

Review Article

Nephrolithiasis: Molecular Mechanism of Renal Stone Formation and the Critical Role Played by Modulators

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Urinary stone disease is an ailment that has afflicted human kind for many centuries. Nephrolithiasis is a significant clinical problem in everyday practice with a subsequent burden for the health system. Nephrolithiasis remains a chronic disease and our fundamental understanding of the pathogenesis of stones as well as their prevention and cure still remains rudimentary. Regardless of the fact that supersaturation of stone-forming salts in urine is essential, abundance of these salts by itself will not always result in stone formation. The pathogenesis of calcium oxalate stone formation is a multistep process and essentially includes nucleation, crystal growth, crystal aggregation, and crystal retention. Various substances in the body have an effect on one or more of the above stone-forming processes, thereby influencing a person's ability to promote or prevent stone formation. Promoters facilitate the stone formation while inhibitors prevent it. Besides low urine volume and low urine pH, high calcium, sodium, oxalate and urate are also known to promote calcium oxalate stone formation. Many inorganic (citrate, magnesium) and organic substances (nephrocalcin, urinary prothrombin fragment-1, osteopontin) are known to inhibit stone formation. This review presents a comprehensive account of the mechanism of renal stone formation and the role of inhibitors/promoters in calcium oxalate crystallisation.

1. Introduction

Renal stones have afflicted humans for millennia. Many researchers are attempting to elucidate the mechanism of CaOx renal stone formation. Archeological findings give profound evidence that humans have suffered from kidney and bladder stones for centuries [1]. The risk of developing urolithiasis in adults appears to be higher in the western hemisphere (5–9% in Europe, 12% in Canada, and 13–15% in the USA) than in the eastern hemisphere (1–5%), although the highest risks have been reported in some Asian countries such as Saudi Arabia (20.1%) with lifetime recurrence rates of upto 50% [2]. The interval between recurrences is variable, with approximately 10% within one year, 35% in five years, and 50% by 10 years [3]. However, approximately 75% of stones are primarily calcium oxalate, but up to 50% of these include calcium hydroxyl phosphate (brushite or calcium hydroxyapatite) in trace or greater amounts; 10–20% are

composed of magnesium ammonium phosphate (struvite or triple phosphate); 5% are composed of urate; and 1–2% are composed of cystine [4, 5]. With its multifactor etiology and high rate of recurrences, urinary tract stone disease provides a medical challenge [6]. There is thus a pressing need to prevent this disease and its recurrence. The physiochemical mechanism of stone formation via precipitation, growth, aggregation, and concretion of various modulators in urine is represented in Figure 1. In addition, some researchers have recently emphasized that the interaction between crystals and renal tubular epithelial cells, including the adhesion or endocytosis of crystals by cells, is an important factor in stone formation [7, 8]. Long-standing interest in the possible role of macromolecules in nephrolithiasis stems from the observation that all human kidney stones consist of a complex amalgam of mineral and organic material [9]. The study of stone matrix has come a long way in recent years, but the wealth of knowledge we have gained has been offset

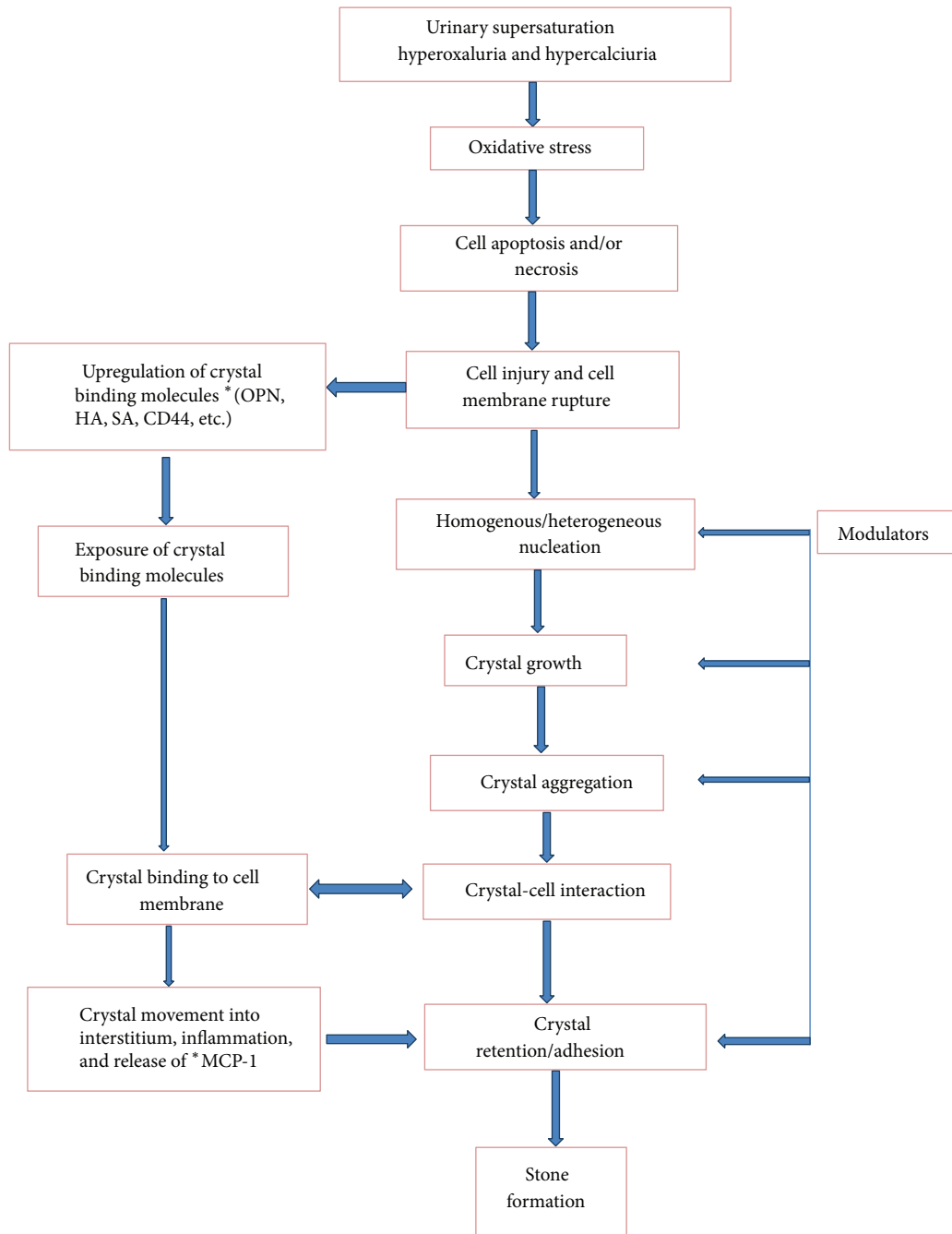


FIGURE 1: Schematic representation of various cellular and extracellular events during stone formation. * (OPN: osteopontin, HA: hyaluronic acid, SA: sialic acid, MCP-1: monocyte chemoattractant protein-1.)

to a large extent by conflicting findings, some of which have simply served to deepen the mystery of the role of matrix in stone formation. New technology has enabled us to strip macromolecules of their anonymity so that now we can identify individual components of matrix, but in every case we cannot say with real certainty just why they are there whether they are good, bad, or indifferent towards the crystallisation process. Perhaps the major reason for this is the use of inappropriate methodology for testing the effects of urine and matrix macromolecules on crystallization

processes. Since we are only now equipped with the requisite tools to identify individual matrix constituents, to some extent we may consider the study of stone matrix just beginning. So it is important at the outset to avoid a problem that has tended to plague the study of proteins. As each new component of matrix is added to the list it is becoming increasingly apparent that there is no single, magic ingredient that alone will carry the blame for the fact that some of us suffer from stones, or take the credit for the fact that the majority of us, happily, do not. Every component of matrix

is potentially an active protagonist in stone pathogenesis until proven otherwise. Doyle et al. reasoned that the study of crystals enabled the study of urinary proteins directly involved in the crucial crystal nucleation phase of stone formation, free of any macromolecular contaminants that might be introduced into a stone by cellular injury [10]. Adopting an approach, Morse and Resnick found that despite the enormous array of proteins present in urine, the crystals precipitated from it contained relatively few proteins [11]. However, although the presence of these proteins may imply that they fulfill some function in stone formation, it is equally possible that their inclusion in the stone structure may simply have been fortuitous or may have resulted from the injurious effects of the stone itself. Many proteins have been reported to be from the renal stone matrix, but the study of function of only few has been done. The common occurrence of urine supersaturation and crystalluria has prompted studies on modulators of the processes beyond supersaturation. To reduce the occurrence of urolithiasis, elucidation of the mechanism of lithogenesis through fundamental research is essential. This review summarises what is currently known or is hypothesised about the influences of urinary macromolecules, especially proteins, on the formation of calcium oxalate crystals. Although a list of proteins is provided that have either been detected in stones or have been implicated by virtue of their effects on crystallization, only a select handful, which have been intensively studied, have been singled out for individual discussion.

