Review Article

Involvement of Kallikrein-Related Peptidases in Normal and Pathologic Processes

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Human kallikrein-related peptidases (KLKs) are a subgroup of serine proteases that participate in proteolytic pathways and control protein levels in normal physiology as well as in several pathological conditions. Their complex network of stimulatory and inhibitory interactions may induce inflammatory and immune responses and contribute to the neoplastic phenotype through the regulation of several cellular processes, such as proliferation, survival, migration, and invasion. This family of proteases, which includes one of the most useful cancer biomarkers, kallikrein-related peptidase 3 or PSA, also has a protective effect against cancer promoting apoptosis or counteracting angiogenesis and cell proliferation. Therefore, they represent attractive therapeutic targets and may have important applications in clinical oncology. Despite being intensively studied, many gaps in our knowledge on several molecular aspects of KLK functions still exist. This review aims to summarize recent data on their involvement in different processes related to health and disease, in particular those directly or indirectly linked to the neoplastic process.

1. Introduction

Human kallikrein-related peptidases (KLKs) are a subgroup of serine proteases that have important roles in regulating normal physiological functions, such as immune response, skin desquamation, enamel formation, and semen liquefaction, and the corresponding pathological conditions. There is growing evidence in the literature supporting the view that KLKs are also implicated in tumorigenesis by activating proteolytic processes associated with the neoplastic phenotype. The potential mechanisms involved include the modulation of growth factor bioavailability and activation of hormone and protease-activated receptors (PARs) resulting in proliferative signaling pathways, the degradation of extracellular matrix, cleavage of junction proteins and induction of an epithelial-mesenchymal transition (EMT) phenotype leading to increased tumor cell migration and invasion, and the modulation of interactions between cancer cells and their microenvironment promoting angiogenesis and other protumorigenic processes (reviewed by [1–3]).

The potential of KLKs as cancer markers has been suggested for several members of this protease family [2, 4–6], particularly for kallikrein-related peptidase 3 or prostate-specific antigen (PSA) [7]. PSA is well accepted for assessing recurrence risk in patients with prostate cancer, but its predictive power for diagnosis has been questioned, since several factors other than malignancy may be associated with its high levels in serum, such as preanalytical variables, benign diseases, and drugs [8, 9]. Biomarker panels combining PSA and other promising markers, including members of the KLK family, are expected to improve prostate cancer screening and reduce unnecessary treatments, a strategy that may also be used for detection and monitoring of other malignancies and nonmalignant diseases.

In this paper, we review the current knowledge about the evolution and functions of human kallikrein-related
peptidases, their substrates, and their role in health and disease, particularly in the context of cancer.

2. The Human Degradome

Protein synthesis is essential for living, metabolically active cells, but its counterpart, protein degradation, is no less important. Proteolytic mechanisms driven by proteases maintain appropriate protein levels and recognize and degrade the misfolded or mislocalized ones. In addition to acting in nonspecific catabolism, proteases are involved in selective cleavages and activations, modulating protein-protein interactions and contributing to cell signaling both as catalytic units and as multicatalytic complexes. Due to their broad-spectrum actions, proteases play critical roles in regulating normal biological processes, including DNA replication and transcription, cell proliferation, differentiation, and apoptosis. When altered, they may facilitate the development of pathological conditions such as inflammatory and degenerative disorders (reviewed by [10]). The importance of these hydrolytic enzymes is reflected by the number of genes already identified in several mammalian species, with more than 500 in human and primates and even more in rodents [11–14].

The complete set of human proteases—named the human degradome—is distributed in aspartic-, threonine-, cysteine-, serine-, and metalloprotease classes according to the chemical group involved in their catalytic activity [15, 16], and the latter three are the most populated classes [10]. Their substrate cleavage patterns may be specific for a single peptide, as in the case of proteases involved in signaling pathways, or common for a broad range of peptides, which is well exemplified by digestive enzymes [17]. Otherwise, inactive proteases or pseudoproteases bind to their cognate substrate without cleaving them, thus exerting a regulatory function [18].

Detailed information on proteases in prokaryotes and eukaryotes, protease families, pseudogenes, the sequences derived from endogenous retroviruses, 3D structures, substrates, and proteolytic events has been accumulated in different databases such as MEROPS [19] and Degradome [20].

