Novel autosomal dominant mutation in loricrin presenting as prominent ichthyosis

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DEAR EDITOR, Loricrin keratoderma (syn. Camisa syndrome, OMIM 604117) is a rare autosomal dominant genodermatosis characterized by palmoplantar keratoderma and ichthyosis. It is caused by mutations in loricrin, a small basic protein synthesized in the upper granular layer, which becomes a major constituent of the cornified cell envelope. Seven distinct mutations in loricrin have been reported in 15 unrelated pedigrees to date. We report a multi-generation family with prominent ichthyosis and palmoplantar involvement due to a novel mutation in loricrin.

The proband was a 14-year-old boy who presented with generalized dryness and scaling affecting his trunk and all four limbs, previously thought to be ichthyosis vulgaris, which was reported from early childhood (Fig. 1a). Clinical examination revealed widespread, prominent ichthyosis and mild diffuse transgredient hyperkeratosis of palms and soles. There was no evidence of atopic dermatitis or keratosis pilaris. His mother and eight other family members were similarly affected (Fig. 1b). Subsequently, a further child was born with a colloidion membrane followed by generalized ichthyosis.

Biopsies of affected skin were processed for light and electron microscopy by standard methods (upper back of the proband’s mother) or for electron microscopy only (affected acral skin from the proband’s grandfather). Following informed consent, genomic DNA was extracted from blood or saliva samples from 10 affected and unaffected family members (Fig. 1a). A whole exome sequencing approach was taken to analyse the proband’s DNA (Methods S1; see Supporting Information).

Fig 1. (a) Pedigree of family with loricrin keratoderma. Filled symbols represent affected individuals. Whole exome sequencing was performed on one affected family member. * marks individuals who were screened for loricrin mutation by Sanger sequencing. (b–d) Clinical pictures of (b) the proband: ichthyosis of upper back with brawny appearance and knuckle pads; (c) proband’s mother: transgredient hyperkeratosis of palms and soles; (d) proband’s grandfather: widespread ichthyosis of forearm and trunk.
Light microscopy of skin from the proband’s mother showed mild hyperkeratosis, a normal granular layer and no significant parakeratosis (Fig. 2a). Electron microscopy of (i) affected acral skin demonstrated mild intracellular oedema, abundant keratohyaline granules in upper layers, with desmosomes and keratin filaments appearing intact and of (ii) affected upper back skin, vacuolar changes and disruption of suprabasal keratinocytes (Fig. 3). Whole exome sequencing directed at relevant epidermal genes revealed a novel heterozygous duplication mutation in the loricrin gene in exon 2 (designated c.806dupG), with an insertion of a single base pair resulting in a frameshift leading to a delayed termination codon and elongation of the protein by 22 amino acids (Fig. 2d). The mutation was confirmed by Sanger sequencing (Methods S2; see Supporting Information) and was present in affected individuals but was not in unaffected family members (Figs 1a, 2b,c). This mutation is not on the dbSNP database or NHLBI Exome Variant Server (http://evs.gs.washington.edu/EVS/).

Six different heterozygous insertion mutations in loricrin in 14 unrelated pedigrees have previously been reported and one heterozygous deletion in a further pedi-
All six insertion mutations are single base-pair insertions leading to delayed termination codons with the most frequent mutation 730insG being present in eight of the 14 published families.2,4,8–13 This region of the loricrin gene is thought to be a mutation hotspot because of the presence of six consecutive guanine nucleotides.12 All single-base-pair insertion and deletion mutations lead to a frameshift and delayed termination, thus elongating the protein by 22 amino acids and changing the Gly-Lys-rich domain into an Arg-Leu-rich terminal domain,2 except for two pedigrees of Brazilian origin, where the new protein is 25 amino acids longer than wild-type protein.5 The mechanism of action of these mutations is thought to relate to preferential localization of mutant loricrin in the nucleus due to the formation of nuclear localization sequences within the arginine-rich mutant loricrin.14 It has been suggested that the abnormal nuclear protein may disrupt the apoptotic process in terminal differentiation of keratinocytes in mouse models, thus supporting the hypothesis that the phenotype of loricrin keratoderma is caused by the synthesis of mutant loricrin rather than by the lack of wild-type loricrin.14,15 No clear genotype-phenotype associations for pedigrees with specific mutations have currently been identified.4,5,13

The phenotype of loricrin keratoderma is heterogeneous. The common clinical features in both the 15 previously reported pedigrees and our new pedigree are palmoplantar keratoderma, usually of a honeycomb pattern, and generalized ichthyosis. Other features, including knuckle pads, pseudoainhum/hyperconstricting bands with autoamputation of digits and colloidion babies, are variably reported. Previously, Gedicke et al.13 have suggested that the term ‘mutilating keratoderma with ichthyosis’ is not entirely suitable, due to the variation in phenotypes previously reported. Similarly, given the prominence of generalized ichthyosis with lesser palmoplantar involvement in this pedigree, and the presence of generalized ichthyosis in all previously reported pedigrees, we suggest that the condition could be described as loricrin ichthyosis rather than loricrin keratoderma.

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References


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Conflicts of interest: None.

Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher’s website:

Methods S1. Whole exome sequencing.

Methods S2. Confirmation of mutation in exon 2 by Sanger sequencing.

Table S1. Clinical features of families with loricrin keratoderma.