2. The Stone

The main components of the stone matrix account for 2-3% of their total dry weight and consists of macromolecules generally present in the urine [12, 13]. They are described by Boyce as 64% protein, 9.6% nonamino sugars, 5% hexosamine as glucosamine, 10% bound water, and the remainder as inorganic ash [14]. Although not detected by Boyce, lipids have also been shown to be significant components of stone matrix [15]. Nonetheless, proteins comprise the major part of matrix, an observation confirmed by Sugimoto et al. [16]. It was inevitable therefore that protein would tend to dominate the study of matrix, and consequently, considerably more is known about them than the other two principal groups, namely, lipids and glycosaminoglycans (GAGs).

Boyce [14] defined and established the importance of stone matrix in nephrolithiasis, proposing that the matrix actively participates in the assembly of kidney stones. In their view, the matrix acts as a template and controls crystallization within its bounds. An opposite hypothesis was advanced by Vermeulen et al., who viewed the matrix and its ubiquitous presence as merely coincidental, because stones form by crystallization in urine in the presence of large macromolecules [17, 18]. Proteins formed a discontinuous coat around the crystals ranging in thickness from 10 to 20 nm. It has been suggested that newly formed crystals with a macromolecular coat are less likely to dissolve during the routine urinary ionic and pH changes and therein may lay the importance of matrix in stone formation [19].

Urinary molecule that affects the mass of CaOx deposited from urine or the size of the crystal particles produced has the potential to influence the likelihood that crystalline particles are retained in the renal collecting system, and thereby, the development of stone disease [20]. Some promote CaOx crystal nucleation in inorganic solutions and in concentrated whole urine [21]; others like albumin appear to exert no significant effect on crystallization in urine [22], but are, nonetheless, found in stones. Many studies, have shown that a variety of urinary proteins inhibit CaOx crystal growth [23] and aggregation [22]. More surprisingly, some can actually do more than one of these. Tamm-Horsfall mucoprotein can inhibit CaOx crystal aggregation, but can also act as a promoter of crystal deposition, depending upon experimental conditions [24]. It has also been demonstrated that polyelectrolytes and proteins that inhibit crystallization in solution can act as promoters when they are immobilized on to surfaces [25]. And the issue is further complicated by the fact that the potency of urinary macromolecules increases inversely in relation to the prevailing ionic strength [26]. The effects of macromolecules are manifold, unpredictable, and paradoxical. Above all, they are certainly not amenable to generalization; knowledge of their roles in stone formation will therefore be obtained only by laboriously teasing out the information for each individual macromolecule. And in the following sections, that is what we will attempt to do.

3. Mechanism of Calcium Oxalate Renal Stone Formation: Urinary Supersaturation and Crystallization

The formation of renal stones is a consequence of increased urinary supersaturation with subsequent formation of crystalline particles. Supersaturation is the driving force for crystallization in solutions like urine. When a salt is added to a solvent it dissolves in the solvent until a particular concentration is reached, beyond which no further dissolution is possible. At this point, the solvent is said to be saturated with the salt. If more salt is added it crystallizes in solution, provided the temperature and pH are unchanged. The concentration at which saturation is reached and crystallization begins is called the thermodynamic solubility product (K_{sp}). If inhibitors of crystallization were not able to act, the final result will be nephrolithiasis [27]. Inhibitors allow higher concentration of calcium salts to be held in solution than in pure solvents. Urine is thus metastable with respect to calcium salts. Indeed, stone formers tend to excrete urine that is more supersaturated than that of nonstone formers [13, 28]. It has been suggested that with a transit time across the kidney of 5 to 10 min, residence time is too short for crystals to nucleate and grow large enough to be trapped in a normal person [29].

3.1. Crystal Nucleation. The initial step in the transformation from a liquid to a solid phase in a supersaturated solution is called nucleation. This process begins with the combination of stone salts in solution into loose clusters that may increase in size by addition of new components or clusters [30].

Nuclei form the first crystals that do not dissolve and have a characteristic lattice pattern. In urine, nuclei usually form on existing surfaces, a process called heterogeneous nucleation. Epithelial cells, urinary casts, RBCs, and other crystals can act as nucleating centers in urine. The saturation necessary for heterogeneous nucleation is much less than for homogeneous nucleation [31]. Once a nucleus is created and principally if it is anchored, crystallization can occur at lower chemical pressures than required for the formation of the initial nucleus. Renal tubular cell injury can promote crystallization of CaOx crystals by providing substances for their heterogeneous nucleation. *In vitro* cell degradation following renal tubular cell injury produces numerous membrane vesicles, which have been shown to be good nucleators of calcium crystals. *In vivo* crystals observed in the renal tubules of hyperoxaluric rats are always associated with cellular degradation products [32, 33].

3.2. Crystal Growth. Once a crystal nucleus has achieved a critical size and relative supersaturation remains above one, the overall free energy is decreased by adding new crystal components to the nucleus. This process is called crystal growth. Crystal growth is one of the prerequisites for particle formation and thus for stone formation [34]. In each step of stone formation, crystal growth and aggregation have important functions. Honda et al. reported that the crystal surface binding substance, which is found in CaOx crystals generated from whole human urine, is a strong inhibitor of CaOx crystal growth and contains proteins like human serum albumin, retinol binding protein, transferrin, Tamm-Horsfall glycoprotein, and prothrombin [35]. However, it has been suggested that the importance of crystal growth for CaOx, the most abundant stone component, is questionable. Since the rate of CaOx crystal growth is low and the transit time of tubular fluid through the kidney amounts to only several minutes, it has been calculated that the probability of a single particle achieving a pathophysiologically relevant size by the process of crystal growth alone is extremely low, even if growth proceeds at an uninhibited rate of 2 mm per minute [29]. The inhibitory effect of fibronectin (FN), distributed throughout the extracellular matrix and body fluids, on CaOx crystal growth is small, considering the quantity normally excreted.

3.3. Crystal Aggregation. The process whereby crystals in solution stick together to form larger particles is called aggregation. Some researchers have proposed that crystal aggregation is the most important step in stone formation. Although crystal growth is definitely a step in CaOx renal stone formation, the process of growth is so slow that crystals cannot become large enough to obstruct the renal tubules and be retained there by this mechanism alone, as several minutes are required for the tubular fluid to pass through the kidney. For this reason, the more critical step is thought to be crystal aggregation. All models of CaOx urolithiasis concede that crystal aggregation is probably involved in crystal retention within the kidneys, since aggregation of crystals can have a considerable effect on particle size and aggregated crystals

are commonly found in urine and renal stones [36]. Crystal aggregation is promoted by viscous binding, implying that crystal-foreign compounds with multiple binding sites, such as abnormally self-aggregating Tamm-Horsfall glycoprotein or other macromolecules, attach to crystal surfaces and act as a kind of glue [37].

3.4. Crystal-Cell Interaction. The mechanisms of crystal-cell interaction are thought to be very complex, and many of them remain unexplored. Crystallization is caused by the condition of urinary supersaturation. Then, the crystals that have formed attach to renal tubular epithelial cells and are taken into them. The process of attachment or endocytosis of crystals to renal tubular cells is what is generally meant by crystal-cell interactions. These structural and functional studies of crystal-cell interactions in culture indicate that COM crystals rapidly adhere to microvilli on the cell surface and are subsequently internalized. Khan et al. concluded that crystal-cell interaction is an essential element in the development of urinary stone disease [38]. Kohjimoto et al. reported that crystal-cell interactions may be among the earliest processes in the formation of kidney stones [39]. Finlayson and Reid hypothesized that it was unlikely that CaOx crystals could grow large enough to be retained within the renal tubules, and that attachment of crystals was necessary for initiation of stone formation [29]. There have been many reports on crystal attachment. Animal model and tissue culture studies have provided evidence for crystal retention within the kidneys via attachment to renal epithelial cells. Kok and Khan observed crystal attachment to the brush border of proximal tubules in rats. Experimental induction of CaOx urolithiasis starts with hyperoxaluria followed by crystalluria and deposition in the kidney [36, 40]. Some urinary macromolecules have an inhibitory effect on CaOx crystal attachment. Lieske et al. reported that diverse polyanionic molecules in urine, such as specific glycosaminoglycans, glycoproteins, and citrate, block the binding of COM crystals to the cell membrane. One common feature of molecules that inhibit COM crystal adhesion to cells is their polyanionic character. They mentioned that although polyanions present in tubular fluid may coat crystals and thereby inhibit their adhesion to tubular cells, a distinct and separate set of signals acts on the cells to regulate their response to crystals that do bind [41, 42].

