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Extracellular matrix mineralization in periodontal tissues: Noncollagenous matrix proteins, enzymes, and relationship to hypophosphatasia and X-linked hypophosphatemia

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Abstract

As broadly demonstrated for the formation of a functional skeleton, proper mineralization of periodontal alveolar bone and teeth – where calcium phosphate crystals are deposited and grow within an extracellular matrix – is essential to dental function. Mineralization defects in tooth dentin and cementum of the periodontium invariably lead to a weak (soft or brittle) dentition such that teeth become loose and prone to infection and are lost prematurely. Mineralization of the extremities of periodontal ligament fibres (Sharpey's fibres) where they insert into tooth cementum and alveolar bone is also essential for the function of the tooth suspensory apparatus in occlusion and mastication. Molecular determinants of mineralization in these tissues include mineral ion concentrations (phosphate and calcium), pyrophosphate, small integrin-binding ligand N-linked glycoproteins (SIBLINGs), and matrix vesicles. Amongst the enzymes important in regulating these mineralization determinants, two are discussed at length here with clinical examples given, namely tissue-nonspecific alkaline phosphatase (TNAP) and phosphate-regulating gene with homologies to endopeptidases on the X chromosome (PHEX). Inactivating mutations in these enzymes in humans and in mouse models lead to the soft bones and teeth characteristic of hypophosphatasia (HPP) and X-linked hypophosphatemia (XLH), respectively, where levels of local and systemic circulating mineralization determinants are perturbed. In XLH, in addition to renal phosphate wasting causing low circulating phosphate levels, phosphorylated mineralization-regulating SIBLING proteins such as matrix extracellular phosphoglycoprotein (MEPE) and

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osteopontin (OPN), and the phosphorylated peptides proteolytically released from them such as the acidic serine- and aspartate-rich motif (ASARM) peptide, may accumulate locally to impair mineralization in this disease.

Introduction

In the craniofacial region, the tooth and its periodontium represent a remarkable tooth-suspension and masticatory apparatus, functionalized by four key mineralized tissues – enamel, dentin, cementum and bone –; and a periodontal ligament (Fig. 1), the loss of any one of which soon renders the entire apparatus nonfunctional. Loss of functionality within teeth and periodontal tissues can be inherited or caused by degenerative or infectious disease, by trauma, by dietary deficiencies, or as a consequence of surgical, radiological or chemical/drug treatments. Maintaining the integrity of the periodontium as a whole is central to retaining teeth in the oral cavity and to keeping them appropriately positioned for the proper occlusion. Proper positioning of teeth requires not only an intact and structurally and functionally sound suspensory periodontal ligament, but also bone modeling and remodeling events in the surrounding alveolar bone that initially facilitate tooth eruption in children, and then act to maintain and stabilize the tooth via the periodontal ligament during adulthood.

Essential to the proper development and functioning of these key tooth and periodontal structures (including bone) is mineralization – the deposition of inorganic, calcium- and phosphate-containing crystals (calcification) into the extracellular matrices of teeth and bone (120, 121). Mineralization of teeth and periodontal tissues has as their key supportive structural/functional element nanosized apatitic crystals acting collectively in large numbers to harden and stabilize the collagenous matrices within which they reside (with the exception of enamel, which has only noncollagenous matrix proteins). The inorganic phase that mineralizes tissues by permeating their extracellular matrices serves to counteract compressive forces (47, 172). Any deviation from normal in crystal number, size, shape, orientation and/or ultrastructural matrix location leads to tissue fragility that compromises tooth and periodontal tissue function.

Overview of extracellular matrices of the teeth and periodontium

In mature erupted tooth enamel, whose pre-existing organic matrix component essential to its formation and mineralization are almost completely removed by enzymatic degradation, the final mineralized state of the (very hard) enamel is critical for resisting mechanical abrasion and chemical (mostly dietary and bacterial) attack. This unique and incredible hardness of enamel (~96% mineral) (159) is quite unlike the other “softer” mineralized tissues of the tooth (54, 136), and bone, whose extracellular matrices have a permanently resident, intermingled and fibrillar ductile collagenous protein phase which along with other noncollagenous proteins provides for the substantial deformability required for these tissues (15, 16). Tooth crown dentin must flex readily when considerable masticatory forces are placed upon the enamel, and the amalgamation of root dentin and cementum across the cemento-dentinal junction likewise must accommodate the strains placed upon it by masticatory forces transduced along the suspensory periodontal ligament (82, 86, 116, 132). Interfaces between these distinct tissues also play an important role in maintaining tooth integrity, just as they do in remodeling bone (118). The embedded and mineralized portions of the extremities of the periodontal ligament fibres (Sharpey's fibres) that insert into both cementum and alveolar bone complete the union of the suspensory apparatus and allow for the dissipation of potentially disruptive masticatory forces across the whole periodontium. None of this would be achieved without Nature's hardening strategy – mineralization – for vertebrate extracellular matrices.

Described briefly below in a categorical way are three of the four extracellular matrices related to the periodontium that mineralize – dentin, cementum and bone [enamel extracellular matrix will not be covered here, but has been recently reviewed by (67, 88)]. Periodontal ligament structure, organization and function have recently been reviewed (20). However, some discussion is given here concerning the terminal ends of periodontal ligament collagen fibres known as Sharpey's fibres as they mineralize at their extremities where they insert into alveolar bone at one end, and into tooth root cementum at the other end.

Jaw bone in the craniofacial complex is generally not unlike bone elsewhere (121), but its origins are different, with much of it deriving from a neural crest cell contribution (130). Another unique characteristic is its high turnover (remodeling) rate (24, 168), presumably resulting from substantially large and frequent mastication forces exerted primarily by the masseter muscle. Such forces transduced in part via the tooth and the suspensory periodontal ligament to the bone result in the requirement for particularly ductile bone lining the tooth alveolus. The bulk of the alveolar bone likely has both an organic and inorganic composition similar to bone found elsewhere (121), but the bone immediately lining the osseous alveolus has a unique structure appearing variably as either a thin “fringe” of bone accommodating the many insertion sites of the periodontal ligament (Fig. 1), or as so-called bundle bone (14) where it is thicker and more developed. Whereas the extensive attachment of the periodontal ligament insertions as Sharpey's fibres deep into the alveolar bone to form bundle bone is evident in terms of its providing a robust suspensory attachment function for bony anchorage of the tooth, the functional attachment mechanism for the “fringe” bone is not so readily obvious. Given what is likely a common adhesion mechanism for the two extremities of Sharpey's fibres which mineralize, the alveolar bone fringe resembles in several ways the acellular cementum found at the tooth root surface – both have a similar thickness, ultrastructural organization and noncollagenous protein composition (116). In particular, both acellular cementum and this surface-residing alveolar bone “fringe” layer are rich in osteopontin (Fig. 1) (32, 36, 84, 101, 116, 119, 186), where it is thought that this protein guides mineralization locally in such a way as to be optimal for this type of attachment. Alternatively, or in addition, osteopontin at these insertion sites might be part of creating a robust, tough and flexible organic extracellular matrix by virtue of it being a substrate for the homo- and heterotypic covalent crosslinking activity of transglutaminase enzymes (93, 94).

