PCR assay for a polymorphic *PvuII* site in the LPL gene

J.P.Johnson, P.M.Nishina* and J.K.Naggert
Children's Hospital Medical Center, Children's Hospital Oakland Research Institute, 747 52nd Street, Oakland, CA 94609, USA

Source/Description: Two oligonucleotides derived from the sequence flanking the polymorphic PvuII site in the intron between exon 6 and 7 of the LPL gene (1) were used to amplify the region and generate a fragment of the predicted size of 319 bp. Polymorphism was detected by PvuII digestion of the PCR product.

Primer Sequences:
LPL-1: AGGCTTCACTCATCCGTGCCTCC
LPL-2: TTATGCTGCTTTAGACTCTTGTC

Frequency: Estimation corresponds to previously observed frequencies (2).

	Current work n = 15	Fisher, *et al.* (2) n = 49
Allele D1: −	0.43	0.41
Allele D2: +	0.56	0.59

Chromosomal Location: The LPL gene has been assigned to chromosome 8p22 (3).

Other Comments: The PCR reaction was performed on genomic DNA as described by Saiki,R.K. *et al.* (4) with some modifications: (a) 50 μM tetramethylammonium chloride was added to the reaction mix to decrease the amplification of nonspecific bands caused by LPL-1 (5), (b) denaturation at 94°C for 1 min, (c) annealing at 62°C for 2 min, (d) extension at 72°C for 2 min, and (e) 30 cycles were used. The PCR products were fractionated in a 6% nondenaturing polyacrylamide gel.

Acknowledgements: Work supported by grant BG88−192 from the National Dairy Promotion and Research Board.

References: 1) Oka,K. *et al.* (1989) *Nucl. Acids Res.* **17**, 6752. 2) Fisher,K.L. *et al.* (1987) *Nucl. Acids Res.* **15**, 7657. 3) Sparkes,R.S. *et al.* (1987) *Genomics* **1**, 138−144. 4) Saiki,R.K. *et al.* (1988) *Science* **230**, 487−491. 5) Hung,T. *et al.* (1990) *Nucl. Acids Res.* **18**, 4953.

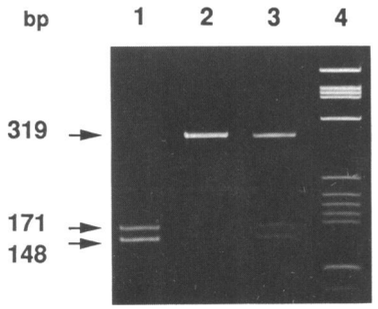


Figure 1. Examples of individuals who are homozygous for presence (lane 1) or absence (lane 2) of the PvuII restriction site or are heterozygous (lane 3). DNA molecular weight marker pBR322 cut with HaeIII shown in lane 4.

* To whom correspondence should be addressed

BamHI RFLP of the inhibin beta B (INHBB) chain gene on chromosome 2

G.Chenevix-Trench*, M.Southall[1], S.Healey[1], A.Stewart[2], R.Forage[2] and N.G.Martin[1]
Queensland Institute of Medical Research and Joint Oncology Program, Department of Pathology, University of Queensland, Herston Medical School, Herston, Q 4006, [1]Queensland Institute of Medical Research, Bramston Terrace, Herston, Q 4006, and [2]Biotech Australia Pty Ltd, 28 Barcoo Street, Roseville, NSW 2069, Australia

Source and Description of Clone: pBTA528 contains 920 bp of the inhibin β_B genomic sequence inserted into pBR322 (1).

Polymorphism: BamHI identifies two alleles: Allele A1—4.4 kb, Allele A2—3.4 kb.

Frequencies: Allele A1: 0.11, Allele A2: 0.89 in 51 unrelated Caucasians.

Not Polymorphic For: EcoRI, HindIII, MspI, TaqI, PstI, SstI, BglII in 9 unrelated Caucasians.

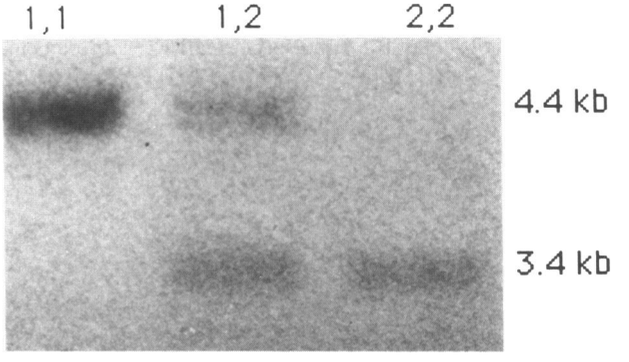
Chromosomal Localisation: Inhibin β_B has been mapped to 2cen−2q13 (2).

Mendelian Inheritance: Mendelian inheritance was demonstrated in 6 families (12 meioses).

Probe Availability: Contact Dr. R. Forage.

References: 1) Stewart,A. *et al.* (1986) *FEBS Lett.* **206**, 329−334. 2) Barton,D.E. *et al.* (1989) *Genomics* **5**, 90−99.

Acknowledgements: This work was supported by the National Health and Medical Research Council of Australia.



* To whom correspondence should be addressed