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Enamel malformations associated with a defined *DSPP* mutation in two families

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Abstract

Dentin sialophosphoprotein (*DSPP*) mutations cause dentin dysplasia type II (DD-II) and dentinogenesis imperfecta (DGI) types II and III. We identified two kindreds with DGI-II exhibiting vertical bands of hypoplastic enamel. Both families had a previously reported *DSPP* mutation that segregated with the disease phenotype. Oral photographs and dental radiographs of four affected and one unaffected participant in one family and the proband in the second family were used to document the dental phenotypes. We aligned the 33 unique allelic *DSPP* sequences showing variable patterns of insertions and deletions (indels), generated a merged DPP sequence that includes sequences from all *DSPP* length haplotypes, and mapped the known *DSPP* mutations in this context. Analyses of the *DSPP* sequence changes and their likely effects on protein expression, as well as published findings of the dental phenotype in *Dspp* null mice support the hypothesis that all *DSPP* mutations cause pathology through dominant-negative effects. Noting that *Dspp* is transiently expressed by preameloblasts during formation of the dentino-enamel junction, we hypothesize that *DSPP* dominant-negative effects potentially cause cellular pathology in preameloblasts that, in turn, causes enamel defects. We conclude that enamel defects can be part of the dental phenotype caused by *DSPP* mutations, although *DSPP* is not critical for dental enamel formation.

Keywords

enamel; dentin; *DSPP*; *dentinogenesis imperfecta*; genetics

The principal organic components in forming enamel are amelogenin, ameloblastin and enamelin (1). In tooth dentin they are type I collagen and dentin sialophosphoprotein (*Dspp*) (2). During formation of the dentino-enamel junction, when the initial dentin and enamel layers mineralize, there is transient expression of enamel proteins by odontoblasts and dentin proteins by preameloblasts (3). *Dspp* is only transiently expressed by preameloblasts, but is

secreted by odontoblasts throughout dentin formation (4, 5). Despite the transient expression of dentin and enamel proteins by opposing cells during formation of the DEJ, it is clear that enamel proteins such as amelogenin and enamelin are not critical for dentinogenesis and *Dspp* is not critical for amelogenesis. Patients with amelogenesis imperfecta (AI) caused by mutations in *AMELX* or *ENAM* do not exhibit a dentin phenotype (6). In addition, there is a loss of selection to maintain the integrity of enamel protein genes in vertebrates that have lost the ability to form dental enamel during evolution (7). *Dspp* is not expressed by secretory or maturation stage ameloblasts and enamel volume and density are normal in *Dspp* null mice (8). In humans, mutations in *DSPP* cause inherited dentin malformations, such as dentin dysplasia type II (DD-II), and dentinogenesis imperfecta types II and III (DGI-II and DGI-III). Dental enamel often undergoes rapid attrition in patients with dentinogenesis imperfecta (9, 10), which is generally ascribed to a lack of support by the defective underlying dentin.

To date, 35 different *DSPP* mutations have been shown to cause inherited dentin defects in humans (11). All show an autosomal dominant pattern of transmission, which means that only one *DSPP* allele is defective. This contrasts with the recessive pattern of transmission observed in mice following total disruption of the *Dspp* gene (12). Tell-tale characteristics of the reported human mutations led to the hypothesis that *all* of the disease-causing *DSPP* mutations lead to the production of a mutant protein that damages the expressing cell and/or the extracellular matrix (13). If this compelling hypothesis is true, *DSPP* mutations cause inherited dentin defects through a dominant-negative mechanism, and not by a loss of function or a reduction in the amount of normal *DSPP* protein (haploinsufficiency), which is the pathogenic mechanism at work in the *Dspp* knockout mice. We use the term “dominant-negative” to indicate the phenotype is caused by the pathological effects of the mutant protein, although the actual pathological mechanism might be better described as a “gain of function”.

***DSPP* 5-prime Mutations**

Fifteen different disease-causing mutations have been reported in the 5' end of *DSPP* (Fig. 1). Five of the mutations are in exon 2, which encodes the signal peptide (amino acids 1 to 15) plus two amino acids from the N-terminus of *DSPP* (amino acids 16 and 17). The first two mutations are within the signal peptide and must cause a problem with protein targeting, as the sequence of the secreted protein is identical to the wild-type. The next three mutations alter the amino acids in the +2 and +3 positions relative to the signal peptide cleavage site. The remaining ten mutations cluster around the splice boundaries of exon 3. Where experimental evidence is available, the result of a defective splicing junction was the skipping of exon 3, rather than intron retention (14, 15). All of the *DSPP* 5-prime disease-causing mutations (either directly or by skipping of exon 3) alter the context of the signal peptide cleavage site. Six of the 15 mutations have been reported more than once, so many of the *DSPP* 5' mutations that potentially cause inherited dentin defects may have been identified. None of the *DSPP* 5' mutations alter the protein at the many conserved sites that are involved in potentially important posttranslational modifications (16), suggesting that heterozygous loss of function mutations in *DSPP* do not cause inherited dentin defects. A reasonable explanation for the dominant-negative effects is that the 5' mutations interfere with protein targeting (secretion) and cause cell pathology (13).

