Kallikreins on Steroids: Structure, Function, and **Hormonal Regulation of Prostate-Specific Antigen** and the Extended Kallikrein Locus

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The 15 members of the kallikrein-related serine peptidase (KLK) family have diverse tissue-specific expression profiles and putative proteolytic functions. The kallikrein family is also emerging as a rich source of disease biomarkers with KLK3, commonly known as prostate-specific antigen, being the current serum biomarker for prostate cancer. The kallikrein locus is also notable because it is extraordinarily responsive to steroids and other hormones. Indeed, at least 14 functional hormone response elements have been identified in the kallikrein locus. A more comprehensive understanding of the transcriptional regulation of kallikreins may help the field make more informed hypotheses about the physiological functions of kallikreins and their effectiveness as biomarkers. In this review, we describe the organization of the kallikrein locus and the structure of kallikrein genes and proteins. We also focus on the transcriptional regulation of kallikreins by androgens, progestins, glucocorticoids, mineralocorticoids, estrogens, and other hormones in animal models and human prostate, breast, and reproductive tract tissues. The interaction of the androgen receptor with androgen response elements in the promoter and enhancer of KLK2 and KLK3 is also summarized in detail. There is evidence that all kallikreins are regulated by multiple nuclear receptors. Yet, apart from KLK2 and KLK3, it is not clear whether all kallikreins are direct transcriptional targets. Therefore, we argue that gaining more detailed information about the mechanisms that regulate kallikrein expression should be a priority of future studies and that the kallikrein locus will continue to be an important model in the era of genome-wide analyses. (Endocrine Reviews 31: 407-446, 2010)

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ISSN Print 0021-972X ISSN Online 1945-7197 Printed in U.S.A. Copyright © 2010 by The Endocrine Society

doi: 10.1210/er.2009-0034 Received August 28, 2009. Accepted December 24, 2009. First Published Online January 26, 2010

Abbreviations: AP-1, Activator protein-1; AR, androgen receptor; ARE, androgen response element; BLTX, blarina toxin; CBP, cAMP-responsive element-binding protein binding protein; ChIP, chromatin immunoprecipitation; ER, estrogen receptor; ERE, estrogen response element; ERG, ETS-related gene; ERR α , estrogen receptor-related receptor α ; ETV1, ETS variant 1; GR, alucocorticoid receptor: GRE, alucocorticoid response element: HDAC, histone deacetylase: HRE, hormone response element; IGFBP, IGF binding protein; KLK, kallikrein-related serine peptidase; KLKB1, plasma kallikrein; KLKP1, kallikrein pseudogene 1; MSR1, minisatellite repeat 1; NCoR, nuclear receptor corepressor; PAR, protease-activated receptor; PPARγ, proliferator-activated receptor γ; Pol II, RNA polymerase II; PR, progesterone receptor; PSA, prostate-specific antigen; RXR, retinoid X receptor; SMG, submandibular gland; TSS, transcription start site; UTR, untranslated region; WFDC, whey acidic protein four disulfide core.

- XVI. Future Challenges
 - A. Are kallikreins direct targets of hormone receptors?
 - B. Where are the hormone response elements?
 - C. Do kallikreins have shared enhancers?
 - D. Is the kallikrein locus relevant in the era of genome-wide analyses?

XVII. Conclusion

I. Introduction

he 100th anniversary of kallikrein research was celebrated in 2009 (1). From humble beginnings, the kallikrein family is now studied across a remarkable range of human diseases because it has a broad expression profile (2–5). At least one of the 15 kallikreins has been detected in all tissue samples except nerves (6). The expression patterns of kallikreins have always been of immense interest and importance to the field. Tissues that express high levels of kallikreins, like the salivary gland and prostate, were used to clone new members of the kallikrein family (7, 8). Knowledge of the tissue-specific expression profiles of kallikreins has helped identify potential substrates and also underpins their use as disease biomarkers. In many tissues, kallikrein expression is regulated by steroids and other hormones. Indeed, the kallikrein locus is exceptionally hormone responsive because every kallikrein is up-regulated by multiple hormones. For this reason, many researchers use kallikreins as markers of hormone receptor activity. In particular, the actions of the androgen receptor (AR) are often measured through changes in KLK2 or KLK3 levels (9). Our laboratory reviewed the tissue-specific expression and hormonal regulation of kallikreins 20 yr ago when just three human genes had been described (10). We now return to this topic to re-examine early reports, analyze the progress that has since been made, and discuss the challenges that still remain.

II. Historical Background

The first observation of kallikrein activity was made when Abelous and Bardier (1, 11, 12) discovered that an alcohol-insoluble fraction of human urine caused peripheral vasodilation and hypotension in dogs. The depressor substance was named "urohypotensine," and the experiments were later confirmed by other laboratories (13–15). In seminal studies during the 1930s, Frey, Kraut, and Werle (16) showed that this factor was abundant in pancreatic extracts, so it was renamed "kallikrein" stemming from the Greek synonym for pancreas, *kallikreas* (16, 17). The hypotensive effect of the kallikrein enzyme, now known as KLK1, was subsequently attributed to its ability to liberate

vasoactive kinin peptides from kiningens (17-19). Therefore, kiningenase activity was initially used as the defining characteristic of kallikreins (20). This definition encompassed two distinct enzymes, tissue or glandular kallikrein (KLK1) and plasma kallikrein (KLKB1), which have different expression profiles, protein structure, and substrate specificity (21–23). KLK1 is a 25- to 40-kDa glycoprotein related to trypsin and the founding member of the kallikrein-related serine peptidase (KLK) family. It is highly expressed in a range of visceral organs and able to process kiningeens, growth factors, and extracellular matrix molecules (18, 21, 24). KLKB1 is an 85- to 88-kDa multidomain serine peptidase that is structurally related to factor XI. It is secreted by the liver into the blood system, where it activates clotting, fibrinolysis, and inflammation (18, 25). The human *KLKB1* gene spans 15 exons on 4q35 and does not belong to a multigene family (26, 27). *KLKB1* falls outside the scope of this article but has been comprehensively reviewed elsewhere (25, 28).

The use of the term kallikrein evolved with the understanding of the structure and function of the kallikreinrelated peptidase locus. Once the amino acid sequence for porcine KLK1 and nucleotide sequence for rat KLK1 were described, their considerable homology to other serine peptidases suggested that KLK1 might be part of a multigene family (29, 30). Before long, 24 mouse kallikrein genes were cloned, including 10 pseudogenes (31, 32). At least 12 genes were identified in rats, 10 of which were shown to be transcriptionally active (33, 34). At the time, only three kallikreins were thought to exist in humans: *KLK1* and the recently described prostatic serine peptidases KLK2 and KLK3 (35-39). These genes were shown to be clustered together at syntenic loci in humans and rodents, but their evolutionary relationship was enigmatic because *KLK1* was the only gene present in all species (31, 34, 40, 41).

In the 1990s, it became apparent that the human kallikrein family was larger than first described when several other genes encoding serine peptidases were found close to the kallikrein locus. With the help of the draft human genome sequence, three laboratories showed that the extended human kallikrein locus contains 15 genes (42–44). Because they were described earlier, human KLK1-3 and the rat and mouse genes became known as classical kallikreins, but KLK1 remained the prototypical kallikrein gene. Whereas KLK2 and KLK3 have 62-67% amino acid identity with KLK1, the more recently identified kallikreins, KLK4-15, have only 27-39% identity with KLK1 (43). This explains why the extended kallikrein family eluded researchers for many years. Orthologs of *KLK4-15* have subsequently been identified in several mammalian species, and it is now clear that most classical kallikreins are closely related, species-specific genes within the expanded kallikrein locus (45–48). Importantly, unlike KLK1, many kallikreins do not have kininogenase activity (49–53). To acknowledge this discrepancy, KLK2–15 are now formally named kallikrein-related serine peptidases (54). Yet for simplicity, we will continue to refer to them as kallikreins in this review. Previous names of human, rat, and mouse kallikreins are listed in Table 1.

III. Organization of the Human Kallikrein Locus

The human kallikrein locus spans approximately 265 kb on chromosome 19q13.3–13.4 and is the largest contiguous cluster of peptidases in humans (42-44). The centromeric end of the kallikrein locus is bordered by several hypothetical small nucleolar RNAs and C19orf48, a minor histocompatibility antigen of unknown function (55, 56). The CD33rSiglec gene family of IgG-like lectin receptors borders the telomeric end of the kallikrein locus (57). Intergenic spacing between kallikrein genes is quite variable, ranging from approximately 1.5 kb between *KLK1* and *KLK15* to 32.5 kb between *KLK4* and *KLK5*. Nevertheless, all but KLK2 and KLK3 are transcribed from telomere to centromere. This organization is disrupted in some tumor cells. For example, fusion between KLK2 and ETV4, an ETS family transcription factor on 17q21, was identified in a specimen of prostate cancer (58). The fused gene contains exon 1 of KLK2 and generates a novel chimeric transcript of unknown function. In addition, copy number gains of the kallikrein locus have been noted in breast, bladder, and ovarian cancer cell lines and ovarian cancer tissues (59-61). Unlike the KLK2 fusion, the copy number gains are due to large unbalanced translocations of 19q rather than rearrangements within the kallikrein locus.

Repetitive elements comprise 34–52% of the kallikrein locus, whereas protein coding regions make up only 4.3% (42, 62). This is typical for chromosome 19, which is exceptionally rich in repetitive elements (63). The most common repeats in the kallikrein locus are short interspersed nuclear elements (SINEs), such as ALUs and mammalianwide interspersed repeats (MIRs), which account for about 22% of the total sequence (42, 62). A simple minisatellite repeat, MSR1, is particularly interesting because it is predominantly, although not exclusively, located within the q13.2–13.4 region of chromosome 19 (62, 64). There are MSR1 elements in the 3' untranslated regions (UTRs) of KLK4 and KLK14, introns of KLK6, 7, and 14, and several intergenic regions (62, 65-67). Of note, the number of MSR1 repeats within the KLK4 and KLK14 3' UTRs varies between matched normal and malignant

