</sup>-PGD<sup>B/B</sup>* and *GPI<sup>A/A</sup>-PGD<sup>B/B</sup>* genotypes in these breeds. The high frequency of the *PGD<sup>B/B</sup>* genotype in Durocs led to increased frequency of *GPI<sup>B/B</sup>-PGD<sup>B/B</sup>* and *GPI<sup>A/B</sup>-PGD<sup>B/B</sup>*, but even in this population the animals of *GPI<sup>A/A</sup>-PGD<sup>B/B</sup>* genotype were the least frequent.

In conclusion, investigated breeds of pigs demonstrated great differences in the genes analysed. The available literature shows that the frequencies of alleles and genotypes given in this report were within the ranges reported for other populations of the breeds analysed. Within-breed similarities and between-breed differences observed may result from selection targeted at obtaining specific breeding goals.

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## Charakterystyka świń hodowanych w Polsce pod względem występowania izomerazy fosfoglukozowej i dehydrogenazy fosfoglukonianowej

### Streszczenie

W badaniach uwzględniono 2969 loszek rasy wielkiej białej polskiej, polskiej białej zwisłouchej, hampshire, duroc, pietrain i linii 990. U świń wszystkich badanych ras w *locus GPI* i *PGD* stwierdzono występowanie dwóch alleli – *A* i *B*. W większości ras (z wyjątkiem wbp), częstość allelu *GPI<sup>A</sup>* była niższa niż allelu *GPI<sup>B</sup>*. Najniższe częstości allelu *GPI<sup>A</sup>* występowały u świń pietrain, hampshire oraz pbz, a nieco wyższe u świń duroc i linii 990. Wśród badanych grup rasowych, świnię rasy duroc charakteryzowały się najniższą częstością allelu *PGD<sup>A</sup>*. W pozostałych grupach częstość allelu *PGD<sup>A</sup>* była wyższa niż allelu *PGD<sup>B</sup>*. Z analizy częstości występowania genotypów *GPI* wynika, że u świń ras pbz, hampshire, duroc, pietrain i linii 990 najmniejszy udział stanowią zwierzęta o genotypie *GPI<sup>A/A</sup>*, a największy o genotypie *GPI<sup>B/B</sup>*. Częstość genotypu *AA* w *locus PGD* była wysoka u świń rasy wbp i hampshire, a najniższa u świń rasy duroc. Oznaczenie częstości genotypów występujących w obu *loci* jednocześnie wykazało brak genotypu *GPI<sup>A/A</sup>-PGD<sup>B/B</sup>* u świń rasy hampshire i pietrain oraz niską jego frekwencję u świń pozostałych ras.