***DSPP* 3-prime Mutations**

Twenty different disease-causing mutations have been reported in the 3' end of *DSPP*, within the coding region for dentin phosphoprotein (DPP), the C-terminal cleavage product of *DSPP* (17–19). *Dpp* is the most acidic protein known, having an isoelectric point near 1.1 (20). Its sequence is highly repetitive and the length of the repeat region varies greatly

among different mammalian species and even within species, which is reflected in the size of the Dpp protein (21). The first studies to successfully characterize the DPP coding region in patients with inherited dentin defects reported therein 22 (13) and 13 (22) different patterns of insertions and deletions (indels). McKNIGHT *et al.* (13) identified 22 DPP indel patterns in 188 normal human chromosomes, while SONG *et al.* (22) reported 13 DPP indel patterns from 220 normal human chromosomes. Only two of the DPP indel patterns were identical between the two studies, so 33 unique indel patterns are known for human DPP coding region, with the deduced amino acid sequences ranging from 770 to 902 amino acids. The DPP region of the DSPP reference sequence (GB# NM_014208.3) has 839 amino acids. We carefully aligned the DPP coding region from each of the 33 haplotypes having novel indel patterns and noted the positions of the 20 disease-causing mutations in the DSPP 3-prime region (Supporting Fig. S1). This allowed us to construct a merged DPP coding region that includes all of the sequences found within the 33 known DPP length haplotypes (Fig. S2). The currently known DPP length haplotypes and the locations of the 20 disease-causing mutations in the merged DPP coding region are charted in Fig. 2. The 20 3-prime disease-causing mutations and their associated phenotypes are listed in Fig. 3.

Because the DPP coding region is so repetitive, an unusual thing happens when a genetic alteration causes a shift in its reading frame. A deletion or insertion that causes a shift to the -2 reading frame (i.e., a deletion of two nucleotides or the insertion of four) will find an in-frame translation termination codon after introducing only a few extraneous amino acids (Fig. S3). A deletion or insertion that causes a shift to the -1 reading frame however, continues without hitting a translation termination signal until downstream of the natural DPP stop codon. Removing the first nucleotide at the beginning of the DPP coding region in the DSPP reference sequence replaces DPP with an 850 amino acid missense protein that is comprised of 35% alanine, 23% valine, 20% threonine, and 12% isoleucine. Any -1 reading frame shift starting 47 or fewer codons before the start of DPP in exon 5 or within the DPP coding region itself will terminate translation at the same stop codon downstream of the normal DSPP termination codon. The length of the missense peptide in each case is a function of the location of the frame-shift and which DPP length haplotype it occurs in. It turns out that all 20 of the disease-causing mutations in the DPP coding region shift the reading frame to the -1 frame. Mutations that shift all or part of the DPP coding region into the -2 reading frame terminate translation without producing much of a missense peptide. Such changes reduce the amount of DPP protein (haploinsufficiency) or generate a truncated DPP protein (loss of function), but these types of mutations have not been observed, presumably because they do not cause inherited dentin defects. This analysis supports the hypothesis that disease-causing mutations in DSPP are the result of dominant-negative effects and that haploinsufficiency secondary to the loss of a single DSPP allele does not cause disease in the heterozygous condition.

We have identified two DGI-II kindreds that show dentin defects typical of this condition, but they also display pathological malformations of their dental enamel. We have characterized the dental condition in these families and identified the same DSPP mutation in both, which was previously reported to cause DGI (23), but without documenting the dental phenotype. We hypothesize that transient expression of the mutated DSPP protein may have caused a dominant-negative effect in preameloblasts that resulted in the observed enamel malformations.