Bone and dentin are similar in several respects, especially regarding the composition of their respective extracellular matrices. However, unlike bone, dentin is not resorbed as part of a remodelling process, and thus it is not involved in the regulation of systemic mineral ion homeostasis as occurs through release of mineral ions during osteoclastic resorption of bone (134). Bone, dentin and cementum are all rich in type I collagen as the scaffolding base of the extracellular matrix, and all are 50-70% calcified with a carbonate-substituted apatitic mineral phase (136). During osteogenesis, dentinogenesis and cementogenesis, extracellular matrix assembly and subsequent mineralization occur through successive, highly ordered steps with a lag time existing between matrix deposition and mineralization. As part of this process, extracellular matrix proteins are secreted, sometimes modified or cleaved by enzymes, and organized in some cases into macromolecular assemblies, which altogether is then structured into a mature fibrillar matrix receptive to mineral deposition (120). These remarkable tissue construction events are orchestrated by the tissue-forming “blast” cells – the osteoblasts, the odontoblasts (a misnomer, in fact should be dentinoblasts) and the cementoblasts – with each being associated with a thin layer of unmineralized matrix which subsequently mineralizes at the “mineralization front” to form the completed tissue. Additional mineralization and mineral changes (such as further carbonate substitution into the hydroxyapatite lattice) (40) slowly occur over time (30), along with changes in the

organic phase of the extracellular matrix (93, 94, 171) and proteolytic degradation, in a maturation process that ultimately provides an adequate final functional state to provide for the biomechanical demands placed upon each tissue.

General concepts for mineralization of collagenous matrices

The hardness and toughness of the collagenous mineralized tissues derive from their being composite materials, with each consisting of an interconnected (and often crosslinked) organic matrix network of proteins whose macromolecular assemblies interweave as a scaffold for mineral deposition (120). Calcium and phosphate complex together as crystalline salts to mineralize (calcify) extracellular matrix in bones and teeth. This biomineralization process is not haphazard, but in fact occurs in a way that is incredibly controlled at the molecular level – indeed, not surprisingly – like most cellular processes. The inorganic phase (mostly a crystalline, substituted form of hydroxyapatite) (144) that forms in the skeleton provides exactly the required hardness, while at the same time ensuring requisite toughness by intimate intercalation of nanocrystals of mineral with the organic scaffolding extracellular matrix (120). In fact, it is precisely this nanoscale deposition of (at least) billions of inorganic, tiny plate-like crystallites within a softer organic matrix that provides for the inherent flexibility of tough bones that allows deformation during mechanical challenge, and then a return to their original shape characteristic for any given skeletal element.

Heterogeneous mineral deposition events occur at discrete locations within, at the surface of, and between, collagen fibrils (100, 120) during mineralization of the teeth and of the alveolar bone of the periodontium (and bone elsewhere). The composite nature of these mineralized tissues is thus determined in a way that spans most dimensional scales starting from the protein/organic-nanocrystal interface and extending into the anatomical macroscale structure of skeletal and tooth structures. The collagen fibrils with interwoven noncollagenous protein assemblies, together with interconnected pores extending throughout the structured extracellular matrix that are ultimately filled with apatitic crystals, all have nanoscale dimensions. Mineral is nucleated not only in nanoscale volumes within fibrillar collagens, but also interfibrillarly where crystal dimensions are slightly larger and where noncollagenous proteins are abundant (117). These two structurally and biochemically distinct extracellular compartments provide different constraints on biomineralization, yet despite this, at each site, mineral is nucleated and crystal growth is subsequently regulated such that bone crystals do not grow beyond the nanometre range. Initially, to reach an apatitic mineral phase, critical nuclei of mineral ions reach a size and stability that subsequently mature to form crystals having some degree of long-range order that ultimately possess welldefined crystallographic faces characteristic of apatite. Initial nucleation events are controlled locally by concentrations of mineral ions and by the presence, or absence, of mineral nucleators and inhibitors.

In bones and teeth, mineral crystals typically are platelet-shaped crystallites with dimensions that vary depending on their physical location within the structure of the preestablished extracellular matrix (100) where there are different local chemical environments defined by matrix composition that will in part define crystal properties at those sites. Charge groups and matrix interaction domains in fibrillar type I collagen have been characterized (158), and mineral identified within the holes zones in the interior of the collagen fibrils, but much less is known about the chemical environment contributing to mineral crystal nucleation and propagation between the fibrils. Of interest, the mineral-binding proteins comprising the SIBLING family of proteins (see below), that are generally thought to guide the mineralization process in bones and teeth, are located primarily between the collagen fibrils. A recent high-resolution transmission electron microscopy study of dense, human cortical femur bone sections prepared by cryogenic ion-milling both parallel and perpendicular to

the long axis of the bone revealed that most of the mineral (approximately 80%) is located external to the collagen fibrils in the form of plate-like mineral structures with dimensions of 5 nm thick, 65 nm wide and over 200 nm long (123). While crystal deposition within the collagen fibril is generally thought to occur independently from that occurring between the fibrils, a recent proposal suggests that crystals formed at the surface of collagen fibrils might migrate to locations within the fibril (166), but further work needs to be done to confirm this unusual possibility.

Protein/genes related to skeletal and dental mineralization are listed in Table 1, and are discussed in greater detail below.

