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LETTER TO THE EDITOR

A Variation in the *HindIII* Restriction Pattern of the Dystrophin Gene DMD With cDMD Probe 11–14

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To the Editor:

The normal restriction pattern of the dystrophin gene (DMD; MIM# 310200) with 8 cDMD probes (1–2a, 2b–3, 4–5a, 5b–7, 8, 9, 10 and 11–14) has been described in about 60 normal individuals of mixed ethnic origin, mainly Caucasians [Darras and Francke, 1988a]. A similar restriction pattern in Indian subjects (40 DMD patients, their family members, and 20 normal healthy controls) was observed with 7 cDMD probes (1–2a, 2b–3, 4–5a, 5b–7, 8, 9, and 10). The eighth probe, 11–14, showed a polymorphism in these subjects with a gain of a new 2.8-kb *HindIII* fragment, and a loss of 1.9- and 1.8-kb fragments [Mital et al., 1998]. Since no population is fixed for different alleles, we reassessed the *HindIII* restriction pattern of the dystrophin gene with probe 11–14 in a fresh set of 112 Indian subjects (74 males and 38 females); 51 individuals from unrelated families suffering from neuromuscular disorders, Duchenne (DMD), Becker (BMD), and Limb girdle (LGMD) muscular dystrophy, Spinal muscular atrophy (SMA) and Quadriceps myopathy (QM), their family members (44) and control (17) DNA samples. We also assessed 9 control DNA samples (6 males and 3 females) from individuals of other ethnic origin, British (3), German (1), Belgium (1), African (2), and Korean (2).

We observed a total of 10 fragments (10.0, 7.8, 6.8, 6.0, 5.9, 2.8, 2.1, 1.9/1.8, 1.5, and 1.45 kb) with probe 11–14 (Fig. 1). A strongly hybridising fragment of 2.8 kb is present in each of the subjects, while the 1.9- and 1.8-kb bands appear as a single faint co-migrating fragment.

X-chromosomal origin for all the fragments was confirmed by dosage, with female DNA (lane 5) showing two-copy intensity and male DNA (lanes 1, 2, 3, 4 and 6) showing single-copy intensity (Fig. 1). A strongly hybridising fragment of 2.8 kb is present in each of the subjects, while the 1.9- and 1.8-kb bands appear as a single faint co-migrating fragment.

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1). In addition to these 10 fragments hybridizing strongly with cDMD 11–14, there was no lane background with faintly hybridizing bands, presumably of autosomal origin as described in Caucasians earlier [Darras and Franke, 1988a, b].

Our observations in Indian subjects with respect to other ethnic groups have shown similar results, indicating that the Indian population in fact does not differ from other populations.

Our finding is important as it suggests that fragment of 2.8 kb belongs to the dystrophin gene, since it hybridized strongly with cDNA probe 11–14 and showed X dosage. This 2.8-kb fragment was not detected by Darras and Francke [1988a], and was mistaken for a polymorphism by Mital et al. [1998].

To conclude, this communication thus sets forth a slightly different standard pattern of restriction fragments that are detected when human DNA, normal or disease-risk, is cleaved with HindIII and hybridized with probe 11–14. Since a few deletions have been mapped to this region with probe 11–14 in DMD patients [Darras and Franke, 1988b; McCabe et al., 1989; Bies et al., 1992], a complete restriction map is important when screening for deletions is undertaken for the dystrophin gene.

REFERENCES


