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Phosphate sensing

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Abstract

Human phosphate homeostasis is regulated at the level of intestinal absorption of phosphate from the diet, release of phosphate through bone resorption, and renal phosphate excretion and involves the actions of parathyroid hormone (PTH), 1,25-dihydroxy-vitamin D (1,25-(OH)₂-D), and fibroblast growth factor 23 (FGF23) to maintain circulating phosphate levels within a narrow normal range, which is essential for numerous cellular functions, for the growth of tissues and for bone mineralization. Prokaryotic and single cellular eukaryotic organisms such as bacteria and yeast “sense” ambient phosphate with a multi-protein complex located in their plasma membrane, which modulates the expression of genes important for phosphate uptake and metabolism (pho pathway). Database searches based on amino acid sequence conservation alone have been unable to identify metazoan orthologs of the bacterial and yeast phosphate sensors. Thus little is known about how human and other metazoan cells sense inorganic phosphate to regulate the effects of phosphate on cell metabolism (“metabolic” sensing) or to regulate the levels of extracellular phosphate via feedback system(s) (“endocrine” sensing). Whether the “metabolic” and the “endocrine” sensor use the same or different signal transduction cascades is unknown. This chapter will review the bacterial and yeast phosphate sensors, and then discuss what is currently known about the metabolic and endocrine effects of phosphate in multicellular organisms and humans.

Introduction

Inorganic phosphate, the variably charged anion of phosphoric acid, i.e. [H₂PO₄¹⁻] and [HPO₄²⁻] (for the purpose of this review referred to as “phosphate” or Pi) is required for cellular functions such as DNA/RNA and membrane phospho-lipid synthesis, generation of high-energy phosphate esters, and intracellular signaling (1). The intracellular inorganic phosphate concentration can be measured using ³¹P-NMR, which is a non-destructive method with little artifactual hydrolysis of labile organophosphates such as phosphocreatine; phosphocreatine is typically present intracellularly at 20 times the apparent free intracellular phosphate concentration of 0.5–5 mM (2). In contrast, the methods used to measure serum phosphate are usually based on a photometric approach using ammonium molybdate, which forms a chromogenic complex with inorganic phosphate (3).

The intracellular concentration of inorganic phosphate is maintained by membrane transporters, which accumulate phosphate at concentrations larger than would be predicted,

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if phosphate were distributed passively across the membrane by coupling with plasma membrane H^+ (4) or Na^+ gradients (5). Concentrations of intracellular phosphate are influenced by pH, hormones, and subcellular compartmentalization; levels in these compartments may be regulated by separate transporters in mitochondria (6,7), lysosomes(8,9), and the endoplasmic or sarcoplasmic reticulum (10). Many enzymes of key metabolic pathways are regulated by phosphate; these pathways include those for anaerobic glycolysis, gluconeogenesis, mitochondrial metabolism, glutamine, purine and nucleic acid metabolism. Although most studies were performed with purified enzymes *in vitro*, some enzymes respond to phosphate concentrations that could reasonably be expected intracellularly in the organs/cells from which they were isolated ($K_d=1-10$ mM), and thus these enzymes may also be regulated by intracellular phosphate *in vivo* (1). Intracellular phosphate levels are elevated in pathological conditions such as ischemia, hypoxia, and skeletal muscle fatigue, as well as in some inherited disorders such as mitochondrial myopathies. Conversely, decreased intracellular levels of phosphate are observed in disorders with severe hypophosphatemia, such as X-linked hypophosphatemia. In addition to the metabolic changes phosphate appears to activate distinct nutrient sensing pathways. These are best understood in unicellular organisms like bacteria and yeast, which will be described in detail below. In mammals circulating phosphate, in addition to serving to maintain intracellular phosphate levels for cell metabolism and growth, serves to regulate extracellular mineralization (complexes of phosphate with calcium). To control mineralization and cellular delivery, extracellular phosphate levels and total body phosphate content are tightly regulated by a number of hormones, including parathyroid hormone (PTH), 1,25-dihydroxy vitamin D ($1,25(OH)_2D$), and fibroblast growth factor 23 (FGF23) and serum phosphate feeds back to regulate these factors in an endocrine fashion (11): high phosphate reduces secretion of PTH and increases secretion FGF23, while low phosphate stimulates the synthesis of $1,25(OH)_2D$, the active form of vitamin D.

Misregulation of phosphate homeostasis can cause serious human disorders (11): the clinical consequences of severe hypophosphatemia for example in tumor-induced osteomalacia or familial forms of rickets, such as X-linked hypophosphatemia, involve disruption of both the metabolic and mineralization functions of phosphate and result in hemolysis, skeletal muscle myopathy, cardiomyopathy, neuropathy, and osteomalacia; in some cases it can contribute to death. Hyperphosphatemia on the other hand leads to tissue calcifications and metabolic changes, which are to date poorly understood. Hyperphosphatemia is encountered most frequently in patients with chronic kidney disease (CKD)(12–14), which affects 20 Million Americans today and the serum phosphate level is an important predictor of mortality in this population. Furthermore, mouse models with hyperphosphatemia due to loss-of-function mutations in *Klotho* or *FGF23* die prematurely. This early lethality can be rescued and their life-spans extended when fed a phosphate-restricted diet (15,16). A similar benefit is seen with dietary phosphate-restriction in humans with CKD and it is possible that similar mechanisms are at work in mice and men. An understanding of the molecular basis underlying the metabolic and endocrine phosphate effects is therefore of great significance for human disease.

