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Mutations in *TNNT3* Cause Multiple Congenital Contractures: A Second Locus for Distal Arthrogryposis Type 2B

To the Editor:

We recently reported that distal arthrogryposis type 1 (DA1 [MIM 108120]) and distal arthrogryposis type 2B (DA2B [MIM 601680]), both of which are characterized by congenital contractures of the hands/wrists and feet/ankles (Bamshad et al. 1996), are caused by mutations in *TNNI2* and *TPM2*, respectively (Sung et al. 2003). *TNNI2* encodes an isoform of troponin I; this isoform and the isoforms of troponin T (TnT) and troponin C constitute the troponin complex of fast-twitch myofibers. This complex is the primary sensor of intracellular Ca^{+2} ion concentration in skeletal muscle, and, consequently, it is an important regulator of muscle contraction. The troponin complex of fast-twitch myofibers exerts its effect on muscle contraction by binding to actin and β-tropomyosin, the product encoded by *TPM2* (Clark et al. 2002). These findings led us to hypothesize that mutations in genes encoding other contractile-apparatus proteins specific to fast-twitch myofibers might also cause multiple congenital contractures. We now report the discovery of a mutation, in *TNNT3* (the gene encoding TnT specific to fast-twitch myofibers), that causes DA2B.

We sequenced *TNNT3* in 47 families with either DA2A (classical Freeman-Sheldon syndrome [MIM 193700]) or DA2B. We found a G→A missense mutation, at nucleotide position 188 in exon 9 of the *TNNT3* cDNA (GenBank accession number NM_006757), that causes an arginine-to-histidine substitution at amino acid residue 63 (R63H) of TnT in a mother with DA2B and her two affected children (fig. 1). For several reasons, this mutation is probably disease causing. First, the mutation identified in the proband was also present in all affected family members (fig. 1). There is, however, a probability of 1/4 that this pattern occurred by chance. The inference that R63H causes DA2B would be strengthened by demonstrating that this mutation did not occur in the unaffected parents of I-2 (i.e., that it is a de novo mutation). However, the only living parent of I-2 is unavailable for study. Second, this change was not found in 488 chromosomes from an ethnically matched control group that we screened. Third, R63H results in the substitution of an amino acid residue that is conserved in all known isoforms of TnT (fig. 2), implying that this difference is likely to have structural and/or functional consequences. Fourth, substitution of the homologous amino acid residue in the cardiac-specific form of TnT causes cardiomyopathy (Varnava et al. 1999).

Because mutations in *TNNI2* have been found in only ~10% of cases of DA2B, we suspected that DA2B is a genetically heterogeneous condition (Sung et al. 2003). To date, however, linkage studies have not identified any candidate regions other than chromosome 11p15.5 (Krakowiak et al. 1997). The observation that DA2B can be caused by mutations in either *TNNI2* or *TNNT3* confirms that DA2B is genetically heterogeneous. Because *TNNI2* and *TNNT3* are located within several hundred kilobases of one another on chromosome 11p15.5, this conclusion is also consistent with the results of our prior linkage studies (Sung et al. 2003). Nevertheless, the absence of mutations in *TNNI2* or *TNNT3* in most cases of DA2B suggests either that regulatory regions of these genes harbor mutations or that mutations in genes yet to be identified also cause DA2B.

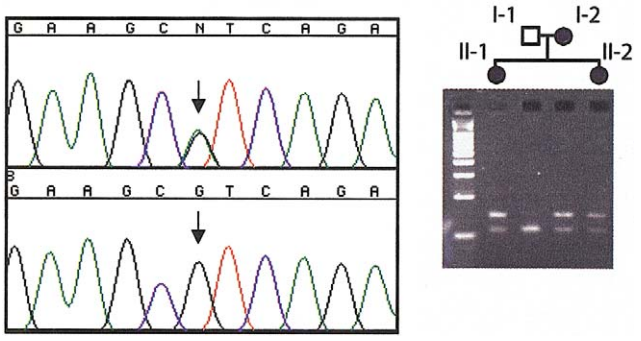

Figure 1 Electropherogram demonstrating heterozygosity for a G→A missense mutation at nucleotide position 188 in exon 9 of *TNNT3* in a family with DA2B. To confirm the presence of this mutation, we incorporated a *Mlu*I restriction site into the amplicon by mismatch PCR. The presence of the mutation eliminates this site, producing fragments of 144 bp and 110 bp in the affected mother and her two affected children (*blackened symbols*), whereas the unaffected father is homozygous for the 110-bp fragment.

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TNNT3, human (fast twitch)  …DDIQKKRQNKDLMELQALIDSHFEARKKEEEEL…
TNNT3, mouse                …DDIQKKRQNKDLMELQALIDSHFEARKKEEEEL…
TNNT3, bird                 …DDIQKKRQNKDLIELQALIDSHFEARRKEEEEL…
TNNT1, human (slow twitch)  …DDIHRKRMEKDLLELQTLIDVHFEQRKKEEEEL…
TNNT2, human (cardiac)      …DDIHRKRMEKDLNELQALIEAHFENRKKEEEEL…
                                      R63H
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Figure 2 Amino acid sequences of fast-twitch TnT in human, mouse, and bird, aligned with amino acid sequences of human slow-twitch TnT and human cardiac TnT.

Although the cause of DA2B can be distinguished by direct testing of *TNNT3* and *TNNI2,* there appear to be few, if any, ways to distinguish, on the basis of only clinical characteristics, which gene is responsible. There may, however, be sufficient phenotypic differences between DA2B and DA1 to distinguish between them. In addition to the facial features (e.g., small mouth and prominent nasolabial folds) common to DA2B but lacking in individuals with DA1, several characteristics (e.g., vertical talus and scoliosis) are more frequent in DA2B than in DA1. Additionally, the hand and foot contractures in patients with DA2B appear to be more resilient to medical intervention (e.g., occupational therapy and casting). It should be cautioned, however, that mutations have been found in too few families with both DA1 and DA2B to lend much credibility to broad generalizations about genotype-phenotype relationships.