3. The Serine Protease Group

Approximately one-third of proteolytic enzymes are serine proteases, usually endopeptidases. These enzymes use the serine residue present in their active site as a nucleophile to attack the peptide bond of the substrate [21]. In humans, many serine proteases are involved in extra- and intracellular processes mainly related to food digestion, blood coagulation, and immunity (reviewed by [1, 22]). Although these processes are essential for the purposes of catabolism or selective cleavages required for cell signaling, serine protease activity (as well as that of other proteases) is potentially devastating, and several cellular mechanisms were selected to modulate and keep them within limits. For example, they are stored as inactive zymogens or inside granules and can access the substrates only through controlled actions. In addition, serpins, a superfamily of serine protease inhibitors, antagonize their activities in many metabolic pathways, arresting the proteases into an irreversible complex (reviewed by [1]).

Although tightly controlled, several serine proteases have been associated with human diseases. For example, high granzyme levels (granule-secreted enzymes found in cytotoxic T cells and natural killer cells) have been observed in chronic inflammatory diseases such as rheumatoid arthritis [23], asthma [24], diabetes [25], atherosclerosis [26], and chronic obstructive pulmonary disease [27] and cardiovascular diseases [28]. They have also been implicated in susceptibility to skin tearing and disorganized collagen as observed in chronic wounds and aged/sun-damaged skin (reviewed by [29]). The role of granzymes in these conditions resides in their ability to cleave many substrates, inducing apoptosis through caspase-dependent and caspase-independent pathways [30]. Their potential to create or destroy autoimmune epitopes [31] and be improperly regulated in chronic wounds or released nonspecifically from immune cell into extracellular spaces also contributes to chronic inflammation or extracellular matrix disorganization [27, 32].

Increased levels of neutrophil proteases such as elastase, cathepsin G, and myeloblastin have also been correlated with the severity of cystic fibrosis and chronic obstructive pulmonary disease [33]. Similarly, trypstatin and chymase, two serine proteases stored in mast cell granules, take part in the pathophysiology of asthma [34], psoriasis [35], atherosclerosis [36], and fibrotic [37] and inflammatory kidney diseases [38].

With respect to cancer, several serine proteases have been linked to tumor development and progression by activating proteolytic processes that are associated with the neoplastic phenotype (reviewed by [1]). Specifically, a family of serine proteases expressed and secreted in many tissues participates in complex networks of cell signaling pathways that are related to cancer [4–7]. One of the most useful cancer biomarkers in clinical medicine is kallikrein-related peptidase 3 or PSA, which is a member of this family (reviewed by [7]), and there is evidence that other KLKs are also deregulated in cancer and other diseases [4, 39–147] as summarized in Table 1.

4. The Human Kallikreins

Human kallikreins, initially detected at high levels in pancreas, *kallikreas* in Greek, include plasma and tissue serine proteases, which are two categories that differ in molecular weight, substrate specificity, and gene structure. The unique plasma kallikrein (PKK) is a glycoprotein encoded by the *KLKB1* gene on chromosome region 4q35 and is predominantly synthesized in the liver as an inactive precursor. After activation by the coagulation factor XII, PKK cleaves high molecular weight kininogen to release bradykinin, a mediator of blood coagulation, inflammation, blood pressure, and thrombosis risk [148].

4.1. Kallikrein-Related Peptidases at DNA Level: Genomic Organization and Evolutionary Aspects. The 15 tissue kallikreins or kallikrein-related peptidases (KLKs) are encoded by genes that are tightly clustered in an approximately
**Table 1:** Kallikrein-related peptidases. Gene expression pattern, SNPs, and promoter methylation related to cancer and other diseases. CSF = cerebrospinal fluid.