The ability of organisms to detect presence and levels of various metabolites (“metabolic sensing”) is important for their normal physiology. G protein-coupled receptors have been shown to play an important role in metabolic sensing of metabolites like glucose in yeast (17), or for calcium in multicellular organisms (18). Amino acids activate metabotropic G protein-coupled receptors, but also rely on import by specialized proton assisted transporters to activate the intracellular TSC (tuberous sclerosis complex)/TOR (target of rapamycin) sensing system (19). While the TSC/TOR pathway is highly conserved between yeast and multicellular organisms, glucose sensing has evolved from use of an extracellular membrane sensor, to an intracellular sensing mechanism, which requires import of glucose by Glut2

transporters in pancreatic beta cells of multicellular organisms (20). Based on these considerations it is possible that the molecular components of the human phosphate sensor are conserved, although new mechanisms could likewise have evolved. Phosphate sensing in bacteria and yeast appears to involve uptake of extracellular phosphate, activation of an intracellular sensor composed of a kinase/kinase inhibitor complex, which leads to transcriptional events mediated by phosphate-specific transcription factors (Fig. 1A). Emerging evidence suggests that similar events are at work to mediate the cellular effects of phosphate in metazoan species including humans. However, the exact molecular nature of these mechanisms is still unclear. This chapter will review the bacterial and yeast phosphate sensors and then discuss what is currently known about the metabolic and endocrine effects of phosphate in multicellular organisms and humans.

Phosphate sensing in Bacteria

In bacteria Pi is sensed by binding to the four-component Pst transporter (PstS, PstA, PstB, PstC). Phosphate thereby activates a two component signaling system composed of the sensory histidine kinase PhoR (an integral membrane protein) and the transcription factor, PhoB. This interaction is modified by a chaperone/Hsp70-like PhoR/PhoB inhibitory protein called PhoU. Excess phosphate turns the system off, while the default state is active. Thus, phosphate sensing in bacteria appears to involve a negative feed-back mechanism, which permits the pho operon to get up-regulated under conditions of phosphate limitation (21,22).

PhoR is required for the activation (phosphorylation) of PhoB under conditions of Pi limitation. It is comprised of five domains, a domain important for anchoring in the membrane, a positively charged linker region, a Per-Arnt-Sim (PAS) domain, a dimerization and histidine phosphoacceptor domain, and a catalytic domain. The transmembrane domain anchors PhoR in the membrane, which is necessary for interaction with the Pst transporter. The PAS domain of PhoR interacts directly with the PstB component of the Pst transporter and binds PhoU. Binding of phosphate to the PstS portion of the transporter in the periplasmic space leads to inhibition of PhoR, resulting in deactivation, i.e. dephosphorylation, of phospho-PhoB (Fig. 1B, Table 1). Cellular phosphate-uptake per se is not required for phosphate-dependent signaling by the Pst system, since mutations that abolish Pi-uptake still allow for inhibition of PhoR by phosphate (21).

PhoB belongs to the OmpR/PhoB subfamily of response regulators in *E. coli*, and, like transcription factors in higher species, it is comprised of a N-terminal regulatory receiver domain and a C-terminal DNA-binding domain. Other (non-PhoR) histidine kinases or small molecule phosphoryl donor(s) such as acetyl phosphate can activate (phosphorylate) PhoB (23), which may be important for integrating different steps of Pi metabolism and other metabolic pathways. Estimates for the number of Pi-regulated genes vary but may involve as many as 400 proteins (almost 10% of the *E. coli* proteome) based on proteomic data (24) and computational predictions (25). These genes encode the above phosphate sensing complex, and other genes important for phosphate scavenging and metabolism such as aldolases, phosphonate transporter subunits, carbon-phosphorus lyase complex subunits, bacterial alkaline phosphatase, glycerol-3-phosphate transporter subunits, and glycosyl transferases (as reviewed in (21)).

In addition to the Pst system, bacteria express a second family of phosphate transporters, which are related to eukaryotic type III sodium-phosphate co-transporters (Pit). However, the high-affinity Pst system appears to be the predominant system for bacterial phosphate-uptake both in conditions of phosphate limitation and abundance, while the low affinity phosphate transporters of the Pit system (i.e. PitA) serve primarily as a transporter of divalent metal cations (Zn^{2+}) that are transported in complex with Pi (26).

The bacterial Pst transporter shows similarity to the large group of mammalian ABC-transporters, however, no specific mammalian ortholog has been identified. Furthermore, an apolipoprotein highly similar to the phosphate binding protein PstS was purified from human plasma (27), but it was later realized that this likely represents a bacterial contaminant (28). Likewise, no orthologs were identified for PhoR or PhoB. Interestingly, PhoU contains a domain similar to eukaryotic type II sodium-phosphate co-transporters, the significance of which is unclear.

Phosphate sensing in Yeast

As in bacteria, phosphate controls a specialized transcription factor, called Pho4, in yeast (29,30). However, unlike the bacterial transporters, the phosphate transporters in yeast belong to the major facilitator superfamily (MFS) or Pit-family and the activity and subcellular localization of Pho4 is regulated by the cyclin-dependent kinase (CDK) complex, Pho80–Pho85 (31). When cells are starved of phosphate, the CDK inhibitor Pho81 inactivates Pho80–Pho85, thereby allowing unphosphorylated Pho4 to associate with the nuclear import receptor Pse1 and to enter the nucleus and bind to a phosphate response element (PRE)(32) in genes belonging to the yeast Pho-regulon (Fig. 1C, Table 1) (33) The yeast Pho-regulon includes genes coding for high affinity phosphate transporters (PHO84, PHO89) and secreted acid phosphatases (PHO5, PHO11, PHO12), which permit the cell to better assimilate phosphate from the surroundings (34).

High-affinity uptake of extracellular phosphate under phosphate-limited growth conditions is mediated by Pho84 (4). Pho84 belongs to the major facilitator superfamily of transporters, and studies of intact yeast cells (4) and inverted plasma membrane vesicles (35) have shown that the Pho84 transporter catalyses a bi-directional proton-coupled Pi uptake, where the direction of transport is determined by the directionality of the driving force rather than by the orientation of the protein. Expression of Pho84 is de-repressed when the external phosphate concentration of the growth medium decreases to about 100 μ M (30). Low intracellular phosphate may serve as an activation signal for the Pho-pathway, since the disruption of Pho84 results in the constitutive expression of Pho5 in Δ pho84 yeast strains (4,36).

