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Is There a PGM_1 4 Allele Specific to Amerindian Populations?

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Summary. Rare PGM_1 variants in Macushi and Wayampi Amerindian populations have been compared electrophoretically and by means of electrofocusing. They appear to be identical. The findings are discussed.

Introduction

In a previous article, we reported finding of a rare PGM_1 variant in an Amerindian population of French Guiana, the Wayampi tribe (Tchen et al., 1978b). This variant, whose electrophoretic pattern is comparable to that of PGM_1 4 (Hopkinson and Harris, 1966), has many similarities to the $PGM_1\ 10_{Mac\ 1}$ variant found in the Macushi of Venezuela (Neel et al., 1977). We have compared the Macushi and Wayampi variants to see if any differences could be detected electrophoretically.

Materials and Methods

Hemolysates of Macushi and Wayampi sera had been stored in liquid nitrogen. For control samples, hemolysates were prepared from fresh red blood cells (RBC), of the following common PGM_1 phenotypes[1]: a_1, a_2, a_2-a_1, a_3-a_1, and a_4-a_2.

Starch gel electrophoresis was performed according to the technique of Spencer et al. (1964), with some modifications as described previously (Tchen et al., 1978a).

Electrofocusing was performed on Ampholine PAG plates, pH 3.5–9.5 and pH 4–6.5 (LKB Catalog Nos. 1804–101 and 1804–102), using a LKB "Multiphor." The self-regulating stabilized power supply (LKB 2103) was set at 1200 V, 50 mA, and 25 W. Runs of 85 min were done in all the experiments. Small filter papers (Whatman No. 3, 5 × 10 mm) were soaked in 10 µl of hemolysate, applied to the gel surface 1.5 cm from the anodal strip, without prefocusing, and removed 25 min before the end of the run.

Staining was done in the dark at 37°C, using the technique of Spencer et al. (1964) for a period of 60 min in the case of starch gels and 30 min in the case of the Ampholine PAG plates. After staining, the PAG plates were preserved by soaking them in a solution of 25% methanol, 8% acetic acid, and 10% glycerol at 4°C for 2 h in the dark, dryed, and covered with a plastic sheet.

Results and Discussion

Fig. 1 shows the starch gel electrophoresis pattern. Using this technique, the Macushi and Wayampi PGM_1 molecules migrate the same distances. Using the relative intensity of the bands as a criterion, the Wayampi variant seems to have an activity close to that of allele 1, while the Macushi variant seems to be less active, but this could be due to different conditions of preservation.

For electrofocusing, we routinely use a running time of 85 min, since this gives a pattern which is reproducible and easily interpreted. Due to a malfunction in our photographic equipment, the original records of the experiments were lost. Fig. 2 shows the pattern obtained with pH 3.5–9.5, but the plate was photographed several weeks after the experiment and the bands had already faded a good deal. Runs with $PGM_1\ a_2$; $PGM_1\ a_3$, and $PGM_1\ a_3-a_1$ control samples showed that the genotypes of the individuals studied were as follows: Macushi—$PGM_1\ a_1/PGM_1\ 10_{Mac\ 1}$; and Wayampi—$PGM_1\ a_3/PGM_1\ (4/10)_{Wayampi}$.

Whether the electrofocusing pattern of the $PGM_1\ 10_{Mac\ 1}$ allele is identical to that of $PGM_1\ (4/10)_{Wayampi}$ is not absolutely certain. The arrow in Fig. 2 indicates the position of a very faint band which was clearly visible on the Macushi sample and

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[1] We use the terminology proposed by Kühnl and Spielmann (1978)

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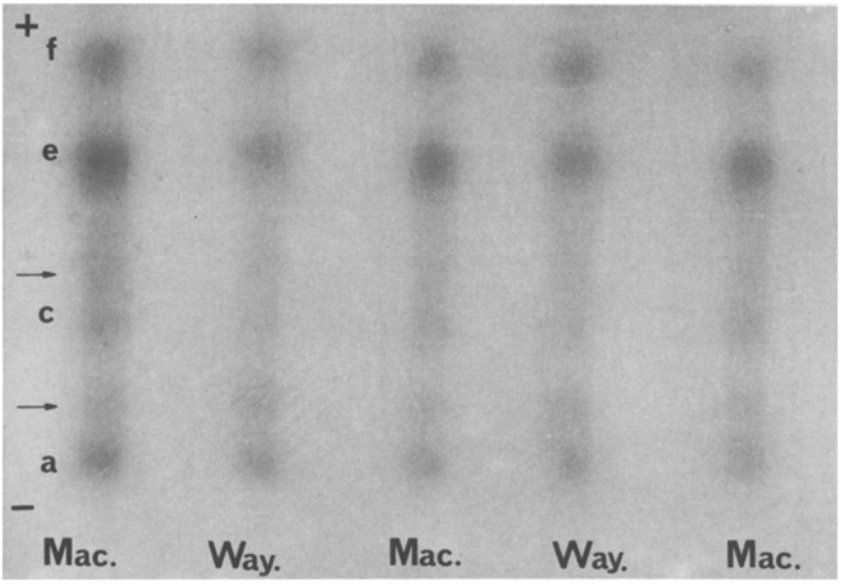