Materials and methods

The study protocol and subject consents were reviewed and approved by the Institution Review Board at the University of Michigan and appropriate informed consent was obtained from all subjects. Two families were recruited. Medical and dental histories were obtained

and pedigrees constructed that span four generations. Oral photographs and radiographs were taken for five members of family 1 (III:7, III:8, IV:1, IV:2, IV:3) and the proband of family 2 (IV:2). Copies of previous dental radiographs were obtained for members IV:1, IV:2, and IV:3 of family 1 and members II:4, III:7, III:8, and IV:3 of family 2. Dental phenotypes were assessed by oral examination and by inspection of dental radiographs. In total 15 persons were recruited: 11 affected and 4 unaffected. The subjects ranged in age from 9 through adult.

DNA Isolation

Ten ml of peripheral whole blood was obtained from participating family members. In family 1 we were able to obtain DNA from five affected (II:6; III:7; IV:1, age 18; IV:2, age 17; and IV:3, age 16) and two unaffected (I:2 and III:8) members. In family 2 we were able to obtain DNA from six affected (II:3; III:4; III:7; IV:1; IV:2, age 13; and IV:3, age 9) and two unaffected (II:4, III:8) members. Genomic DNA was isolated using the QIAamp DNA Blood Maxi Kit (Qiagen, Valencia, CA, USA). Ages of adults were not specified.

Polymerase Chain Reaction (PCR)

PCR amplifications were done using the Platinum® PCR SuperMix (Invitrogen, Carlsbad, CA, USA). The reactions had a 5 min denaturation at 94 °C, followed by 35 cycles each with denaturation at 94 °C for 90 s, primer annealing at 56–59 °C for 60 s, and product extension at 72 °C for 90 s. In the final cycle the 72 °C extension was for 7 min. PCR amplification products were purified by QIAquick PCR Purification Kit and protocol (Qiagen).

Exons 2 through 4 were amplified along with their adjoining intron sequences. Exon 5 was characterized up to the repetitive region. Exon 2 was amplified with forward 5'gatgtcccccataaacacacc and reverse 5'ctccatgactctctgggcatt primers to generate a 596 bp product (annealing 56 °C; extension 72 °C/90 s). Exons 3 and 4 were amplified together as a 1490 bp product using the forward 5'caagccctgtaagaagccact and reverse 5'acatggatgctgtcatggt primers (annealing 59 °C; extension 72 °C/90 s). The 5' part of exon 5 was amplified using the forward 5'cctatggcaacttttcccagt and reverse 5'tgtcattgtcatcattcccatt primers (annealing 56 °C; extension 70 °C/90 s) to generate a 589 bp product.

DNA Sequence Analysis

DNA sequencing was performed at the University of Michigan DNA sequencing core. The original PCR primers used to generate each amplicon were used for sequencing reaction. In addition, for the larger exon 3–4 amplification product, two sense primers 5'-ggaccatgggaagaagatg and 5'-gcattcagggacaagtaagc, and three antisense oligonucleotides 5'-cattcccttctccttctgga, 5'-cctcgtttctacagaattctca and 5'-tggaggctctgtctccatca were used for sequencing reactions.

Alignment of 33 DPP indel patterns

Haplotype sequences from McKnight *et al.* (13) were imported from GenBank and provided the haplotype sequences starting with *DSPP* nucleotide 2572 encoding Arg³⁹⁶. Each sequence can be obtained by searching the National Center for Biotechnology Information (NCBI) database with “DSPP haplotype #”. For the purpose of this analysis, the reference sequence (NM_014208.3) was used to complete the DPP sequences 5-prime to this position, with the exception of Clone 37, where the short sequence 5' to nucleotide 2572 was obtained from Hap37A to ensure correct positioning of indel 1. The SONG *et al.* (22) haplotype sequences were not available in GenBank. These sequences were obtained by altering the *DSPP* cDNA reference sequence (NM_014208.3) according to Tables 2 and 3 in SONG *et al.*

(22). *SONG et al.* reported 15 haplotypes that showed 13 different indel patterns. The *SONG et al.* haplotype designations are in bold. One Song haplotype from each of the 13 groups was used in the alignment: **1** (803 aa), **2** (839 aa), **3** (788 aa), **4** (788 aa), **5** (790 aa), [**6**, **6T**, (797 aa)], [**6(2)**, **6(2)T** (796 aa)], **7** (782 aa), **102** (791 aa), **130** (794 aa), **106** (806 aa), **72** (785 aa), **110** (782 aa). Song haplotype **2** has the same indel pattern as McKnight haplotypes 9 and 14 as well as the reference sequence. Song haplotype **3** has the same indel pattern as McKnight haplotypes 19, 21, and 22.