3.5. Endocytosis of CaOx Crystals by Renal Tubular Epithelial Cells. Many studies of the endocytosis of crystals by cells have been reported. Lieske et al. noted engulfment of crystals into tubular epithelial cells and cell proliferation in a transplanted kidney in a patient with primary hyperoxaluria [43] and confirmed this phenomenon experimentally using calcium-containing crystals and tubular cells in culture [44]. Various substances have an inhibitory effect on CaOx crystal endocytosis. Tamm-Horsfall protein (THP) leads to [45], decreased COM crystal endocytosis by 34%, suggesting that THP in distal tubular fluid may block the uptake of COM crystals by cells of this portion of the nephron and thereby prevent renal crystal retention and stone formation [46].

The inhibitory effect of FN on CaOx crystal endocytosis was only 18.4% at the physiological concentration of excreted FN (0.5 mg/mL), though morphological examination revealed that FN clearly inhibited the endocytosis of crystals by renal tubular cells [47, 48]. Lieske and Toback reported that the internalization of CaOx crystals by BSC-1 and MDCK cells is a regulated event that can be modified by various signals [49]. In addition, they reported that the adsorption of nephrocalcin, a urinary glycoprotein of renal cell origin, to COM crystals prevented attachment of the crystal to the plasma membrane, engulfment, or both and thereby prevented mitogenic effects.

3.6. Relationship between Crystal-Cell Interaction and Renal Tubular Cell Injury. Some investigators have obtained evidence that oxalate and CaOx crystals may be injurious to renal tubular cells. Cultured renal tubular cells exhibited evidence of damage after exposure to CaOx crystals. Addition of CaOx crystals to monolayers of Madin-Darby canine kidney (MDCK) cells led to a marked increase in the release of lysosomal enzymes, prostaglandin E₂, and, to a lesser extent, cytosolic enzymes [40, 50]. In animal models of renal stone disease produced by the administration of high oxalate loads, the presence of CaOx crystals within the renal tubules is associated with renal tubular damage, as evidenced by enzymuria and the presence of membranous debris within the tubular lumina [51]. This membranous debris appears together with focal loss of the brush border from proximal tubular cells and the appearance of proximal tubular enzymes in the urine, suggesting that proximal tubular cells are the source of the membranous debris [51–53]. Thus, in this animal model of stone disease, CaOx crystals or the high concentrations of oxalate ion in proximal tubular fluid appear to be toxic for renal tubular epithelial cells.

Some reports have suggested the involvement of renal tubular epithelial cell injury in the crystal-cell interaction process. Wiessner et al. reported that individual cell injury and generalized cell monolayer injury result in the presentation of different cell surfaces, and that both types of injury result in increased affinity for crystal adhesion. They also stated that both mechanisms could be important, either independently or together, for the retention of microcrystals adhering to renal collecting duct cells in nephrolithiasis. Furthermore, they mentioned that the mechanism of adhesion of crystals to renal tubular cells is based on crystal interaction with basolateral or basement membrane components. These components may become exposed as a result of the loss of cell polarity seen in several disease states in association with tissue injury, ischemia in kidney tubules, microvillus inclusion disease, and polycystic kidney disease [54]. Injury to the renal tubular epithelial cells results in cellular degradation and the production of membranous vesicles. The crystals are either passed as crystalluria particles or are endocytosed by the epithelial cells to be processed by their lysosomal system or transported to the interstitium. CaOx crystal deposition in the kidneys upregulates the expression and/or synthesis of macromolecules that can promote inflammation and lead to fibrosis. Mild hyperoxaluria is a known risk factor for CaOx

uroolithiasis [55]. Mild hyperoxaluria promotes increased production of crystallization modulators, such as Sosteoportun, bikunin [56], and FN [57]. These macromolecules are involved in controlling not only crystal nucleation, growth, and aggregation, but also crystal interaction with the renal tubular epithelial cells and crystal retention within the kidney [9, 58].

4. Matrix Components

4.1. Lipids. The matrix of all stones examined to date, including struvite, uric acid, CaOx, and CaP, contains lipids [59]. Phospholipids account for 8.6% of the total lipid, which in turn represents approximately 10.25% of stone matrix [15]. Various identified phospholipids and glycolipids include sphingomyelin (SM), phosphatidylcholine (PC), phosphatidylethanolamine (PE), cardiolipin (CL), and trace amounts of phosphatidylserine (PS) in all stone matrices [60]. Occasionally, the stone matrix also contains phosphatidylinositol (PI), lyso-PC, lysophosphatidic acid (PA) and lyso-PE. In all stones glycolipids include gangliosides, sphingosine and glucocerebrosides. Lipids play a more active role since cell membranes [33, 61] and the lipids of CaOx stone matrix [59] can catalyse the nucleation of CaOx from a metastable solution. Cell membranes and their lipids play critical roles in the process of calcification. Particular membrane phospholipids promote the formation of calcium oxalate and calcium phosphate and become a part of the organic matrix of growing calcification [60].

4.2. Glycosaminoglycans (GAGs). The presence of GAGs in stone matrix was inferred by Boyce and Garvey as long ago as 1956 [62]. Nishio et al. reported that between 0.19 and 0.58% of a stone's weight consists of GAGs, thereby providing us with the evidence that GAGs may account for up to 20% of the weight of matrix [63]. This alone is sufficient to suggest that they may fulfill some function in stone formation.

GAGs occurring in the urine of normal individuals typically consist of 55% chondroitin sulphate (CS), 20% heparan sulphate (HS), 11% low sulphated CS, and 4–10% hyaluronic acid (HA) [64]. It is therefore somewhat surprising that only HS and, to a lesser extent, HA have been reported to be present in CaOx stones [63]. CS, the most abundant GAG in urine, though present in small amounts in magnesium ammonium phosphate and apatite stones has not been detected in CaOx stones [63, 65]. These results strongly suggest that the incorporation of GAGs into stones is a selective process, a notion supported by the finding that inclusion of GAGs into CaOx crystals freshly precipitated from human urine is also highly selective. Like stones, such crystals contain only HS [65]; CS is incorporated into CaOx crystals only in the absence of HA [66], indicating that they probably compete for the same binding sites on the crystal surface. Similar results have been reported for uric acid stones and crystals, with HS being the only GAG detected [67].

However, the simple fact of their presence in stones or crystals tells us nothing about the mechanism by which GAGs came to be there. However, recent evidence suggests

that urinary GAGs can fulfill both roles, promoting CaOx crystal nucleation and reducing the final size of the crystals produced, thereby lessening their chance of retention within the urinary tract [68]. On the basis of present evidence, it would appear that CS, though present in urine in larger quantities than HS, plays no significant role in CaOx crystallization or in stone formation. HS, on the other hand, may act as an inhibitor, although confirmation of such a role must await the results of further studies. What is quite clear, however, is that the routine measurement of total urinary GAGs excretion is unlikely to be of any practical benefit in the diagnosis and management of nephrolithiasis. With the benefit of hindsight, it is not surprising that comparisons of urinary GAG excretion in stone formers and normal subjects have produced conflicting findings [68–71].

4.3. Proteins. Despite the fact that stone matrix has been shown to contain an ever increasing list of proteins, in most cases it is not possible to say with any certainty why they might be there. One can speculate of course. For instance, the presence of superoxide dismutase may perhaps be explained by the fact that the enzyme acts as a protector of tissue damage by scavenging the toxic superoxide anion [72]. Could the enzyme's presence be explained by release of this radical in response to cellular injury caused by the kidney stone itself—an example of a macromolecule incorporated as a secondary matrix component? However, speculation alone will not unravel the mystery of why proteins are in stone matrix, but detailed study of individual proteins may. We will now discuss what is known about several urinary proteins that have been subjected to rigorous study because they have been found to occur in stones or because they have been isolated from urine and shown to influence the crystallization of CaOx. And we will begin with Tamm-Horsfall glycoprotein because it has the longest historical association with stones, and, as a consequence, has been subjected to the most intense experimental scrutiny. A detailed table (Table 1) has been provided to show the effect of the modulators (protein) on stone formation.

4.3.1. Tamm-Horsfall Protein (THP). The most extensively investigated urinary macromolecule in nephrolithiasis research Tamm Horsfall glycoprotein (THP), enjoys a distinct position, perhaps because it is the most abundant protein in human urine and was one of the first components of stone matrix to be identified by Boyce and Garvey [62]. THP is a renal protein of all placental invertebrates [73, 74]. It is known to have a monomeric molecular weight of 80 kDa. THP is present in urine in polymeric forms measuring up to several million Da. In humans, daily excretion ranges between 20 and 100 mg/day [75] with a daily urinary volume of 1.5 litres, and in rats it ranges between 552 and 2,865 μ g/day with a daily urinary volume of 16.5 mL [76]. It is its extraordinary ability to self-associate due to presence of carbohydrates in urine into large structures visible to the naked eye that probably accounts for its known effects on CaOx crystallization [77], and it is these effects to which we will now primarily confine our discussion. THP may be

involved in the pathogenesis of nephropathy, nephrolithiasis, and tubule interstitial nephritis [78]. Mo et al. by ablating the murine THP gene established that THP is on the first line of host defences against both renal stone formation and bacterial infection [79].