<table>
<thead>
<tr>
<th>Disease</th>
<th>Kallikrein</th>
<th>Factor</th>
<th>Observation</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alzheimer’s disease</td>
<td>KLKs 6 (CSF), 10</td>
<td>Increased expression</td>
<td>Increased expression</td>
<td>[39–42]</td>
</tr>
<tr>
<td></td>
<td>KLKs 6 (brain, blood), 7</td>
<td>Decreased expression</td>
<td>Decreased expression</td>
<td></td>
</tr>
<tr>
<td>Amelogenesis imperfecta</td>
<td>KLK4</td>
<td>Mutation</td>
<td>Disease-causing mutation</td>
<td>[43–45]</td>
</tr>
<tr>
<td>Aneurism</td>
<td>KLK6</td>
<td>Decreased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[46, 47]</td>
</tr>
<tr>
<td></td>
<td>KLK8</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
<td></td>
</tr>
<tr>
<td>Asthma</td>
<td>KLK3</td>
<td>SNP</td>
<td></td>
<td>[48]</td>
</tr>
<tr>
<td>Atopic dermatitis</td>
<td>KLK5</td>
<td>Decreased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[49, 50]</td>
</tr>
<tr>
<td>Coronary artery disease</td>
<td>KLK1</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[51]</td>
</tr>
<tr>
<td></td>
<td>KLK1</td>
<td>Increased expression</td>
<td>Predictor of disease</td>
<td>[52, 53]</td>
</tr>
<tr>
<td>Kidney disease</td>
<td>KLK1</td>
<td>SNP</td>
<td>Disease-associated SNP</td>
<td></td>
</tr>
<tr>
<td>Lupus nephritis</td>
<td>KLK1</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[54–56]</td>
</tr>
<tr>
<td>Acute kidney injury</td>
<td>KLK1</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
<td></td>
</tr>
<tr>
<td>Diabetic nephropathy</td>
<td>KLK1</td>
<td>Increased expression</td>
<td>Tubular inflammation</td>
<td></td>
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<tr>
<td>Multiple sclerosis</td>
<td>KLK6</td>
<td>Increased expression</td>
<td>Advanced disease</td>
<td>[57–59]</td>
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<tr>
<td>Dementia with Lewy bodies</td>
<td>KLK6</td>
<td>Decreased expression</td>
<td>Suggestion of diagnostic marker</td>
<td>[60]</td>
</tr>
<tr>
<td>Other neurodegenerative diseases</td>
<td>KLKs 1, 5, 6, 7, and 9</td>
<td>Increased expression</td>
<td>Suggestion of disease-associated marker</td>
<td>[61–63]</td>
</tr>
<tr>
<td>Other skin diseases</td>
<td>KLKs 5–8, 10–13, and 15</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[64–73]</td>
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<tr>
<td>Netherton syndrome</td>
<td>KLK5</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td></td>
</tr>
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<td>Psoriasis</td>
<td>KLK8</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[74, 75]</td>
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<tr>
<td></td>
<td>KLKs 6, 8, 10, and 13</td>
<td>Increased expression</td>
<td>Severity of skin lesions</td>
<td></td>
</tr>
<tr>
<td>Parkinson’s disease</td>
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<td>Disease-associated marker</td>
<td>[76]</td>
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<td>Siogren disease</td>
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<td>Increased expression</td>
<td>Suggestion of disease-associated marker</td>
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<tr>
<td>Breast cancer</td>
<td>KLKs 2, 4</td>
<td>SNP</td>
<td>Breast cancer risk Association with less aggressiveness</td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLK3</td>
<td>SNP</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLKs 5, 10, and 14</td>
<td>Increased expression</td>
<td>Potential diagnostic biomarkers</td>
<td>[4, 47, 78–83]</td>
</tr>
<tr>
<td></td>
<td>KLKs 6, 12 variant 3, and 15</td>
<td>Increased expression</td>
<td>Suggestion of favorable prognosis</td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLKs 3, 8, and 12</td>
<td>Decreased expression</td>
<td>Suggestion of favorable prognosis</td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLKs 5, 7</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLK10</td>
<td>Methylation</td>
<td>Suggestion of favorable prognosis</td>
<td></td>
</tr>
<tr>
<td>Cervix cancer</td>
<td>KLK7</td>
<td>Increased expression</td>
<td>Controversial prognosis</td>
<td>[84, 85]</td>
</tr>
<tr>
<td>Colorectal cancer</td>
<td>KLKs 4, 6, 7, and 10</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
<td>[86–90]</td>
</tr>
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</table>
Table 1: Continued.