Pyrophosphate and the phosphate/pyrophosphate ratio in mineralization

Homeostasis of inorganic phosphate is essential for the normal development and maintenance of the mineralized tissues of the skeleton and dentition (55). Pyrophosphate (PP_i) – composed of two molecules of phosphate (P_i) – pivotally regulates physiologic mineralization and pathologic calcification by acting as a potent inhibitor of crystal precipitation and growth (5, 53, 124, 128). Local tissue concentrations of pyrophosphate are controlled by a number of regulatory enzymes and transporters. The ectoenzyme tissue-nonspecific alkaline phosphatase (TNAP) hydrolyzes pyrophosphate (126), thus providing a mechanism to control the concentration of this potent mineralization inhibitor. TNAP is highly expressed by cells resident in bones and teeth, and it is critical for proper skeletal mineralization (128, 175). Loss-of-function mutations in the human TNAP gene *ALPL* cause hypophosphatasia (HPP), a disease marked by poor bone mineralization, rickets, and osteomalacia, as well as tooth phenotypes (143, 177). Ablation of the homologous mouse gene *Apl* leads to increased inhibitory pyrophosphate and osteopontin leading to (76, 77) mineralization defects that closely phenocopy human infantile HPP (125, 131). Furthermore, two proteins can increase pyrophosphate locally in tissues – the progressive ankylosis protein (ANK) and the enzyme ectonucleotide pyrophosphatase phosphodiesterase 1 (NPP1). ANK encodes a multipass transmembrane protein that regulates transport of intracellular pyrophosphate to the extracellular space (75, 85, 92). NPP1 increases extracellular PP_i by hydrolysis of nucleotide triphosphates (91). Pyrophosphate removal by TNAP activity thus antagonizes provision of PP_i by ANK and NPP1, thereby creating a concerted regulation of phosphate and pyrophosphate levels to ultimately regulate mineralization (76). TNAP also can remove phosphate from osteopontin, reducing its mineralization-inhibiting function (5). Thus, in the extracellular matrix of bone, TNAP's enzymatic degradation of pyrophosphate (together with dephosphorylation of osteopontin and potentially other matrix proteins) controls the phosphate/pyrophosphate (P_i/PP_i) ratio to favor proliferation of hydroxyapatite crystals outside the matrix vesicles (for matrix vesicles, see next section) and along and between the collagen fibrils. Indeed, mineralization in bone is determined partly by the ability of osteoblasts (and possibly early osteocytes as well) to remove inhibitory pyrophosphate from their adjacent extracellular matrix via expression of TNAP, and by the presence of a fibrillar collagen-rich matrix network (128). Thus, the co-expression of TNAP and a fibrillar collagenous scaffold appear to be necessary and sufficient to cause mineralization of an extracellular matrix. Enamel, which will not be discussed at length here, appears to be an interesting exception to this general rule, where TNAP function is likewise important for mineralization (185) but where a collagenous matrix is lacking.

Matrix vesicles and mineralization

Mineralization of bones and teeth occurs by a series of physicochemical and biochemical processes that together facilitate the deposition of apatitic crystals at specific sites within the extracellular matrix. Crystals reside within and between collagen fibrils of the extracellular

matrix (68), and also within the lumen of chondrocyte-, osteoblast- and odontoblast-derived matrix vesicles shed from the cells (8, 9, 70, 182). Early studies on matrix vesicles used transmission electron microscopy and serial sections of growth plate cartilage to show that matrix vesicles form through exfoliation of vesicles from the plasma membrane of growth plate chondrocytes (26), findings which were subsequently confirmed by freeze-fracture analyses (27, 41, 183). Additional evidence that matrix vesicles arise from the plasma membrane derives from comparative lipid and protein studies of the vesicles and the plasma membrane of the epiphyseal chondrocyte and osteoblasts (181). Overall, cell membranes contain similar components to matrix vesicles, but in different proportions. While investigators in the bone mineralization field are divided between accepting collagen-mediated and matrix vesicle-mediated mechanisms of mineralization, there is no obligatory incompatibility between these two mechanisms. Biochemical and genetic studies (10, 11, 45, 76, 77, 83, 128, 184), using single- and double-knockout mice to probe the function of key molecules involved in the control of phosphate/pyrophosphate ratio including TNAP, NPP1, ANK, and phosphatase orphan 1 (PHOSPHO1), are compatible with a sequence of events involving both mechanisms described briefly as follows. Initially, formation of hydroxyapatite crystals inside matrix vesicles is favored by phosphate accumulation through two mechanisms, PHOSPHO1-mediated intravesicular production and transporter-mediated influx of extravesicular phosphate produced primarily by the adenosine triphosphatase activity of either TNAP or NPP1 (184). Organophosphate compounds such as adenosine triphosphatase, polyphosphates and perhaps also pyrophosphate might be the source of phosphate for this initial step of mineralization (133, 184). TNAP and NPP1 also support the next phase of collagen-mediated extravesicular calcification, although it is the pyrophosphatase, rather than the adenosine triphosphatase or polyphosphatase, activity of these enzymes that is predominant in this step (184). Extravesicular mineralization is then driven by the extracellular phosphate/pyrophosphate ratio and by the presence of a collagenous fibrillar scaffold, with further regulation of crystal growth by noncollagenous proteins of the SIBLING family (see below), most notably osteopontin. This model, which is compatible with most available experimental data, takes into account the roles of both organic and inorganic phosphates in skeletal and tooth dentin mineralization, and unifies the matrix vesicle-mediated and collagen-mediated models of mineralization as two separate, but linked, steps during osteogenesis and dentinogenesis. These interactions regulating mineralization are summarized in Figure 2.

Noncollagenous extracellular matrix proteins and mineralization

While the local removal from the extracellular matrix of mineralization inhibitors such as pyrophosphate is central to the induction of mineralization, the exquisite biological control regulating crystal growth in mineralized tissues appears to reside at the molecular/atomic level of mineral-nucleating and mineral-inhibiting noncollagenous proteins (and their released peptides) (63) to transform unmineralized “oid” matrix into mineralized matrix (137). Many of the noncollagenous proteins in the skeleton and in teeth (and also in many other biomineralized invertebrate tissues) are highly acidic phosphoproteins that bind strongly to mineral – often through negatively charged phosphate groups – to regulate crystal growth. Substantial evidence now exists for the role of acidic, negatively charged mineral-binding proteins (and their peptides) as being important in regulating at least the interfibrillar mineralization process, and this family of proteins (also having cell-signaling properties) is referred to as the SIBLING family (small integrin-binding ligand N-linked glycoproteins) (52), being a subcategory of the secreted calcium-binding phosphoprotein (SCPP) family (95).

The SIBLING family, encoded by a series of genes located on chromosome 4 in humans (loci 20-21), includes dentin sialophosphoprotein (DSPP), dentin matrix protein 1 (DMP1),

bone sialoprotein (BSP), osteopontin (OPN), statherin, and matrix extracellular phosphoglycoprotein (MEPE). In various mineralized tissues (including pathologically mineralizing soft tissues), once initiated, crystal growth is regulated (inhibited) by direct binding of certain inhibitory SIBLING proteins/peptides (for example, osteopontin and its ASARM-containing peptides; see below) to crystal surfaces (4, 66). Some SIBLING proteins are associated with specific sites on collagen molecules, possibly to promote the nucleation and growth of apatite crystals related to collagen (81, 167). SIBLING genes are well-conserved during the evolution of vertebrates, especially genomic regions coding for the arginine-glycine-aspartate (RGD) motif and for long stretches of acidic amino acids, with these motifs having proven roles in cell adhesion and mineral binding, respectively (17, 18, 112, 148). In MEPE, the arginine-glycine-aspartate tripeptide is associated with a glycosaminoglycan attachment motif serine-glycine-aspartate-glycine (SGDG) to form a region called dentonin, and a synthetic dentonin peptide has been shown to stimulate new bone formation (80) and to enhance dental pulp progenitor proliferation (104, 160). Finally, transgenic mouse studies on the SIBLINGs, together with the identification of human SIBLING gene mutations linked to diseases showing mineralization defects, have confirmed the importance of these proteins in regulating bone and tooth mineralization (7, 48, 71, 161-163).