Following the addition of repressive amounts of phosphate (10mM) to low-Pi-grown cells, Pho84 is rapidly internalized from the plasma membrane and degraded within 60 minutes, a process that involves PKA signaling (30,37,38). Endocytosis and vacuolar processing of Pho84, like many other plasma membrane proteins in yeast, may require phosphorylation and/or ubiquitination (37). Down-regulation and degradation of Pho84 is also triggered by the non-metabolized phosphate analogue methylphosphonate (MP) at a concentration of 10 mM (38). MP appears to be recognized as a Pho84 substrate and to mimic phosphate's inhibition of the phosphate-response at the level of Pho84 protein expression and degradation within 60 minutes and causes repression of Pho5 activity by 120 minutes. Lack of Pho84 (Δ pho84) can be rescued by over-expression of the high-affinity Pho89 and low-affinity Pho87, Pho90, and Pho91 inorganic phosphate transporters, or the glycerophosphoinositol transporter (Git1). This supports the idea that intracellular phosphate is the regulatory signal. However, de-repression of secreted acid phosphatase Pho5 does not require activation of the PKA signaling pathway (39) and is not rescued by over-expression of the Pho89, Pho87, Pho90 and Pho91, and thus binding of phosphate to Pho84 alone may be sufficient to cause some down-stream effects of phosphate.

Under conditions of high phosphate (above 100 μ M), the Pho80–Pho85 cyclin/CDK complex is gradually activated to phosphorylate the transcription factor Pho4. Phospho-Pho4 associates with the nuclear export receptor Msn5, leading to the rapid export of Pho4 from

the nucleus to the cytoplasm and thus to repression of the Pho-regulon (Fig. 1C). The multiple ankyrin-repeat containing CDK inhibitor Pho81 has been proposed as the intracellular phosphate sensor because of its regulatory activity in the Pho-pathway (40,41), and because a minimal domain of Pho81 containing 80 amino acids is both necessary and sufficient to inhibit Pho80–Pho85 CDK activity (41). Inhibition of Pho81 in conditions of phosphate excess requires accumulation of myo-d-inositol heptakisphosphate (IP7) (42), which appears to involve binding of IP7 to the Pho80/81/85 complex (43). Pho81 is also required to control trehalose metabolism, the postdiauxic shift stress-response (44), and the activity of the protein kinase Rim15, which plays a central role in the integration of phosphate, glucose, nitrogen and amino acid availability during the cell cycle (45). Thus, Pho81 may integrate several nutrient-sensing pathways to control the cell cycle in yeast. Further indication for a cross-talk between several nutrient sensing pathways is that limitation in carbon sources results in rapid degradation of Pho84 despite the presence of de-repressing levels of Pi (38,46).

Pho84 belongs to the major facilitator family, which comprises more than 200 members in humans and includes the type I sodium-phosphate transporters (SLC17A1-9). Pho87, 90, 91 are related to metazoan sodium-sulfate transporters (SLC13A1-4), and Pho89 is related to the type III sodium-phosphate transporters SLC20A1 (Pit-1) and SLC20A2 (Pit-2) (47,48). Using DNA footprint analysis, Kido et al. identified a phosphate responsive element (PRE) in the mouse NaPi-IIa promotor, which has similarity to the yeast PRE and isolated a transcription factor mE3 (TFE3), which is similar to yeast Pho4, and may mediate the up-regulation of NaPi-IIa gene expression in response to low-phosphate diet (49).

Regulation of phosphate sensing by intracellular phosphate stores

Inorganic polyphosphate (Poly P) is a linear polymer comprising ten to many hundred phosphate residues; these are linked by the same phosphoanhydride bonds found in ATP. It is present in intracellular vacuoles in all cell types, where it functions as a phosphate store.

In bacteria, Poly P can serve both as a phosphate reservoir and as an energy source in different biological processes, where it substitutes for ATP in phosphorylation reactions by kinases to trigger signal transduction by inhibiting or activating effector molecules (50,51). The poly P kinase gene PPK, which is involved in poly P synthesis, appears to be under the control of the PhoR/PhoB two component signaling system (52,53). Conversely, poly P is able to regulate PitA expression, and furthermore, PPK, Pst and PitA are able to compensate for each other to regulate cellular phosphate uptake (54).

Similarly in yeast, Poly P is synthesized and accumulated in the vacuole and represents a phosphate reserve used during periods of phosphate starvation (55–57). This is illustrated in cell culture experiments when transfer of cells to a phosphate-deficient medium results in a rapid decrease of poly P content (58). In addition to serving as a buffer that can be mobilized during periods of Pi limitation (59), the capacity to synthesize Poly P, furthermore, exerts control on the rate at which Pi is taken up, possibly via a transient increase in the level of phosphate in the cytosol (38). Finally, Poly P strongly influences the expression of Pho5, the main secreted acid phosphatase (36) by which yeast mobilizes phosphate from extracellular sources.

Little is known about Poly P in animal cells beyond its widespread abundance in tissues and subcellular compartments (60). Poly P, at the concentrations of 0.15–1.5 μM found in mammalian cells (61) and with Poly P chain lengths ranging from 15 to 750 phosphate residues, appears to stimulate mTOR (mammalian target of rapamycin), a ser-thr protein kinase that is at the center of signaling pathways in cell growth and proliferation and is

activated by autophosphorylation (62). mTOR function is controlled by nutrient availability to ensure that protein synthesis is repressed when the supply of precursor amino acids is insufficient. The key downstream targets of mTOR are PHAS-I (also called eukaryotic initiation factor 4E binding protein (eIF4E-BP)), and the kinase for the 40S ribosomal S6 protein (p70 S6 kinase) (63). PHAS-I is inhibited by mTOR, while S6K is activated. PHAS-I in its unphosphorylated state sequesters eIF4E, a mRNA cap-binding protein in the eIF4G elongation complex (64,65). Via activation of mTOR polyP thus stimulates global protein translation. Poly P also appears to enhance the mitogenic activities of acidic fibroblast growth factor (FGF-1) and basic fibroblast growth factor (FGF-2) in human fibroblasts by functioning as co-activator similar to heparin (66). Finally, addition of Poly P to human plasma cells (PCs) inhibited secretion of immunoglobulin and stimulated apoptosis by activating caspase-3 and arresting the cell cycle (67), suggesting that poly P plays a role in immunity.

