

Conflict of interest

The authors declare no conflict of interest.

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Sir,

A possible genetic answer to a recently reported novel phenotype

We read with interest the recent article of Shen *et al*, who report a unique Chinese pedigree with the features of ectopia lentis and varicose great saphenous vein. Marfan's syndrome (MFS), clinically diagnosed by characteristic multiple-system abnormalities, lies at one end of a phenotypic spectrum. At the other end of that spectrum are members of the general population who have one feature common to those with MFS.² Of those patients who fulfil the modified Ghent criteria for full MFS, up to 97% are found to have FBN1 mutations.3 However, the patients presented by Shen et al are atypical. An alternative approach would be to try to postulate an all-encompassing molecular diagnosis that best fits the clinical signs. Venous varicosity is usually secondary to valvular incompetence, a condition that has been strongly associated with heterozygous mutations in the FOXC2 gene on chromosome 16.4 Similarly, a range of anterior segment phenotypes have been described, with mutations in FOXC2 inherited in a dominant manner.5 When aiming for a genetic diagnosis in this family, we would therefore advocate including FOXC2 in the screening set of genes. If a FOXC2 mutation were found in this family, this would represent an interesting extension to the associated phenotype.

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Sir,

Response to Khan et al

We thank Khan et al¹ for their insightful comments on our recent paper.² Their suggestion of including FOXC2 in the screening set of genes is very interesting. It opens a possibly new aspect of an interesting extension to the associated phenotype in the reported Chinese family. We have already collected 18 genomic DNA samples from three generations of this family. Linkage to FBN1 locus cannot be ruled out by microsatellite markers. A novel missense mutation was identified in FBN1 gene, which co-segregated with the ocular phenotype (data not published). Association of single-nucleotide polymorphisms in $TGF\beta R2$ gene was not confirmed. Obviously, this is different from the features associated to disposition to a rtic dilatation and dissection of a UK family reported by Law et al.3 FOXC24,5 or other genes may be the possible genetic factors as Khan et al pointed out. Whole-genome scanning using single-nucleotide polymorphism chips is our future strategy, which we hope can answer the question shortly.

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