<table>
<thead>
<tr>
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<th>Observation</th>
<th>Reference</th>
</tr>
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<tbody>
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<td>KLKs 6, 7, and 10</td>
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<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK13</td>
<td>Increased expression</td>
<td>Suggestion of favorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK11</td>
<td>Decreased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td>Head and neck cancer</td>
<td>KLK10</td>
<td>Methylation</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK 4–8, 10</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td>Intracranial tumor</td>
<td>KLKs 6–8</td>
<td>Increased expression</td>
<td>Controversial prognosis</td>
</tr>
<tr>
<td>Lung cancer</td>
<td>KLK 10</td>
<td>Methylation</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLKs 5–7</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLKs 11, 13, and 14</td>
<td>Increased expression</td>
<td>Diagnostic marker</td>
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<td>KLKs 8, 12</td>
<td>Decreased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td>Melanoma</td>
<td>KLKs 6, 8, and 13</td>
<td>Increased expression</td>
<td>Suggestion of favorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK7</td>
<td>Increased expression</td>
<td>Advanced stage</td>
</tr>
<tr>
<td></td>
<td>KLKs 4–6, 11, 13, 14</td>
<td>Increased expression</td>
<td>Suggestion of favorable prognosis</td>
</tr>
<tr>
<td>Ovarian cancer</td>
<td>KLKs 5, 7</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK10, KLKP1</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
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<td></td>
<td>KLKs 3, 15</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
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</tr>
<tr>
<td></td>
<td>KLK3</td>
<td>Increased expression</td>
<td>Disease monitoring and recurrent prediction</td>
</tr>
<tr>
<td></td>
<td>KLKs 1, 2, 4, and 15</td>
<td>Increased expression</td>
<td></td>
</tr>
<tr>
<td></td>
<td>KLKP1</td>
<td>Decreased expression</td>
<td>Controversial prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK7</td>
<td>Increased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK11</td>
<td>Decreased expression</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLKs 2, 3, 4, and 10</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
<tr>
<td></td>
<td>KLK12</td>
<td>SNP</td>
<td>Cancer predisposition</td>
</tr>
<tr>
<td></td>
<td>KLKs 4, 14, and 15</td>
<td>SNP</td>
<td>Suggestion of unfavorable prognosis</td>
</tr>
</tbody>
</table>

300 kb sequence of the 19q13.33–13.41 chromosome region, all containing 5 coding exons with comparable lengths and sequence homology [149, 150]. A pseudogene (KLKP1) has also been assigned to this region [151], as well as multiple repetitive elements such as ALU, Tigger2, MER8, and MSR1 [152]. The large contiguous human KLK gene cluster is limited by the ACPT (testicular acid phosphatase) gene and the Siglec (sialic acid-binding immunoglobulin-like lectin) family of genes at centromeric and telomeric positions, respectively, and other less characterized genes (SNORD88C, CI9orf48, MGC45922, and CTU1) (Figure 1).

The colocation and sequence conservation in a wide variety of species make this human tissue serine proteinase family a very interesting target for evolutionary studies [153]. The phylogenetic analysis of KLKs performed by the Maximum Likelihood method [154], using the transcript isoforms of 15 KLK genes, the pseudogene-1 (KLKP1) sequence, and the PRSSI (trypsin 1) transcript sequence as an external group,
Figure 1: KLK gene cluster and schematic representation of the human KLK gene and protein structure. (a) KLK gene cluster on the 19q13.33–13.41 chromosome region including the pseudogene KLKP1 and the transcriptional direction from centromere to telomere, except for KLK2 and KLK3, which have the opposite transcriptional direction. The classic KLK genes (KLKs 1–3) are turquoise, KLK4–KLK15 are medium purple, and the Ψ KLK1 processed pseudogene is silver; the arrowheads represent the neighboring genes: ACPT (testicular acid phosphatase) and the Siglec (sialic acid-binding immunoglobulin-like lectin) gene family as well as other less characterized genes (SNORDs, C19orf48, and CTU1). (b) The human KLK gene consists of 5 coding exons (orange boxes represent coding exons; silver boxes represent noncoding exons) and their 4 intervening introns. The positions of the catalytic residues are highly conserved with the histidine (H), aspartic acid (D) 3, and serine (S) codons on coding exons 2, 3, and 5, respectively. Most KLK genes demonstrate alternative splicing, which generates several transcript variants. Alternative 3’ splice sites or skipped exons (shown in green) result in short variants of KLKs 2, 3, 5, 8, and 12 genes. Alternative 5’ splice sites or start sites (shown in blue) also generate short variants of KLKs 2, 3, 6, 7, 8, and 11 genes. Utilization of the alternative exon 6 generates a long transcript encoding a variant of KLK12 gene (shown in blue). (c) KLK proteins are single-chain proteases that are synthesized as preproenzymes and are proteolytically processed to pro-KLKS and secreted after removal of the terminal signal peptide (Pre). The KLK sequence also includes a propeptide (Pro) that maintains the inactive state of the enzyme, as well as a serine protease domain.

