Hum Genet (1995) 96:626–627

DNA VARIANTS

Jorge Azofeifa · Ramiro Barrantes · Marion Cremer

Lack of a *Bgl*II site at the 5′ region of the PGK 1 locus: a new variant discovered in two Chibchan Amerindian groups from Costa Rica

Received: 15 March 1995 / Revised: 9 May 1995

Abstract A new 3.8-kb allele at the 5′ region of the PGK 1 locus detected by the probe pSPT/PGK is reported. This variant was discovered in the Cabecar and Guaymi, two Chibchan Amerindian groups of Costa Rica. So far, a polymorphism that consists of an *Eco*RI/*Bgl*I (1.3-kb) variable site within an *Eco*RI/*Bgl*II (1.7-kb) fragment when DNA is simultaneously digested with *Eco*RI, *Bgl*I and *Bgl*II is known to occur in black and Caucasian populations. These two alleles were also found in the Amerindians tested. The newly described band is due to the lack of the *Bgl*II site situated 1.7 kb downstream from the *Eco*RI site and to the cleavage of another *Bgl*II site 2.1 kb downstream from the lacking one. This variant might be restricted to some Amerindian groups and perhaps also to Asiatic populations. Thus, it could be a useful marker in evolutive studies and for forensic applications. Moreover, the presence of a third allele in populations with Amerindian ancestry can increase the heterozygosity of the region disclosed by the pSPT/PGK probe, thus improving its application in issues dealing with X-chromosome activation ratios in females.

Description of the probe. pSPT/PGK is an 812-bp *Eco*RI-*Bam*HI fragment cloned in the plasmid pSP64 and encompasses the 5′ region of the X-linked PGK1 locus (Keith et al. 1986).

Polymorphism. pSTP/PGK detects an *Eco*RI/*Bgl*I (1.3-kb) variable site located within an *Eco*RI-*Bgl*II (1.7-kb) fragment when genomic DNA is cleaved with the three enzymes (Fearon et al. 1987; Vogelstein et al. 1987). By using this combination of enzymes, a new 3.8-kb band was detected in two Chibchan Amerindian groups from Costa Rica: the Guaymi from the Peninsula de Osa Indian Reservation and the Cabecar from Ujarrás (Barrantes et al. 1990).

Determination of the origin of the new variant. DNAs of four males having the 3.8-kb band, of a female homozygous for the 3.8-kb band, of a female heterozygous for the 3.8- and 1.3-kb bands and of a control female heterozygous for the 1.7- and 1.3-kb bands were digested with *Eco*RI, *Eco*RI + *Bgl*I, and *Eco*RI + *Bgl*II. The *Eco*RI digests showed bands in the range between 12 and 20 kb. The 3.8-kb band was present only in the *Eco*RI + *Bgl*II digests of all individuals tested except in the female heterozygous for the 1.7- and 1.3-kb bands who instead showed the 1.7-kb band. The 1.3-kb band was only observed in the heterozygous females in the *Eco*RI + *Bgl*I digests. Evidence indicating that the *Bgl*II and not the *Eco*RI site was missing was provided by digestion with *Bst*XI, *Bst*XI + *Bgl*I, and *Bst*XI + *Bgl*II. Two *Bst*XI sites, separated approximately 2 kb from each other, bracket the *Bgl*II site that originates the 1.7-kb fragment. (Fig. 1) (Vogelstein et al. 1987). All *Bst*XI digests showed the 2-kb band which was modified by neither the *Bgl*I nor the *Bgl*II enzyme in double digests of DNAs from the persons carrying the 3.8-kb fragment. Thus, the 3.8-kb band is the result of cleavage by *Eco*RI, lack of the *Bgl*II site situated 1.7 kb downstream from the *Eco*RI site and cleavage of another *Bgl*II site lying 2.1 kb downstream from the one which was lacking (Fig. 1).