Fig. 1. Starch gel electrophoresis of Macushi (*Mac.*) and Wayampi (*Way.*) samples. *Arrows* indicate the locations of the bands

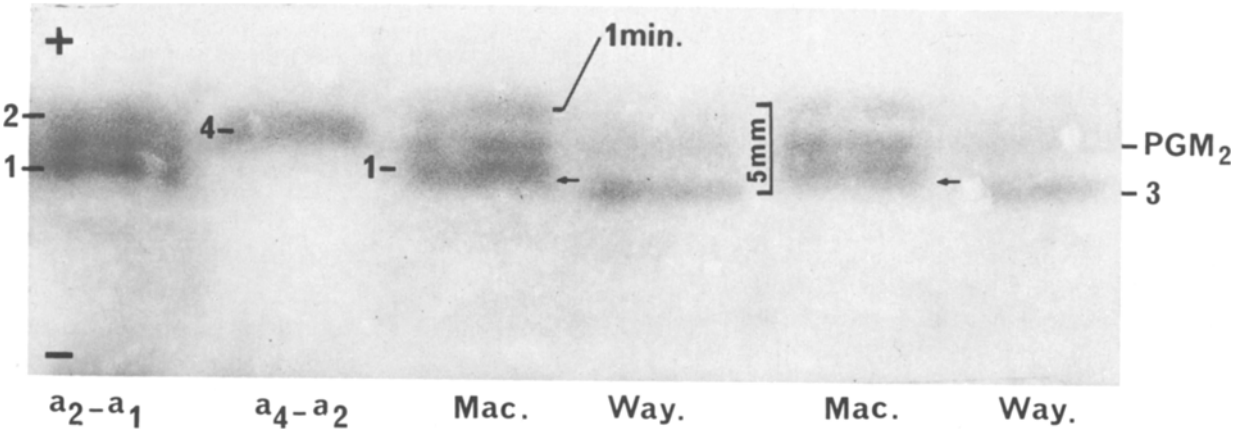

Fig. 2. Results after 85 min of electrofocusing, pH 3.5—9.5. Phenotypes of the control samples: a_2–a_1 and a_4–a_2. *Mac.* = Macushi sample; *Way.* = Wayampi sample. The bands are numbered according to Kühnl and Spielmann (1978). *Arrow* indicates the location of the faint band visible in the Macushi sample

is still somewhat visible on the picture. This faint band, which is cathodal to band 1, may also exist in the Wayampi sample but, due to the intensity of band 3 in this sample, it could not be distinguished.

The presence of a PGM_1 4 variant in the Amerindian inhabitants of the village of Socaire in northern Chile has been reported recently (van der Does et al., 1978). Such a variant has also been found in the Chilean Aymara studied by Ferrell et al. (1979). That genetic exchanges might have occurred between Macushi and Wayampi is not impossible, although it is unlikely and not confirmed by historical or ethnologic studies. Before settling in the interior of French Guiana three centuries ago, the Wayampi lived near the mouth of the Amazon, in a region which was then further away from the Macushi territory than is the present Wayampi territory. The hypothesis of a genetic exchange between the Aymara or Atacamanians of Chile and the Macushi of Venezuela or the Wayampi of French Guiana is even more unlikely.

The identity of the electrophoretic mobility does not imply the identity of the molecules, but it is a striking coincidence to encounter the same electrophoretic variants in such widely separated groups. Thus there is a possibility that the molecules have a common origin. As fas as we can determine, PGM_1 4 variants are not frequent in any population, and if the PGM_1 variants found in Amerindians arise from different

mutational events, then the probability of finding identical electrophoretic mobilities is very low. However, other considerations argue for a separate origin of some and perhaps all of these similar electromorphs. The variant has thus far been detected in low frequency in four different linguistic groups which, as noted above, are widely separated. Although Amerindian chronology leaves much to be desired, an ancestral population common to all four groups cannot have existed prior to 3000 B.C., or 200 generations ago. We must presume that the gene frequency was low at the time this hypothetical ancestral population became subdivided into the groups that developed into the four tribes in which the allele is now found. For Amerindian tribes, Thompson and Neel (1978) have developed the expected number of copies of a "neutral" mutant allele at any given generation following its origin. Very simply, under reasonable population growth schedules (including no growth), the vast majority of mutants have been lost after 200 generations, but those that survive are apt to have achieved numbers that would be recognized as a genetic polymorphism in the tribe in question. A rigorous extension of this argument to the present situation is impossible for a number of reasons, but, by analogy, it seems unlikely that the same variant could have persisted in all four populations but could not in any one of them have "drifted up" to the number of copies which would result in a polymorphism. The increasing ability to characterize definitively small samples of the protein should soon make this type of speculation unnecessary, although in this case there is the additional need to obtain repeat samples from rare individuals in widely dispersed populations.

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