reveals five major branches: (a) the classic KLKS (KLKS 1–3), (b) KLKS 4, 5, 7, and 14 and KLKP1, (c) KLKS 9 and 11, (d) KLKS 8, 10, and 15, and (e) KLKS 12 and 13, and a separate branch with KLK6. The tree (Figure 2) is similar in several aspects to other phylogenetic analyses of this cluster [150, 153, 155–157] but also includes the isoforms and reinforces the idea that all KLK genes evolved from a single gene by successive tandem duplications and genomic rearrangements facilitated by repetitive elements.

The high similarity between KLK2 and KLK3 sequences and the highest support value also suggest that they might have formed by duplication later in evolution. The data grouping KLK4/KLK5 and KLK9/KLKL1 also corroborate previous studies [153, 156]. The isolated position of KLK6 in this phylogenetic tree, unlike the findings of other authors, may explain the apparent distance of the remaining family members in respect to normal and pathological functions.

4.2. Kallikrein-Related Peptidases at RNA Level: Transcriptional Regulation Mechanisms. Kallikrein-related peptidase expression is regulated at transcriptional, translational, and posttranslational levels. At the transcriptional level, several response elements (REs) have been identified in the KLK promoters such as an estrogen-related receptor γ (ERRγ) response element [158], a GATA binding motif in KLKI [159], and functional retinoic acid response elements (RAREs) in
Figure 2: Phylogenetic relationships within the human tissue KLK gene family in humans. Phylogenetic analysis was performed using the MEGA5 [205] and Maximum Likelihood methods based on the GTR model (General Time Reversible) [154] with Gamma distribution. The bootstrap method was used (with 1000 data set replicates) to investigate node robustness [206]. The phylogenetic tree includes 15 KLK transcripts, the pseudogene-1 (KLKP1) sequence, and the trypsin 1 gene sequence (PRSS1) [155, 156]. The sequences were obtained from the NCBI Reference Sequence (RefSeq) database (http://www.ncbi.nlm.nih.gov/). Numbers indicate the percentage of 1000 bootstrap replicates at each node in the consensus. Bootstrap value ≤ 95.

KLK10 [160]. Due to the importance of KLK3 expression in prostate cancer, a number of REs have already been described for its promoter, including Sp1/Sp3 [161] and WT1 transcription factor-binding sites [162], a putative p53 RE [163], an XBE (X-factor-binding element that binds specifically to the NF-kappaB p65 subunit) in the AREc (androgen response element enhancer core) [164], and androgen-responsive elements (AREs), the last of which were also present in the KLK2 promoter (reviewed by [127, 165]).

KLK gene expression can also be regulated by epigenetic mechanisms, including histone modifications such as DNA methylation as well as microRNAs (reviewed by [166]), which can affect normal cell physiology and facilitate tumorigenesis if altered. In fact, aberrant promoter methylation leading to KLK10 downregulation has been described in acute lymphoblastic leukemia [167] as well as in breast [168], gastric [91], and prostate cancer [169]. Similarly, abnormal histone acetylation at KLK2 and KLK3 sequences and deregulated expression of miRNAs targeting KLK genes have also been reported in kidney, prostate, and breast cancer cell lines (reviewed by [166]).

In addition to epigenetic events, polymorphisms in regulatory sequences can potentially alter RNA transcription rates and protein levels, as was observed for the homozygous G base substitution (rs266882) in the androgen response element (ARE-1) of the KLK3 promoter [170] and for polymorphic alleles in the 5′-flanking region of the KLK1 gene [171]. KLK gene activity is likewise affected by polymorphisms in
The KLKs are involved in several normal processes including blood pressure, coagulation, semen liquefaction, and skin desquamation and can also protect against cardiac injury and ischemia. These proteases may also participate in skin inflammation, neurodegeneration, and autoimmune diseases.