Hypophosphatasia, tissue-nonspecific alkaline phosphatase and the periodontium

Deficiency of TNAP activity characterizes hypophosphatasia (HPP), which is a heritable disorder featuring hypomineralization of the skeleton and teeth (58, 176, 178). Clinical manifestations of hypophosphatasia vary from stillbirth with complete absence of skeletal mineralization, to early tooth loss as the only symptom. The typical and striking oral manifestation of hypophosphatasia is premature loss of primary teeth (176, 178). Expression of TNAP in bone, dentin, and cementum has been well-characterized by immunohistochemistry and in situ hybridization (22, 72, 79, 87, 169, 180). Dysplasia or aplasia of cementum has been well-documented histologically in hypophosphatasia, and this abnormality is considered the cause for the early exfoliation of teeth (38, 50, 89). Irregular dentin mineralization and enlarged pulp chambers have also been described (25, 50, 90).

Cementum was first linked to pyrophosphate metabolism in the condition hypophosphatasia, where premature tooth exfoliation was discovered to result from developmental cementum aplasia or hypoplasia, and thus poor periodontal ligament attachment (38, 170, 175). Intriguingly, studies to date suggest the acellular cementum (acellular extrinsic fiber cementum) of the cervical portion of the root is the most severely affected by the pyrophosphate dysregulation, while the apically located cellular cementum (cellular intrinsic fiber cementum) is generally unaffected, or at least much less so. Proper cementum formation is critical for dento-alveolar function, though cementogenesis remains relatively poorly understood (compared to other mineralized tissues) in terms of associated cells and their origin, their activities and the regulatory factors involved in cementum formation and mineralization. This is especially true with regard to differences between the acellular and cellular varieties of cementum, and how cementum differs developmentally from the other hard tissues. Pyrophosphate serves as an essential regulator of tooth root acellular cementum development and mineralization, and is a key determinant defining the hard-soft interface between the cementum and the periodontal ligament (56). Loss of TNAP caused severe underdevelopment, or even an absence of acellular cementum, and this was prevented by enzyme replacement therapy with mineral-targeting TNAP (122). In contrast, loss of either ANK or NPP1 results in loss of control of cementum apposition and mineralization, causing an extensive hypercementosis (56). With TNAP, ANK and NPP1 adjusting extracellular pyrophosphate levels, the observations described above strongly support pyrophosphate as being a key mechanistic factor uniting the cementum phenotypes in all three mouse models,

together suggesting that pyrophosphate regulates acellular cementum in a molecular “rheostat” fashion, *i.e.* that cementum thickness relates inversely to pyrophosphate production.

While one might suspect that enamel mineralization could also depend on the local regulation of phosphate and pyrophosphate metabolism, there have been no conclusive reports of enamel defects in hypophosphatasia patients, although some papers have alluded to enamel hypoplasia in this disease (89, 111, 143, 174). Recently, Yadav et al. mapped the expression of TNAP in amelogenesis in healthy mice to maturation stage ameloblasts and to the stratum intermedium cell layer (185). Furthermore, these authors showed that deficiency of TNAP in *Alpl*^{-/-} mice leads to enamel defects. Of note here is that enzyme replacement therapy with mineral-targeting TNAP can prevent the dentin (125), cementum (122) and enamel defects (185) in the *Alpl*^{-/-} model of infantile hypophosphatasia. Clinical trials of mineral-targeting TNAP (Asfotase Alfa) in patients with life-threatening hypophosphatasia indicate improved survival and correction of the rickets in these patients (179). A study of changes in the teeth, and tooth retention, as a result of enzyme replacement therapy, is yet to be conducted in these subjects.

The ASARM peptide and mineralization

Proteins of the SIBLING family have an acidic serine- and aspartate-rich motif (ASARM) which is highly conserved across species (114, 148). The ASARM region contains serine residues which can be phosphorylated, and which are interspersed with abundant acidic aspartate and glutamic acid residues (149). The conserved ASARM motif is located in the C-terminal region of all SIBLINGs except osteopontin where it is located in the mid-region of the protein. In most vertebrates, ASARM appears to have evolved to regulate mineralization, extending from eggshell to mammalian bone (17). In mammals, its function appears to have been extended to both transduce and suppress fibroblast growth factor 23 (FGF23) signalling (105, 148). In normal osteogenesis and dentinogenesis, MEPE can be enzymatically cleaved resulting in the release of free ASARM peptide into the extracellular matrix (114), and related recent work for osteopontin also shows enzymatic cleavage to produce ASARM-containing peptides (19). These acidic peptides are generally highly resistant to proteolysis, and are potent inhibitors of bone and dentin mineralization (4, 6, 151). However, ASARM peptides can be selectively cleaved and thus cleared from the local matrix environment where mineralization is destined to occur by the enzyme PHEX (phosphate-regulating gene with homologies to endopeptidases on the X chromosome), a transmembrane zinc-dependent endopeptidase highly expressed by osteoblasts, osteocytes and odontoblasts (4, 6, 19). PHEX can bind to MEPE (and possibly also to other SIBLING proteins(49)) at the ASARM site, protecting these proteins from proteolytic cleavage by other enzymes (74, 150). Once released, the ASARM peptide itself becomes a substrate for PHEX with multiple internal cleavage sites (4, 6), thus promoting mineralization. In this way, together with our recent report on the essentially complete degradation of inhibitory full-length osteopontin by PHEX (19), this enzyme tightly controls mineralization at the local level in the extracellular matrix (4, 150). Furthermore, PHEX can negatively or positively influence FGF23 expression through binding DMP1 or through cleaving ASARM, respectively, which in turn influences systemic circulating phosphate levels (49, 114, 115). In addition, it has also been suggested that PHEX indirectly influences cleavage of FGF23, probably via KLOTHO, thus controlling the negative effects of this hormone on phosphatemia (13, 115, 148). However, the complex links between PHEX, FGF23, DMP1, ASARM, KLOTHO and MEPE in the control of phosphate homeostasis still need further study.

In chronic inflammatory diseases that affect bones and teeth, and more specifically in the case of periodontal disease, excessive pathologic bone resorption occurs in the alveolar bone

of the periodontium (46). In this disease process, bone mineral is dissolved, extracellular matrix is degraded, and total bone volume is lost, all of which threatens the stability and longevity of adjacent teeth. As part of this extensive matrix degradation and mineral dissolution, mineral-bound proteins and peptides such as ASARM might be released, redistribute in tissue fluids and ultimately circulate systemically (35). While tissue-resident PHEX may be able to degrade some of this increased inhibitory ASARM (4, 6) to promote bone healing and mineralization, and positively influence phosphatemia, on other occasions the enzymatic capacity of PHEX might be overwhelmed such that bone healing is impaired and circulating phosphate levels are negatively affected. In this context, ASARM peptides might be considered as target molecules for the treatment of chronic inflammatory diseases of bone.