THP is often detected in stones, regardless of crystal components [80]. THP is absent from CaOx crystals precipitated from whole urine [10], which would seem to indicate that THP binds only weakly, if at all, to CaOx crystals. Since it has been accepted for some time that inhibitors act by binding to crystal surfaces, we might expect THP to be a poor inhibitor of CaOx crystallization—at least in urine, where stones form. The protein has been reported to act as an inhibitor [22, 24, 81–83] and a promoter [24, 84, 85] of crystallization. The picture is further complicated by the fact that conflicting findings were obtained in the only studies in which the effect of THP was tested in undiluted urine. Rose and Sulaiman [84] found that THP enhanced the deposition of CaOx crystals from urine concentrate by evaporation to high osmolalities, whereas Ryall et al. [22] and Grover et al. [83] found that the protein was a potent inhibitor of CaOx crystal aggregation, although having no effect on CaOx deposition. An explanation for these opposing findings is to be found in a study by Grover et al. [24] who tested the effect of THP in the experimental systems used by the two research groups and found that while THP undoubtedly promotes CaOx precipitation under conditions of high osmolality, where it also links CaOx crystals together into large, loosely connected agglomerates, it is a very effective inhibitor of crystal aggregation at more usual urinary concentrations. It is also apparent that THP inhibits crystal aggregation by steric hindrance rather than by binding to the crystal surfaces [22]; binding might therefore not be a prerequisite for inhibitory potency after all. Moreover, however potent an inhibitor it may be, it cannot account for the total inhibitory effect of urinary macromolecules on CaOx crystal aggregation in centrifuged and filtered urine [86], because it is removed from urine by centrifugation and filtration. Thus, there can be no doubt that other urinary macromolecules contribute to this inhibition [22]. A reflection of the disagreement surrounding the role of THP as a promoter or inhibitor, of CaOx crystallization is to be found in similar conflict relating to its urinary excretion. If indeed THP does play a directive role in stone formation, we might expect that its excretion would be different in stone formers and normal subjects. But it is not [87]. Contrary to this, rat model studies have provided controversial results for THP. One study shows decreased renal expression of THP during CaOx crystal deposition [88], while results of another study show upregulation of the THP gene [89]. However, it may be that stone formation is related more to the type of THP excreted than to the quantity. This fact led them to hypothesize that THP of stone formers is structurally different from that of the healthy subjects [90]. THP isolated from the urine of stone formers contained less carbohydrate (mainly sialic acid) than the THP obtained from control subjects [91]. Studies have also shown differences in sialic acid contents and surface charge between THP from stone formers and normal individuals. Isoelectric focussing (IEF) studies have shown that THP from healthy

TABLE 1: List of Urinary/Stone matrix protein modulators of crystallization in Nephrolithiasis.

S. no	Name of protein	Mol. Wt. (kDa)	pI	Role in crystallization (I: inhibitor/P: promoter)				References
				Nucleation	Growth	Aggregation	Adhesion	
1	Nephrocalcin (NC)	14	4.5–6.0	I	I	I	—	[95, 98, 116]
2	Tamm-Horsfall Protein (THP)	87	4.8	P	—	I/P	—	[45, 46, 79, 80, 117–121]
3	Osteopontin/Uropontin (OPN)	42–80	3.5	I	I	I	I/P	[80, 120–124]
4	Albumin	66.5	4.8	P	—	I	—	[80, 118, 120, 121, 125–127]
5	Urinary prothrombin fragment 1 (UPTF1)	31	5.0–5.4	I	I	I	—	[80, 123, 128–131]
6	Alpha-1-microglobulin Calgranulin	26	4.2	—	—	I	—	[126, 132]
7	S100A ₈	A-10.9	A-6.5	—	I	I	—	[80, 120, 121, 133–135]
	S100A ₉	B-13.2	B-5.7					
	S100A ₁₀	C-10.6	C-5.8					
8	Inter-alpha-inhibitor IαI	Heterotrimer 180–240	5.95	I	I	I	I	[136–138]
9	Bikunin	39	2.1	I	I	I	I	[139–141]
10	Renal lithostathine	23	4.2	—	I (CaCO ₃)	—	—	[117, 142–144]
11	α-Defensin	10.2	6.5	—	P	P	—	[121, 134]
12	Human phosphate cytidyltransferase 1, choline, beta	42	6.3	—	I	—	—	[145, 146]
13	Myeloperoxidase	83.9	9.19	—	P	P	—	[120, 121, 134]
14	Nucleolin	76	4.39	—	—	—	P	[120, 147]
15	Histone-lysine N methyltransferase	53	9.9	—	I	I	—	[148]
16	Inward rectifier K channel	44	5.84	—	I	I	—	[148]
17	Protein Wnt-2	42	9.06	—	I	I	—	[148]
18	Alpha-2HS glycoprotein	50	5.43	P	I	—	—	[120, 121, 123]
19	Crystal adhesion inhibitor (CAI)	39	—	—	—	—	I	[149]
20	Hyaluronic acid (HA)	50–800	8.6	—	—	—	P	[150–152]
21	Chondroitin sulphate (CS)	50	—	—	I	I	—	[66]
22	Heparin sulphate (HS)	16	—	—	I	—	—	[65, 66]
23	Human urinary trefoil factor 1	13.2	—	—	I	—	—	[153, 154]
24	Monocyte chemoattractant protein-1 (MCP 1)	5–20	—	—	—	—	P	[155, 156]
25	Annexin II	37	—	—	—	—	P	[157]
26	CD44	81.5	5.13	—	—	—	P	[151, 152]
27	Matrix Gla Protein (MGP)	10.6	—	—	I	—	I	[158–162]
28	Histone H1B	62	11.03	—	P	—	—	[163]
29	Fibronectin	230	5.39	—	—	I	I	[51, 68, 69]
30	Collagen	180	4.7–7.7	P	—	—	—	[121]

individuals has a pI value of approximately 3.5, while THP from recurrent stone formers has pI values between 4.5 and 6, and the two exhibit completely different IEF patterns [92].

Self-aggregation of THP may promote either heterogeneous nucleation or formation of a protein and crystalline mass large enough to block the tubular lumen. Further studies are still required to elucidate its real contribution, if any, to nephrolithiasis and its interaction, if any, with its urinary companions. And it is to those companions that we will now direct our attention.

4.3.2. Nephrocalcin (NC). Second to THP, nephrocalcin (NC) has been the most widely studied protein reported in the stone literature. In 1978, Nakagawa and his colleagues described it as an unidentified acidic polypeptide [93] and then for a number of years as a glycoprotein inhibitor of CaOx crystal growth [94–97]. In 1987, after the first report of its isolation from urine, the protein was named nephrocalcin [98]. NC holds a prominent position in urolithiasis research, having been claimed to be the principal inhibitor of CaOx crystallization in urine [95], its activity reportedly accounting for approximately 90% of urine's total inhibitory effect on CaOx crystallization [94, 95, 97]. The molecular weight of NC varies widely depending upon the state of aggregation of the protein, with the molecular weights of the monomer, dimer, trimer, and tetramer being reported as 14–15, 23–30, 45–48, and 60–68 kDa, respectively [94, 96]. There are at least four isoforms of nephrocalcin, that is, NC-A, NC-B, NC-C, and NC-D. Mustafi and Nakagawa explained mechanism of inhibition of COM crystal growth by NC and characterised the Ca²⁺-binding sites present in nephrocalcin [99]. Nakagawa, in 1997-described that nonstone-forming people excrete more NC-A and NC-B isoforms in urine, but more NC-C and NC-D isoforms were found in stone formers' urine. The organic matrix of calcium oxalate kidney stone was found to have greater quantities of NC-C and NC-D isoforms than those of NC-A and NC-B isoforms. Isoforms A and B changed their conformation upon Ca²⁺ binding, but there was no change in the conformation of C and D. All these observations suggest that isoforms A and B are strong inhibitors of calcium oxalate monohydrate (COM) crystal growth and aggregation, whereas isoforms C and D act as promoters for COM crystal growth [100].

The protein is located in the epithelium of the proximal tubules and thick ascending limb of the loops of Henle, in both human and mouse kidneys [101]. NC was originally isolated from human urine [93, 95–97] and has also been detected in tissue culture medium of human kidney cell lines [94, 102] and kidney stones [98, 103]. A glycoprotein, NC has been reported to occur in urine at concentrations ranging from 5 mg/L [102] to 16 mg/L [103] and to contain 2–3 residues of γ -carboxyglutamic acid (Gla) in its primary structure [94–96]. The Gla component confers the protein's potent ability to inhibit CaOx crystallization, previously reported to be deficient in this amino acid. A lack of Gla in NC isolated from kidney stones was suggested as the reason why the stones had formed [98].