TABLE 1. Previous designations of kallikrein genes and proteins

Symbol	Other designations
KLK	
KLK1	Tissue/renal/pancreatic kallikrein, hK1, mGK-6 (mouse), pMAK3 (mouse), rGK-1 (rat), PS (rat), RSK1105 (rat)
KLK2	Glandular kallikrein, hGK1, hK2
KLK3	Prostate-specific antigen (PSA), APS, KLK2A1, hK3
KLK4	PRSS17, KLK-like 1, enamel matrix serine protease 1 (EMSP1), androgen-regulated message 1 (ARM1), PSTS, prostase, pemB, enamel serine proteinase (pEMS), hK4
KLK5	KLK-like 2, stratum corneum tryptic-like enzyme (SCTE), hK5
KLK6	PRSS9, PRSS18, brain and skin serine protease (BSSP), protease M, zyme, neurosin, myelencephalon specific protease (MSP), hK6
KLK7	PRSS6, stratum corneum chymotrypsin-like enzyme (SCCE), hK7
KLK8	PRSS19, neuropsin, HNP, ovasin, tumor-associated differentially expressed gene-14 (TADG-14), brain serine protease 1 (BSP1), hK8
KLK9	KLK-like 3, hK9
KLK10	PRSSL1, normal epithelial-Specific 1 (NES1), hK10
KLK11	PRSS20, trypsin-like serine protease (TLSP), hippostasin, hK11
KLK12	KLK-like 5, hK12
KLK13	KLK-like 4, hK13
KLK14	KLK-like 6, hK14
KLK15	Prostinogen, ACO protease, HSRNASPH, hK15
Klk1b ^a	Name and the factor and mait according to CN 2
Klk1b3	γ Nerve growth factor subunit, pSM676, mGK-3
Klk1b4	α Nerve growth factor subunit, 2A4, mGK-4
Klk1b8 Klk1b9	pMF-2, mGK-8 Epidermal growth factor-binding protein C (EGF-BP C),
	MBI-73, mGK-9
Klk1b16	γ-renin, mGK-16
Klk1b22	β Nerve growth factor endopeptidase, epidermal growth factor-binding protein type A (EGF-BP A), enzyme A, mGK-22
Klk1b26	Epidermal growth factor-binding protein type B (EGF-BP B), Egfbp2, pSGP-2, prorenin converting enzyme, pPRECE, pPRECE-2, mGK-26, mGK13
Klk1c	
Klk1c2	rGK-2, RSKG-5, S2, rKLK2, tonin
Klk1c3	rGK-3, RSKG-50, S1, rKLK3
Klk1c4	rGK-4, rKLK4
Klk1c6	rGK-6, rKLK6
Klk1c7	RSKG-7, rKLK7, K1, rK7, esterase B, proteinase A
Klk1c8	rGK-8, rKLK8, P1, rK8
Klk1c9	rKLK9, S3, KLKP-S3, rK9, SEV
Klk1c10	rKLK10, rK10, endopeptidase k, T-kininogenase, proteinase B, antigen D3b region
Klk1c12	RSKG-3, rKLK12

^a All classical mouse genes previously had the prefix mGK (mGK-1 is KLK1b1, mGK-2 is Klk1b2-ps, etc.).

specimens of breast and prostate (62). The functional consequences of these polymorphisms have not been investigated, but could include changes in the stability of kallikrein mRNA transcripts.

Further interest in repetitive elements within the human kallikrein locus was sparked by the identification of a new

kallikrein-like gene, kallikrein pseudogene 1 (KLKP1) (68–70). KLKP1 lies between KLK2 and KLK4 and contains three "exonized" repetitive elements: an AluY repeat for exon 1, a MLT2A2 long-terminal repeat for exon 2, and an ERVL endogenous retrovirus-related repeat for most of exon 5 (69). Exons 3 and 4 are homologous to a segment spanning intron 1 to intron 2 of KLK1-3, suggesting that *KLKP1* was created by genomic duplications within the kallikrein locus. At least four different transcripts arise from KLKP1, including \(\psi KLK1\), KLK31Pshort, KLK31P-long, and KRIP1 (68-70). None of these transcripts encode a serine peptidase; however, a 143amino acid intracellular protein is translated from KRIP1 and possibly *KLK31P-long* (68). The *KLKP1* transcripts may not be the last novel transcripts to be identified in the kallikrein locus. Based on expressed sequence tag alignments, it seems that some other regions outside kallikrein genes are also transcribed (our unpublished observations). This suggests that current understanding of the kallikrein

locus may still not be complete.

IV. Structure of Kallikrein Genes

In addition to their colocalization in the genome, similarities in form and function unify the kallikrein-related serine peptidase family. As shown in Fig. 1A, all kallikrein genes have five coding exons, which are conserved in size and arrangement (42, 71). Exon 1 contains the 5'UTR and the start codon, whereas exon 5 contains the termination codon and 3'UTR. The histidine, aspartate, and serine residues of the catalytic triad are encoded by exons 2, 3, and 5. The intron phases (1, 2, 1, 0) and splice site sequences between coding exons are also consistent between kallikrein genes (72). The only exception is a variant splice site for intron 4 of *KLK10* (73).

In contrast to the coding regions, there are substantial differences between the untranslated regions of kallikrein genes. For example, the size and sequence of introns varies considerably between kallikreins (42). Furthermore, most human kallikrein genes have one to three additional upstream exons arising from alternative transcription start

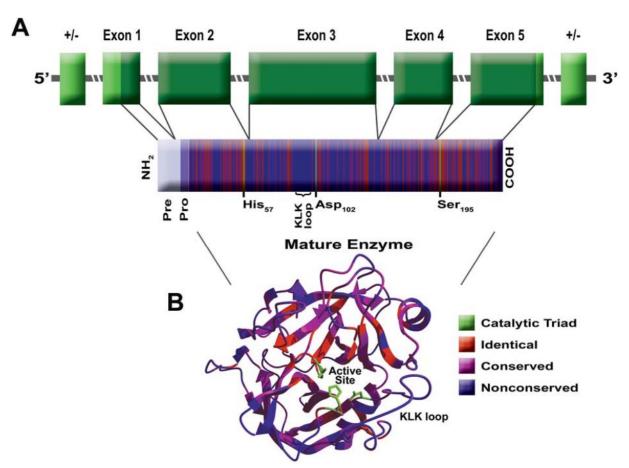


FIG. 1. The structure of kallikrein genes and proteins. A, Kallikrein genes contain five coding exons (*dark green*) and a variable number of noncoding exons (*light green*). Kallikrein proteins have a predomain, required for intracellular trafficking and a prodomain that must be cleaved for proteolytic activity. B, The structure of a mature kallikrein protease is based on the crystal structure of KLK1 reported by Laxmikanthan *et al.* (125). The histidine, aspartate, and serine residues of the catalytic triad are shown in *green*. The position of the kallikrein loop is also noted. The amino acids that are identical among all kallikreins are *red*, whereas those that are conserved in at least eight kallikreins are *purple*. Nonconserved amino acids are *blue*. The residues surrounding the active site are more highly conserved than the surface exposed loops.

sites (TSS) (3). Some of these noncoding exons need to be experimentally validated using rapid amplification of cDNA ends because they have only been predicted in silico. KLK1, 2, and 3 do not have additional 5' exons but instead have TSSs near putative TATA boxes 20 to 30 bp upstream of exon 1 (72). Unlike the 5'UTR, the 3'UTR is contained within a single exon for all kallikrein genes except KLK14, which has an additional downstream exon (65). Yet the length of the 3'UTR is quite variable, ranging from 45 bp for *KLK8* to 748 bp for *KLK7* (3). Differences in the 5' and 3'UTRs may affect the relative stability and translational efficiency of kallikrein transcripts as well as their susceptibility to microRNA (74). Further research into noncoding regions and posttranscriptional regulation of kallikreins will help clarify the relationship between transcriptional regulation and protein abundance.

V. Evolution of the Kallikrein Locus

The evolution of the kallikrein family may underlie similarities in transcriptional regulation and proteolytic function. Kallikreins belong to the S1A family of the PA clan of serine peptidases, which is the largest group of enzymes in the human degradome (75). PA peptidases have a characteristic trypsin-like structure with most S1A subset being secreted proteins (76). The origin of S1A peptidases is contentious but likely occurred in lower eukaryotes before the family underwent substantial duplications and divergence during the evolution of higher metazoates (77). Based on both phylogenetic trees and active site evolutionary markers, kallikreins are most closely related to trypsins and granzymes within the S1A family (78, 79). Kallikrein genes have the same structure as trypsin, but vary from other serine peptidases that have different intron phasing or additional coding exons (80). Indeed, it has been suggested that kallikreins could have easily been classed as trypsins had they not shared a locus with KLK1 (5). The clustering of kallikreins at a single locus differs from the dynamic evolution of most peptidase families where paralogous genes have translocated to different chromosomes after their duplication (81).

It is possible that kallikreins first arose some time during chordate evolution because they are present in mammals and some reptiles (45, 82, 83). Using bioinformatics, no kallikrein genes were detected in the chicken or frog genomes (45). In placental mammals, the kallikrein family has been described at syntenic regions to the human locus in the mouse (chromosome 7 B2), rat (chromosome 1q21), pig (chromosome 6q12–21), dog (chromosome 1), chimpanzee (chromosome 20), and other species (45–48, 84). Only *KLK5-15* are present in the opossum, which is a

marsupial (45). It is not clear whether the lack of *KLK1* and *KLK4* in the opossum means that these genes arose later in mammalian evolution or were deleted in this species.

Given that all placental mammals have *KLK1* and *KLK4-15*, it is likely that these kallikreins have important physiological functions. As shown in Fig. 2, the position and orientation of these genes are highly conserved. Phylogenetic analyses from most studies agree that KLK4 and KLK5 segregate from other kallikreins, as do KLK9 and KLK11, and KLK10 and KLK12 (43, 45–47, 81, 83–86). This implies, for example, that a duplication of *KLK9* and *KLK10* generated *KLK11* and *KLK12*, or vice versa. Currently, there is no consensus on other members of the extended kallikrein locus, but the resolution of phylogenetic trees may improve as kallikreins are identified in other species.

Further comparisons of the kallikrein locus between species suggest that KLK2 and KLK3 have a distinct evolutionary history from other human kallikrein genes. KLK2 and KLK3 are closely related to KLK1 because they segregate with *KLK1* in phylogenetic analyses and are the only other genes that encode the kallikrein loop (Fig. 1B) (87). It is likely that a duplication of *KLK1* created the progenitor of KLK2 in the early evolution of eutherian mammals. It seems this gene was silenced in rats and mice to become Klk2-ps and deleted in other species like the cow and pig (83). Humans, dogs, and many primates still have KLK2, but it is a pseudogene in some species throughout the primate order (37, 45, 88–91). It is likely that KLK3 arose through duplication of KLK2 during primate evolution. In keeping with their close evolutionary relationship, KLK2 and KLK3 have highly homologous coding, noncoding, and promoter regions. KLK3 is present in humans and various species of apes and Old World monkeys, but not New World monkeys or the dog (36, 92–95). Given that high levels of KLK2 and KLK3 are secreted by the prostate, the loss of KLK2 and gain of KLK3 in particular mammals may reflect differences in reproductive biology. The major substrates of KLK2 and KLK3 in seminal plasma, semenogelin I and II are coagulum proteins that are unique to primates (96). The semenogelin genes are rapidly evolving with many differences between species (92). KLK2 may also be under positive selection in primates at certain residues that could alter its substrate specificity, whereas KLK3 appears to be under weak or variable selection (90, 92).