Results

Two apparently unrelated Caucasian families of Northern European ancestry with inherited defects of dentin were examined at a University of Michigan dental clinic. There was no history of any unusual bone brittleness or unexplained hearing loss in either family. Affection status (the presence of inherited dentin defects) was oral ascertained by routine examination and pedigrees of the two kindreds going back four generations were constructed following interviews with multiple family members (Fig. 4). Mutational analyses of *DSPP* 5-prime region identified the same disease-causing mutation in both families: IVS3+1G>A; c.135+1G>A. This transition mutation changes the first nucleotide of intron 3, which is absolutely required for mRNA splicing. The mutation was identified in all ten of the affected members that donated samples for mutation analyses. The enamel surfaces of the probands, particularly in the anteriors, appeared shriveled, with vertical lines of hypoplastic enamel Fig. 5.

Dental phenotyping: Family 1

In family 1, the proband was an 18 yr old female (IV:1) exhibiting translucent and chalky-colored crowns with vertical grooves of hypoplastic enamel and spaces between the maxillary and mandibular anterior teeth (Fig. S4). The enamel was more opaque on radiographs than dentin. The pulp chambers and many of the root canals were already obliterated. The roots of many teeth were noticeably shorter than normal, particularly in the anteriors. Some of the molar crowns had a bulbous morphology. Attrition was apparent along the incisal edges of the anteriors and the buccal cusp tips of the mandibular cuspids and premolars.

The proband's youngest brother (IV:3) at age 16 already had extensive attrition of all anterior teeth, and detectable attrition on the buccal cusp tips of the mandibular premolars (Fig. S5). The crowns were translucent or chalky, with some vertical grooves still evident in cervical areas that had not yet abraded, such as the buccals of #12 and #13. The pulp chambers and root canals were obliterated and the molar and premolar crowns appeared bulbous. The enamel was more radiopaque than dentin. The proband's other brother (IV:2) at age 17 had extensive attrition of the anterior teeth, and lesser attrition on the buccal cusp tips of the mandibular premolars and second molars (Fig. S6), presumably worsened by failure of the crowns on three of the first molars. Like his siblings, the crowns were translucent and chalky, the pulp chambers and root canals were obliterated, the molar and premolar crowns were bulbous (which appeared to play a role in the impaction of the lower left third molar), and the enamel was more radiopaque than dentin. Vertical grooves were evident on the buccal cervical areas of the premolars, which were not yet destroyed by attrition. The father (III:7) had a very similar dentition, although the crowns were mostly translucent rather than chalky (Fig. S7). Attrition was most severe in the maxillary anteriors, but was not as bad as his sons' condition. The radiographs showed obliterated pulp chambers and root canals, bulbous crowns and enamel that was more radiopaque than dentin. The enamel surfaces had a polished appearance. The mother (III:8) was not affected and had a normal and healthy dentition (Fig. S8). The expression of the DGI-II phenotype in the four affected members of this family was remarkably consistent.

Dental phenotyping: Family 2

The proband of family 2 (IV:2) at age 12 was the youngest affected person to be characterized. Like family 1, the proband of family 2 had classic DGI-II (Fig. S9). The crowns alternated between chalky and translucent in color and had vertical grooves in the enamel. The pulp chambers and most of the root canals in the incisors and first molars had obliterated. The crowns of the posterior teeth were bulbous. The enamel was more radiopaque than dentin. Attrition was evident on the incisal edges of the anterior teeth. The affected mother had maxillary and mandibular complete dentures. Taking the differences in age between the subjects in the two families, the dental phenotypes of these patients with the IVS3+1G>A; c.143+1G>A mutation in *DSPP* were very similar.

Discussion

We characterized the dental phenotype of two families with a classic DGI-II phenotype and observed enamel defects in the form of vertical grooves in both probands. Both families had the same *DSPP* transition mutation (IVS3+1G>A). This mutation might cause the retention of intron 2, or the skipping of exon 3. Retention of intron 2 would lead to premature translation termination and delete all but two amino acids of the DSPP secreted protein. Such a transcript would likely be degraded by nonsense mediated decay (24), potentially causing haploinsufficiency but not dominant-negative effects. Skipping of exon 3 would delete amino acids 18 through 45 and potentially alter the context of the signal peptide cleavage site after Ala¹⁵. This is the most likely predicted scenario and has experimental support (14, 15). Ten of the disease-causing *DSPP* 5' mutations localize along the splice junctions of exon 3. We hypothesize that during RNA splicing of transcripts expressed from the mutant *DSPP* allele, exon 3 is skipped all or part of the time, and the resulting protein is not targeted properly and causes cell pathology.