4.3. Kallikrein-Related Peptidases at Protein Level. The KLKs are proteins of 230 amino acids and 28 to 33 kDa, although some small isoforms reach only 3 kDa. Their standard tertiary structure consists of two juxtaposed six-stranded antiparallel \( \beta \)-barrels and two \( \alpha \)-helices with the active site between the barrels [173, 174]. They are synthesized as preproenzymes, which are proteolytically processed to pro-KLKs and secreted after removal of the terminal signal peptide. Their ability to release kinins was initially viewed as the definition of a true kallikrein. However, besides plasma kallikrein, only KLK1 has the ability to cleave kininogen (in this case, low molecular weight kininogen) to release kinin. The tissue kallikrein-kinin system can protect against cardiac injury and ischemia/reperfusion-induced cardiomyocyte apoptosis as well as against oxidative stress-induced renal cell apoptosis via stimulation of kinin B2 receptor-Akt [175]. Otherwise, this system appears to be involved in the development of lupus nephritis by increasing local tissue damage triggered by autoimmune inflammation [176] (Figure 3).

As mentioned above, KLK promoters have several hormone response elements, and their expression can be regulated by steroid hormones [177]. Therefore, KLK levels in different tissues are dependent not only on the presence of specific transcriptional and translational regulators, but also on proteolytic mechanisms, as previously referred to in the degradome section. Shaw and Diamandis [178] detected distinct expression profiles for several kallikrein-related peptidases: KLK1 was highly expressed in the pancreas and salivary gland, KLKs 2, 3 (also observed in seminal plasma), and 11 were highly expressed in the prostate, KLK5 was expressed in the skin, KLK6 was expressed in the brain, KLK9 was expressed in the heart, and KLK12 was expressed in several anatomical sites. KLKs 4, 8, 14, and 15 exhibited a more homogeneous profile or were not detected in various tissues. Komatsu et al. [179] analyzed the skin stratum corneum and identified the presence of many KLKs (KLKs 5–8, 10, 11, 13, and 14). Generally, expression patterns are compatible with their origins—duplicate genes have similar expression patterns in the same tissues, and coexpression patterns are compatible with their physiological functions [153].

5. Kallikrein-Related Peptidases and Their Relationship to Health and Disease

5.1. Normal Physiological Processes and Nonmalignant Diseases. Similar to what has been observed for other proteases, several regulatory mechanisms protect tissues from harmful proteolysis by KLKs. In addition to controlled proenzyme activation and endogenous inhibitors (such as \( \alpha_2 \)-macroglobulin and serpins), there are also inactivating cleavages and allosteric regulation (reviewed by [165]). Regulatory steps may be performed by other proteases including members of the KLK family, which are supported by their
coexpression in the same tissue. For example, a KLK cascade including KLK2, KLK14, and probably other KLKs activates pro-KLK3 to generate the mature protease that directly cleaves the semenogelins SgI and SgII resulting in seminal clot liquefaction and spermatozoa release [180]. Recently, Yoon et al. [181] observed that MMP-20, which is usually expressed only in dental enamel, processes the prosequence of nine different KLKs and may be a nonspecific activator of the KLK family in pathological conditions.

Another proteolytic cascade has been described for the skin desquamation process in which KLK5 may be autoactivated or activated by KLK14 at neutral pH and then process KLK7, regulating skin desquamation. This cascade may start by KLK6 autoactivation following the cleavage of KLK11, which in turn activates KLK14. Although not completely understood, skin desquamation also depends on other proteases, including cathepsins, aspartic proteases, urokinase, plasmin, and the inflammatory metalloproteinases. Because KLK regulation is critical for proper desquamation, various endogenous inhibitors participate as attenuators of their activities, mainly LEKTI (serine protease inhibitor Kazal-type 5), a protein encoded by the SPINK5 gene. Other factors such as an acidic environment and UV irradiation (and resulting inflammation) may inhibit LEKTI, also contributing to increased KLK expression and enhanced desquamation [64]. The lack of LEKTI expression in Netherton syndrome, a rare genetic skin disease characterized by congenital ichthyosis and severe allergic manifestations, indeed results in increased proteolytic activities of KLK5 and KLK7, which trigger an inflammatory process by activating protease-activated receptor-2 (PAR-2) and stimulating cytokine production [70] (Figure 3).