Further duplications within the centromeric end of the kallikrein locus have led to divergent evolution of this gene family in some species. To avoid confusion, current nomenclature classifies kallikreins into subfamilies when they are only present within a single species or in highly

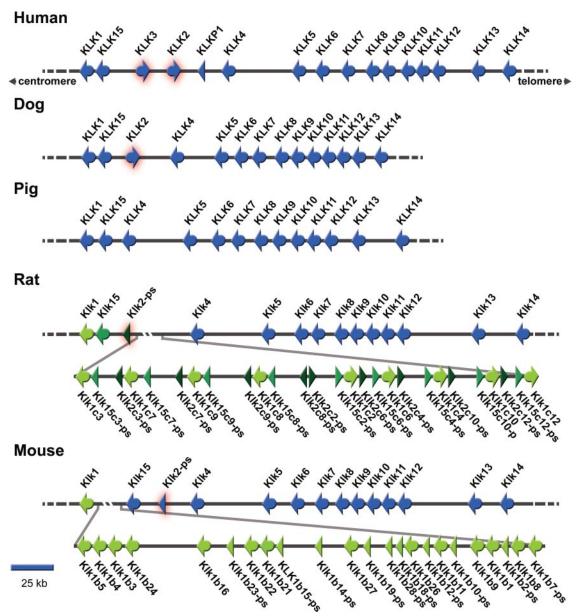


FIG. 2. The organization of the kallikrein locus. The orientation and approximate position of kallikrein genes are shown for mammalian species (human, dog, pig, rat, mouse) where the hormonal regulation of kallikreins has been studied. Kallikrein genes are shown as *arrows*, whereas pseudogenes are shown as *arrowheads*. *KLKP1* is also shown as an *arrowhead* because it does not encode a serine peptidase. The classical rat and mouse kallikrein gene subfamilies are shaded *green* to show whether they are paralogs of *Klk1*, *Klk2-ps*, or *Klk15*. *KLK2*, *KLK3*, and *Klk2-ps* genes are highlighted *red* to emphasize their close evolutionary relationship. This figure is adapted from Refs. 45, 46, 54, and 83.

related species (54). So far these subfamilies include the b-family in the mouse, c-family in the rat, and d-family in the horse. Based on Southern blots with a human *KLK1* probe, at least six classical kallikrein genes have been detected in the horse (47). One of these genes was initially classified as an ortholog of *KLK3*, but recent phylogenetic analyses suggest that *KLK1D2* is more likely to be a paralog of *KLK1* (47, 97). The functions of these horse kallikreins are unknown; however, the presence of *KLK1D1* in stallion seminal plasma further implies that there is a link between reproduction and the evolution of the kallikrein locus.

The selective pressures on the kallikrein locus seem to have been different in the shrew, which has three paralogs of *KLK1: blarina toxin (BLTX), blarinasin-1*, and *blarinasin-2* (98). These proteins have a higher level of amino acid identity with human KLK1 than it has with human KLK4–15. Like KLK1, BLTX and blasrinasin-1 are secreted from the salivary gland and have kininogenase activity (99, 100). BLTX is a constituent of shrew venom and has acquired toxic properties through small insertions and mutations that are predicted to increase its efficiency as an enzyme (98). Strikingly, venomous snakes and lizards also have KLK1-like enzymes that act as toxins, some with similar insertions to BLTX,

suggesting that particular kallikreins have undergone convergent evolution in reptiles and mammals (82, 98, 101).

The most dramatic differences in the kallikrein locus are in murine rodents. In the mouse, a 290-kb region between Klk1 and Klk15 contains 24 Klk1 paralogs, although 10 are pseudogenes (31, 48). A KLK2-like pseudogene, Klk2-ps, occupies a similar position to human KLK2, between KLK15 and KLK4, but does not have the reverse orientation of human KLK2. In rats, a 30-kb segment spanning Klk1, Klk2-ps, and Klk15 has been duplicated nine times between Klk2-ps and Klk4 (47). The Klk1 paralogs encode potentially functional proteins, whereas the Klk2-ps and Klk15 paralogs are all pseudogenes. In contrast to rats and mice, the guinea pig, a cavian rodent, is only estimated to have two or three classical kallikreins including *KLK1* and a prostatic kallikrein (47, 102). The functional relevance of the expanded kallikrein locus in rats and mice is unclear, and research into these classical kallikreins has waned now that it is known that they lack human orthologs. One theory is that murine kallikreins are involved in wound healing through licking because they are highly expressed in the salivary gland and can activate some growth factors. For example, Klk1b9, Klk1b22, and Klk1b26 can activate proepidermal growth factor, and Klk1b3, Klk1b4, and Klk1b22 are part of the 7S nerve growth factor (NGF) complex that cleaves pro-NGF (103). Yet murine kallikreins are also expressed in a range of other tissues where their functions are unknown. It has also been suggested that the expansion of the kallikrein locus is linked to the evolution of the whey acidic protein four disulfide core (WFDC) family of serine protease inhibitors, which have homology to semenogelins and a role in immunity (104). Like the kallikrein locus, the WFDC cluster has undergone separate expansion in mice and rats compared with humans.

VI. Structure of Kallikrein Proteins

Like most members of the S1A peptidase family, kallikreins are produced as preproenzymes (Fig. 1A) and must be correctly processed to become proteolytically active. Newly synthesized kallikreins are first directed to the endoplasmic reticulum and secretory pathway by the 16- to 33-amino acid signal peptide or predomain. After secretion, kallikreins remain as inactive proenzymes or "zymogens" until the 3- to 37-amino acid prodomain is removed. This induces a conformational change in the substrate binding pocket that allows kallikreins to capture and cleave their substrates (105). The prodomain is cleaved at an arginine₁₆ or lysine₁₆ residue in most kallikreins, indicating that they are activated by peptidases with trypsin-like specificity, including other kallikreins (106–108). KLK4 is the only exception. It has a glutamine₁₆ residue and may instead be activated by enzymes such as matrix metallopeptidase-20 and dipeptidyl peptidase I, a cysteine peptidase (109, 110). In general, KLK1, 2, 3, 5, 9, and 11, which have an arginine₁₆ residue, are more efficiently activated by other kallikreins than those with a lysine₁₆ residue (106, 108). KLK2, 5, 11, 12, and 14 also have the ability to autoactivate (53, 108, 111–114). Several peptidases in the thrombostasis axis including plasmin, tissue plasminogen activator, urokinase-type plasminogen activator, factor Xa, thrombin, and KLKB1 can also cleave the prodomain of particular kallikreins (107).

Once activated, kallikreins function as endopeptidases to cleave bonds within polypeptide chains. Like all members of the PA clan, the proteolytic activity of kallikreins depends on the catalytic triad of histidine 57, aspartate 102, and serine₁₉₅ residues (standard bovine chymotrypsin numbering) that span the active site (Fig. 1B) (76). Crystal structures have been solved for human KLK1 and KLK3-7, pig KLK1, horse KLK1D2, rat Klk1c2, and mouse Klk8, Klk13, Klk1b3, and Klk1b4 (85, 115–128). They show that the catalytic triad is brought together from separate parts of the protein by two asymmetric sixstranded β -barrels with "Greek key" topology that is typical of PA clan peptidases (Fig. 1B). The catalytic serine₁₉₅ initiates proteolysis by attacking a carbonyl moiety within a peptide bond of the substrate (105). The substrate specificity of kallikreins depends on residue 189, which lies at the base of the substrate binding pocket. KLK1, 2, 4, 5, 6, and 10–14 all have an aspartate₁₈₉ residue that confers them with trypsin-like specificity to cleave after arginine or lysine residues (83, 129). KLK15 also has trypsin-like specificity, but has a glutamate at position 189 (106, 130). KLK3, with a serine₁₈₉, and KLK7, with an asparagine₁₈₉, both have chymotrypsin-like specificity for tyrosine, leucine, and phenylalanine residues (39, 131). It is difficult to predict the specificity of KLK9 because its glycine₁₈₉ residue is rare among serine peptidases. It is possible that KLK9 has similar specificity to human neutrophil elastase, which also has a glycine 189 residue and tends to cleave after valine and alanine residues (132, 133). The substrate specificity of kallikreins is further refined by residues in eight loops surrounding the mouth of the active site and charged exosites on the surface of the proteins (Fig. 1B) (129).

Based on multiple sequence alignments, almost half the amino acids (122 residues) are conserved in at least half of the human kallikrein proteins (3). Of the 39 amino acids that are identical between human kallikrein proteins, 37 are also present in human trypsin and 33 in bovine chymotrypsin. The amino acids involved in proteolytic ac-

tivity and protein folding are highly conserved between kallikreins, whereas residues associated with substrate specificity are more divergent. The catalytic triad and several adjacent residues are identical among kallikreins, as are 10 disulfide bridge-forming cysteine residues. KLK4-12 and 15 have an additional pair of cysteine residues (137 and 232) that are unique to kallikreins compared with other S1A peptidases (79). Glycine₁₉₃ is present in all kallikreins except for KLK10, which has a glutamate instead. This residue is highly conserved among serine peptidases because it helps form the oxyanion hole that stabilizes negatively charged intermediates during proteolysis (105). The substitution in KLK10 may account for its apparent lack of proteolytic activity against traditional kallikrein substrates (134). The sequence of kallikrein proteins is most divergent in the eight surface-exposed loops surrounding the active site. The 99 loop is the most extreme example where KLK1-3 have an 11-amino acid insertion known as the "kallikrein loop." KLK8-11 and 13 also have small insertions in this region. The 148 loop also varies between kallikreins, most notably for KLK15, which has a 10-amino acid insertion. Notwithstanding the variation between surface-exposed loops, the core structure of kallikrein proteins is conserved. This suggests that kallikreins can cleave different substrates, but through the same mechanism.

VII. Proteolytic Functions of Kallikreins

Some serine peptidases like trypsin, thrombin, and plasma kallikrein are centrally produced and systemically active. Kallikreins, in contrast, may be locally produced and locally active or secreted as bioactive components of bodily fluids. Because the kallikrein family has a diverse expression profile, it is associated with a broad range of physiological functions. The many potential kallikrein substrates fall into several categories including growth factors and signaling molecules, extracellular matrix proteins, cell adhesion proteins, and cell surface receptors. A complete list of putative substrates is shown in Table 2. It is important to note that many candidate substrates have only been tested in binary biochemical assays where they are combined with purified or recombinant kallikreins. Consequently, the predicted physiological and pathophysiological roles of most kallikreins in most tissues are quite speculative. It is expected that more definitive and biologically relevant substrates will be identified in the next few years due to the increased use of proteomics and in vivo models.

Low molecular weight kininogen was the first kallikrein substrate to be identified and is still one of the most extensively studied. KLK1 cleaves low molecular weight kiningen at two sites to release kallidin, a decapeptide also known as lys-bradykinin, which can be further processed by other peptidases into a nonapeptide, des-Arg¹⁰kallidin (135). Kallidin and des-Arg¹⁰-kallidin are kinins that mediate the cellular effects of KLK1 by binding to bradykinin receptors 1 and 2. These G protein-coupled receptors subsequently stimulate the production of nitric oxide, prostaglandins, and other secondary mediators that trigger vasodilation, smooth muscle contraction or relaxation, inflammation, and pain (18, 135). This means that the kallikrein-kinin system has a protective role in cardiovascular disease, stroke, and renal dysfunction but exacerbates inflammatory conditions such as asthma (136). KLK2, 5, 8, and 14 cleave either high or low molecular weight kiningen in vitro; however, only KLK2 has been shown to generate the kinin peptide, and with a 1000-fold less efficiency compared with KLK1 (6, 52, 53, 137, 138).