DSPP has a signal peptide and is translated into the endoplasmic reticulum (ER) for secretion. Following translocation into the ER, the DSPP signal peptide is cleaved by the ER signal peptidase complex (SPC). Secretory proteins have a distinct secondary structure requirement at their cleavage site for processing by ER SPC (25–28). The flanking amino acid residues around the signal peptide cleavage site significantly influence this cleavage process (28). The *DSPP* IVS3+1G>A mutation, which alters the consensus sequence of a splice donor site, presumably leads to skipping of exon 3. Although exon 3 skipping of *DSPP* does not cause a frameshift or premature termination, it significantly changes the C-terminal flanking amino acid residues of signal peptide cleavage site, which could disturb signal peptide cleavage and interfere with normal DSPP folding and secretion. Mutations in or near the signal peptide coding region of other genes are known to cause diseases by inducing ER stress and cell pathology (29–32). Different proteins have different specific requirements for targeting. Recently it has been shown that a proline in the +2 position, which is specifically altered in three of the *DSPP* 5' mutations, is critical for the export of nucleobindin 1 (33). A mouse amelogenin missense mutation (p.Y64H) induced extensive ER stress and ameloblast cell pathology (34).

During enamel formation, *DSPP* is transiently expressed in preameloblasts. To explain the enamel defects in our patients, we hypothesize that the *DSPP* IVS3+1G>A mutation interferes with DSPP secretion and causes ER stress and cell pathology in pre-ameloblasts leading to developmental enamel defects. However, this pathogenic concept does not suggest that *DSPP* plays an important role in enamel formation. Any genetic or environmental aberration that induces ameloblast pathology will potentially cause developmental enamel defects. DSPP is transiently expressed at a sensitive transition period in ameloblast differentiation when the basal lamina is being degraded, enamel proteins are starting to be expressed, and cell-matrix interactions are in a state of flux (1). Pathology of

secretory stage ameloblasts could explain the thin enamel. The vertical grooves might relate to buckling of the ameloblast layer during transition/early maturation because of ameloblast over-crowding on the pathologically small enamel surface. The scarcity of reports of enamel defects in persons with *DSPP* related dentin malformations might be due to the rapid attrition of enamel in DGI patients, so the enamel defects are seldom observed.

The finding that disease-causing mutations cluster at the borders of exon 3 and that improper splicing can potentially be caused by mutations at the edges of the exon (i.e. in the coding sequence) or 6 nucleotides into the intron suggests that this exon might be particularly susceptible to skipping, despite the fact that inclusion of this exon is critical to avoid pathological consequences. Perhaps this exon has undergone recent changes during evolution. *DSPP* belongs to the secretory calcium binding phosphoprotein (SCPPs) family of genes that all evolved from *SPARCL1* (secreted protein, acidic, cysteine-rich related) (35). In humans there are seventeen SCPP genes in the enamel/milk/saliva group and five in the evolutionarily older dentin/bone group, which includes *DSPP* (36). *DSPP* exon 3 is unusual in that it is longer than the exon 3 of its homologues and does not encode a Golgi casein kinase phosphorylation site.

We assembled data concerning natural and pathological variations in *DSPP*. Alignment of the 33 known DPP indel patterns (Fig. S1) allowed us to produce a merged sequence and to chart the 20 frame-shift mutations (Fig. 2). Such a merged sequence should prove helpful in localizing the positions of indels in yet to be discovered length variations in the DPP code. As only two of the DPP indel patterns were the same in the two studies that reported them, there are likely to be many more the DPP indel patterns in the population as a whole.

Recently reported *DSPP* mutations and their associated phenotypes strengthen our previously stated hypothesis that autosomal dominant dentin defects caused by *DSPP* mutations should be considered a single disease, with a continuous spectrum of phenotypes that can be subclassified according to their severity into DD-II, DGI-II, and DGI-III, with DD-II being the least, and DGI-III being the most severe (37). Patients with the fifteen disease-causing 5' *DSPP* mutations have been diagnosed as having DD-II, DGI-II, and DGI-III. The p.P17S, p.PV18F and p.V18D mutations have been identified in persons diagnosed with DGI-II and DGI-III. The twenty disease-causing 5' *DSPP* -1 frame shift mutations have been identified in patients diagnosed with DD-II and DGI-II. All of the 35 characterized disease-causing *DSPP* showed a dominant pattern of inheritance. The pathogenesis in all cases (which is currently based upon logic and not scientific demonstration) seems to occur by a similar mechanism: dominant-negative effects induced by the mutant DSPP protein.

