New SacI RFLP for human liver glutathione-S-transferase

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Source/Description: Ha is a class of subunit of human liver enzyme glutathione-S-transferase (GST). The pGTH1 DNA contains a GST cDNA encoding the human GST subunit 1 of the Ha class in the pUC19 vector. It is 810 nucleotides long and contains a 66 nucleotide unit at the 5' non-coding region, a 222 amino acid open reading frame, and a complete sequence of 78 bp at the 3' non-coding end (1, 2).

Polymorphism: SacI identifies a polymorphism which detects bands of 8.3 kb and 11.0 kb.

Frequency:

		Allele Frequency		Genotype Frequency	
SacI	N = 46	A1	A2	A1 A1	A1 A2
*C=44	***B=0				
A=1	**NA=1	.435	.565	4 (.087)	32 (.696)
A1 = 11.0 kb					10 (.217)
A2 = 8.3 kb					
*C = Caucasian **A = Asian ***B = Black ****NA = Native American					

Not Polymorphic For: EcoRI, HindIII, BamHI, BclI, BglI, BglII, HincII, PstI, KpnI, ApaLI, PvuII, XbaI, RsaI, AvaII, Sau3AI, EcoRV.

Chromosomal Localization: 6p12 (3, 4).

There was no statistically significant deviation from Hardy-Weinberg equilibrium.

Probe Availability: Contact C.-P.D. Tu.

References: (1). Tu, C.-P.D., Matsushima, A., Li, N., Rhoads, D.M., Srikumar, K., Reddy, A.P. and Reddy, C.C. (1986) *J. Biol. Chem.* **261**, 945–954. (2). Tu, C.-P.D. and Qian, B. (1986) *Biochem. & Biophys. Res. Com.* **141**, 229–237. (3). Board, P.G. and Webb, G.C. (1987) *Proc. Natl. Acad. Sci. USA* **84**, 2377–2381. (4). Chow, N.-W.I., Whang-Peng, J., Kao Shan, C.-S., Tam, M.F., Lai, H.-C.J. and Tu, C.-P.D. (1988) *J. Biol. Chem.* **263**, 12979–12800.

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Single copy probe CRI-L1065 (D6S21) maps to 6cen-6q21

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Source/Description: The probe was isolated from a genomic lambda charon 4A library (1). Insert size 10–15 kb.

Polymorphism: The probe detects a VNTR polymorphism with RsaI. Variable fragments range in size beginning at 10.5 kb. Invariant bands are seen at 1.9, 1.5, and 0.8 kb. The probe detects polymorphisms with all enzymes tested. These include ApaI, BamHI, BglII, BstEII, EcoRI, HindIII, HaeIII, MspI, StyI, and TaqI. All RFLPs appear to be in linkage disequilibrium.

Chromosomal Localization: The probe has been localized to 6cen–6q21 by somatic cell hybrids. Cri-L1065 is linked by twopoint analysis to other chromosome 6 markers (2):

Interval	Recombination Fraction	Maximum LOD
CRI-L1065–CRI-L1077	0.05	16.74
CRI-L1065–CRI-T22	0.00	15.65

Mendelian Inheritance: Co-dominant inheritance of the RsaI RFLP was seen in 22 multigenerational CEPH families.

Probe Availability: Probe is available for research use. Contact G. Voivis, Collaborative Research, Inc.

Other Comments: PIC = 0.74, Heterozygosity = 0.74.

References: 1. Lawn *et al.* (1978) *Cell* **15**, 1151–1174. 2. Donis-Keller *et al.* (1987) *Cell* **51**, 319–337.