A particularly important group of kallikrein substrates are other peptidases. KLK2, 4, 5, 12, and 14 are the most efficient at activating other kallikreins (106, 107). Yet kallikreins do not always only activate one another. KLK5 and KLK14 initially activate KLK3, before inactivating it by cleaving sites within the mature protein (139, 140). Some kallikreins have also been shown to activate other classes of peptidases. For example, KLK1 may activate matrix metallopeptidases 2 and 9, whereas KLK2, 4, and 8 may activate urokinase-type plasminogen activator (141–145). Collectively, these observations suggest that kallikreins participate in enzyme cascades. This means that the proteolytic response to a stimulus may be amplified or modified depending on the particular kallikreins that are present. Indeed, multiple kallikreins are thought to be involved in enzyme cascades in the skin and seminal plasma (111, 140, 146). Therefore, a greater understanding of the substrate specificity and gene expression profiles of kallikreins is needed to predict their biological functions in each tissue.

Kallikreins also have a well-characterized role in skin homeostasis (5). KLK1 and 4–14 are all expressed in skin, but the actions of KLK5, 7, and 14 have been studied in the most detail (147–151). Kallikreins facilitate skin desquamation by degrading desmosomal adhesion proteins such as corneodesmin, desmoglein, and desmocolin in the outermost layer of the skin (146, 152). In addition, KLK5 and KLK7 may bolster innate immunity within the skin by activating antimicrobial cathelicidins (153). The activity of kallikreins within the skin is regulated by the pH gradient, enzyme cascades with other kallikreins, and the levels of protease inhibitors such as lymphoepithelial kazal type inhibitor, which arises from the *Spink5* gene (146, 154). A range of pathologies develop when the balance of kallikrein activity is disrupted in mouse models. *KLK7*

TABLE 2. Putative kallikreins substrates (version 1)

	3003110103 (10131011 1)
Substrate	Kallikrein/s
Blood pressure regulation	
Angiotensinogen	KLK1
Atrial natriuretic peptide	KLK1
Bradykinin B2 receptor	KLK1
Fibrinogen	KLK2-6, 8, 14
Low molecular weight kininogen	KLK1, 2, 5, 14
High molecular weight kininogen	KLK1, 5, 8, 14
Plasminogen	KLK3, 5, 6, 13, 14
Tissue plasminogen activator	KLK1
Prorenin Cell-cell adhesion molecules	KLK1
Corneodesmin	KLK5, 7
Desmocollin	KLK5, 7 KLK5, 12
Desmoglein 1	KLK1, 3, 5, 6, 12, 14
Desmoglein 2	KLK5
E-cadherin	KLK6, 7
Cell surface receptors	RERO, /
PAR1	KLK1, 2, 4, 14
PAR2	KLK2, 4, 5, 6, 14
PAR4	KLK14
Urokinase receptor	KLK4
Cytokines, growth factors, and hormone	es
GH	KLK4-6, 8, 13, 14
GHRH	KLK1
IGFBP1	KLK5
IGFBP2	KLK5, 14
IGFBP3	KLK1-5, 11
IGFBP4	KLK4, 5
IGFBP5	KLK4, 5
IGFBP6	KLK4, 5
Insulin A and B chains	KLK1, 3
pro-IL-1β	KLK7
IL-2	KLK3
PTHrP	KLK3
Somatostatin	KLK1
Latent TGFβ1	KLK1, 2, 5, 14
Latent TGF β 2 Vasoactive intestinal peptide	KLK3 KLK1
Enzymes and proteases	KLK I
β -glucocerebrosidase	KLK7
proHGF activator	KLK4, 5
proKLK1	KLK2-8, 11-15
proKLK2	KLK2-8, 12-14
proKLK3	KLK2-8, 11-15
proKLK5	KLK2, 4–6, 8, 11, 12, 14, 15
proKLK6	KLK4, 5, 11, 14
proKLK7	KLK5, 12, 15
proKLK8	KLK5, 12, 15
proKLK9	KLK1-6, 12-15
proKLK10	KLK14
proKLK11	KLK2-6, 8, 11-15
proKLK12	KLK4, 5, 8, 11, 12, 14
proKLK13	KLK4, 5, 12, 14
proKLK14	KLK4, 5, 11, 12, 14
proKLK15	KLK4, 5, 12, 14, 15
proMeprin $oldsymbol{eta}$	KLK4
proMMP2	KLK1, 3
proMMP9	KLK1
Sphingomyelinase	KLK7
proUrokinase	KLK2, 4, 6, 8
	(Continued)

TABLE 2. Continued

Substrate	Kallikreins
Extracellular matrix	
Aggrecan	KLK6
Amelogenin	KLK4
Collagen I	KLK5, 6, 13, 14
Collagen II	KLK5, 13, 14
Collagen III	KLK5, 6, 13, 14
Collagen IV	KLK1, 5, 6, 8, 14
Enamelin	KLK4
Fibronectin	KLK1-3, 5-8, 13, 14
Laminin	KLK3, 5, 6, 13, 14
Vitronectin	KLK5, 6, 14
Immune defense	
Cathelicidin hCAP18	KLK5, 7
Defensin α	KLK5
Lysozyme	KLK3
Mucin 4 and 5B	KLK5, 12
Neuronal biology	•
Amyloid precursor	KLK6
L1 adhesion molecule	KLK8
Mylein basic protein	KLK6
α -Synuclein	KLK6
Seminal plasma	
Prostatic acid phosphatase	KLK4
Seminogelin I and II	KLK2, 3, 5, 14
Miscellaneous	
Apolipoprotein B-100	KLK1
Casein	KLK1, 3, 5, 6, 8, 14
Gelatin	KLK1, 3, 4-8, 14
Myoglobin	KLK3
Ovalbumin	KLK3

References for these substrates are provided in Version 2 of Table 2 in Supplemental Data. Please note that some experiments with purified kallikreins may contain contaminating peptidases.

overexpression causes inflammation and itching, *KLK8* knockout delays the recovery of the epidermis from UVB-induced inflammation, and *Spink5* knockout leads to a loss of skin barrier function (155–157). Moreover, *Spink5* mutations in humans cause Netherton syndrome, which is a severe autosomal recessive skin disorder (158). These observations suggest that kallikreins are potential therapeutic targets for skin diseases.

As previously mentioned, kallikreins have a functional role in reproductive biology through the postejaculatory cleavage of seminogelin I and II. Seminogelins are produced by the seminal vesicles and are the major structural gel-forming proteins in human semen (96). All kallikreins are present in seminal plasma; however, KLK2, 3, and 11 are by far the most abundant (159, 160). Interestingly, seminogelins regulate their own degradation by chelating the high concentration of zinc ions in seminal fluid that would otherwise inhibit kallikrein enzyme activity (140, 161–163). Degradation of seminogelins by kallikreins causes liquefaction of seminal fluid which facilitates sperm motility (164). So far, KLK2, 3, 5, and 14 have all been shown to cleave seminogelins (140, 161, 165, 166). Other kallikreins might also cleave seminogelins, other constit-

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uents of seminal plasma such as fibronectin and prostatic acid phosphatase, or simply participate in enzyme cascades (144, 167).

Hormonal Regulation of the KLK Family

In addition to their normal physiological functions, there has been great interest in the potential roles of kallikreins in cancer progression (2). For example, kallikreins are thought to enhance the invasion of tumor cells by cleaving cell-cell adhesion proteins like E-cadherin and degrading extracellular matrix molecules including fibronectin, laminin, vitronectin, and collagen I-IV. Indeed, KLK1, 3–10, and 13 all increase the *in vitro* invasiveness of tumor cell lines through reconstituted extracellular matrix solutions like Matrigel (61, 168-175). KLK6 also promotes the invasion of MCA3D keratinocytes through chicken chorioallantoic membranes (176). KLK1, 2, 4, 5, 6, and 14 may also facilitate the dissemination of tumor cells through protease activated receptors (PARs), a family of G protein-coupled receptors that initiate downstream signaling and cellular migration upon protease cleavage (177-186).

The functions of some putative substrates imply that kallikreins might also stimulate the proliferation of tumor cells. For example, IGF binding proteins (IGFBPs) are cleaved by KLK2-5, 11, and 14 (6, 138, 140, 187-192). Because cleaved IGFBPs have reduced affinity for IGF-I, it is possible that kallikreins increase the bioavailability of this mitogenic, antiapoptotic growth factor in the tumor microenvironment (193). Degradation of IGFBP3 by KLK3 increases the proliferation of prostate stromal fibroblasts (194), but there is no clear correlation between kallikrein levels and the proliferation of tumor cells. KLK3, 4, and 6 increase the *in vitro* proliferation of some cell lines, but not others (176, 195-199). Therefore, the biological significance of IGFBP degradation by kallikreins is unclear. This emphasizes that the relevance of kallikrein substrates identified in biochemical assays needs to be confirmed in biological contexts.

In addition to invasion and proliferation, kallikreins have been suggested to have several other functions in cancer progression, although many of the substrates involved have not been identified. KLK3 is the most extensively studied kallikrein in tumor progression, and its putative functions are quite varied. For instance, KLK3 may regulate oxygen balance in tumors. It inhibits the migration and tube formation of endothelial cells in vitro (200, 201) and stimulates the production of reactive oxygen species in prostate cancer cells (202). It is also possible that KLK3 modulates the immune response. For example, KLK3 has immunosuppressive effects, by inhibiting T cell proliferation and dendritic cell maturation (203, 204), as well as proinflammatory effects, by stimulating interferon γ secretion by natural killer cells (205). KLK3 has also been implicated in the metastasis of prostate cancer cells to bone. Overexpression of KLK3 increases the migration of prostate cancer cells through epithelial to mesenchymal transition (199). KLK3 also stimulates the proliferation and osteoblastic differentiation of bone cells (206–210), perhaps in part by activating latent TGFβ2 and degrading PTHrP (208, 211, 212). In turn, conditioned medium from bone cells up-regulates KLK3 expression in prostate cancer cells (213). Finally, it has been proposed that KLK3 enhances androgen-regulated gene expression in castrate-resistant prostate cancer cells by binding to a cofactor of the AR, ARA70 (197). These data show that even within one type of tumor, the functions of kallikreins depend on the context. Similarly, KLK6 and KLK10 either increase or decrease the aggressiveness of cancer cells depending on the tumor models that are tested (134, 173, 176, 198). This means that kallikreins cannot easily be classified as tumor promoters or suppressors without detailed functional studies.