Phosphate sensing in multicellular organism

Metabolic effects of activation of MAPK by phosphate

It has long been recognized that differentiation of primary or immortalized osteogenic cells requires the addition of inorganic phosphate in the form of hydroxyapatite (68–70) or beta-glycerophosphate (71) along with ascorbic acid, which is believed to support formation of collagen matrix (72). Expression of several bone-cell specific genes, such as dentin matrix protein 1 (*DMP1*), osteopontin (*OPN*), and matrix-gla-protein (*MGP*), is stimulated by phosphate at the transcriptional level, while expression of alkaline phosphatase (*TNSALP*) is suppressed (73–75). Cellular uptake of phosphate by specialized transporters appears to be required since addition of phosphonoformic acid (PFA, forscarnet), an inhibitor of sodium-phosphate co-transporters, blocks these effects of Pi (75–77). The downstream effects that result in suppression of TNSALP may require BMP-signaling in ST2 murine bone marrow stromal cells (78). In contrast, dependence of phosphate signaling on the p42/p44-MAPK/ERK pathway was shown in ATDC5 cells (79). Likewise, induction of OPN and MGP requires activation of the p42/p44-MAPK/ERK pathway and can be blocked by UO126, a specific inhibitor of MAPK-kinase, MEK (80,81).

Activation of MAPK by calcium-phosphate crystals in primary fibroblasts was initially described by Nair and colleagues (82). Beck and colleagues subsequently showed that phosphate at concentrations between 5–10 mM alone is sufficient to activate MAPK in MC3T3 mouse fibroblast cells (80), and subsequently activation of MAPK by inorganic phosphate was demonstrated in multiple other cell lines, including chondrogenic ATDC5 cells, MC3T3-E1 osteoblasts and ST2 murine bone marrow stromal cells (81), HEK293 human proximal tubular cells (83), and lung alveolar cells (77) (Fig. 1D). Although some cell lines, for example C2C12 or L929 cells, were less responsive than others (81), activation of MAPK by phosphate appears to be quite universal in metazoans. This mechanism is furthermore conserved evolutionarily, since similar observations were made in *Drosophila* S2R+ hemocyte cells (84). Addition of PFA (76,85) or siRNA-mediated knockdown of Pit1 sodium-phosphate co-transporters blocks activation of MAPK by phosphate (83) indicating that cellular uptake of phosphate is required for the activation of MAPK. Furthermore, using cell lines expressing a Pi-transport-deficient Pit1 transporter, Beck and colleagues recently reported that Pit1 may have transport-independent effects on cell proliferation and tumor growth *in vitro* and *in vivo*, although it remains to be shown whether these effects depend on phosphate-binding to Pit1 (86). Pit1 together with its mammalian paralogue Pit2, the bacterial pitA, and yeast pho89 transporters belongs to the NaPi-III class of sodium-phosphate co-transporters (47,48).

Phosphate appears to induce phosphorylation of FRS2alpha, a mediator of FGF receptor action (79,83). In addition siRNA-mediated knockdown of FGFR1 is able to interfere with Pi-induced MAPK (79,83). Furthermore, phosphorylation of Akt and c-Raf by phosphate was shown in human bronchial epithelial cells (77) and proliferating chondrocytes (79), respectively, suggesting that phosphate interacts with the MAPK pathway relatively close to the cell membrane. Activation of p42/p44-MAPK by phosphate is rapid and occurs within 5 min., but biphasic up-regulation with a second peak after 8–12 hrs. has been reported in some cell lines, while the related kinases JNK and p38-MAPK appear not to be affected by phosphate at least in those cell lines reported to date (80,81).

It is possible that binding of extracellular phosphate to Pit1 activates the MAPK pathway. However, since knockdown of members of the MFS family (i.e. NaPi-I) blocks phosphate-induced MAPK at least in *Drosophila* S2R+ cells (84), intracellular phosphate after uptake via multiple transporter classes may be the signal for MAPK and the activation of possibly other pathways. Furthermore, blocking phosphate-induced MAPK by knockdown of FGFR1 or FRS2alpha either suggests a cooperative interaction between Pit1 and FGFR1 to sense extracellular phosphate after binding to Pit1 or that intracellular phosphate acts to modulate flow through the MAPK pathway at one or multiple levels downstream of the FGFR1/FRS2alpha.

Egr-1 was shown to be a downstream effector of phosphate-induced MAPK (87,88). Pi also induces the expression of Fra-1 (87) and Nrf2 (89,90), although dependence of these factors on MAPK as the intermediary has only thus far been demonstrated for Fra-1 (87). Phosphate-induced MAPK has been implicated in proliferation of the chondrogenic cell line ATDC5, possibly by activating cyclin D1 (79). Finally, activation of MAPK by phosphate stimulates apoptosis of hypertrophic chondrocytes (91), which also requires changes of the mitochondrial membrane potential and activation of caspase-9 (92). Conversely, inhibition of phosphate uptake or phosphate restriction prevent apoptosis of hypertrophic chondrocytes *in vitro* (85,93,94), and lead to a 2.5-fold increase in parathyroid hormone-related protein mRNA expression pointing to an important role for phosphate in regulating growth plate maturation (92). Both effects may explain expansion of the growth plates in the growing skeleton *in vivo*, for example in children with hypophosphatemic rickets (95).