Frequency. Out of a total sample of 29 Cabecars analyzed, 22 females and 2 males (46 X chromosomes) can be considered independent. Among them four 3.8-kb, three 1.7-kb and thirty nine 1.3-kb alleles were counted. The total Guaymi sample was 26, but only 5 females and 4 males (14 X chromosomes) are independent since the other 17 are members of 6 families. Twelve 3.8-kb, one 1.7-kb and one 1.3-kb alleles were found. As the sample sizes are not

J. Azofeifa · M. Cremer
Institut für Humangenetik und Anthropologie der Universität, Im Neuenheimer Feld 328, D-69120 Heidelberg, Germany

J. Azofeifa (✉) · R. Barrantes
Instituto de Investigaciones en Salud (INISA) and Escuela de Biologia. Universidad de Costa Rica, Ciudad Universitaria Rodrigo Facio, San José, Costa Rica

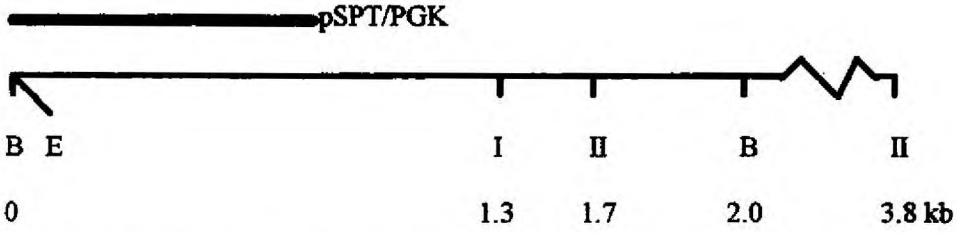

Fig. 1 Restriction sites of the enzymes employed to detect the described polymorphism at the 5′ region of the PGK1 locus (modified from Vogelstein et al. 1987) (*B BstXI*, *E EcoRI*, *I BglI*, *II BglII*). The newly described 3.8-kb band is an *EcoRI-BglII* fragment resulting from lack of the *BglII* site lying 1.7 kb downstream from the *EcoRI* site. The *shorter and wider line* represents the probe pSPT/PGK at its hybridization site

representative of the groups in which the variant was found, an estimate of allelic frequencies cannot be given.

Mendelian inheritance. The 3.8-kb band cosegregates with the 1.7-kb and the 1.3-kb bands in one family (mother and two daughters, 3.8/1.7, daughter of a different father, 3.8/1.3) and with the 1.3-kb band in another independent family (mother and two daughters, 3.8/1.3, one daughter, 3.8 and one son, 1.3).

Chromosomal localization. PGK1 has been mapped to the Xq13.3 band (Willard et al. 1985).

Comments. Since this band has not been reported in Caucasians and Blacks, it could be a variant restricted to some Amerindian groups and perhaps also to Asiatic populations as is the case of the transferrin D-China (Azofeifa and Barrantes 1991; Barrantes et al. 1990), and as such it would serve as a useful marker to trace phylogenetic relationships, to determine racial admixture and in forensic applications. Additionally, the presence of this allele probably increases the heterozygosity of the region detected by the probe pSPT/PGK in these populations, thus improving its application in studies determining X-chromosome activation ratios in females.

Acknowledgements Part of this investigation was financed by the Universidad de Costa Rica and by the Consejo Nacional de Investigaciones (CONICIT) of Costa Rica. The stay of J.A. in Germany was supported by a fellowship of the Deutscher Akademischer Austauschdienst (DAAD) and of the Universidad de Costa Rica.

References

Azofeifa J, Barrantes R (1991) Genetic variation in the Bribri and Cabecar Amerindians from Costa Rica. Rev Biol Trop 39: 249–253

Barrantes R, Smouse PE, Mohrenweiser HW, Gershowitz H, Azofeifa J, Arias TD, Neel JV (1990) Microevolution in lower Central America: genetic characterization of the Chibcha-speaking groups of Costa Rica and Panama, and a consensus taxonomy based on genetic and linguistic affinity. Am J Hum Genet 46:63–84

Fearon ER, Winkelstein JA, Civin CI, Pardoll DM, Vogelstein B (1987) Carrier detection in X-linked agammaglobulinemia by analysis of X-chromosome inactivation. N Engl J Med 316: 427–431

Keith DH, Singer-Sam J, Riggs AD (1986) Active X-chromosome DNA is unmethylated at eight CCGG sites clustered in a guanine-plus-cytosine-rich island at the 5′end of the gene for phosphogylcerate kinase. Mol Cell Biol 6:4122–4125

Vogelstein B, Fearon ER, Hamilton SR, Preisinger AC, Willard HF, Michelson AM, Riggs A, Orkin SH (1987) Clonal analysis using recombinant DNA probes from the X-chromosome. Cancer Res 47:4806–4813

Willard HF, Goss SJ, Holmes MT, Munroe DL (1985) Regional localization of the phosphoglycerate kinase gene and pseudogene on the human X chromosome and assignment of a related DNA sequence to chromosome 19. Hum Genet 71:138–143