Despite its long history, there has been no report in the literature of its primary amino acid sequence and the exact

nature of the protein remains unknown. Hochstrasser et al. suggested the identity of NC isolated from human urine with fragment HI-14 of the light chain (bikunin) of inter- α -trypsin inhibitor (ITI) [104]. They concluded that NC represents a portion of the bikunin chain of ITI.

The inhibitory activity of NC should now perhaps be reappraised, particularly since a recent paper by Worcester et al. reassessed its contribution to be no more than 16% [105]. Moreover, all existing estimates of the protein's inhibitory potency have been obtained from crystallization systems based on inorganic metastable solutions. Although NC is undoubtedly a potent inhibitor of CaOx deposition in an inorganic metastable solution, observations [106, 107] have confirmed using material tentatively identified as NC. It is becoming increasingly apparent that this potency is shared with a number of other urinary proteins, for example, uropontin, urinary prothrombin fragment 1, and UAP, and so forth.

4.3.3. Osteopontin (OPN). Osteopontin is a protein important in bone mineralization, where it is thought to anchor osteoblasts to bone [108]. Osteopontin is originally isolated from rat bone matrix as a 44 kDa phosphorylated protein. It is rich in acidic amino acids like serine, aspartic acid and glutamic acid, which are commonly found in proteins involved in biomineralization [109]. It has an amino acid sequence that serves as a recognition signal for interacting with cell-surface receptor molecules known as integrins, which are involved in cell adhesion [110], and is a member of a family of proteins rich in aspartic acid that have been shown *in vitro* to have stereospecific activity at the surface of crystals [111].

Osteopontin (OPN) is a negatively charged aspartic acid rich protein and is intimately involved in the regulation of both physiological and pathological mineralization. OPN is a phosphorylated protein of wide tissue distribution that is found in association with dystrophic calcification including in the organic matrix of kidney stones. OPN is synthesized within the kidney and is present in the human urine. The bone-derived and kidney-derived forms of this protein appear to be very similar in amino acid sequence. It is involved in various biological processes like inflammation, wound healing, cell survival, and leukocyte recruitment [112]. In 1992, Shiraga et al. reported the isolation from human urine of a protein which they called uropontin (UP) [113]. It was isolated by immune affinity chromatography using a monoclonal rat antibody and had exhibited maximal inhibition of CaOx crystal growth in an inorganic metastable solution. Total amino acid analysis of OPN revealed a high proportion of aspartic acid residues [113]. Molecular weight estimations of UP, which has an apparent molecular weight of 50 kDa in 16% SDS-PAGE gels and 72 kDa in 5–18% gradient gels, were also similar to UP [109]. These similarities, together with identical nucleotide sequences of cDNAs encoding UP from human kidney [113] and bone [114], indicate that UP is not a distinct protein, but rather a urinary form of OPN. OPN has been referred to by a variety of names including secreted phosphoprotein [115], 44 kDa bone phosphoprotein [109], and uropontin.

The distribution of OPN in humans was recently reported by Brown et al. [164]. UP is present in normal adult urine at a mean concentration of approximately 6×10^{-8} molar [165]. The protein is widely distributed on the luminal surfaces of specific epithelial cells in the gall bladder, pancreas, urinary tract, reproductive tracts, gastrointestinal tract, lung, breast, salivary glands, and sweat glands. OPN was specifically found in the cytoplasm of many epithelial cells of the distal tubules and collecting ducts. Others have reported OPN to be present in mice, but only in the thick ascending limbs of the loop of Henle and the distal convoluted tubules in a subset of nephrons [26]. It might perhaps be argued that the widespread distribution of OPN in humans militates against it having a specific function in stone formation, but its potent effect on CaOx crystal growth would suggest that it may influence the course of the disease. Certainly, it is present in kidney stones, with quantities in those composed principally of CaOx dehydrate being considerably less than in calculi comprising mainly CaOx monohydrate [165], and recently, OPN has also been detected in uric acid stones along with COM and COD crystals [80], where its abundance is substantially greater than that reported for NC [98]. *In vitro* studies suggest that OPN may inhibit the nucleation, growth, and aggregation of calcium oxalate crystals. In addition, it also inhibits the crystal adhesion to cultured epithelial cells [122]. Wesson et al. observed that it may direct CaOx crystallisation to the CaOx dehydrate phase rather than the CaOx monohydrate (COM) phase, the dehydrate being less adherent to renal tubular epithelial cells [166]. Clinical studies to date are inconclusive regarding the relationship between OPN and renal stone disease. Some investigators have reported decreased concentrations of OPN in urine from stone formers compared to normal individuals [123], while others have not [167]. A single-base mutation in the OPN gene is seen at significantly higher incidence in patients with recurrent stone formation or familial nephrolithiasis [168]. The role of OPN in nephrolithiasis is though somewhat unclear; due to very high content of aspartic and glutamic residues, OPN is subjected to significant post translational modification, which may function as regulatory switches in promotion or inhibition of mineralization [124]. The proportional contribution of UP to the inhibitory activity of urine has not been assessed [165], but the fact that it is present in stones in greater quantities than NC, despite its lower concentration in urine, might suggest that it binds more avidly to the CaOx crystal surface and may consequently be a more potent inhibitor. However, like NC, its inhibitory effect on CaOx crystallization has not been tested in urine, so it is not presently possible to assess its likely effects on CaOx crystallization *in vivo*. Thus, like all proteins currently under investigation for their possible roles in stone formation, significantly more information must be obtained before it will be possible to state with certainty that the presence of UP in urine is related specifically to its ability to inhibit CaOx crystallization, and thereby, stone pathogenesis.

4.3.4. Urinary Prothrombin Fragment 1 (UPTF1). Urinary Prothrombin Fragment-1 was discovered from CaOx crystals

freshly precipitated from urine. With a molecular weight of 31 kDa and staining characteristics of a glycoprotein, it was selectively incorporated into the crystals in quantities far exceeding those of any other, and in amounts disproportionately greater than its concentration in the urine from which the crystals had been derived. It was not possible to identify the protein by western blotting using commercial antibodies such as crystal matrix protein (CMP). However, it has since been shown, both immunologically and by amino acid sequence analysis, that the protein is related to human prothrombin [128, 169]. The link between nephrolithiasis and blood clotting was recently confirmed when its close identity with the FI activation peptide of human prothrombin was demonstrated [170]. To avoid confusion, the name crystal matrix protein has been abandoned and the protein is now known as urinary prothrombin fragment 1 (UPTF1). The known characteristics of UPTF1 and its presence in calcium oxalate stones indicate that it may fulfill some function in stone pathogenesis. UPTF1 is one of the principal constituents of CaOx stones. Most notably, it was not found in two struvite stones, indicating that its presence in CaOx stones is a consequence of direct inclusion into the crystalline architecture rather than a secondary product of tissue injury. Suzuki et al. studied the expression of prothrombin in human and rat kidneys [171]. Analysis of the matrix of calcium phosphate crystal reveals that UPTF1 is a major component, while in urate crystals it is only a very minor constituent, which reflects the known relationship between this protein and calcium ions [172]. Immunohistochemical studies have mapped its location in the human kidney, specifically to the epithelial cells of the thick ascending limb of the loops of Henle and the distal convoluted tubules [173]. The protein was not detected in any other human tissue, with the exception of the cytoplasm of hepatocytes. Limited data also demonstrated that the amount of UPTF1 in the kidneys of stone formers is significantly greater than in those of healthy subjects [173, 174].

UPTF1 is the most prominent protein in the organic matrix of CaOx crystals precipitated from fresh human urine [10]. This combined with the observation that the organic matrix is the most potent macromolecular inhibitor of CaOx crystallization induced in human urine that has yet been described led to the presumption that this inhibitory activity was likely to be attributable to its component UPTF1 [20]. This presumption was largely justified since UPTF1 purified by RPHPLC is now known to be a potent inhibitor of CaOx crystal aggregation in undiluted urine [129], a feature that currently distinguishes it from its peers, whose inhibitory activities, with the exception of THP, have only ever been tested in inorganic solutions. When crystallization inhibitory potential of all the prothrombin-related peptides, the PT, thrombin (T), and fragments 1 and 2 was tested using a simple inorganic solution, both prothrombin and fragment 1 were found to inhibit crystal aggregation [130]. However, when similar experiments were conducted using undiluted, centrifuged, and ultrafiltered human urine [131], crystal aggregation was inhibited only by PT fragment 1. There seems to be little doubt that the potent inhibitory effect of UPTF1 on CaOx crystallization can be ascribed to the Gla domain

of the peptide, which is absent from thrombin and F2 and both PT and F1 fragments [131]. Along with that of its peers, UP and UAP, the study of UPTF1 is still in its early stages. Certainly, preliminary data would indicate that it possesses all the features expected of a significant macromolecular urinary inhibitor, including potent activity in undiluted urine. Nonetheless, like all other proteins presumed to fulfill some function in urolithiasis, the true role of UPTF1 must remain speculative until such time as a cause and effect relationship between the protein and stone pathogenesis can be unequivocally demonstrated.