In this study we provided a detailed summary and analysis of the normal polymorphic structures of *DSPP* and the 35 *DSPP* mutations that cause DD-II, DGI-II and DGI-III. Current evidence supports the interpretation that *DSPP* mutations cause these dominant forms of inherited dentin defects by a dominant-negative mechanism, and that the three disease designations reflect varying levels of severity of a common disease. We characterized the dental phenotypes and the mutation that causes them in two DGI-II families. The dental phenotypes in these two families were similar, and both showed linear vertical defects in the enamel. We interpreted these enamel defects as likely being developmental in origin, rather than being caused by damage to the weakened structure during or following eruption. In a recent case, a 5' *DSPP* mutation (c.53T>A, p.V18D) caused enamel defects that were evident on radiographs even before tooth eruption (38).

If enamel defects can occur when *DSPP* is mutated, is DSPP necessary for proper dental enamel formation? Because Dspp is not expressed by ameloblasts during dental enamel

formation and no enamel defects are observed in *Dspp* null mice, the answer is almost certainly no. No dental phenotype is observed in *Dspp* heterozygous mice (where only one *Dspp* allele is deleted) (8). In contrast, *all* of the 35 reported disease-causing *DSPP* mutations show a dominant pattern of inheritance. Analyses of these mutations strongly suggest that the resulting dental phenotype is *not* caused by a loss of *Dspp* function, but is due to poorly understood pathological mechanisms that we have referred to simply as “dominant-negative effects”. As *Dspp* is transiently expressed by preameloblasts, we propose that enamel defects associated with *DSPP* mutations are probably the result of cell pathology induced by this transient expression.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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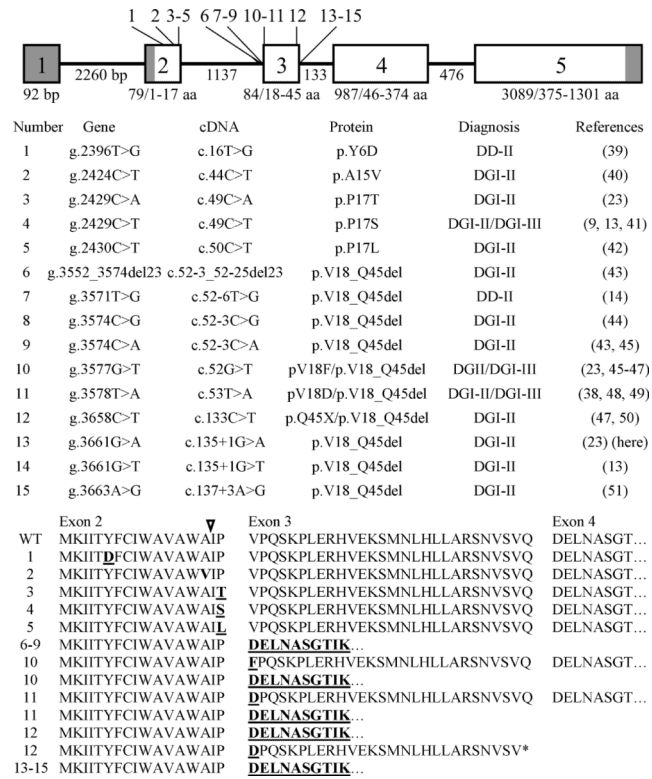


Figure 1.

Mutations in the 5-prime end of *DSPP* causing inherited dentin defects. *Top:* The intron/exon structure of *DSPP*. The five *DSPP* exons are indicated by numbered boxes; the four introns are the lines connecting the exons. The numbers below each intron show the number of basepairs (bp) in that intron. The numbers below each exon show the number of bp in that exon followed by the range of amino acids encoded by it. Locations of the 15 reported *DSPP* 5' mutations are indicated by numbered lines, starting at the 5' end of *DSPP*. The first five mutations are in exon 2. We hypothesize that these mutations directly interfere with signal peptide function or cleavage. The other ten mutations cluster around the splice boundaries of exon 3. Skipping of exon 3 might affect cleavage or functioning of the *DSPP* signal peptide of (amino acids 1 to 15). Signal peptide malfunction is presumed to interfere with protein secretion and cause cell pathology. *Middle:* List of the 15 reported *DSPP* 5' mutations and their dental phenotypes. Note that six of the fourteen *DSPP* 5' mutations have been reported more than once and that the diagnoses of DGI-II or DGI-III have both been used to describe the phenotype of persons with the same *DSPP* mutation. *Bottom:* Wild-type (WT) and mutant predicted amino acid *DSPP* sequences. Changed amino acids are in bold and underlined; the signal peptide cleavage site is indicated by an arrow.