Endocrine effects of phosphate

1. Human phosphate homeostasis—Over the last two decades, information derived from genetic analyses of familial disorders has led to the discovery of novel genes involved in the regulation of phosphate homeostasis, which in contrast to the regulation of calcium homeostasis (96,97), remains less well understood to date. Among these novel genes is fibroblast growth factor 23 (*FGF23*), named after its similarity to members of the fibroblast growth factor family. Different from most other members of this family, it is a circulating hormone and acts at the level of the kidney to regulate phosphate reabsorption (98). *FGF23* is produced by osteocytes and osteoblasts in bone and up-regulated by an increase in dietary phosphate intake and the active form of vitamin D, 1,25(OH)₂D, while it is down-regulated, through yet unknown mechanisms, by *PHEX*, *DMP1*, *ENPP1* and probably several additional proteins (Fig. 2) (99). *FGF23* acts through one or more FGF receptors, with Klotho as co-receptor (100), to reduce renal phosphate re-absorption (5,101,102), to decrease circulating 1,25(OH)₂D levels, and possibly to inhibit PTH secretion by the parathyroid glands. Its net effect is to lower the serum phosphate concentration. PTH on the other hand acts, like *FGF23*, to decrease renal phosphate re-absorption and thus also reduces the serum phosphate concentration. In contrast to *FGF23*, however, PTH stimulates renal 1-alpha hydroxylase and thus increases serum 1,25(OH)₂D levels. Serum phosphate feeds back to stimulate *FGF23* and PTH secretion (see below). It also appears to be sensed in the

intestinal lumen to regulate renal retention of phosphate independent of FGF23 and PTH, which may involve novel, yet to be discovered factors (103). Through its effect on the regulation of FGF23, it also reduces 1,25(OH)₂D levels (104), although serum phosphorus may also have direct effects on 1-alpha-hydroxylase and/or 24-hydroxylase (105). 1,25(OH)₂D acts through VDR/RXR heterodimers to enhance the intestinal absorption of phosphate (106) and to stimulate FGF23 synthesis and secretion by osteocytes; it furthermore inhibits PTH synthesis and secretion by the parathyroid glands. The net 1,25(OH)₂D effect is an increase in the serum phosphate concentration. For detailed discussion of the receptors and signal transduction cascades for PTH, 1,25(OH)₂D, and FGF23 the reader is referred to several recent reviews (98,99,107–115).

2. Regulation of Parathyroid hormone secretion by phosphate—The major physiological role of the parathyroid glands is to function as a “calciostat” (116–119). Consequently, parathyroid hormone (PTH) secretion by the parathyroid glands is tightly regulated by extracellular calcium on a transcriptional and post-transcriptional level. Similarly, 1,25(OH)₂D suppresses *PTH* gene expression via vitamin D responsive elements in the PTH promoter (120). Acute infusion of phosphate has little effect on PTH secretion in dogs (121) and cows (118). However, chronic elevation of serum phosphate stimulates PTH secretion by direct and indirect mechanisms: persistent hyperphosphatemia stimulates PTH-secretion presumably by lowering extracellular calcium (122,123), while hypophosphatemia suppresses PTH-secretion indirectly by up-regulation of 1,25(OH)₂D. Up-regulation of 1,25(OH)₂D production also induces of FGF23 synthesis, which acts at the parathyroids to suppress PTH mRNA synthesis (as already mentioned above) and secretion *in vitro* and *in vivo* in an alpha klotho (KL)-dependent fashion (124–127). Finally, KL may also have an FGF23-independent role by facilitating PTH-secretion through maintenance of membrane Na/K-ATPase activity in the setting of hypocalcemia and KL null mice are thus desensitized to hypocalcemic stress (128).

In addition to these indirect effects, phosphate directly acts on the parathyroids to stimulate PTH synthesis through posttranscriptional mechanisms, which have been elucidated in recent years. Using Northwestern blot analysis, RNA electrophoretic mobility shift and affinity cross-linking studies of parathyroid extracts, cytosolic transacting factors were identified that bind to a 63 bp cis-acting instability element in the PTH mRNA 3'-untranslated region (UTR) (122,129) (Fig. 3). It appears that there is a balanced interaction of the PTH mRNA with the stabilizing proteins AUF1 (AU-rich element binding protein, isoforms p37, p40, p42 and p45) and Unr (upstream of N-ras) (130) and the destabilizing protein KSRP (K-homology splicing regulator protein) *in vivo* (131). In the setting of hypocalcemia or chronic kidney disease the peptidyl-prolyl isomerase Pin1 is inactive (132), resulting in KSRP phosphorylation and hence its inactivation. This presumably allows AUF1 and Unr to bind the PTH mRNA 3' UTR ARE with a greater affinity, leading to increased PTH mRNA stability. Conversely, hypercalcemia and hypophosphatemia lead to destabilization of the PTH mRNA, which then is targeted for degradation by the exosome. Because parathyroid cells that sense phosphate, as they do *in vivo*, have not been established as stable cell lines, the mechanistic links between the regulation of PTH mRNA stability by phosphate *in vivo* and the Pin1/KSRP pathway remain to be established.

3. 1-alpha hydroxylase regulation by phosphate—Cholecalciferol is generated from its precursors 7-dehydrocholesterol and ergosterol in the skin, subjected to 25-hydroxylation in the liver and converted to the active 1,25-dihydroxycholecalciferol (1,25(OH)₂D) in the kidney (133,134). 1-alpha-hydroxylation in the kidney is tightly regulated. It is induced by PTH, hypocalcemia and hypophosphatemia, which all appear to induce expression of *CYP27B1*, the gene encoding 1-alpha hydroxylase (135) (Fig. 4). FGF23, hypercalcemia and hypophosphatemia, on the other hand, reduce *CYP27B1* expression (135,136). Also FGF7

and sFRP-4 appear to inhibit synthesis of 1,25(OH)₂D (137,138). FGF23 and 1,25(OH)₂D also increase renal CYP24 activity (136,139,140), which converts 25-OH-vitamin D and 1,25(OH)₂D into inactive metabolites. It will be of interest to elucidate the upstream sensing mechanism and whether phosphate regulates CYP27B1 at a transcriptional or posttranscriptional level, as these two events are not properly understood.