4.3.5. Inter- α -Inhibitor (I α I). Inter- α -inhibitor (I α I) belongs to the Kunitz-type protein superfamily, a group of proteins possessing kunitin as a common structural element and the ability to inhibit serine proteases [175]. I α I is a plasma glycoprotein normally synthesized in the liver and is composed of a combination of heavy chains, H1 (60 kDa), H2 (70 kDa), and H3 (90 kDa) covalently linked via a chondroitin sulphate bridge to a light chain called bikunin (35–45 kDa) [106]. The heavy and light chains also exist independently as single molecules. I α I (180–240 kDa) is a heterotrimer consisting of bikunin linked to heavy chains H1 and H2. Pre- α -inhibitor (P α I, 125 kDa) is composed of bikunin and heavy chain H3. The macromolecule consisting of bikunin linked to heavy chain H2 is called I α I-like inhibitor (I α LI). I α I and related proteins have been linked to various pathological conditions such as inflammatory diseases [176], cancer [177], renal failure [178], and more recently the urinary stone disease. A possible role of I α I in stone disease can be traced as far back as 1909, when Bauer and Reich demonstrated that the proteolytic activity of trypsin was inhibited by urine [179]. Atmani et al., in 1993, isolated uronic acid-rich protein (UAP) from human urine by three gel filtration chromatographic steps and, in the reduced form, had an estimated molecular weight of 35 kDa on an 8–20% SDS gradient gel [107]. UAP earned its name because of its high content of uronic acid; D-glucuronic and L-iduronic acids are major constituents of GAGs, carbohydrate accounts for 8.5% of its weight, and amino acid analysis reveals a protein rich in glutamic and aspartic acids, glycine, and valine and it contains no Glu. N-terminal amino acid sequence analysis has demonstrated homology with the light chain of inter- α -trypsin inhibitor (ITI), that is, bikunin [136, 180]. This supposition is further vindicated by the fact that the urinary derivative of ITI is also known to be a GAG adduct [175] and has a relative molecular weight of 35 kDa on SDS-PAGE under reducing conditions [104]. Bikunin is a broad-spectrum protease inhibitor and an acute-phase reactant. It is excreted in urine where it degrades further to fragments HI14 and HI8. Both heavy and light chains have also been identified in the urine [107, 181, 182]. The average concentration of I α I in the plasma of healthy human subjects is approximately 450 mg/L [137]. Urinary excretion is 2 to 10 mg/day, but can increase to 50–100-fold or more in certain pathological conditions such as cancer. Plasma concentration of I α I is, on the other hand, reduced during various pathological conditions including renal failure. Bikunin is expressed mainly in the proximal

tubules and the thin descending segment near the loop of Henle. Tissue-culture studies have shown that human renal proximal tubular epithelial cells constitutively express genes for bikunin and H3 components [183]. Bikunin gene is also expressed in MDCK cells and was upregulated when they were exposed to oxalate [119]. In normal rat kidneys, staining of the I α I-related proteins is mostly limited to the proximal tubules and generally to their luminal contents [184]. Iida et al. investigated renal and urinary expression of various members of the I α I family in male rats with or without experimentally induced hyperoxaluria and CaOx crystal deposition. The expression of bikunin mRNA increased in renal epithelial cells exposed to oxalate and CaOx crystals [184]. As a result, an increase in CaOx inhibitory activity is anticipated. However, this was not the case, as there might be some structural abnormalities in stone formers' bikunin. It was shown that bikunin isolated from the patients contained less sialic acid and exhibited less crystallization inhibitory activity than that purified from the urine of healthy subject [138]. Western analysis showed that a significantly higher proportion of stone patients had a 25 kDa bikunin in their urine in addition to the normal 40 kDa species. 25 kDa bikunin was similar to the deglycosylated bikunin and was less inhibitory. In a separate study, mean urinary bikunin to creatinine ratio was found to be significantly higher in stone formers than in nonstone-forming healthy male and female controls [185]. Contrary to this, another study found decreased urinary excretion of bikunin by stone-forming patients. Mean urinary excretion of bikunin in 18 healthy individuals was $5.01 \pm 0.91 \mu\text{g/mL}$ and $2.54 \pm 0.42 \mu\text{g/mL}$ in 31 stone patients [139].

The inhibitory activity of this protein from human urine was determined in an inorganic CaOx crystallization system, where it strongly retarded CaOx crystal growth. It was reported that this activity is reduced in stone formers compared with normal controls [138]. I α I proteins have been shown to inhibit CaOx crystallization *in vitro* [107, 136, 139, 180, 186, 187]. The inhibitory activity is confined to the carboxy terminal of the bikunin fragment of I α I [187]. Both rat and human urinary bikunin inhibited nucleation and growth of CaOx crystals. Treatment with chondroitinase AC had no effect on this inhibitory activity which was destroyed by pronase treatment, indicating that the activity lies not with the chondroitin chain but with the peptide. In 1999, Atmani and Khan showed that urinary bikunin, at concentrations of 2.5 to 20 $\mu\text{g/mL}$, retarded crystal nucleation by 67 to 58% and inhibited crystal aggregation by 59 to 80% [140]. These results were confirmed later when inhibition of CaOx crystal growth and aggregation by I α I, its heavy chains, light chain (bikunin) with or without chondroitinase treatment, and bikunin's carboxy terminal domain (HI8) was tested in an *in vitro* crystallization assay [187]. I α I was a weak inhibitor while heavy chains showed no discernible activity. Bikunin and HI effectively inhibited the crystallization. Chondroitinase treatment had no effect on the inhibitory activity of bikunin. I α I molecule itself is also an effective inhibitor of CaOx crystal growth [136] and in another study was shown to be more efficient than another crystal growth inhibitor, prothrombin fragment 1 [186]. Ebisuno et al. showed inhibitory effect of

bikunin on adhesion of calcium oxalate crystals to renal tubular cells in human urine [141]. MDCK cells were exposed in culture to CaOx monohydrate crystals in the presence or absence of various protein fractions isolated from normal human urine. A single fraction with a molecular weight of 35 kDa was found to be most inhibitory of crystal adhesion. This protein, on sequencing found, to be homologous to bikunin, inhibited crystal adhesion at the minimum concentration of 10 ng/mL, and completely blocked it at 200 ng/mL. It may contribute to the modulation of crystal adhesion and retention within tubules during kidney stone formation [188].

Despite having been the subject of investigation for many years, the true physiological function of IαI remains somewhat a mystery, although it may play a role in cancer, adult respiratory distress syndrome, and septic shock and may be a useful therapeutic agent in such conditions [183]. Furthermore, the potent inhibition of CaOx crystal growth by these proteins, coupled with the known presence of bikunin and its fragments in urine, suggested the possible existence of a relationship between IαI and CaOx stone formation [189]. Then it is possible that its clinical usefulness may also extend to the treatment of human kidney stones.

4.3.6. Calgranulin. Calgranulin is a 28 kDa calcium-binding protein, member of S100 protein family, which are small, ubiquitous, and acidic proteins involved in normal developmental and structural activities. This group of calcium-binding proteins are also implicated in a number of diseases [190]. There are 3 monomers of calgranulin (A, B, and C) all mapped to chromosome 1. It is present in the kidney and human urine and can inhibit growth of CaOx crystals, which is the major component of kidney stones. The protein was isolated from human urine at a concentration of 3.5–10 nM. Purified urinary calgranulin inhibited both CaOx crystal growth (44%) and aggregation (50%) in nanomolar range. The inhibitory properties of calgranulin may be due to its ability to bind to the crystal surface [133]. Western analysis of rat and human kidneys as well as renal epithelial cell lines including BSC-1 and MDCK confirmed its renal presence. Calgranulin has also been identified in matrices of different type of stones, for example, calcium oxalate stones [120, 121, 134], uric acid stones [80], and infectious or struvite stones [135], and in CaP deposits formed by MDCK cells [191]. Calgranulin is abundant in both rat and human kidney homogenates, and Pillay et al. isolated the cDNA of calgranulin by screening a human kidney expression library. Its renal presence was further evidenced by western and northern analysis of two renal epithelial cell lines. The inhibitory properties of calgranulin may be shared and expressed by other urinary S100 proteins; bovine brain S100 protein inhibits COM growth and aggregation. The expression of calgranulin by renal cells indicates that urine calgranulin could be produced by kidney cells and may be regulated by them in ways that are important in defense against crystallization [133]. Calgranulin has also been detected in the matrices of different types of stones, for example, calcium oxalate stones [120, 121, 134], uric acid stones [80], and infectious or struvite stones [135], and in CaP deposits formed by MDCK cells [191].