X-linked hypophosphatemia, PHEX and the periodontium

Familial hypophosphatemic rickets (*e.g.* X-linked hypophosphatemic rickets, or X-linked hypophosphatemia, XLH) are genetic disorders whose major symptom is a soft (hypomineralized) skeleton and dentition. In 1995, the *PEX* gene located on chromosome Xp22.1-22.2 in humans and later renamed *PHEX* (phosphate-regulating gene with homologies to endopeptidases on the X chromosome) was identified as the cause of XLH (MIM-307800) (1). Recently, *PHEX* mutations have been diagnosed in 87% of familial cases, and also in 72% of sporadic cases, in a large cohort of 118 pedigrees representing 56 familial cases and 62 sporadic cases of X-linked hypophosphatemia (61). Regarding other genes associated with familial hypophosphatemic rickets, *FGF23* mutations were identified as the cause of autosomal dominant hypophosphatemic rickets (2), and *DMP1* mutations (108) and *SLC34A* mutations (23, 107) as causes of recessive autosomal hypophosphatemic rickets. In addition, loss-of-function mutations in the *NPP1* gene and a translocation involving the *KLOTHO* gene were assumed to be also associated with hypophosphatemic rickets (37, 102, 106).

In X-linked hypophosphatemia, impaired bone mineralization manifests in children as rickets with severe skeletal deformities, and in adults as osteomalacia (39). A major feature in these same patients is the occurrence of spontaneous tooth abscesses both in the deciduous and permanent dentition, and in teeth without any signs of trauma or decay (43, 156) (Fig. 3). Despite the fact that teeth of patients with X-linked hypophosphatemia look clinically normal, X-rays show a thin enamel layer and a radiolucent dentin layer, the latter associated with enlarged pulp chambers resembling classic taurodontism and prominent pulp horns extending up to the dentino-enamel junction (43) (Fig. 3). Histologic examination show extensive enamel cracking and fissuring, and unmerged dentin calcospherites separated by large nonmineralized interglobular spaces (42, 127) where the dentin matrix contains degraded fragments of MEPE, DMP1 and osteopontin, and also the MEPE-ASARM peptide (33). Abnormal dentin mineralization and enamel cracks may lead to rapid pulp necrosis with periapical complications, and with bacterial ingress into the pulp being facilitated to cause infections of the teeth and surrounding periodontium (44).

The major dental focus in X-linked hypophosphatemia patients has been on the tooth abnormalities alone, and only a few studies have extended this by exploring their overall periodontal status. Recently, a study has reported the periodontal condition of ten adults with familial hypophosphatemic rickets (188). They showed that 60% of the patients presented periodontal bone loss – a figure much higher than reported values for periodontitis prevalence of 3.6% to 7.3% (28, 29) – suggesting that patients with hypophosphatemic rickets are prone to increased periodontal bone loss and thus require more comprehensive examination by dental care providers. Our unpublished clinical data support the results of this study, and we generally observe symptoms of periodontal disease in roughly 70% of our adult X-linked hypophosphatemia patients (data from the “Centre de Référence des maladies

rares du métabolisme du phosphore et du calcium,” Assistance Publique-Hôpitaux de Paris, France). Consistent with this, mice lacking DMP1 develop severe periodontal defects related to defective alveolar bone and cementum (187). Of note in this regard, proteolytic processing of DMP1 results in two major fragments (139) (a C-terminal 57 kDa and a 37 kDa N-terminal fragment) having different functions, the former inhibiting FGF23 expression (109), and both promoting hydroxyapatite formation (65).

Since the 1970s, a treatment has been introduced for X-linked hypophosphatemia which combines the administration of oral phosphate salts and 1,25-dihydroxyvitamin D₃, the hormonal form of vitamin D (in X-linked hypophosphatemia, vitamin D metabolism is perturbed). This treatment for X-linked hypophosphatemia patients has considerably improved their growth and bone mineralization, and it has decreased or prevented bone malformations thus reducing the need for surgical intervention (39, 69). This combined treatment has also had a substantial beneficial impact on oral health, especially for the permanent teeth, which mineralize after birth and for which the treatment has some effect. In 2003, we reported that the decayed, missing and filled teeth index of patients treated since early childhood was similar to the index of healthy, age-matched controls (43). Moreover, we showed that tooth examination formed an important part of the evaluation of the benefits of systemic treatment on mineralization (34, 44, 62). Indeed, permanent tooth analysis from patients treated since early childhood showed a rescue by this treatment resulting in normal dentin and a generally healthy overall tooth phenotype. In terms of periodontal disease, more work is required to determine the treatment effects on the periodontal status of these patients.

Specifically referring to X-linked hypophosphatemia, and as discussed in detail in the preceding section, PHEX is involved in mineral ion homeostasis and in the binding and proteolytic processing of the proteins and peptides regulating mineralization. Important to this are the high levels of expression of these proteins (relative to other cells types) by osteoblasts, osteocytes and odontoblasts (153, 165). In normal conditions, it has been described that PHEX protectively binds to MEPE to prevent ASARM peptide release by other proteases (74, 105), but when free inhibitory ASARM has been released, PHEX degrades it to promote mineralization (4, 6). PHEX also completely degrades full-length inhibitory osteopontin to promote mineralization, and in the absence of PHEX activity, an osteopontin protein fragment accumulates in Hyp mouse bone (19) – the murine mouse homolog of X-linked hypophosphatemia. With *PHEX* mutations in X-linked hypophosphatemia, excessive ASARM and inhibitory osteopontin fragments accumulate to inhibit mineralization. High levels of ASARM peptide have been detected in the serum of patients with X-linked hypophosphatemia, and in Hyp mice (35), and the peptide accumulates in the kidneys (35) where it impairs phosphate uptake from the urine and consequently induces hypophosphatemia (49). More recently, MEPE-derived ASARM peptides have been shown to inhibit in a dose-dependent manner the mineralization of human primary osteoblast cultures grown under differentiating conditions (13). Consistent with this, experiments both *in vivo* and *in vitro* have confirmed the capacity of MEPE-derived ASARM peptides to inhibit both dentin mineralization and odontoblast differentiation (unpublished data). In schematic format, key determinants of normal mineralization are summarized as they relate to X-linked hypophosphatemia (Fig. 4).

Conclusions

The structure and function of the periodontium – including the teeth, bone and the soft surrounding tissues – act collectively to provide for occlusion and mastication. Essential to these activities is mineralization of bone and tooth extracellular matrices, and mineralization of the extremities of the periodontal ligament fibres where they insert either into alveolar

bone at one end, and into cementum at the other end. The proper function of this suspensory apparatus relies on this essential mineralization, and diseases where bone and tooth mineralization is altered – such as X-linked hypophosphatemia and hypophosphatasia – invariably lead to malformed and weak bones and teeth, and premature tooth loss and tooth infections. Substantial progress has been made in recent years in understanding the underlying mechanisms contributing to mineralization diseases where bones are soft (hypomineralized), and some new clinical treatments are showing great promise in promoting mineralization, particularly of bone. Additional work is now required to extend this progress to the treatment of diseased dental tissues.