4. Regulation of FGF23 secretion by phosphate—The main sources of FGF23 are osteocytes and osteoblasts in the skeleton (141). The phosphate-regulating gene with homologies to endopeptidases on the X chromosome (PHEX) and dentin matrix protein 1 (DMP1), bone-specific proteins which were discovered in genome-wide linkage studies of hypophosphatemic disorders (108,142), suppress expression of FGF23 in bone most likely through indirect mechanisms (99). Intact DMP1 is cleaved into a 35 and a 57 kDa fragment, possibly by bone morphogenic protein 1 (BMP1) (143), which, in turn, is activated by a complex consisting of the subtilisin propeptide convertase SPC2 and the co-activator 7B2 (144). Transgenic over-expression of the C-terminal 57 kDa DMP1 fragment is both necessary and sufficient to rescue the bone phenotype (and probably the hypophosphatemia) resulting from increased FGF23 secretion in *Dmp1*-null mice (145). This 57 kDa DMP1 fragment appears to have nuclear effects, which may be required for suppression and/or feedback regulation of FGF23 gene transcription and/or FGF23 secretion (145,146). Recently, ecto-nucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1) was found to be another negative regulator of FGF23 secretion. ENPP1 is a membrane-bound ecto-enzyme responsible for the generation of the mineralization inhibitor pyrophosphate (PPi) (147). Loss-of function mutations in this enzyme can cause generalized arterial calcifications of infancy (GACI) (148,149) and/or hypophosphatemic rickets due to FGF23-dependent renal phosphate-wasting (150,151). FGF23 excess may be directly related to lack of PPi production, or may be due to accumulation of precursors of PPi, such as ATP in the extracellular space. However, presence of mild hyperphosphatemia in individuals and carriers suffering from hypophosphatasia, which is caused by loss-of-function mutations in the PPi-degrading enzyme, namely tissue non-specific alkaline phosphatase (TNALP) (152), suggests that PPi is the intermediary suppressing FGF23 production.

In contrast, dietary phosphate and serum 1,25(OH)₂D stimulate FGF23 synthesis in human (153) (154,155) or animal studies (156); both factors appear to regulate FGF23 expression independently from each other. For example, injection of 1,25-dihydroxyvitamin D₃ increases serum FGF23 levels within hours in rodents without significant increase in serum phosphate levels, indicating that vitamin D can increase FGF23 independently of phosphate (156). The effect of 1,25-dihydroxyvitamin D₃ is via its nuclear vitamin D receptor (VDR), which heterodimerizes with RXR, another nuclear receptor. The VDR-RXR heterodimer in turn binds to the promoter region of the FGF23 gene and transactivates its expression (109). Similarly, phosphate positively regulates FGF23 expression, although the exact mechanisms need to be defined. VDR-deficient mice have low serum levels of phosphate and FGF23, but when placed on a calcium and phosphate-rich “rescue” diet serum FGF23 levels are restored to normal, indicating that phosphate can increase FGF23 independent of the actions of vitamin D (157).

Due to the lack of suitable *in vitro* cell culture models, which show regulation of FGF23 secretion by phosphate, it remains unclear, whether the *in vivo* effects of phosphate on FGF23 transcription and/or secretion are cell autonomous or mediated via intermediary factors. Insights from cell lines transfected with plasmids encoding the full-length human hormone indicate that FGF23 is subjected to post-translational modification, and that this modification may be regulated by phosphate (Fig. 5): After the cleavage and removal of the signal sequence comprising 24 amino acids, FGF23(25–251) is O-glycosylated by UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyl-transferase 3

(GALNT3). O-glycosylation is essential for secretion of FGF23 by CHO cells (158). Similar observations are made for the secretion of FGF7 by human embryonic kidney cells (HEK293) (159). Mutations that impair O-glycosylation of FGF23 lead to hypophosphatemic familial tumoral calcinosis in humans (160,161) and similar observations are made in mice (162) due to the lack of bioactive FGF23. Expression of GALNT3 appears to be stimulated by extracellular phosphate and is suppressed by extracellular calcium and 1,25(OH)₂D in HEK293 cells (159). It also appears to be stimulated by cAMP-mediated mechanisms *in vitro* (163) and by fibrous dysplastic lesions that are caused by gain-of-function mutations of Gs- α *in vivo* (164). This suggests that GALNT3 may be an important component of the regulatory mechanism of FGF23 secretion by phosphate and cAMP.

Summary and outlook

Phosphate sensing in bacteria and yeast requires binding and cellular uptake of phosphate by transporters of the ABC and MFS superfamilies, respectively. Intracellular phosphate acts to negatively regulate histidine or cyclin-dependent kinases in these species. These kinases, in turn, control specialized transcription factors that are required for the expression of phosphate-scavenging genes, which are collectively referred to as Pho-regulon, and encode secreted phosphatases, phosphate transporters, along with members of the phosphate signal transduction cascade. Database searches based on sequence homology have so far been unsuccessful in identifying metazoan orthologs of the bacterial and yeast phosphate sensors and the Pho-regulon. However, there is growing evidence indicating that binding and cellular uptake of phosphate by specialized sodium-phosphate transporters is required also for phosphate effects in mammalian cells. This suggests that similar processes govern phosphate sensing in higher species. Elevated intracellular phosphate leads to the activation of MAPK, which is required for the regulation of gene expression and apoptosis by phosphate in mammalian cells. Furthermore, phosphate appears to have post-transcriptional and post-translational effects on PTH mRNA stability and O-glycosylation of FGF23 protein, respectively, two important endocrine regulators of phosphate homeostasis. We currently perform functional screens using genome-wide siRNA technology to identify components of the mammalian phosphate-sensing pathway. An important unanswered question is whether the regulators of the metabolic functions of intracellular phosphate and the regulators of the extracellular functions of phosphate are similar. For this purpose, generation of PTH-, FGF23- and CYP27B1 producing cell lines will be helpful to further characterize the transcriptional, post-transcriptional and post-translational control of these hormones by phosphate.