4.3.7. Renal Lithostathine. Lithostathine is a glycoprotein synthesized by acinar cells and secreted in pancreatic juice. Pancreatic juice is naturally supersaturated at calcium and bicarbonate ions, and lithostathine plays an important role in inhibiting calcium carbonate crystal growth. A protein immunologically related to lithostathine and is actually present in urine of healthy subjects and in renal stones renal lithostathine (RL) [192]. Western blot analysis of proteins extracted from concentrated normal urine or kidney stones demonstrated the presence of a protein with molecular weight of 23 kDa [142]. Because of its structural and functional similarities with pancreatic lithostathine, it was called renal lithostathine. Renal lithostathine seems to control growth of calcium carbonate crystals. Several reports showing the presence of calcium carbonate (CaCO₃) in renal stones suggested that crystals of CaCO₃ might be present in the early steps of stone formation. Such crystals, therefore, might promote CaOx crystallization from supersaturated urine by providing an appropriate substrate for heterogeneous nucleation [143, 144].

4.3.8. Albumin. Albumin is one of the most abundant proteins in the urine [62, 118] and has been detected in the matrix of both urinary stones [14, 62, 80, 118] and crystals [189, 193] made in the whole human urine. It is known to bind to CaOx as well as uric acid crystals [116, 126] but does not inhibit their growth [22, 116]. However, it has been shown to inhibit CaOx crystal aggregation in concentration dependent manner [194]. When immobilized to surfaces and exposed to metastable solutions, albumin promotes crystal nucleation [127, 195]. When dissolved in solution albumin exists either in monomeric and/or polymeric form [127]. In metastable CaOx solutions both monomeric and polymeric forms promote nucleation of CaOx. In addition, nucleation by albumin leads exclusively to the formation of COD crystals. Urinary albumin purified from healthy subjects contained significantly more polymeric forms and was a stronger promoter of CaOx nucleation than albumin from idiopathic calcium stone formers. Promotion of CaOx nucleation and formation of large number of COD crystals might be protective. Nucleation of large number of small crystals would allow their easy elimination and decrease CaOx saturation preventing crystal growth and aggregation and subsequent stone formation. COD crystals are more common than COM crystals in nonstone formers' urine and are generally found in less quantities in stones than COM crystals. In addition, crystals present in the urine from nonstone formers are significantly smaller than those in stone formers urine. Albumin also exhibits the capacity to bind some of the urinary proteins. Interestingly, urinary proteins that show great affinity for albumin are also those that are included in the stone matrix. It is suggested that proteins become a part of stone matrix by binding to the albumin coating of the CaOx crystals. It is also suggested that unlike other calcium-binding urinary proteins, albumin promotes nucleation by interacting with calcium through the carboxyl group. Strong nucleation activity was observed at pH 7 but was totally eliminated at pH 4 when carboxyl groups are no

longer ionized. In addition, morphological studies showed CaOx crystals to nucleate through calcium-rich face [127].

4.3.9. Human Urinary Trefoil Factor 1 (THF1). Human urinary trefoil factor 1 (THF1) belongs to the trefoil factor family proteins. It is synthesised by mucosal epithelial cells and is expressed in gastric mucosa. It has been described as an antiapoptotic agent with mitogenic activities [196]. It may also act as a potent inhibitor of CaOx crystal growth. Functional studies of urinary THF1 demonstrated that its inhibitory potency was similar to that of nephrocalcin. The inhibitory activity of urinary THF1 was dose dependent and was inhibited by THF1 antisera. Concentrations and relative amounts of THF1 in the urine of patients with idiopathic CaOx kidney stone were significantly less (2.5-fold for the concentrations and 5- to 22-fold for the relative amounts) than those found in controls [153]. Urinary trefoil factor 1 has the ability to inhibit growth and aggregation of calcium oxalate crystals and can transform calcium oxalate monohydrate crystals to the dihydrate type [154].

4.3.10. Hyaluronic Acid (HA). HA is a linear glycosaminoglycan (GAG) that is composed of multiple units of glucuronic acid and N-acetylglucosamine (1, 4-GlcUA-1, 3-GlcNAc-)_n. It is an extremely large and high molecular weight GAG, that is, >10⁶ Da, one disaccharide is approximately 400 Da; high molecular weight HA is a chain of >2500 disaccharide repeats. HA chains occupy huge tissue domains and can entrap large amounts of solvent due to its expanded random coil structure [197]. HA is produced by HA synthase (HAS) proteins that are located at the inner face of the plasma membrane, where it is extruded across the membrane into the extracellular space. HA is a major component of the extracellular matrix (ECM) in the renal medullary interstitium and the pericellular matrix (PCM) of mitogen/stress-activated renal tubular cells. Hydrated PCM provides the microenvironment that is conducive to adjustments in cell shape and epithelial architecture during dynamic morphogenetic processes like wound healing, embryonic development, inflammation, and cancer [198]. The size, negative ionic charge, and ability to form hydrated gel-like matrices make HA an excellent crystal-binding molecule. Crystal binding to HA leads to crystal retention in the renal tubules and to the formation of calcified plaques in the renal interstitium (Randall's plaques). HA also directly influences cell behavior through its ability to communicate with the cell interior via cell-surface receptors, such as CD44 and CD168 [197–199].

In a healthy kidney, HA is abundant in the renal medullary interstitium, but in the cortex it is almost undetectable, and renal tubular cells normally do not express HA. HA should be considered an enormous inhibitor of crystallization that efficiently prevents papillary calcification, for the reason that interstitial HA is low during antidiuresis; the highest risk for crystal formation most likely occurs during periods of water deprivation. On the other hand, high fluid intake leads to high interstitial HA which protects against crystallization. Ca²⁺ also becomes associated with the COO⁻ groups in the HA matrix, thereby preventing

CaP precipitation. Precipitated calcium crystals (CaP) may bind to the HA matrix, which could play an important role in interstitial plaque formation (Randall's plaques) [150]. Therefore, it was speculated that HA could be an inhibitor of crystallization as long as calcium salts are in solution because the carboxyl groups of the HA chains race with anions such as phosphate and oxalate for binding to calcium, whereas HA may serve as binding substance for precipitated calcium salts because of the affinity of these crystals for high molecular weight HA. In case of renal cell injury, HA may act as promoter for crystal adhesion to the cell surface, which will ultimately result into stone formation. Crystal retention in the human kidney may depend on the expression of damaged distal tubular epithelium of CD44, OPN, and HA-rich cell coats [151]. HA becomes expressed in areas of the kidney where it is absent under normally conditions, such as in the cortical interstitium and on the luminal surface of renal tubular cells [152]. HA is upregulated in the kidney during inflammatory renal disease states such as interstitial nephritis [200], acute ischemic injury [201], autoimmune renal injury [202], acutely rejecting human kidney grafts [203], acute tubular necrosis [151], and obstructed kidneys and EG poisoning [152]. HA-expressing renal tubular cells invariably also express the HA receptor CD44 [151, 152, 200, 204, 205]. HA is also one of the major constituents of the organic matrix of renal stones. HA is present in kidney stones in fractions that are disproportionate to its urinary concentrations [63].

4.3.11. Annexin II. Annexin II protein is a 37 kDa member of the annexin family, that is, calcium-dependent phospholipid-binding protein family. These family members play a role in the regulation of cellular growth and in signal transduction pathways. As a family, annexins are characterized by a conserved COOH-terminal protein "core" that mediates their membrane and calcium-binding properties. The conserved COOH-terminal core is 70-amino acid-long chains and contains four repeats, each of which consist of a calcium-binding motif G-X-G-T [206]. Members of the annexin family differ in binding specificity of the core for phospholipid headgroups like PS, phosphatidic acid or phosphatidylinositol, as well as the binding specificity of the NH₂-terminal tail.

Annexin II is a calcium-dependent phospholipid-binding protein whose function is to help organize exocytosis of intracellular proteins to the extracellular domain. Annexin II is involved in diverse cellular processes like cell motility, linkage of membrane-associated protein complexes to the actin cytoskeleton, endocytosis, fibrinolysis, ion channel formation, and cell matrix interactions. Ax-II is a pleiotropic protein, meaning that its function is dependent on the place and time in the body. Ax-II has been demonstrated on the surface of many cell types, including keratinocytes [207], endothelial cells, glioma cells, and smooth muscles cells [208], where it can serve receptor-like functions for molecules including lipid A [209], cytomegalovirus [210], 1,25(OH)₂D₃ [211], 2-glycoprotein I [212], and tissue plasminogen activator [213]. Annexin II can bind to the crystals while anchored on the cell surface. Under certain circumstances, Ax-II is

known to interact with membranes via cholesterol molecules in a calcium-independent mechanism, possibly leaving the calcium-binding motifs available to bind calcium oxalate crystals. The NH₂-terminus of Ax-II can bind a p11 dimer and become linked to another Ax-II molecule via its NH₂ tail; a process that can mediate aggregation of membrane vesicles. Ax-II-p11 tetramer might link a crystal to a membrane instead of linking two membranes [206].