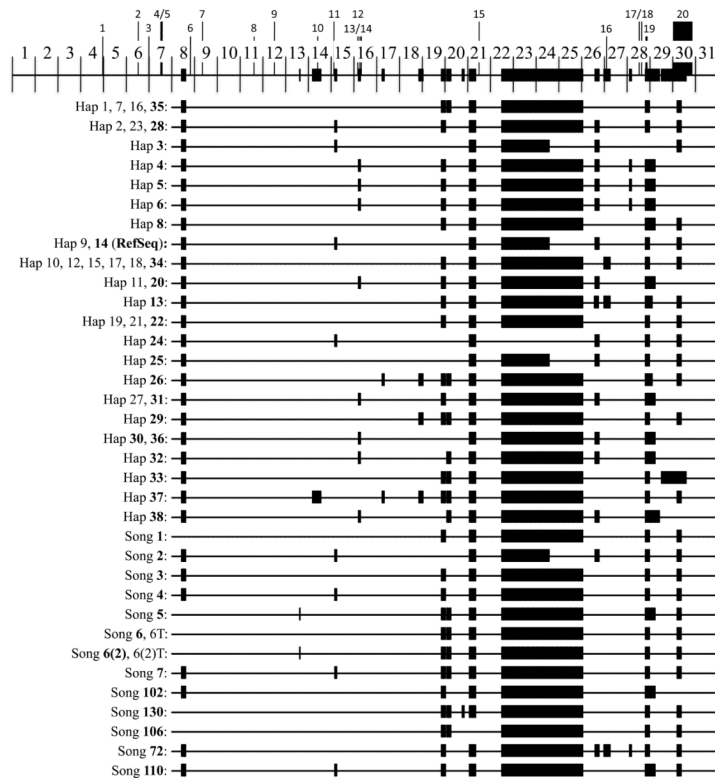


Figure 2.

Human DPP length haplotypes and positions of indels and disease-causing mutations in merged human DPP. *Top:* The merged DPP sequence (from Fig. S2) is shown divided into a little over 31 equal, numbered segments corresponding to 90 bp (30 aa) of DPP. The thin bar represents universal segments found on all DPP length haplotypes; the thick bars are variable regions found only on some DPP length haplotypes. The numbered lines above the merged DPP map mark the locations of the twenty *DSPP* 3-prime disease-causing mutations (listed in Fig. 3). Note that most indels are located in the downstream half of the DPP code. *Bottom:* Maps showing positions of the indels (thick bars) on each of the 33 novel length haplotypes. The first seven segments of DPP show no length polymorphisms and are not included in the diagrams for each length haplotype. There can be multiple DPP haplotypes for each length haplotype because of nucleotide substitutions (polymorphism that don't effect length). The 22 length haplotypes from McKnight *et al.* (13) and 13 length haplotypes from Song *et al.* (22) are shown.

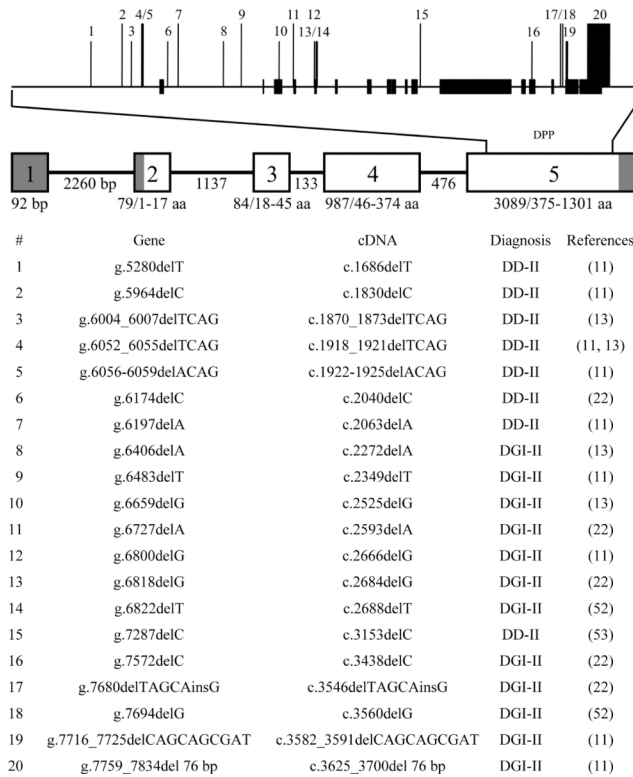


Figure 3.