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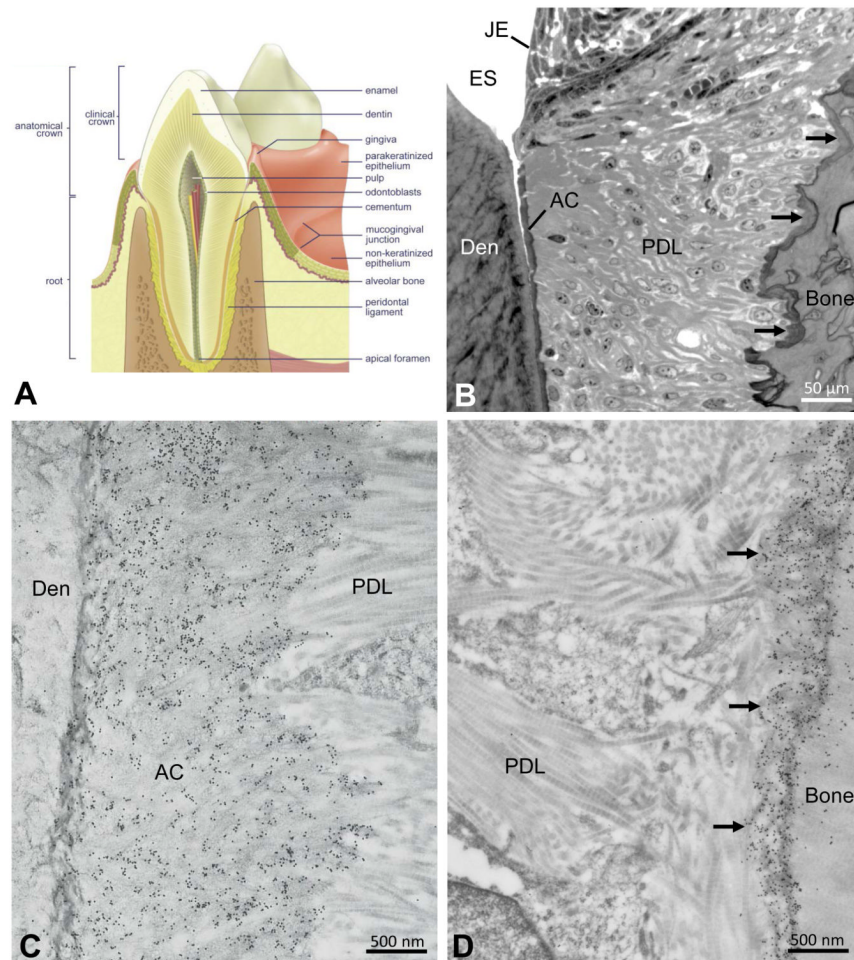
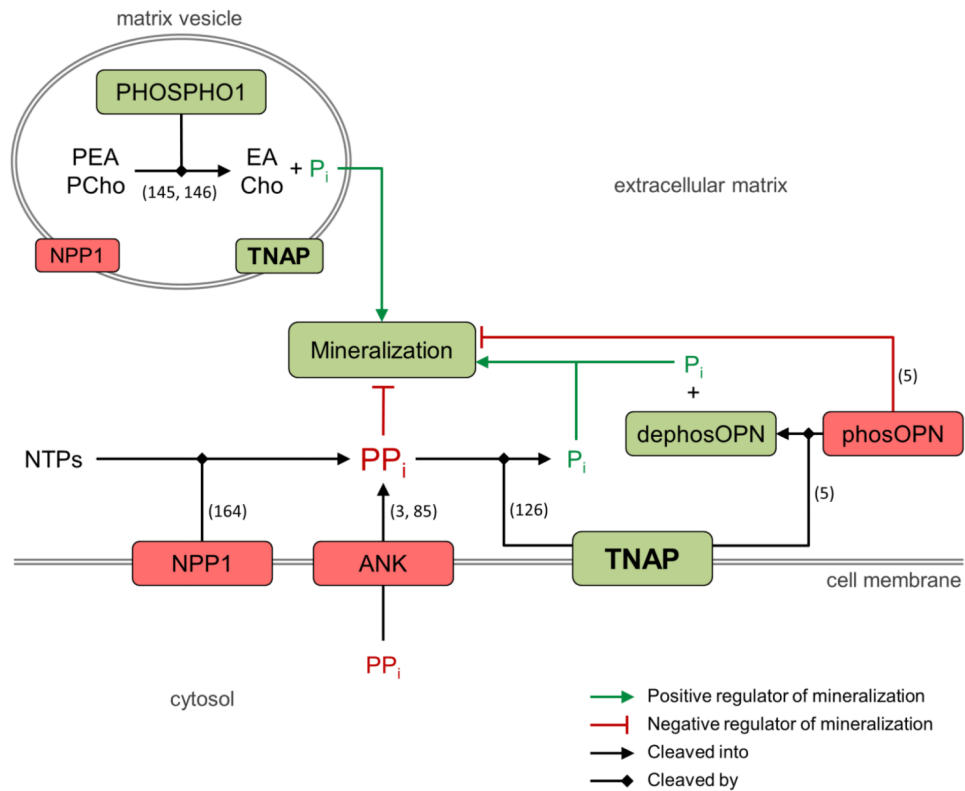


Figure 1.

(A) Anatomical relationships of mineralized tissues of the tooth and surrounding hard and soft tissues of the periodontium. **(B)** Light microscopic relationships of periodontal tissues near the cemento-enamel junction. Junctional epithelium (JE) abuts against the enamel (here enamel space [ES] after sample decalcification), and a thin layer of acellular cementum (AC) interfaces with the dentin (Den) at the dentino-enamel junction. Periodontal ligament (PDL) collagen fibres surround the tooth, inserting at one end into the acellular cementum and inserting at the other end into a fringe of darkly stained bone (arrows) lining the alveolus. **(C,D)** Electron microscopy after colloidal-gold immunolabeling (small black particles) for osteopontin of periodontal ligament (PDL) collagen fibrils inserting into the acellular cementum (AC) apposed to the dentin (Den) at the dentino-enamel junction (left panel), and into the fringe of alveolar bone (arrows) lining the alveolus (right panel). Images obtained from the first molar of a 1-month-old mouse.