VIII. Tissue-Specific Expression Profiles

Kallikreins are expressed throughout the body with distinct expression profiles that often overlap. Figure 3 shows the expression of human kallikrein genes in a broad range of tissues based on microarray data from Gene Atlas (214). The results are consistent with previous Northern blot, RT-PCR, and ELISA data showing that some kallikreins are produced at very high levels in specific tissues (42, 43, 160). For example, KLK2 and KLK3 are two of the most highly expressed genes in the prostate (215). KLK1 is abundant in the kidney, salivary gland, and pancreas, whereas KLK6 is highly expressed in the central nervous system. Yet none of these kallikreins is completely tissuespecific. KLK3 has been detected in salivary gland, brain, breast, and other tissues, albeit at more than 100-fold lower concentrations than the prostate (160, 216–218). Several kallikreins are usually expressed in the same tissue, although at quite different levels. In keeping with previous findings, Fig. 3 also shows that KLK14 and KLK15 are more lowly expressed than other kallikreins (160). Almost all kallikreins are expressed in the salivary gland, including the species-specific rat and mouse kallikrein genes (160, 219, 220). Many kallikreins are also produced in the skin, prostate, female reproductive tract, and other tissues (150, 199, 221). Intriguingly, adjacent genes in the kallikrein locus sometimes have similar expression profiles. For example, *KLK*2, 3, and 4 are all highly expressed in the prostate compared with other tissues. Similarly, KLK5-8 have parallel expression profiles in ovarian cancer (222). This has led some researchers to suggest that kallikreins

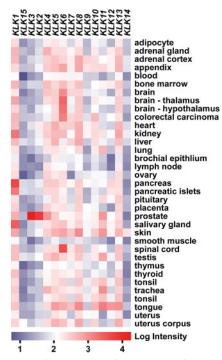


FIG. 3. Tissue-specific expression of the kallikrein family. A heatmap showing the Log_2 intensity of kallikrein gene expression in a selection of tissues from Gene Atlas (214). Data were downloaded from the Genome Expression Omnibus (GDS594 and GDS596). Genes are displayed in their order, from centromere to telomere, within the kallikrein locus. As shown in the key, *darker shades of red* represent highest gene expression. For genes with multiple probes (*KLK2*, 3, 10, 13), the average probe intensity is shown. Please refer to Supplemental Methods for more information about data analysis.

may be coordinately regulated through "cassette-type" expression (223).

Kallikreins are expressed in specific cell types within each tissue. This means that data from whole tissue extracts provide a valuable overview of kallikrein expression but should be complemented by immunohistochemistry experiments. Figure 4A shows that KLK2, 3, 4, 14, and 15 are all expressed in luminal epithelial cells within the prostate, which is in keeping with their secretion into seminal plasma (167). A detailed study by Petraki *et al.* (224) and data on KLK2, 3, 5, 7, 8, 10, 13, 14, and 15 staining from the Human Protein Atlas (225) both show that in visceral organs kallikreins are primarily expressed by glandular epithelial cells. This is consistent with the secretion of kallikreins into a range of bodily fluids.

It is notable that the tissue-specific expression profiles of kallikreins are conserved among different mammalian species. For example, KLK3 is produced in the prostate of humans and various species of Old World monkeys (93, 95, 226). *KLK1* has been detected in the human, pig, dog, cat, rat, and mouse salivary gland and pancreas (24). *KLK4* is expressed during tooth development in humans, mice, and pigs (227). *KLK8* has been studied in the skin and brain of both humans and mice (228–231). Finally,

different splice variants of KLK11 are expressed in the brain and prostate of humans and mice (232, 233). Two conclusions can be drawn from these observations. First, the consistent expression patterns imply that there are evolutionarily conserved regulatory elements within kallikrein promoters. Second, the conserved expression profiles suggest that kallikreins have important and nonredundant functions that might involve different substrates in each tissue. Indeed, KLK1, KLK4, and KLK8 knockout mice have confirmed the functional importance of these kallikreins in some tissues (234–237). KLK1 controls the production of kinins, KLK4 regulates the mineralization of tooth enamel, and KLK8 is involved in synaptogenesis and skin desquamation. Although there are many examples of conserved tissue-specific kallikrein expression between species, the complete expression profile of the extended kallikrein locus has only been reported for humans and the pig (42, 43, 46, 160). More extensive studies with other animal models are needed to determine whether the tissue-specific expression profile of each kallikrein is completely conserved or exhibits some speciesspecific differences.

IX. Kallikreins as Biomarkers of Disease

As a result of their tissue-specific expression profiles, the kallikrein family is a rich source of potential biomarkers (238). Indeed, KLK3 [prostate-specific antigen (PSA)] has been used as the serum biomarker for prostate cancer for more than 20 yr (239, 240). Normally, PSA is only secreted into seminal plasma, and very little enters the bloodstream, but in prostate cancer, it leaks into the circulation due to loss of glandular architecture and breakdown of basement membrane within the tumor (241, 242). Yet PSA is a prostate-specific marker, not a cancer-specific marker. Benign prostatic hyperplasia, a common condition in older men, also disrupts prostatic architecture and increases serum PSA levels (240, 241). Whether PSA screening reduces the rate of deaths from prostate cancer is controversial (243, 244). Furthermore, widespread use of the PSA test has led to stage migration where fewer cases of advanced and metastatic prostate cancer are being diagnosed compared with low grade and clinically insignificant disease (245, 246). The PSA test may be more valuable in younger men where benign prostatic hyperplasia is less common. For men in their forties, small increases in PSA concentration are highly predictive of the development of advanced prostate cancer in future decades (247).

In the search for ways to improve the PSA test, other members of the kallikrein family have been examined as potential adjunct biomarkers (248). There are promising Hormonal Regulation of the KLK Family

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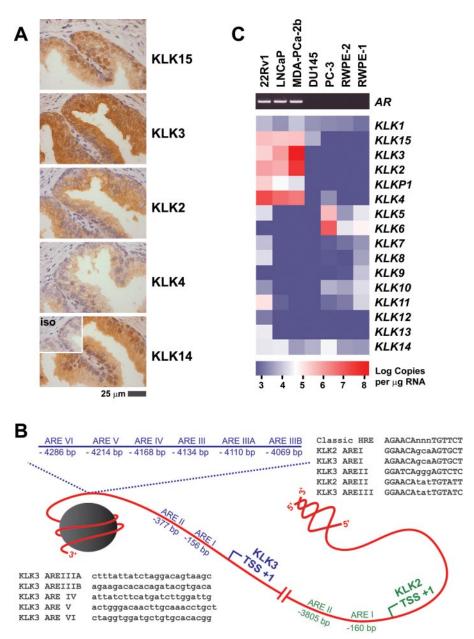


FIG. 4. Expression and androgen regulation of kallikreins in prostate. A, Immunohistochemistry for KLK2, 3, 4, 14, and 15 on serial sections of a sample of benign prostate. All kallikreins are expressed in luminal epithelial cells, but not the stroma. The isotype negative control (iso) is shown as an inset. Tissue specimens were obtained from the Australian Prostate Cancer BioResource. Scale bar, 25 μ m. B, A diagram of functional AREs in the promoter and enhancers of the KLK2 (green) and KLK3 (purple) genes. ARE positions are relative to the TSSs where the first transcribed nucleotide is +1. Typically, the DNA is double-stranded when bound by the AR and histones (circle). The sequences of KLK2 and KLK3 AREI-III are shown, as are the DNase protected regions containing KLK3 AREIIIA, B, IV, V and VI. C, A heatmap of Log copies of kallikrein transcripts per microgram of RNA in a panel of prostate cell lines. Genes are listed in their order in the kallikrein locus from centromere (top) to telomere (bottom). As shown in the color scale, red cells represent higher gene expression. The AR status of each cell line was confirmed using RT-PCR. KLK2, 3, 4, 15, and KLKP1 are highly expressed in the androgen-responsive 22Rv1, LNCaP, and MDA-PCa-2b cell lines. Intriguingly, genes that are adjacent in the kallikrein locus have similar expression profiles.

results for KLK2 that may help distinguish between prostate cancer and benign prostatic hyperplasia (249). KLK2 may also be a useful prognostic marker because its levels have been correlated with increased grade and stage of prostate cancer in several, although not all, studies (248). Serum levels of KLK5, 6, 8, 10, 11, and 14 have also been examined, albeit in comparatively small numbers of patients (250–253). There is a trend of reduced

KLK5, 6, 8, and 10 levels in men with prostate cancer compared with normal controls, but increased KLK11 and KLK14 levels.

Kallikreins have also been studied as biomarkers for a range of other diseases from breast, lung, and ovarian cancer to dermatological diseases and even neurodegeneration. Readers are referred to a recent review by Paliouras *et al.* (238) for a detailed summary of this topic.

It is a significant challenge to determine which kallikreins may be successful biomarkers for particular diseases. The levels of some kallikreins change in several diseases. The serum levels of KLK6, for instance, are increased in ovarian cancer, uterine serous papillary carcinoma, multiple sclerosis, and psoriasis (254–257). Similarly, in some diseases, the levels of multiple kallikreins change. For example, *KLK2-11* and 13–15 are all differentially expressed in ovarian cancer compared to normal or benign tissue (238). Several recent studies suggest that the key to using kallikreins as biomarkers is to test them in combination. Indeed, for colorectal, ovarian, and non-small cell lung cancer, kallikreins are more effective as multiparametric panels of biomarkers than as individual antigens (258– 261). This emphasizes the need for a thorough understanding of which kallikreins are coexpressed in different tissues, cell types, and diseases. More detailed information about the transcriptional regulation of kallikreins would also explain why they are dysregulated in particular diseases and, therefore, the biological changes that they may represent as biomarkers.

X. Steroid Hormone Regulation

Kallikreins are expressed at different levels in a diverse range of tissues. Although many of the factors that coordinate this complex expression profile are unknown, in a subset of tissues it is clear that kallikrein expression is strictly regulated by steroid hormones including androgens, estrogens, progestins, mineralocorticoids, and glucocorticoids. Genomic signaling by steroid hormones is mediated by cognate nuclear receptors. Upon ligand binding, nuclear receptors translocate to the nucleus and stimulate transcription by binding to hormone response elements (HREs) in the promoters of target genes (262). Since the identification of the first glucocorticoid response element (GRE) (263), it has been widely accepted that HREs are composed of palindromic repeats of the 5'-TGTTCT-3' motif separated by a three nucleotide spacer. Classically, the 5'-AGAACAnnnTGTTCT-3' motif is recognized by the glucocorticoid receptor (GR), mineralocorticoid receptor, progesterone receptor (PR), and AR, whereas the estrogen receptor (ER) recognizes the 5'-AGGTCAnnnTGACCT-3' motif (264).

The traditional model of hormone receptor action has recently been overhauled through the results of genome-wide studies. Technological advances have helped develop new chromatin immunoprecipitation (ChIP)-based techniques such as ChIP display, ChIP-on-chip, ChIP with paired-end diTag analysis (ChIP-PET), ChIP-sequencing, and chromatin interaction analyses by paired end tag sequencing (ChIA-PET) that allow the unbiased identification of functional hor-

mone receptor binding sites (265-269). Bioinformatic analyses of these sites have revealed some important findings. First, many hormone receptor binding sites do not contain canonical HRE motifs, but rather 6-bp half-sites. For example, only 7.1-26.8% of AR binding sites have a near consensus androgen response element (ARE), whereas 78–79.2% at least contain an ARE half-site (270–272). ER α binding sites are more likely to contain a consensuslike estrogen response element (ERE) (49-71%), but those that don't usually have an ERE half-site (268, 269, 273). Many PR and GR binding sites are also reported to only have half-site motifs (274, 275). Another significant observation from genome-wide ChIP studies is that hormone receptor binding sites seldom lie in the 5' promoter of hormone-regulated genes. Instead, many binding sites are intragenic, particularly intronic, or at distal sites upstream or downstream from currently annotated genes (266-269, 272, 273, 276, 277). Indeed, only 28% of AR binding sites and 5–7% of ER α sites are located within 5 kb of the TSS (268, 269, 276). This means that many hormone receptor binding sites may be distal enhancers that bridge large distances through extensive chromatin looping to interact with the proximal promoters of target genes (265, 266, 272, 278). Alternatively, future unbiased transcriptome studies using next-generation RNA sequencing platforms may reveal other transcripts that are located proximal to these HREs.