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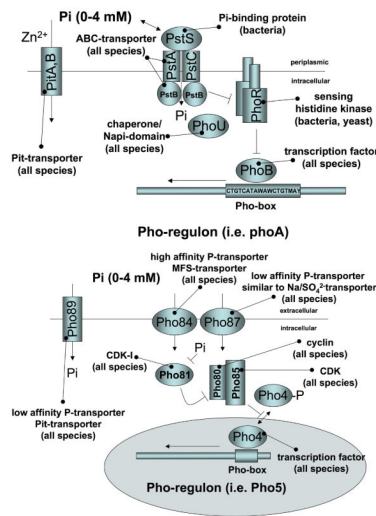
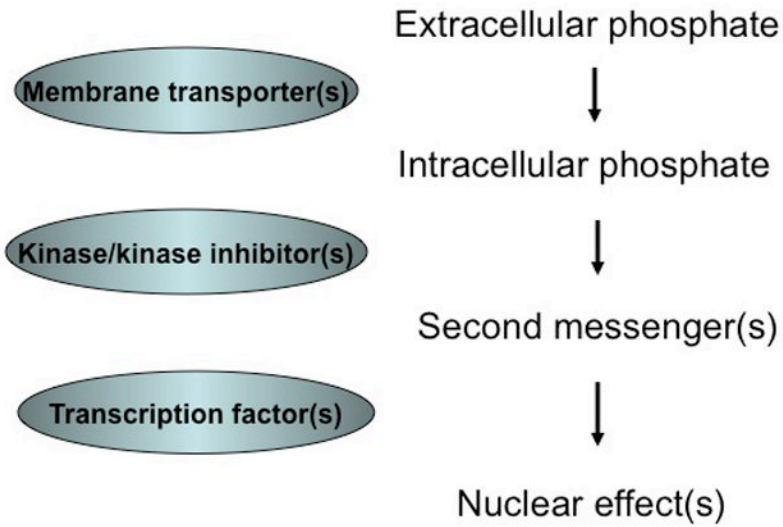
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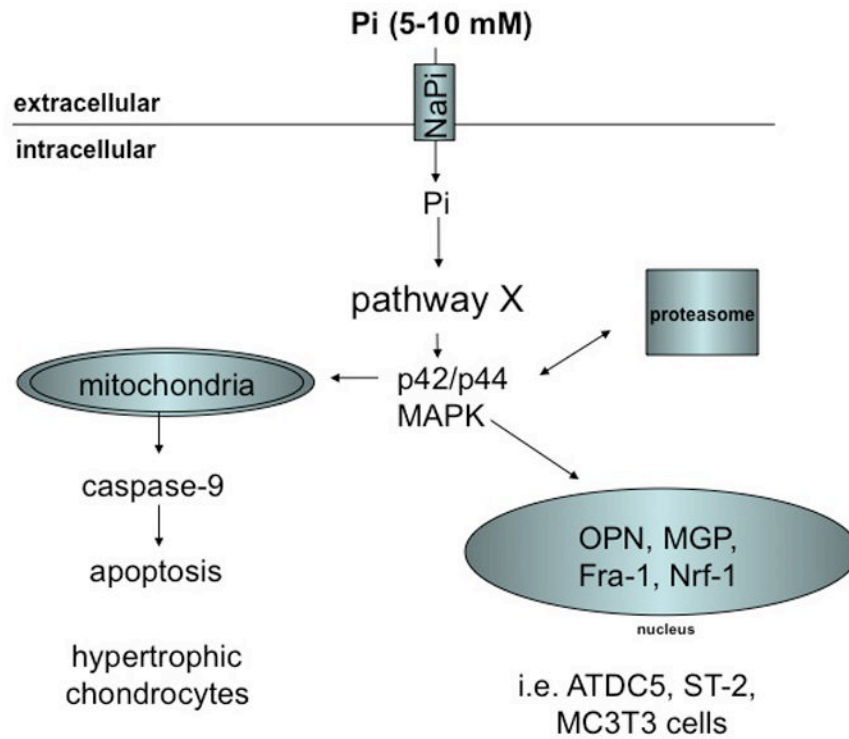


Fig. 1.

Fig. 1A: An evolutionarily conserved mechanism of phosphate sensing

Fig. 1B: Bacterial phosphate sensing

Modified from: (22), see table 1 and text for an explanation of the abbreviations

Fig. 1C: Yeast phosphate sensing

Modified from: (29), see table 1 and text for an explanation of the abbreviations

Fig. 1D: Regulation of MAPK and gene expression by phosphate in murine and human cell lines

See text for an explanation of the abbreviations

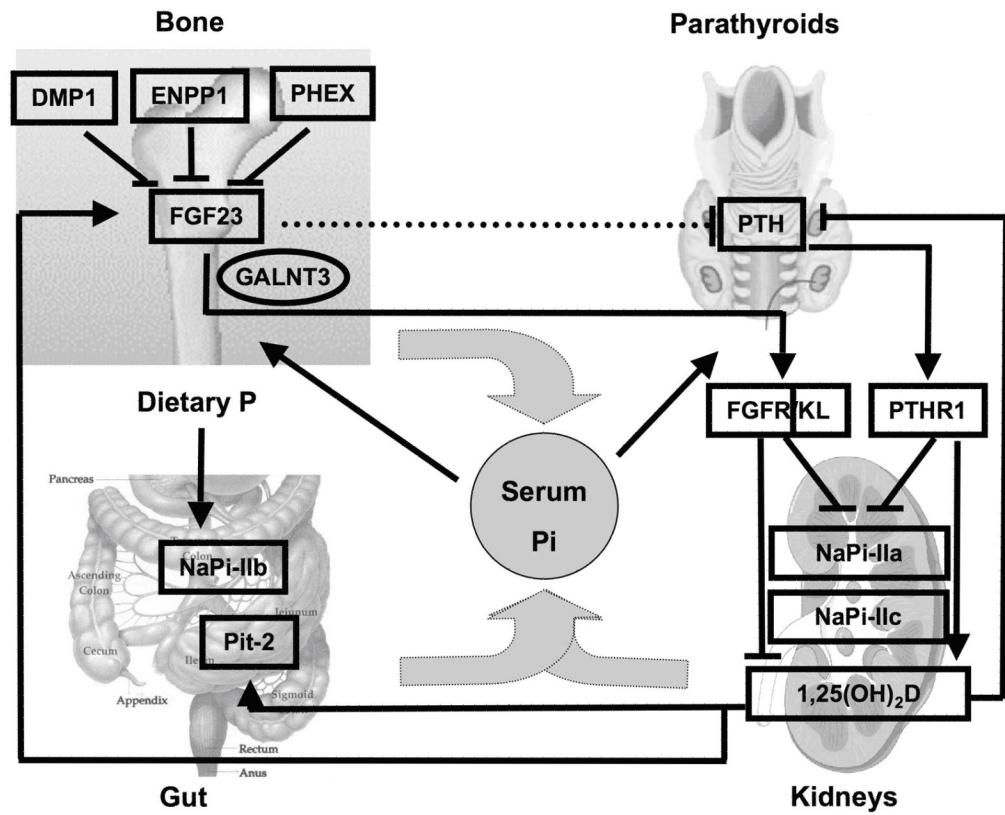


Fig. 2. Endocrine regulation of mammalian phosphate homeostasis
 Modified from: (115), see text for an explanation of the abbreviations