**Figure 2.**

Determinants of normal mineralization relevant to hypophosphatasia. The extracellular phosphate/pyrophosphate ratio is regulated by phosphatase orphan 1 (PHOSPHO1), ectonucleotide pyrophosphatase phosphodiesterase 1 (NPP1), progressive ankylosis protein 1 (ANK), and tissue-nonspecific alkaline phosphatase (TNAP). Inactivating mutations in the enzyme TNAP result in an increase in extracellular pyrophosphate that inhibits mineralization and is a key factor in causing hypophosphatasia. Similar molecular determinants are thought to occur related to matrix vesicles. In the extracellular matrix, phosphorylated osteopontin (phosOPN) inhibits mineralization, and dephosphorylation of osteopontin (dephosOPN; and possibly other matrix proteins) by TNAP may contribute to extracellular phosphate levels. Green boxes indicate positive regulators of mineralization, while red boxes indicate negative regulators of mineralization. Citations supporting the indicated functions are shown by the numbers in parentheses. PEA, phosphoethanolamine; EA, ethanolamine; PCho, phosphocholine; Cho, choline; P_i, phosphate; PP_i, pyrophosphate; NTPs, nucleotide triphosphates.

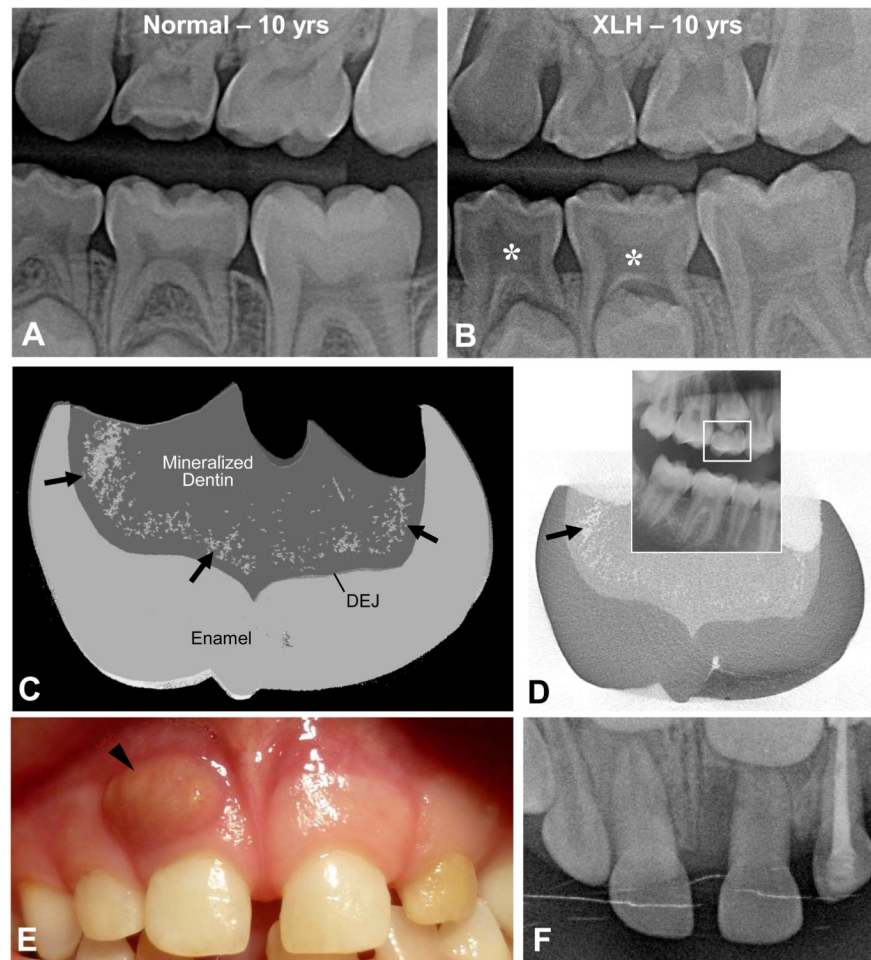


Figure 3. (A,B) Tooth radiographs from a normal, 10-year-old male, and from a 10-year-old male patient with X-linked hypophosphatemia (XLH) caused by an inactivating mutation in the *PHEX* gene. In deciduous molars, note the enlarged pulp chambers (asterisks), the prominent pulp horns, and the radiolucency of the hypomineralized dentin that mineralized prior to the onset of systemic treatment. (C,D) Micro-computed tomography of a crown from the upper-right, second deciduous molar (seen on the panoramic X-ray inset) of a 13-year-old female X-linked hypophosphatemia female patient with a mutation in the *PHEX* gene. Mineralization voids (the spotty areas indicated by the arrows in panel C accumulating in the dentin near the dentino-enamel junction (DEJ) were rendered in grey using 3D reconstruction software to compile volumetric data from the 2D X-ray “slices,” one of which is depicted in panel D where the mineralization voids appear white. (E,F) Photograph and occlusal X-ray of the upper central right deciduous incisor from a 6-year-old X-linked hypophosphatemia male patient with a mutation of the *PHEX* gene. A large abscess (arrowhead) is observed related to the incisor root; the tooth was extracted after systemic treatment with antibiotics.

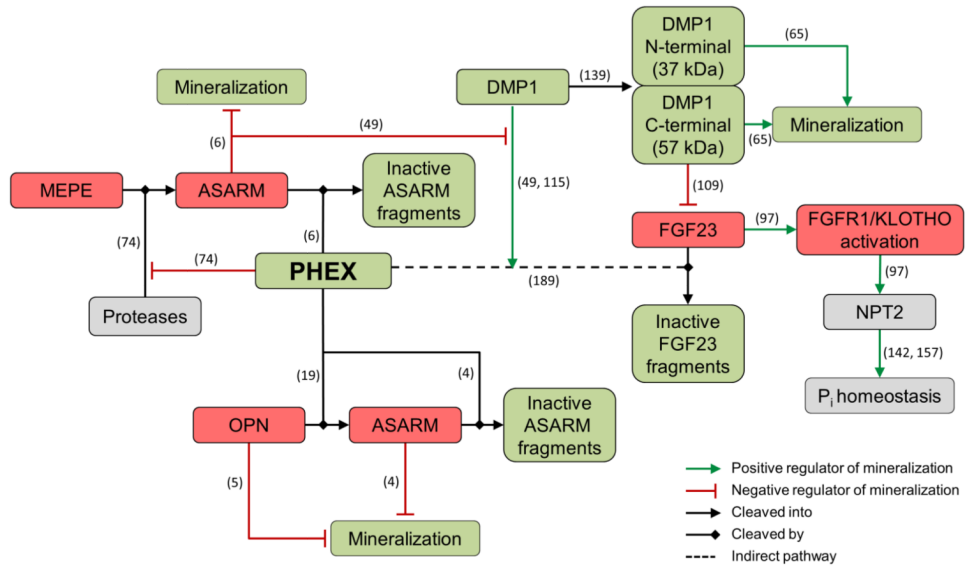


Figure 4. Determinants of normal mineralization relevant to X-linked hypophosphatemia. Local and systemic regulation of mineralization is controlled by phosphate-regulating gene with homologies to endopeptidases on the X chromosome (PHEX). PHEX regulates mineralization locally at the level of the extracellular matrix by directly degrading mineralization inhibitors such as osteopontin and ASARM peptides. Systemic regulation involves influencing phosphate homeostasis indirectly through fibroblast growth factor 23 (FGF23), a key circulating factor that directs sodium-dependent phosphate transporters (NPT2) in the kidney and intestine, thus controlling phosphate reabsorption. Green boxes indicate positive regulators of mineralization, red boxes indicate negative regulators of mineralization, and grey boxes indicate indirect regulators of mineralization. Citations supporting the indicated functions are shown by the numbers in parentheses.