KLK deregulation is also observed in several other pathological conditions, of which neurodegenerative disorders are good examples (Figure 3). Alzheimer’s disease (AD) and Parkinson’s disease (PD) are the most prevalent human neurodegenerative disorders. Both are caused by the aggregation of proteins: AD is characterized by extracellular deposits of amyloid β (Aβ) and intraneuronal aggregates of tau protein in specific brain regions, and PD is characterized by intracellular neuronal deposits (Lewy bodies and neurites) formed by insoluble α-synuclein [182, 183].

There is convincing evidence from the literature on Alzheimer’s disease that KLK6, the most abundant kallikrein-related peptidase in the central nervous system, cleaves the amyloid precursor protein (APP), a transmembrane glycoprotein from which Aβ derives. The proteolytic activity of KLK6 against APP and substrates in the extracellular matrix and perineuronal net places this peptidase as a potential component of AD pathogenesis. KLK6 expression is reduced in brain tissues, as well as in cerebrospinal fluid of AD patients [42, 184, 185], but the mechanisms behind these findings and their functional consequences are not yet known. Actually, other enzymes (α-, β-, and γ-secretases) cleave APP in different sites and generate several fragments; some of them are aggregation-prone [183]. KLKs may, for example, promote a bias toward synthesis of these toxic fragments by β- and γ-secretases.

Besides KLK6, the kallikrein-related peptidases 7 and 10 show decreased and increased levels, respectively, in cerebrospinal fluid of AD patients [39]. Recently, Shropshire and collaborators observed that KLK7 is able to cleave the core of Aβ in vitro, inhibiting Aβ aggregation and reducing neuronal toxicity [186]. This result may open new opportunities towards treatments for AD.

Several studies on Parkinson’s disease have implicated KLK6 in the degradation of intracellular α-synuclein [187]. Recent data suggested that secreted α-synuclein is also involved in the development of PD by affecting neuronal cell viability [188] and activating inflammatory response [189]. Although still controversial with respect to the intracellular type, KLK6 inefficiency in α-synuclein degradation seems to contribute to PD pathogenesis, probably due to an altered trafficking of KLK6 [187, 190] or to the resistance of certain forms of α-synuclein to KLK6-proteolysis [76, 191].

Multiple sclerosis (MS) is another example of neurodegenerative disorder in which KLK6 levels are altered. In MS patients, KLK6 is abundantly expressed and cleaves myelin proteins, resulting in demyelination and oligodendrogiopathy [192].

As may be noted from AD, PD, and MS data, KLK6 seems to be important for the neuronal homeostasis and survival. However, other kallikrein-related peptidases are probably involved in these processes, as can be deduced from the data on overexpression of KLK1 in epilepsy [193] and on the ability of a set of KLKs (KLK1, KLKs 5–7, and KLK9) to promote neural injury [62].

5.2. Malignant Diseases. As evidenced by the literature, particularly in prostate cancer, KLKs participate in proteolytic pathways that contribute to the neoplastic process (Figure 4). With respect to tumor growth, KLK1 facilitates EGFR and ERK1/2 cascade activation, which is involved in cell proliferation [194]. Similarly, KLK1, KLK2, and KLK3 can regulate tumor growth through IGF-binding protein (IGFBP) degradation, thereby allowing the release of the insulin-like growth factors (IGFs) and proliferative signals. However, a negative regulatory role for KLK3 in cancer has also been suggested because this protease can activate latent transforming growth factor-β (TGFβ), a known suppressor of growth and promoter of apoptosis [2].

Recent data have demonstrated that kallikrein-related peptidase 4 and its substrate, promyelocytic leukemia zinc finger protein (PLZF), modulate androgen receptor (AR) and mTOR signaling in prostate cells to regulate cell survival. In fact, KLK4 negatively regulates PLZF, thus preventing its binding and inhibition by AR, which keeps mTORC1 signaling active and ensures cell survival [195].

