BamHI and EcoRI restriction fragment length polymorphisms at the glutathione S-transferase 3 locus

Philip G. Board and Marjorie Coggan

Human Genetics Group, John Curtis School of Medical Research, The Australian National University, Canberra ACT 2601, Australia

SOURCE/DESCRIPTION: A plasmid (pGT3.1) containing a 592 bp cDNA fragment derived from the GST3 gene was used as a probe (1).

POLYMORPHISM: BamHI identifies a two allele polymorphism with variant hybridizing fragments of 5.6 and 5.22 kb. Invariant fragments of ≈37, 17.5 and 2.6 kb are also detected. EcoRI identifies a two allele polymorphism with variant hybridizing fragments of 6.41 and 6.15 kb. Invariant fragments of ≈12.8 and 4.1 kb are also detected.

FREQUENCY: The BamHI (5.6/5.22 kb) and EcoRI (6.41/6.15 kb) allele frequencies were .095/.905 in a sample of 37 Europeans. Both polymorphisms appear to result from the same insertion/deletion event, or are in complete linkage disequilibrium.

NOT POLYMORPHIC FOR: ApaI, BclI, BglII, HaeIII, HindIII, PvuII, Rsal, TaqI and XbaI.

CHROMOSOMAL LOCALIZATION: The GST3 gene has been localized to 11q13 by in situ hybridization (1). A related weakly hybridizing sequence has also been detected at 12q13-14 (1).

MENDELIAN INHERITANCE: Codominant transmission has been demonstrated in one family of five individuals.

PROBE AVAILABILITY: Freely available from Dr P.G. Board.


ACKNOWLEDGEMENTS: This investigation received financial support from the UNDP/World Bank/WHO Special Programme for Research and Training in Tropical Diseases and the Australian Capital Territory Cancer Society.