Table 1

Human proteins/genes associated with mineralization

Protein abbreviation	Gene name(s)	Protein function
TNAP	<i>Tissue-nonspecific alkaline phosphatase (ALPL)</i>	TNAP is a membrane-bound phosphatase prominent in osteoblasts, chondrocytes and odontoblasts, as well as in their matrix vesicles (126). In the skeleton, it hydrolyzes the mineralization inhibitor pyrophosphate, also producing phosphate locally in the matrix. TNAP is also found in other organs (liver, kidney, skin), however little is known about its function in these tissues.
PHEX, PEX	<i>Phosphate-regulating gene with homologies to endopeptidases on the X chromosome (PHEX)</i>	PHEX is a membrane-bound endopeptidase found predominantly in osteoblasts, osteocytes and odontoblasts (21, 73, 152, 153). Mutations in PHEX lead to X-linked hypophosphatemia, which is accompanied by an increase in circulating levels of FGF23 resulting in renal phosphate wasting (141, 147). PHEX protects MEPE from cleavage (74), as well as cleaving the physiologically relevant mineralization inhibitors osteopontin (19) and the MEPE ASARM and OPN ASARM peptides (4, 6).
ANK	<i>Progressive ankylosis protein human (ANKH)</i>	ANK is a transmembrane protein that acts as pyrophosphate transporter, exporting intracellular pyrophosphate into the extracellular space to inhibit mineralization (3). ANK loss-of-function mutations lead to soft-tissue calcification (85) while ANK gain-of-function mutations in humans leads to calcium pyrophosphate disease characterized by the formation of calcium pyrophosphate crystals in cartilage extracellular matrix (3).
NPP1	<i>Ectonucleotide pyrophosphatase phosphodiesterase 1 (ENPP1)</i>	NPP1 is a type II transmembrane ecto-enzyme that hydrolyzes nucleotide triphosphates to generate extracellular pyrophosphate to inhibit mineralization (164). A loss-of-function mutation in the gene encoding this enzyme leads to idiopathic infantile arterial calcification (154).
PHOSPHO1	<i>Phosphatase orphan 1 (PHOSPHO1)</i>	PHOSPHO1 is an enzyme prominent in mineralized tissue cells that exhibits phosphatase activity towards phosphoethanolamine and phosphocholine (146). PHOSPHO1 is also present in matrix vesicles and is therefore thought to play a role in the initiation of matrix mineralization (145).
OPN (Osteopontin)	<i>Secreted phosphoprotein 1 (SPP1)</i>	OPN is produced by many cell types, and in bone by osteoblasts, osteocytes and osteoclasts, and in tooth by odontoblasts and cementoblasts (118). Many <i>in vitro</i> and <i>in vivo</i> studies have shown that OPN has a strong inhibitory role in mineralization that is largely phosphorylation dependent (5, 31, 64). OPN is also thought to play a role in osteoclast development and function (57), cell adhesion and migration (103), as well as several immune-related functions (173).
BSP (Bone sialoprotein)	<i>Integrin-binding sialoprotein (IBSP)</i>	BSP is prominent in mineralized tissue extracellular matrices such as bone, dentin and mineralized cartilage, where it is produced mainly by osteoblasts, osteocytes and chondrocytes (60, 137). Reported functions include hydroxyapatite nucleation (78) as well as promotion of osteoclastogenesis (113).
MEPE	<i>Matrix extracellular phosphoglycoprotein (MEPE)</i>	MEPE is mainly produced by osteocytes (129) and osteoblasts (12), and is upregulated during osteoblast matrix mineralization. MEPE plays a role in matrix mineralization by enhancing osteoblastic activity (71) and indirectly suppressing osteoclastogenesis (48). Its ASARM peptide, derived from a C-terminal cleavage, has been shown to be a potent mineralization inhibitor (6) and an indirect promoter of renal phosphate excretion (151).
DMP1	<i>Dentin matrix protein 1 (DMP1)</i>	DMP1 is a prominent matrix protein in teeth (predentin, dentin and cementum - odontoblasts and cementoblasts), bones (osteocytes) and to some extent in certain soft tissues (108, 138). Generally, it is processed to 37-kDa N-terminal and 57-kDa C-terminal fragments (139). The full-length and fragment forms of DMP1 have been shown to have many biological functions including as a hydroxyapatite nucleator (full-length and C-terminal fragment) (59) and as a promoter of cell differentiation via its RGD interaction with cell surface integrin/CD44 receptors (96). DMP1 is also thought to control phosphate homeostasis through the FGF23 pathway (51), as well as osteogenesis and dentinogenesis (138).
DSPP	<i>Dentin sialophosphoprotein (DSPP)</i>	DSPP is found predominantly in dentin (and to a lesser extent in bone), but is immediately cleaved into its active fragments dentin phosphoprotein and dentin sialoprotein (110, 140). Dentin phosphoprotein contains a large number of aspartic acid and phosphoserine repeats which allows it to bind to hydroxyapatite and is thought to initiate and modulate dentin mineralization (135). The function of dentin sialoprotein is not yet known.

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FGF23	<i>Fibroblast growth factor 23 (FGF23)</i>	FGF23 is a secreted protein mainly expressed by osteoblasts and osteocytes that acts as a circulating factor to control serum phosphate levels (142). FGF23 binds to FGF receptor 1, 3 or 4 and its co-receptor Klotho in the proximal tubule of the kidney, which decreases the expression of sodium-dependent phosphate cotransporter 2, thus reducing phosphate reabsorption (142, 157). It also suppresses 1,25-dihydroxyvitamin D levels by downregulating renal 25-hydroxyvitamin D-1 -hydroxylase.
KLOTHO	<i>KLOTHO (KL)</i>	KLOTHO is produced in a limited number of tissues, with the highest being in the distal convoluted tubules of the kidney (98). Here, KLOTHO acts as a membrane-bound co-receptor for FGF23, allowing it to bind to fibroblast growth factor receptors 1, 3, and 4, and contribute to phosphate homeostasis (99). Although less common, KLOTHO can be found in a secreted form where it is thought to activate cell surface ion channels, ion transporters, and growth factor receptors (97).
SLC34A3, Na/Pi-IIc (NPT2C)	<i>Solute carrier family 34 (sodium phosphate) member 3 protein, Renal sodium-phosphate cotransporter, Na/Pi-IIc (SLC34A3)</i>	SLC34A3 is prominent in the apical membrane of proximal tubular cells in the kidney (155). Like other sodium-dependent phosphate cotransporters, it plays a major role in extracellular phosphate homeostasis.