Fibrodysplasia ossificans progressiva (FOP) [OMIM 135100] is a rare genetic disorder in which ossification of connective tissue leads to severe disability. It is an autosomal dominant trait and affected persons have mutations in the activin A type 1 receptor gene (ACVR1), chromosomal locus 2q23-24.1 ACVR1 is one of the f4 type 1 receptors that mediate in the highly conserved bone morphogenetic protein (BMP) signalling pathway, through a domain rich in glycine and serine (GS-domain) residues.2,3

Diagnosing FOP has depended on recognising characteristic clinical and radiological features, and until recently the causative mechanism remained elusive.3,4 FOP molecular investigations has revealed that most affected individuals have the same single nucleotide change 617G>A in the ACVR1 gene. The base change is a missense mutation that leads to the substitution of arginine with histidine (R206H). The point mutation 617G>A in ACVR1 that occurs in the GS-domain alters the ligand-dependent sensitivity for BMP signalling in connective tissue progenitor cells. Under normal circumstances, type 1 receptors such as ACVR1 are inactive until stimulated by extracellular BMPs through phosphorylation.4,5

**Objective.** Fibrodysplasia ossificans progressiva (FOP) is a rare genetic condition in which progressive ossification of fibrous tissue, tendons and ligaments leads to severe physical handicap. Most affected individuals who have been studied have a recurrent 617G>A mutation in the ACVR1/ALK2 gene that codes for activin A type 1 receptor/activin-like kinase 2. The majority of publications on the genetics of FOP have concerned whites or Asians, and no genetic information is available concerning sub-Saharan blacks. The aim of the project was to determine whether or not this mutation is present in affected persons in South Africa.

**Method.** Molecular mutational analysis was undertaken on genomic DNA from peripheral blood leukocytes from 6 affected South Africans of different population groups (4 Xhosa, 1 coloured, 1 white).

**Results.** The 6 persons with FOP were all heterozygous for the ACVR1/ALK2 617G>A mutation. This mutation was absent in 6 controls.

**Conclusion.** Confirmation of the presence of this recurrent mutation facilitates diagnostic accuracy in affected persons in South Africa, and allows researchers to narrow the search for molecular targets for rational intervention to the ACVR1/ALK2 domain.

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**Fibrodysplasia ossificans progressiva (FOP) is a rare genetic disorder in which ossification of connective tissue leads to severe disability.**

1. ACVR1 is one of the f4 type 1 receptors that mediate in the highly conserved bone morphogenetic protein (BMP) signalling pathway, through a domain rich in glycine and serine (GS-domain) residues.

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3. FOP molecular investigations has revealed that most affected individuals have the same single nucleotide change 617G>A in the ACVR1 gene.

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5. Diagnosing FOP has depended on recognising characteristic clinical and radiological features, and until recently the causative mechanism remained elusive.
The 617G>A mutation in ACVR1 eliminates a Cac8I site and forms a new HphI site (Fig. 1). In addition, each of the samples was subjected to sequence analysis.

Results
The 350 bp PCR product from the normal allele (617G) after digestion with Cac8I showed the 3 bands (139, 114, and 97 bp) while the mutant allele (617A) appeared as 2 bands (253 and 97 bp) in persons with FOP. For HphI, PCR products of the 617G allele (normal) were not digested but PCR products of the 617A allele showed bands of 228 and 122 bp in the FOP patients. All 6 persons with FOP were heterozygous for the 617G>A mutation. The mutation was absent in all 6 controls. Sequence analysis (Fig. 2) revealed the heterozygous genotype in all affected individuals while the controls had the normal homozygous 617G/G genotype.

Discussion
Most individuals with FOP are sporadic, representing new mutations for the determinant gene. Although FOP has a worldwide distribution, there are few previous reports of affected persons in South Africa. Four of the 6 persons investigated in Cape Town are Xhosa. Reports from several other parts of the world have confirmed the presence of the 617G>A specific mutation in persons with FOP. However, the concept of 1 specific mutation in ACVR1 is no longer tenable as evidenced by the reports associating 605G>T, 983G>A, 774G>C and 1067G>A with FOP in the absence of the recurrent 617G>A. Nevertheless, the important feature of these mutations is that their resulting amino acid changes mostly occur in the GS or kinase coding domains. This observation makes molecular sense in that different mutations in the ACVR1/ALK2 receptor gene could lead to different clinical manifestations of FOP. By extrapolation, mutations within the ACVR1/ALK2 receptor gene that cause variable ACVR1/ALK2 receptor activity could also lead to different phenotypes, depending on the sensitivities of the domains in which they occur.
This concept could also argue for the involvement of mutations in ACVR1 receptor gene in other related disorders such as some forms of myositis.\textsuperscript{2,7}

The identification of the recurrent 617G\textsuperscript{A} mutation in almost all FOP patients worldwide, together with the narrowing of all reported mutations to the GS and kinase domains of the ACVR1/ALK2 gene, provides a specific target of intervention in a critical signalling pathway. The prime target in FOP would be inhibition of the BMP signalling pathway, using RNA technology or monoclonal antibodies.\textsuperscript{1,4} In South Africa, confirming the recurrent 617G\textsuperscript{A} mutation in all 6 patients suggests that genetic analysis can aid the diagnosis of suspected FOP, thereby negating the need for invasive procedures that can accelerate its progression.

Conclusions

Demonstrating that 6 affected South Africans with disparate antecedents have the same worldwide documented 617G\textsuperscript{A} mutation provides a firm starting point for establishing a diagnostic molecular testing facility for FOP in sub-Saharan Africa. In turn, awareness of FOP and the feasibility of molecular diagnostic confirmation would positively influence its medical management in Africa. The ubiquity of the 617G\textsuperscript{A} mutation could also facilitate research on identifying molecular intervention strategies that may be applied in FOP patients to slow the progression of the disorder, particularly by targeting the BMP signalling pathway.

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References


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Fig. 2. DNA sequence analysis of a section of the ACVR1/ALK2 gene in South African FOP patients. The arrow indicates position of the gene where the mutation has been reported (c.617G\textsuperscript{A}; R206H). The numbering FOP1.1 to FOP6 refers to the different patients with GA representing the heterozygous genotype at this position.