During neoplastic progression, different KLKs can regulate new vessel formation, which are essential to provide oxygen and nutrients to proliferating cancerous cells. KLKs 1 and 4 stimulate angiogenesis by cleaving kininogen to kinin or activating prometallloproteinases 2 and 9 to their active forms, thereby potentiating extracellular matrix hydrolysis and enabling endothelial cell migration and neovascularization [196–198]. Other kallikrein-related peptidases (KLKs 2 and 4) can stimulate the urokinase plasminogen activator
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KLKs 2, 4, 6, and 14
KLKs 6, 13
KLK3
KLKs 4, 5
KLK4
KLK12

KLKs 1–5, 11, and 14
KLK1

KLKs 2, 4, 6, and 14

MAPK
EGFR
PAR
Plasminogen
Angiostatin

Antiangiogenesis

Pro-HGF
HGF
Pro-HGF

Growth

mTOR
Survival

PLZF
e-cadherin

EMT, migration

Pro-MMP2/9
MMP2/9

Kininogen
Kinin

PDGF
VEGF

uPA-uPAR
Plasmin
Proangiogenesis

ECM

degradation

Invasion
metastasis

Latent TGF\(\beta\)

Active TGF\(\beta\)

Growth
Apoptosis

These examples demonstrate how important kallikrein-related peptidases are in tumor development and progression. The biological processes in which they participate are related to diseases other than cancer but are directly connected with cancer pathways, including cell proliferation, adhesion, inflammation, and apoptosis.

6. Therapeutic Relevance of KLKs

As discussed in previous sections, KLKs have been associated with different pathologic processes, from skin diseases to neurodegenerative disorders and cancer. The progress in our knowledge on all members of this protein family, functions, 3D structures, substrates, and physiological roles, has provided opportunities to develop new therapeutic approaches for different disorders.

KLKs are targeted by several types of inhibitors, including small-molecule inhibitors, antibody-, protein-, and peptide-based inhibitors, KLK-activated prodrugs, interfering RNAs, and immunotherapeutic vaccines (reviewed by [3]). PROSTVAC, for example, is a prostate cancer vaccine consisting of a KLK3 recombinant vector that contains transgenes for three T-cell costimulatory molecules (TRICOM). This vaccine has demonstrated success in inhibiting, with few side effects, cell proliferation and tumor growth and in improving overall survival [203].

Prodrugs activated by KLKs are another strategy that has been investigated. For instance, KLK3-activated peptides have the ability to target the prostate since most KLK3 is expressed in the gland whereas circulating KLK3 is normally inactivated in plasma by endogenous inhibitors [204]. This...
drug has overcome the challenge of specificity, although similar successful results are not always achieved. The reasons for that include the fact that the active sites of members of KLK family are conserved, which hampers drug design. The resolution of 3D structure of KLKs should help in this regard. However, KLKs also have overlapping and even opposing actions, which certainly depend on the physiologic, tissue, and disease context [203].

7. Conclusions

The KLK network is impressive. Its intricate signaling pathways and protein interactions strongly show that this group of proteases contributes to normal and pathological metabolisms. However, despite being intensively studied, there are many gaps in our knowledge on the molecular aspects of the KLK family. For example, there is no doubt that KLK expression deregulation participates in the development of neurodegenerative disorders. But what exactly is its role? Would it be a primary and direct one, promoting erroneously protein degradation, which results in pathogenic fragments? Or would it be one that implies cooperating with specific secretases and other enzymes to generate toxic deposits?

In cancer, it is not clear whether KLKs alterations are driver mutations or deleterious passenger mutations. The fact that similar sets of KLKs are associated with different tumor types and facilitate proliferation, migration, and other cancer hallmarks aligns with driver mutations. Differently, antiproliferative effects of KLKs and similar regulatory factors for different members of this family may argue in favor of random passenger mutations. However, both statements are not mutually exclusive and may occur simultaneously or sequentially. In fact, the idea of sequential occurrence is interesting: considering the complexity of human proteolytic system, it is reasonable to assume that the expression of specific KLKs may counteract the under- or overexpression of other KLKs or enzymes or even that those KLKs are activated, one after the other, to neutralize the expression of a driver mutation, but without success. The analysis of KLK panels in large sets of samples from diverse stages of the disease, including premalignant phases, will probably help to reveal how the expression profile evolves during the course of the disease.

Many questions are still unanswered and the scenario is therefore incomplete. Many more data are necessary to improve our understanding on the function, substrates, and role of KLKs in health and disease in order to distinguish in each case whether they are heroes, villains, or supporting actors.

Conflict of Interests

The authors declare that they have no conflict of interests.

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References


Disease Markers


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