Top: *DSPP* intron/exon structure with the DPP region expanded to show the positions of indels (thick bars) and sites of 20 disease-causing frame shift mutations (numbered).
 Bottom: List of the 20 reported *DSPP* 3-prime mutations, their designations, and their associated dental phenotypes. All twenty disease-causing mutations shift the downstream sequence into the -1 reading frame.

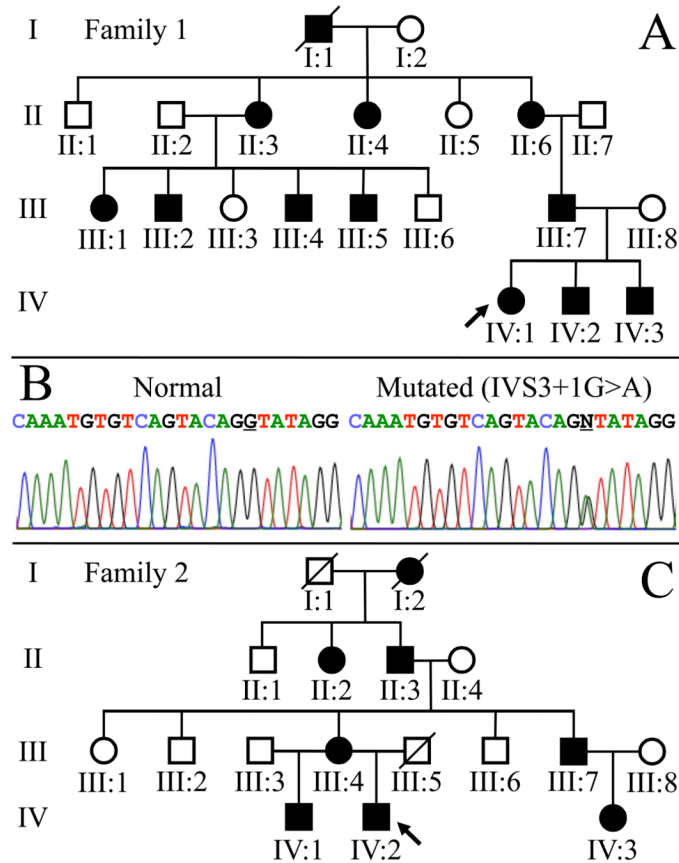


Figure 4.

A & C: Pedigrees of two Caucasian families with dentinogenesis imperfecta type II (DGI-II). The diseases of these two families segregated as an autosomal dominant trait. B: DNA sequencing chromatograms identified the same reported disease-causing mutation (IVS3+1G>A) in both families. This mutation changes the first nucleotide of intron 3 and is predicted to disturb normal proper mRNA splicing, presumably by causing the skipping of exon 3 during RNA splicing.

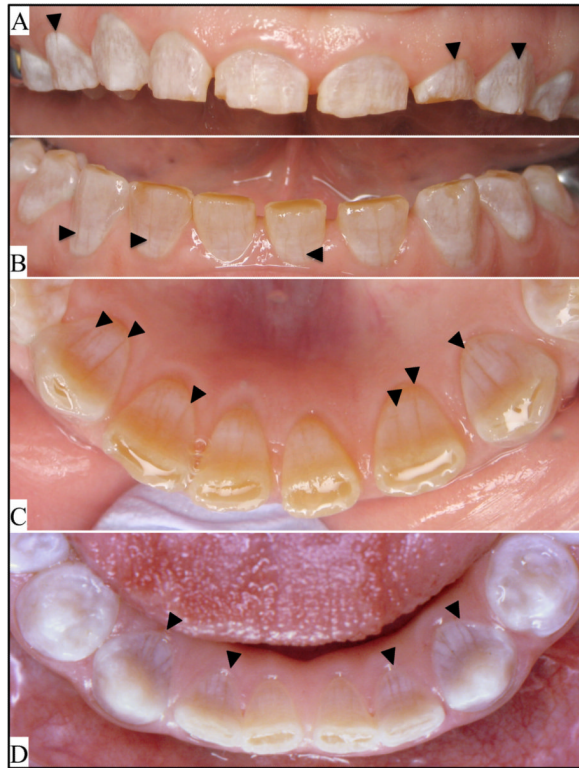


Figure 5.

A–C: Oral photos of the proband of family 1, and D: the proband of family 2. Arrowheads mark the most conspicuous vertical bands of hypoplastic enamel. More complete oral photographic surveys of the probands are provided in Figs. 4S and 9S.