By analyzing large numbers of binding sites, genome-wide studies have been able to explore the mechanisms that regulate the recruitment and activity of hormone receptors. Several non-HRE motifs were found to be overrepresented in steroid hormone binding sites including those for activator protein-1 (AP-1), octomer-binding transcription factor (Oct-1/POU2F1), GATA binding proteins (GATA-2), CCAAT/ enhancer binding protein (C/EBP) and Forkhead (FoxA1) (265, 268, 270, 272, 273, 279, 280). In addition, v-ets erythroblastosis virus E26 oncogene homolog 1 (Ets1) was found to share a subset of AR binding sites in prostate cancer cells (271). Many of these molecules act as pioneer factors to prime the promoters of tissue-specific target genes in readiness for ligand-bound hormone receptors. ChIP-on-chip studies have also shown that epigenetic marks like histone 3 methylation and acetylation colocalize with hormone receptor binding sites (279, 281, 282). Indeed, mono- and dimethylation of histone 3 lysine 4 residues is critical for the recruitment of coactivators, $ER\alpha$, and the AR to enhancers (281, 282). Collectively, the results from genome-wide ChIP studies show that the specificity of hormone receptor binding to distal sites relies on epigenetic marks and coactivators rather than the similarity of the HRE to the consensus motif.

XI. Androgen Regulation of Kallikrein Expression

A. Classical kallikreins in animal models

The most extensively studied and well-characterized aspect of kallikrein gene expression is their androgen responsiveness. Initial studies focused on the mouse and rat submandibular gland (SMG), a rich source of classical kallikreins that is well known to have a sexually dimorphic pattern of cellular differentiation and gene expression (283). Most classical kallikreins in the mouse (*Klk1b1*, *1b3*, *1b4*, *1b5*, *1b8*, *1b9*, *1b11*, *1b16*, *1b21*, *1b22*, *1b26*) and rat (Klk1c2, 1c3, 1c7, 1c8, and 1c9) are more abundant in the SMG of male animals, decrease after castration, and increase after testosterone treatment (284–288). *KLK1* is a notable exception; it does not display sexually dimorphic expression in the rat SMG and may actually be down-regulated by androgens in the mouse (220, 285, 288–292). Importantly, the KLK1 paralogs are unlikely to be direct AR target genes either because it takes up to 1 wk of testosterone treatment to increase the levels of these kallikreins in the rat SMG (288). Instead, the increased expression of KLK1 paralogs is a secondary effect of androgendependent differentiation of the granular convoluted tubule cells in which these kallikreins are expressed (220, 288, 293). Indeed, *KLK1* is expressed in a different subset of cells that are unresponsive to androgens. These early experiments highlight the need to distinguish between direct and indirect hormonal regulation of kallikrein genes.

A subset of classical kallikreins may be direct AR target genes in rodent testes. Rat Klk1c8 and mouse Klk1b9, Klk1b21, Klk1b24, and Klk1b27 are all produced by Leydig cells, which secrete testosterone (220, 294-297). Klk1b21, Klk1b24, and Klk1b27 are all down-regulated in the testes of mice with attenuated androgen or AR levels (295, 298). In contrast, *Klk1b21* is up-regulated by testosterone treatment of primary and immortalized mouse Leydig cells (297). Notably, a KLK1b27 promoter construct is activated by androgens in the MA-10 mouse Leydig tumor cell line (295). Based on the activity of deletion constructs, the androgen-responsiveness of the *KLK1b27* promoter relies on the -175 to -440 region of the promoter, which contains three putative AREs (295). BLAST searches show that this whole region is highly conserved in the promoters of Klk1b21 and Klk1b24, but not human kallikrein genes. Although several human kallikreins are also expressed in the testes, their androgen responsiveness has not been examined (299, 300).

Kallikreins are also highly expressed in the prostate where they are under direct transcriptional regulation by the AR. Canine *KLK2*, originally known as canine arginine esterase, was one of the first prostatic kallikreins shown to be androgen responsive (301, 302). Canine

KLK2 levels decreased more than 100-fold in dogs that were castrated or injected with AR antagonists such as flutamide (303, 304). Nuclear run-on experiments demonstrated that canine *KLK2* was rapidly down-regulated at the mRNA level in castrated animals, implying direct transcriptional regulation by the AR (305). A subset of rat classical kallikrein genes (*Klk1c2*, *Klk1c8*, *Klk1c9*) was also shown to be expressed in the luminal epithelial cells of the prostate in response to androgens (8, 285, 294, 306, 307).

B. Human kallikreins in the prostate

Androgens regulate the prostatic expression of several human kallikreins, in particular KLK2 and KLK3. The earliest evidence for androgen-regulated KLK3 expression came from immunohistochemistry experiments showing that prostatic KLK3 levels mirror serum testosterone concentrations: low in prenatal development and childhood, greater in puberty, and highest in adulthood (308–310). Soon after the KLK2 and KLK3 genes were cloned, their androgen responsiveness was confirmed at the mRNA level using Northern blots of androgen-treated LNCaP prostate cancer cells (38, 311–315). These observations were verified with a range of in vitro and in vivo experiments (316-319). Numerous studies have since used KLK2 and KLK3 as prototypical AR target genes to investigate different aspects of androgen signaling in prostate cells. KLK3 levels are also monitored in patients undergoing androgen ablation therapy for prostate cancer because KLK3 is re-expressed when AR signaling is reactivated in castrate-resistant tumors. KLK3 levels, however, are highly heterogeneous in castrate-resistant prostate cancer and do not directly correlate with tumor growth (320, 321). This variability may be due to the different ways that tumors adapt to castrate androgen levels including overexpression and mutation of the AR, up-regulation of transcriptional coactivators, and intratumoral steroidogenesis (322).

C. The KLK3 promoter and enhancer

AREs were identified within the promoter of *KLK3* soon after its androgen-dependent expression was established. Using DNase I footprinting assays, the Trapman group showed that the *KLK3* promoter is bound by nuclear proteins in LNCaP cells (323). They then identified the first *KLK3* ARE, AREI (AGAACAgcaAGTGCT), at -170 to -156 bp from the TSS using a series of promoter deletion and mutation constructs (323). Other groups confirmed this finding using similar reporter experiments (324) and EMSAs (325). The results from reporter assays suggested that another ARE might be present between -320 and -539 bp from the *KLK3* TSS (323). Subsequently, AREII (GGATCAgggAGTCTC) was identified at -400 bp

from the TSS and found to be a low-affinity AR binding site that cooperates with AREI (326). This was confirmed by other studies that also suggested that Fos-related complexes, distinct from AP-1, might be important in mediating AR transactivation of the *KLK3* promoter (327–329).

KLK3 expression is also regulated by a highly androgen-responsive enhancer located between -5824 and -3738 bp from the TSS (330). Importantly, the KLK3 enhancer is prostate specific, unlike the proximal promoter AREs, which are active in nonprostatic cell lines such as Panc-1 and Ovcar-3 cells (330). The KLK3 enhancer contains AREIII (GGAACAtatTGTATC) at -4148 to -4134 bp as well as GAGATA motifs that bind a putative coactivator (331-334). The observation that AREIII has lower activity in isolation than AREI suggested that other AR binding sites are located within the enhancer (330, 331). Accordingly, AREs IIIA, IIIB, IV, V, and VI were later identified within the enhancer between -3870 bp and -4366 bp from the KLK3 TSS (335). These sites do not contain consensus ARE motifs, but DNase I footprinting assays show they directly bind recombinant AR. The location of all KLK3 AREs is shown in Fig. 4B. Chromatin looping may bring the promoter and enhancer AREs together to form a coordinated transcription complex (336) as supported by ChIP chromosome conformation capture assays (278). It is also possible that there is a separate transcriptional complex at the KLK3 enhancer because reporter constructs spanning the -4685 to -3862 bp region have basal promoter activity in LNCaP cells (337).

ChIP assays have confirmed *in vivo* binding of the AR to the KLK3 promoter and enhancer in LNCaP cells (336, 338). ChIP experiments also show that androgen-induced recruitment of the AR is cyclic and coincides with histone H3 acetylation as well as binding of RNA polymerase II (Pol II) and AR coactivators including cAMP-responsive element-binding protein binding protein (CBP), p300, steroid receptor coactivator-1 (SRC-1/NCOA1), SRC-2 (GRIP1/TIF2/NCOA2), SRC-3 (AIB1/NCOA3), mediator complex subunit 1 (MED1/TRAP220), coactivator-associated arginine methyltransferase 1 (CARM1) and others (278, 336, 338, 339). This may in part be regulated by upstream protein kinase A signaling (340). The AR still occupies the KLK3 promoter in cells that are treated with AR antagonists such as bicalutamide, although this results in the corecruitment of AR corepressors like nuclear receptor corepressor (NCoR), silencing mediator of retinoic acid and thyroid hormone receptors (SMRT), histone deacetylase (HDAC) 1 and HDAC2 instead of Pol II and AR coactivators (278, 336, 338, 339). Notably, IL-6 might have a role as an endogenous AR antagonist because it inhibits androgen-mediated recruitment of AR, CBP, and p300 to the KLK3 enhancer and promoter (341). Generally, Pol II

and AR coactivators are recruited to both the promoter and enhancer of *KLK3*. In contrast, AR corepressors only bind the *KLK3* promoter (278, 336), although one study has shown bicalutamide-mediated recruitment of NCoR to the enhancer (339). Table 3 lists all proteins that have been shown to bind to the *KLK3* gene using ChIP assays, EMSAs, and promoter deletion constructs. Readers are referred to an excellent review (342) for details of all factors that interact with the AR, some of which modulate *KLK3* expression, but have not yet been shown to be directly recruited to the *KLK3* gene.

Two particularly interesting coregulators are ETV1 (ETS variant 1) and ERG (ETS-related gene). Both factors are commonly overexpressed in prostate cancer due to chromosomal rearrangements that fuse their coding regions to the androgen-regulated promoter of *TMPRSS2*. ETV1 and ERG both bind the *KLK3* enhancer, but they have opposing effects; ETV1 synergistically increases ARdependent *KLK3* expression, whereas ERG represses *KLK3* expression (343, 344). Perhaps different gene fusions account for some of the heterogeneity in *KLK3* expression between prostate tumors.

