

DNA VARIANTS

N. German Pasteris · Jerome L. Gorski

An intragenic *TaqI* polymorphism in the faciogenital dysplasia (FGD1) locus, the gene responsible for Aarskog syndrome

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Abstract A *TaqI* polymorphism, located in intron 4 of the faciogenital dysplasia (*FGD1*) gene, the gene responsible for Aarskog syndrome, is described. *FGD1* encodes a putative Rho/Rac guanine nucleotide exchange factor involved in mammalian morphogenesis. The identification of an intragenic polymorphism will facilitate the accurate carrier detection of individuals at risk for Aarskog syndrome.

Description. The *FGD1* probe is a 3.85-kb *EcoRI* cDNA insert, denoted as pFCF3.85, that encodes the complete open reading frame of the faciogenital dysplasia gene, the gene responsible for Aarskog syndrome (Pasteris et al. 1994).

PCR primers. E4-P9: 5'-TGAGGCCTCCCGCTGCCTGTTTC-3'. E5-P21: 5'-CTGATCCAGGAGATGGAGCC-TGG-3'.

Polymorphism. Used as a probe to perform hybridization analyses of *TaqI*-digested genomic DNA, probe pFCF3.85 detected two alleles: A1, 6.0 kb and A2, 3.8 kb. The 6.0-kb fragment represented the 3.8-kb fragment (which included exon 4) and its adjacent 2.2-kb *TaqI* fragment (which included exon 5). To facilitate analysis, a PCR strategy was generated to investigate the presence or ab-

sence of the polymorphic *TaqI* site in intron 4. Genomic DNA was amplified using oligonucleotide primers directed against *FGD1* exons 4 and 5. The polymorphism was identified by digesting the resulting 1.7-kb PCR product with *TaqI*; upon digestion, products containing the *TaqI* site yielded 1.2-kb and 0.5-kb fragments.

Allelic frequency. Estimated from 84 chromosomes of unrelated individuals (40 CEPH females and 2 random unrelated females). A1 = 0.13; A2 = 0.87.

Chromosomal localization. The *FGD1* gene was localized to region Xp11.21 by somatic cell and radiation hybrid analyses (Pasteris et al. 1994).

Mendelian inheritance. Mendelian X-linked inheritance was observed in one family of five individuals.

PCR conditions. Amplifications were performed in 50- μ l volumes containing 50 mM KCl, 10 mM Tris-HCl, pH 8.0, 10 mg/ml BSA, 1.5 mM MgCl₂, 200 μ M each of dATP, dGTP, dCTP, and dTTP, 100 ng of genomic DNA, 0.5 μ M primers, and 2.5 U AmpliTaq (Perkin Elmer/Cetus). Amplifications were performed in a DNA thermal cycler 480 (Perkin Elmer/Cetus); after an initial 10-min denaturation cycle (94°C), 34 cycles followed: 94°C denaturation 1 min, 65°C annealing 1 min, 72°C extension 2 min, with a final extension of 10 min at 72°C.

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N. G. Pasteris · J. L. Gorski
Department of Human Genetics and Pediatrics
and Communicable Diseases,
University of Michigan Medical Center,
Ann Arbor, MI 48109-0688, USA

J. L. Gorski (✉)
Pediatrics and Communicable Diseases,
Division of Pediatric Genetics,
University of Michigan Medical Center,
Ann Arbor, MI 48109-0688, USA

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