The mechanism by which the R63H substitution in TnT in fast-twitch myofibers causes congenital contractures is unknown. Missense mutations in *TNNT2*—a *TNNT3* paralogue, encoding a cardiac-specific form of TnT—cause ~15% of cases of familial hypertrophic cardiomyopathy (Watkins et al. 1995). One of these mutations is an arginine-to-leucine substitution of amino acid residue 94 (R94L), which is homologous to amino acid residue 63 in fast-twitch myofiber TnT (Varnava et al. 1999). The R94L substitution perturbs tropomyosin-dependent functions of TnT, including the binding of tropomyosin to actin (Palm et al. 2001), an effect that might be due, in part, to impaired flexibility of the N-terminal tail of TnT (Hinkle and Tobacman 2003). The R63H substitution may have a similar effect on TnT in fast-twitch myofibers.

The theme that is emerging from this and our previous studies is that perturbation of the function of the contractile apparatus of skeletal muscle during fetal development can cause multiple congenital contractures in individuals with an otherwise normal neuromuscular examination. On the basis of this result, it seems plausible that polymorphisms in one or more of the genes encoding the proteins of the troponin-tropomyosin complex of fast-twitch myofibers may influence an individual's susceptibility to isolated contractures (e.g., idiopathic clubfoot) or modify the phenotype of common myopathic disorders (e.g., Duchenne muscular dystrophy). At minimum, this report underscores the existence of a new class of genetic muscle diseases that lack many of the findings typical of a heritable myopathy.

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Electronic-Database Information

The accession number and URLs for data presented herein are as follows:

GenBank, http://www.ncbi.nlm.nih.gov/Genbank/ (for *TNNT3* cDNA [accession number NM_006757])
Online Mendelian Inheritance in Man (OMIM), http://www.ncbi.nlm.nih.gov/Omim/ (for DA1, DA2B, and classical Freeman-Sheldon syndrome)

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Haploinsufficiency of *TNXB* Is Associated with Hypermobility Type of Ehlers-Danlos Syndrome

To the Editor:

Ehlers-Danlos syndrome (EDS) is a heterogeneous group of heritable connective-tissue disorders, generally affecting skin, joints, and blood vessels. The most recent classification recognizes six subtypes (Beighton et al. 1998), of which the hypermobility type (HT-EDS [formerly EDS type III] [MIM 130020]) is the most common. This type of EDS is similar to benign joint hypermobility syndrome (BJHS), and both are often considered to represent the same hyperlaxity syndrome, since no clear clinical distinction can be made (Grahame 1999). Although various causative genes have been found in all other types of EDS, the genetic basis of HT-EDS or BJHS remains unexplained (Steinmann et al. 2002). One family has been described that has a missense mutation in *COL3A1* (Narcisi et al. 1994), resulting in a phenotype that resembles HT-EDS, without obvious vascular complications. Mutations in *COL3A1* generally result in the severe vascular type of EDS (MIM 130050). To our knowledge, no other cases of *COL3A1* mutations in HT-EDS have been reported.

Recently, we showed that deficiency of the extracellular-matrix protein tenascin-X (TNX), encoded by the *TNXB* gene, causes a new type of recessively inherited EDS (Schalkwijk et al. 2001). Patients with complete deficiency of TNX showed marked joint hypermobility, skin hyperextensibility, and easy bruising. The absence of atrophic scars and recessive inheritance distinguishes TNX deficiency from the classical type of EDS. In our initial report (Schalkwijk et al. 2001), only a few heterozygous family members were available for examination. Here, we have examined all 20 heterozygous family members (individuals from families A–D in table 1) who were available for further study, regardless of clinical symptoms; in all of these individuals, we have found significantly reduced serum TNX levels (56% $\pm$ 6% vs. 100% $\pm$ 14% in the control population; $P < .001$, by Student's t test) (fig. 1*f*), and, in 17 of them, we have confirmed heterozygosity for a truncating *TNXB* mutation (table 1). Clinical examination revealed generalized joint hypermobility in nine family members (45%), using the Beighton score (Beighton et al. 1973), for HT-EDS, or the Brighton criteria (Grahame et al. 2000), for BJHS (table 1 and fig. 1*e*). Skin hyperextensibility and easy bruising, frequently seen in the individuals with complete TNX deficiency, were absent. A number of patients with haploinsufficiency had recurring joint dislocations and chronic joint pain, as are seen in HT-EDS and BJHS. Only four family members carrying two normal *TNXB* alleles were available for study, of whom none had hypermobility. The local medical ethics committee (CMO Regio Arnhem-Nijmegen) approved the study protocol, and informed consent was obtained from all patients.

A striking finding is that 0 of the 6 males with haploinsufficiency fulfilled the clinical criteria for HT-EDS or BJHS, whereas 9 of 14 (64%) females were positive. This finding is in accordance with previous population-based studies that show a female preponderance in joint hypermobility syndromes (Larsson et al. 1987; Rikken-Bultman et al. 1997). In a control group of 30 unaffected females of the same age as the females with haploinsufficiency in the present study, we found no individuals with a Beighton score >4. This indicates that the prevalence of generalized joint hypermobility in a population of females with haploinsufficiency is significantly higher than in a control population ($P < .001$, by χ^2 test). No sex differences in serum TNX levels in unaffected individuals and individuals with haploinsufficiency were found (not shown).

Because our observations in families carrying previously described *TNXB* mutations suggested an association between *TNXB* haploinsufficiency and joint