D. KLK3 as a marker of prostatic differentiation

Kallikreins can be used as markers of particular cell types, especially when their patterns of tissue-specific expression and hormonal regulation converge. KLK3 is a good example because it is one of the most highly expressed genes in the prostate (215). This means that KLK3 may have several clinical applications in prostate cancer. In addition to its use as the serum biomarker, KLK3 has been tested as a marker of circulating tumor cells, as an antigen to prime dendritic cells for targeted immunotherapy, and as an enzyme to activate cytotoxic prodrugs (345-347). Furthermore, the KLK3 promoter and enhancer have been used to design prostate-specific expression vectors for gene therapy (348). KLK3 is more precisely a marker of terminally differentiated luminal epithelial cells of the prostate. It is not produced by stem, transit amplifying, or intermediate cells, which make up the basal layer of the epithelium and express little or no AR(349). Although the prostate stroma is androgen-responsive, it does not express KLK3 (350). This suggests that KLK3 expression in luminal epithelial cells depends on more than just androgens and AR. Recent genome-wide ChIP studies have shown that epigenetic marks, such as histone 3 lysine 4 methylation and pioneer coactivators guide hormone receptors to enhancers of tissue-specific target genes (282). This holds true for AR-mediated expression of KLK3. Prostate cancer cell lines that express endogenous KLK3 have high levels of di- and trimethylated histone 3 lysine 4 at the promoter and enhancer of KLK3 (351). Furthermore, pioneer factors like GATA2 bind to the KLK3 enhancer in prostate cells and are re-

TABLE 3. Factors that bind to the *KLK3* gene and their effect on KLK3 expression (version 1)

Transcription factors			
ATF2	U	GATA3	↑
c/EBP $lpha$	\downarrow	$HIF1\alpha$	^
c/EBPβ	Ţ	NF1	†
CREB [°]	†	p50/p65 complex	†
Fos	\downarrow	p53	į.
c-Jun	^/↓	PDEF/SPDEF	†
c-Rel	1	Oct1/POUF1	†
EGR1	1	RREB-1	Ţ
ERG	\downarrow	Runx1/CBFα1	1
ERRlpha	↑ ↑ ↑/↓	Sp1	1
ETV1	↑	Sp3	1
FOXA1/HNF3 α	↑/ ↓	SREBP-1c	\downarrow
FOXP1	\downarrow	Thyroid hormone	1
		receptor	
FOXO1	\downarrow	USF2	\downarrow
GATA2	1	Wilms tumor 1	U
Chaperone and co-chaperones			
Bag-1L	U/ ↑	Hsp70	U/ ↑
Hsp27	1		
Chromatin remodeling complex			
BAF57/SMARC1	1	SNF5/SMARCB1	U
BRG1/SMARCA4	↓	SRG3/BAF155	1
BRM/SMARCA2	1		
DNA repair		1/ 00 N/DCCF	
Ku70/XRCC6		Ku80/XRCC5	1
Histone acetyltransferases and c			
CBP	Î	SIRT1	<u> </u>
DBC 1/KIAA1967	↑ ↑ ,	SRC-1/NCOA1	\uparrow
HDAC1 and 2	↑ /↓	SRC-2/GRIP1/ TIF2/	↑
200		NCOA2	
p300	Ţ	SRC-3/AIB1/ NCOA3	\uparrow
P/CAF	Ţ	Tip60/KAT5	\uparrow
Sin3a	↓ domoothu	dagag	
Histone methytransferases and CARM1/PRMT4			^
G9a/EHMT2	1	JMJD2C/KDM4C	1
JHDM2A/KDM3a	1	LSD1/KDM1A NSD2/WHSC1	↑ ↑
Kinases and phosphatases	I	NSDZ/VVIISC I	ı
LATS2/KPM	1	PDK1	U/↓
MAK	*	SCP1-3/CTDSP	J
Nuclear receptor co-regulators	ı	JCI I J/CIDJI	V
Alien/COPS2	I	SMRT/NCOR2	1
NCoR	ľ	TRAP220/MED1	Ť
RIP140/NRIP	ľ	u 220/IVILD I	ı
Splicing and RNA metabolism	¥		
Ddx5/p68	↑	p54nrb/NONO	Ţ
PSF/SFPQ	<u> </u>	Sam68/KHDRBS1	Ů/ ↑
p44/WDR77	Ť		1
Signal integrators and transduce	ers. scaf	folds, and adaptors	
Ack1/TNK2	↑	PRK1/PKN1	↑
β-catenin	†	Smad1	Ţ
IRS-1	†	EBP1/PA2G4	Ĭ
Nucleophosmin	†		•
Ubiquitination/proteosome path	nway		
E6-AP/UBE3A	^	PIRH2/ARNIP RCHY1	\uparrow
Mdm2	↓	RNF6	†
Diverse functions			•
CDK6 (cell cycle)	\uparrow	Pdx1 (Antioxidant	\uparrow
-		enzyme)	-
CRIF1/GADD45GIP1 (cell	\downarrow	Pontin/RUVBL1	↑
cycle)	•	(AAA+ ATPase)	'
DACH1 (tumor suppressor)	\downarrow	Prohibitin (Nuclear	\downarrow
(,4 13pp. 65501)	•	and Mitochondrial	•
		Protein)	
HIP1 (endocytosis)	\uparrow	Ubc9/UBE E2I	↑
ini i (chaocytosis)	I		ı
		(Sumoylation)	

Full gene names and references for these transcription factors are provided in Version 2 of Table 3 in Supplemental Data. ↑, Increased KLK3 expression; ↓, decreased expression; U, unknown effect on KLK3 expression.

quired for maximum androgen-regulated gene expression (272, 279, 352). Within the prostate, GATA2 and KLK3 are both produced by luminal epithelial cells, but not the stroma (242, 353). As previously noted, KLK3 is expressed in some other tissues, but at much lower levels. Presumably, these tissues lack the precise combination of methylation, coactivator expression, and AR activity that stimulates such high levels of KLK3 in the prostate.

E. KLK3 promoter polymorphisms

The *KLK3* promoter and enhancer harbor numerous polymorphisms, some of which have been reported to alter androgen responsiveness (354). The G−158A polymorphism (rs266882) in AREI is of particular interest because it may alter AR binding and consequently androgen-induced *KLK3* expression (355). Contrary to two previous reports (355, 356), our laboratory found that the A-allele increases both the binding affinity of AREI for the AR and the transcriptional response to androgens (357). We also contend that the data presented by Shibahara et al. (356) actually support our findings because they show higher binding affinity of the A allele to the AR in EMSAs and a qualitative, but not statistically significant, increase in transcriptional activity for the A allele in reporter assays. The G-158A polymorphism has been associated with higher serum KLK3 (PSA) levels, tumor volume, stage and grade of disease, lymph node invasion, and circulating tumor cells in some but not all studies (358-365). An initial association study found that men with the GG genotype have a 3-fold increased risk of developing prostate cancer that is compounded 5-fold when associated with short AR alleles (364). Subsequent studies have reported increased risk of prostate cancer for either the A (361, 366, 367) or G (358, 364, 368, 369) allele, whereas others have found no significant association for either allele (370-373). Furthermore, a meta-analysis of 12 previous studies found that neither allele is associated with prostate cancer risk, nor any of the clinical parameters previously investigated (374). Other KLK3 promoter polymorphisms have also been examined, but preliminary studies suggest that the G-4643A polymorphism (rs925013) may be the only one to confer increased risk of prostate cancer (366, 370, 373, 375–377). The inconsistencies between studies likely stem from many factors including differences in the size and ethnicity of sample populations, confounding cultural and environmental effects, and the presence or absence of other protective alleles.

F. The KLK2 promoter and enhancer

The *KLK2* and *KLK3* promoters share over 80% sequence identity in the regions between -1 to -196 bp and -1673 to -4165 bp from the KLK2 TSS (Supplemental Fig. 1A, published as supplemental data on The Endocrine Society's Journals Online web site at http:// icem.endojournals.org). Not surprisingly, similar motifs to the KLK3 AREs have been identified within the KLK2 promoter and enhancer. In fact, the sequence (GGAA-CAgcaAGTGCT) and position (-160 bp) of KLK2 AREI is almost identical to KLK3 AREI (Fig. 4B) (319). Promoter constructs spanning KLK2 AREI have also confirmed that it is androgen responsive (324, 327). Like KLK3, much of the androgen responsiveness of KLK2 is mediated by the distal enhancer (378, 379). The data from several studies using a series of deletion constructs collectively show that the *KLK2* enhancer spans the region from -4.4 to -3.8 kb from the TSS (378, 379). This *KLK*2 minimal enhancer region was also identified by Southern blotting with a KLK3 enhancer probe (380). The KLK2 enhancer contains the functionally validated KLK2 ARE (GGAACAtatTGTATT) located at -3819 to -3805 bp from the TSS, which is similar to KLK3 AREIII (Fig. 4B) (378, 379). KLK3 AREs IIIA, IIIB, and IV also seemed to be conserved within the KLK2 enhancer (Supplemental Fig. 1B). ChIP studies have shown that the AR is recruited to the KLK2 promoter and enhancer within 1 h of androgen stimulation in LNCaP cells (338, 339). Furthermore, Pol II is synergistically recruited with the AR in a cyclic event (339). Methylation of histone 3 Arg-17 at the *KLK2* enhancer and androgen-induced recruitment of CARM1, a histone methyltransferase, are also necessary for activation of KLK2 gene expression (381). The AREs within the human KLK2 promoter and enhancer are shown in Fig. 4B.

It is notable that the promoter of canine *KLK2* is similar to its human ortholog. Canine *KLK2* has an ARE in the same position as the human AREI with a similar, although not identical, sequence (AGGACAacaGGTGTT) that binds the AR with 100-fold lower affinity compared with *KLK3* AREI (382). The enhancer ARE is also conserved for canine *KLK2* (GGGAACtatTAATACT) (47). Intriguingly, this motif has been deleted in the cotton-top tamarin where *KLK2* is a pseudogene (84). This implies that the function of KLK2 is intertwined with its transcriptional regulation.

G. Other prostatic kallikreins

In addition to *KLK2* and *KLK3*, other kallikreins are also up-regulated by androgens in the prostate. There has been particular interest in *KLK4* because it is highly expressed in the prostate. *KLK4* expression is up-regulated by androgens at the mRNA and protein level in LNCaP cells, but down-regulated in the CWR22 prostate cancer xenograft in castrated mice (66, 383–386). Our laboratory recently confirmed previous findings that the most abundant *KLK4* transcript in prostate cancer cells arises from an alternative downstream TSS in exon 2 (384, 385).

This truncated transcript and the classical form of *KLK4* are both androgen regulated. Several putative AREs have been identified upstream of *KLK4 in silico* (184). One element located 1005 bp upstream of the exon 2 TSS (GGTGCAggaGATTGT) indirectly binds the AR in EMSAs, but does not mediate androgen-regulated expression in reporter assays (385).

The KLK31P and KRIP1 transcripts of the KLKP1 gene, which lies adjacent to KLK4, are also androgen regulated in LNCaP cells (68, 69). Notably, recent AR ChIPon-chip studies have shown that there is an AR-occupied region close to the KLKP1 gene (279, 282). Of the remaining kallikreins, there are preliminary data that androgens stimulate *KLK12* and *KLK15* gene expression in LNCaP cells as well as KLK5 and KLK8 protein levels in AR-transfected PC-3 cells (387–390). To distinguish between androgen-dependent and androgen-responsive kallikreins, we have examined the expression of all 16 genes in a range of prostate cell lines using quantitative RT-PCR (Fig. 4C). KLK1-4, KLKP1, and KLK15 levels correlate with AR status, implying that the expression of these kallikreins in prostate epithelial cells is AR-dependent. Other kallikreins have AR-independent expression profiles, including *KLK14*, which is ubiquitously expressed.