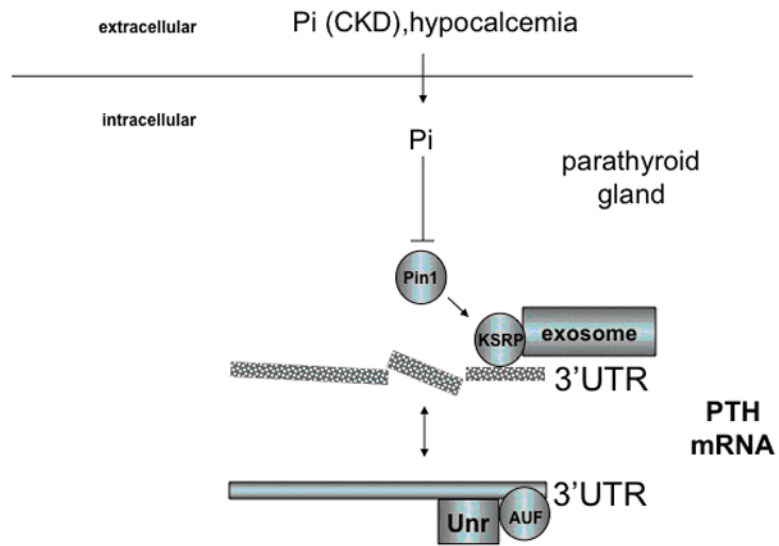


Fig. 3.
 Regulation of PTH mRNA stability by phosphate
 Modified from: (132), see text for an explanation of the abbreviations

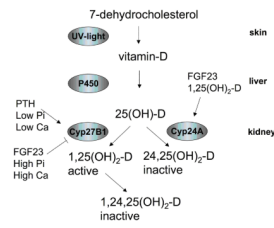


Fig. 4.
 Regulation of 1-alpha hydroxylase by phosphate
 Modified from: (133), see text for an explanation of the abbreviations

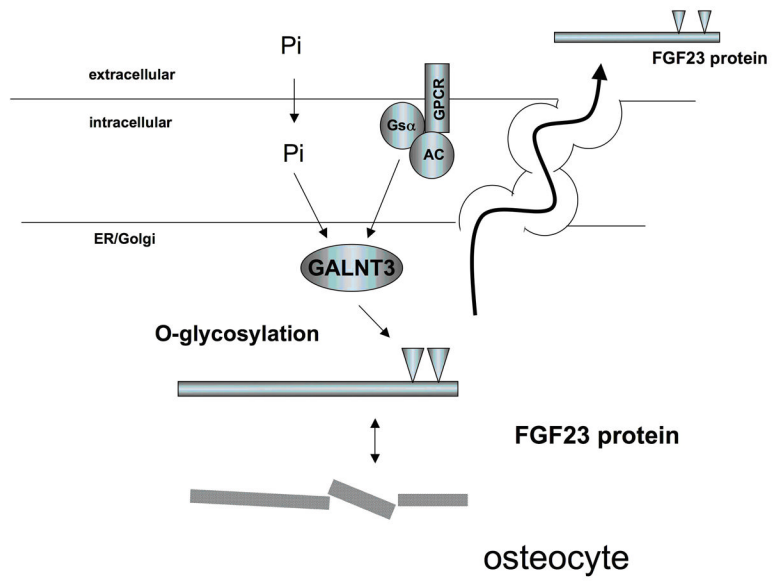


Fig. 5.
 Regulation of FGF23 secretion by phosphate
 Modified from: (159), (163), see text for an explanation of the abbreviations

Table 1

Molecular components of the bacterial, and yeast phosphate sensor

Name	Accession	Species	Function
phoB	ECK0393	<i>E. coli</i> K-12	DNA-binding response regulator
phoR	ECK0394	<i>E. coli</i> K-12	Sensory histidine kinase
phoU	ECK3717	<i>E. coli</i> K-12	Chaperone-like PhoR/PhoB inhibitory protein
pstA	ECK3719	<i>E. coli</i> K-12	Phosphate transporter subunit, membrane component
pstB	ECK3718	<i>E. coli</i> K-12	Phosphate transporter subunit, ATP-binding component
pstC	ECK3720	<i>E. coli</i> K-12	Phosphate subunit, membrane component
pstS	ECK3721	<i>E. coli</i> K-12	Phosphate periplasmic-binding component
PHO80	YOL001 W	<i>S. cerevisiae</i>	Cyclin: inhibitor of Pho4p
PHO81	YGR233C	<i>S. cerevisiae</i>	Cyclin-dependent protein kinase inhibitor
PHO85	YPL031C	<i>S. cerevisiae</i>	Cyclin-dependent protein kinase regulator
PHO4	YFR034C	<i>S. cerevisiae</i>	DNA-binding transcriptional activator
PHO84	YML123C	<i>S. cerevisiae</i>	MFS Pi transporter (H ⁺ -coupled)
PHO89	YBR296C	<i>S. cerevisiae</i>	Pi transporter (Na ⁺ -coupled)
PHO90	YJL198 W	<i>S. cerevisiae</i>	Putative Pi transporter
PHO91	YNR013C	<i>S. cerevisiae</i>	Putative Pi transporter
PHO87	YCR037C	<i>S. cerevisiae</i>	Pi transporter-associated

After: (21) and (30)