Ax-II mediates the adhesion of COM crystals to renal cells and it may also play a role in their subsequent internalization. Kumar et al., in 2003, used COM affinity to identify apical membrane proteins that might mediate crystal adhesion to renal epithelial cells. They found annexin II to be the major COM crystal-binding protein, and it was identified on the apical surface of intact MDCK-I cells. The interaction between crystals and renal tubular cells has been proposed to be a crucial event that elicits subsequent cellular responses, leading to kidney stone formation. Ax-II has a role as a COM crystal-binding molecule on the surface of intact cells as COM crystal adhesion decreased significantly after MDCKI cells were pretreated with a monoclonal antibody against Ax-II. Studies suggest that Ax-II may be one of several cell surface crystal-binding molecules that might modulate crystal retention [157]. Membrane-associated annexin II has also been reported to regulate extracellular matrix (ECM) metalloproteinase inducer (Emmprin) activity [150, 214].

4.3.12. CD44. CD44 is a multifunctional extracellular matrix (ECM) glycoprotein involved in adhesion, migration and cell-cell interactions. CD44 is the main cell surface receptor for hyaluronan or hyaluronic acid (HA) as well as OPN [215] and can also interact with other ligands, collagens, and matrix metalloproteinases (MMPs). CD44 is expressed in a large number of mammalian cell types. It is also found to be associated with adhesion of crystals to renal epithelial cells. Retention of crystals in the kidney is an essential early step in renal stone formation. OPN, rather than HA, is the major ligand for CD44 on bone cells in the remodelling phase of healing of fractures [216]. CD44 plays an important role in calcium oxalate (CaOx) crystal binding during wound healing. Both CD44 and HA are upregulated during injury and inflammation and are involved in the formation of a cell coat or pericellular matrix on surfaces of proliferating and migrating cells. HA is restricted to the inner medullary interstitium of the normal kidneys. Distal collecting duct cells express both CD44 and HA on apical cell surfaces of the proliferating cells. At confluence, however, CD44 is expressed at the basolateral membrane while HA is undetectable. Proliferating cells are receptive to adhesion of CaOx crystals, a property lost when cells become confluent. In addition, removal of pericellular matrix by hyaluronidase treatment also results in loss of crystal adhesion property of the proliferating cells [151]. Asselman et al. studied crystal retention *in vivo*; intratubular crystals were found adhered to injured/regenerating tubular epithelial cells expressing HA, OPN, and CD44 at their luminal membrane [152]. Based on these observations it has been proposed that intact epithelium does not bind crystals because of the absence of a pericellular

matrix and crystal attachment depends upon the expression of CD44, OPN, and HA by the damaged renal epithelial cells [217].

4.3.13. Matrix Gla Protein. Matrix Gla protein (MGP) is a natural inhibitor of vascular calcification. MGP, a vitamin K-dependent extracellular matrix protein, was initially isolated from the bone and is also expressed in lung, heart, vascular smooth muscle cells of the blood vessel wall, and kidney [218]. MGP is an 84-amino-acid protein that contains five γ -carboxyglutamic acid (Gla) residues which have a high affinity for calcium and phosphate ions and hydroxyapatite crystals [158]. The pathological mechanism of kidney stone formation was partly similar to vascular calcification: forming calcific plaques, increasing expression of calcification inhibitors, and regulating actively calcification process. MGP genetic single nucleotide polymorphism was associated with the individual susceptibility of nephrolithiasis [159]. MGP is involved in cell growth, differentiation, and regulation of apoptosis and increase cell density in normal kidney cells [160].

Matrix Gla protein (MGP) is a molecular determinant regulating vascular calcification of the extracellular matrix. MGP is polarly distributed on the apical membrane of renal tubular epithelial cells and binds directly to crystals; it is also found in the ascending thick limbs of Henle's loop and the distal convoluted tubule in hyperoxaluric rats; its expression was present in the medullary collecting duct in stone-forming rats. Crystals with multilaminated structure were formed in the injurious renal tubules with lack of MGP expression [161]. Lu et al. also reported that there was no crystal formation in renal tubules with MGP expression, and crystals only deposit in the damaged renal tubules with lack of MGP expression. MGP mRNA expression was found to be upregulated in renal tubular epithelial cells following exposure to calcium oxalate monohydrate (COM) and oxalate [161, 162]. Luo et al. found that homozygous MGP-deficient mice died within 8 weeks as a result of arterial calcification that led to blood vessel rupture [219]. Vascular calcification in MGP-deficient mice was reversed by overexpressing MGP in vascular smooth muscle cells [220]. These findings imply that MGP may play a cytoprotective role in maintaining cells' survival and inhibiting crystal retention under oxalate and crystal exposure.

4.3.14. Monocyte Chemoattractant Protein-1 (MCP-1). Monocyte chemoattractant protein-1 (MCP-1/CCL2) is a member of the CC chemokine family and belongs to the group of inflammatory chemokines. MCP-1 is a potent chemotactic factor for monocytes [221]. Chemokines are also grouped into two main functional subfamilies: inflammatory and homeostatic. Inflammatory chemokines control the recruitment of leukocytes in inflammation and tissue injury. Homeostatic chemokines fulfill housekeeping functions, such as navigating leukocytes to and within secondary lymphoid organs, in addition to in the bone marrow and the thymus during hematopoiesis [222]. Chemokine activation of cell surface G-protein-coupled receptors results in directed cell migration, that is, chemotaxis [223].

The development of kidney disease involves a complex interplay between neurohormonal, inflammatory, and biochemical changes which act on either intrinsic or extrinsic renal cells or both. This can lead to the development of an innate immune response predominantly characterized by the accumulation and activation of leukocytes, particularly monocytes/macrophages, in the kidney. Chemokine-induced recruitment of peripheral leukocytes into tissues is a critical step in the development of inflammatory responses [224]. MCP-1 plays an important role in various pathophysiological conditions in many organ systems [225]. Even though MCP-1 is involved in various inflammatory diseases and may not be specific for a particular disease, this should not necessarily preclude its use as a biomarker. MCP-1 plays a critical role in the development of kidney diseases. It has been investigated as a potential urinary biomarker in several renal diseases, in a number of studies [155]. However, the exact role of MCP-1 in stone formation is still not clear, but its expression in renal epithelial cells on exposure to oxalate and CaOx crystals indicates a close relationship between inflammation and nephrolithiasis [156].

Our research group has been conducting many studies to explore the organic matrix of renal stone and revealed the presence of a 66 kDa stimulator of calcium oxalate crystal growth in the human renal calculi extract [6]. Later they investigated the activity of high and low molecular weight biomolecules present in the matrix of human CaOx stones not only on the initial mineral phase formation of calcium and phosphate (CaP) but also on its growth and demineralization of the preformed mineral phase [226]. We also purified, identified, and characterized novel proteins from human renal stone matrix. Some of them were potent inhibitors like urobilinubin (14.2–16.2 kDa) [227], a 36 kDa inhibitor protein [228], anionic protein like human phosphate cytidyltransferase-1, β (42 kDa), [145, 146] cationic proteins like histone-lysine N-methyltransferase (53 kDa), inward rectifier K channel (44 kDa), and protein Wnt-2 (42 kDa) [148]. 2D map of >3 kDa fraction from matrix of CaOx stone revealed the presence of disheveled-associated activator morphogenesis (123.9 kDa), glutamate receptor delta-1 subunit (113 kDa), caspase recruitment domain-containing protein (114.8 kDa), ALBU_BOVIN (71.2 kDa), VP7 glycoprotein precursor (37.5 kDa), chymotrypsinogen A (26.2 kDa), and plasminogen (15.7 kDa). Also, our group conducted various cell culture studies to explain the effect of proteins in the stone matrix on oxalate-injured renal cell lines [229].

5. Conclusion

Various theories of pathogenesis of human kidney stones suggest that their formation is too complex for simple understanding. The pathogenesis of calcium oxalate stone formation is a multistep process and essentially includes nucleation, crystal growth, crystal aggregation, and crystal retention. A detailed discussion has been made about several urinary proteins found to occur in stones that modulate the process of stone formation, thereby leading to better

understanding of the pathophysiology and pathogenesis of kidney stone disease. Many aspects of the mechanism of renal stone formation remain unclear at present; hence, a better understanding of this intricate mechanism will lead to the development of a novel strategy for preventing this disease.

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