H. Kallikrein expression in breast

The breast is also a prominent site of androgen-regulated kallikrein expression. Most studies have used BT-474 and T47D breast cancer cells, which express the AR, ER, and PR (391). KLK2, 3, 8, 10, 11, 13, 14, and 15 are all up-regulated by androgens at the mRNA and protein level in breast cancer cell lines (223, 392-396). Based on qualitative RT-PCR, KLK4, 5, 6, 9, and 12 expression may also be stimulated by androgens in breast cancer cell lines, but these observations require further validation (71, 223, 389, 397, 398). Notably, KLK3 has been detected in 98% of breast cancer specimens that express AR (399). Moreover, ChIP experiments have shown that AR is recruited to the proximal promoter of KLK3 in dihydrotestosterone-treated T47D cells (400). These observations suggest that KLK3 expression in breast is predominantly AR-dependent, just as it is in prostate. In contrast, other kallikreins may be regulated by both direct and indirect mechanisms. In BT-474 cells that are co-stimulated with androgens and estrogens, membrane-bound AR indirectly enhances estrogen-dependent KLK10, 11, and 14 expression by increasing Akt phosphorylation and downstream ER activity (401). An AR antagonist blocks the synergistic effect of androgens, whereas an ER antagonist completely inhibits kallikrein expression. In T47D cells treated with androgens alone, the AR may directly mediate a more modest increase in KLK10 and KLK11 levels (400). ChIP experiments suggest that the AR binds within two regions of the KLK10 (-2000 to -2500 bp and +1000 to +1500 bp) and KLK11 (-1000 to -1500 bp and +1 to +500 bp) promoters, which contain predicted AREs. Yet a reporter construct spanning the -2000 to -2500 bp region of KLK10 is not responsive to androgens in T47D cells (394). This is similar to our observations for KLK4 in prostate cells (385). Perhaps AR-mediated induction of KLK4, 10, and 11 involves indirect interactions of more distal AR complexes.

XII. Progestin Regulation of Kallikrein Expression

Like androgens, progestins coordinately stimulate the expression of multiple kallikreins. KLK2 and KLK3 are both up-regulated by progestins in breast cancer cell lines (392, 395, 402). KLK2 (-493 to +27) and KLK3 (-620 to +40) reporter constructs are also activated by progesterone in PC-3 prostate cancer cells cotransfected with PR (327). Therefore, it is tempting to speculate that the PR is recruited to AREI and AREII. A reporter construct spanning the KLK3 promoter and enhancer was also stimulated by progestins in T47D cells (331). Yet, a construct only containing the KLK3 enhancer was not responsive to progesterone in PR-transfected BHK cells (335). This is consistent with the KLK3 enhancer being more AR-dependent and prostate-specific than the promoter. Progesterone also stimulates KLK4 expression in KLE endometrial cancer and T47D breast cancer cell lines, possibly through a functional progesterone response element (AGAACAtgagagAGAACA) located 2419 bp upstream of the primary TSS in breast cells (385, 403). The KLK4 progesterone response element has two strong half-site motifs rather than the classical 15-bp HRE sequence. Although this element binds the PR in EMSA and ChIP experiments, it is only moderately responsive to progesterone in luciferase reporter assays. In addition to KLK2, 3, and 4, preliminary data suggest that KLK6 and 8-15 expression are also up-regulated by progestins in breast cancer cells (71, 388, 389, 393, 396, 404-407). Progestins may also stimulate kallikrein expression in the female reproductive tract because KLK5, 6, 7, 11, and 12 levels in human cervico-vaginal fluid all peak in the secretory phase of the menstrual cycle (221). Furthermore, KLK5 and KLK6 may be direct PR target genes because they are up-regulated in the uteri of wild-type mice, but not PR knockout mice, within 4 h of progesterone treatment (408). Collectively, these observations show that progestins regulate kallikrein expression in different tissues, in some instances through direct binding of the PR to kallikrein promoters.

XIII. Corticosteroid Regulation of Kallikrein Expression

Unlike androgens and progestins, glucocorticoids either activate or repress kallikrein expression, particularly in breast and cervical cancer cell lines. For example, KLK10 levels are increased by dexamethasone treatment of MCF7, T47D, and MDA-MB-468 breast cancer cells, but decreased in MCF-10A cells (388, 409). The effect of dexamethasone on KLK5, 6, 8, and 11 expression also varies between cell lines. Generally, these kallikreins are coordinately regulated and exhibit the same response to glucocorticoids in each cell line (388). The GR can activate or repress gene expression in cis by directly binding to different types of GREs, or in trans by interacting with other transcription factors (410). The mechanisms underlying kallikrein expression and their differences between cell lines remain to be determined. Numerous GRE half-sites have been identified in the promoters of KLK5, 6, 7, 8, 10, and 13 in silico, but none have been experimentally verified (388). Notably, KLK2 and KLK3 promoter constructs are just as responsive to dexamethasone as androgens, so it is possible that the GR binds AREI and AREII (326, 327). Yet androgens are much more potent than glucocorticoids at increasing endogenous KLK2 and KLK3 levels, probably because the KLK2 and KLK3 enhancers are only activated by androgens (392, 395). Overall, there is mounting evidence that glucocorticoids modulate kallikrein expression, but more research is required to define the molecular mechanisms and in vivo significance of these findings.

The effects of adrenal hormones on *KLK1* expression have been more extensively studied. Initial reports suggested that mineralocorticoids directly regulate renal KLK1 expression. Urinary KLK1 levels are sometimes, although not always, increased in patients with primary hyperaldosteronism, a condition where the adrenal glands overproduce the potent mineralocorticoid aldosterone (411, 412). Normal patients on low-salt diets that stimulate endogenous mineralocorticoid production also have increased urinary KLK1 levels, but not if they are treated with mineralocorticoid receptor antagonists (413, 414). Yet experiments with animal models yielded conflicting results. Studies that measured the amount of KLK1 protein or activity after extended mineralocorticoid treatments reported an increase in renal or urinary KLK1 levels (415, 416). In contrast, studies that used acute mineralocorticoid treatments or measured KLK1 mRNA levels found no change in KLK1 expression (417, 418). Therefore, the increase in KLK1 protein may be due to posttranscriptional regulation or simply a secondary effect of changes in renal physiology.

In contrast to mineralocorticoids, glucocorticoids are generally associated with decreased renal KLK1 expres-

sion. Yet differences in the dose and duration of hormone treatments and methods of measuring KLK1 levels have led to conflicting data between studies. Nevertheless, experiments with short time points, which are arguably the most informative, suggest that glucocorticoids have a direct effect on KLK1 expression. For example, a low physiological dose of the glucocorticoid methylprednisolone reduces in vivo protein synthesis of rat renal KLK1 within 2 h (419). Renal KLK1 levels in the rat are also inversely proportional to diurnal changes in corticosterone concentrations (419). In addition, dexamethasone decreases *KLK1* mRNA and protein levels in AR42] rat pancreatic cancer cells within 12 h of treatment (420). Although these observations suggest that corticosteroids modulate KLK1 levels, they do not regulate basal KLK1 expression. KLK1 is still expressed in the rat kidney, pancreas, and SMG when adrenalectomy is used to abolish endogenous mineralocorticoid and glucocorticoid production (418, 421).

XIV. Estrogen Regulation of Kallikrein Expression

The first studies to examine the effect of estrogens on kallikrein expression focused on the rat anterior pituitary, where there is greater kininogenase activity in female animals (422). KLK1 is produced by lactotrophs within the rat anterior pituitary, which also secrete prolactin in response to estrogens (423). KLK1 and prolactin levels follow similar trends; both are produced after the onset of puberty, increase in animals treated with 17β -estradiol, but decrease in ovariectomized animals (294, 424–426). Yet changes in KLK1 and prolactin expression have different kinetics. High doses of the nonsteroidal estrogen diethylstilbestrol cause lactotroph proliferation and anterior pituitary adenomas in rats. There is a rapid 250-fold increase in KLK1 levels in these tumors, but KLK1 levels subsequently plateau, even as prolactin levels and tumor size continue to increase (427, 428). There is also discordance between KLK1 and prolactin levels in human pituitary specimens and immortalized rat pituitary cell lines (429, 430). These discrepancies might be due to the mixture of direct and indirect mechanisms that seem to contribute to estrogen-regulated *KLK1* expression. Estrogens increase the number of lactotrophs in the anterior pituitary, so changes in KLK1 levels are partly a secondary effect of variations in cellular differentiation (431). Based on immunohistochemistry experiments, estrogens also increase the intensity of KLK1 staining in each lactotroph, suggesting that KLK1 may indeed be a direct ER target gene (431). Potential EREs have been noted in the proximal promoter of rat KLK1, but have not been experimentally analyzed (431, 432).

The effect of estrogens on kallikrein expression has also been investigated in the female reproductive tract. KLK1 expression in the human endometrium fluctuates with the menstrual cycle, peaking with maximum estrogen concentrations in the mid to late proliferative phase (433). There is a similar trend in rats and mice where endometrial KLK1 levels are highest in the estrogen-regulated proestrous phase (434–436). KLK1 may be a direct ER target gene because it is up-regulated in the endometrium of ovariectomized mice within 3 to 6 h of estradiol treatment (435, 437). There are some species-specific differences because *KLK1* levels do not change across the estrous cycle in the pig (438). In all species, however, endometrial KLK1 expression increases at sites of embryo implantation, possibly due to estrogen secreted by blastocysts (436, 439, 440). Estrogen also stimulates KLK1 expression in the vagina of ovariectomized mice (437).

KLK8 has a similar expression pattern to KLK1. It is highly expressed in the human endometrium during the proliferative phase of the menstrual cycle and up-regulated by estrogen in the mouse vagina (441, 442). Yet *KLK8* levels in the mouse do not change until 48 h of estrogen treatment, suggesting that this response is a secondary effect of changes in cellular differentiation (442). Little is known about the effect of estrogens on the other kallikreins in the female reproductive tract. Preliminary data suggest that estrogens upregulate KLK4 expression in KLE human endometrial cancer cells and OVCAR-3 human ovarian cancer cells (403, 443). Estrogen stimulates KLK11 secretion from Me-180 cervical cancer cells, but it slightly decreases KLK6, 10, and 11 secretion from VK2 vaginal epithelial cells (221).

Estrogen has different effects on kallikrein expression in the breast compared with the reproductive tract. Unlike the endometrium and vagina, KLK1 expression is not upregulated by estrogen in the mouse mammary gland (437). Interestingly, estrogen actually inhibits the androgen-dependent expression of KLK2 and KLK3 in human breast cancer cell lines (392, 402). In contrast, KLK5, 6, 8, 10, 11, 13, and 14 mRNA and protein levels are all stimulated by estrogen (223, 250, 388, 393, 401, 404, 405). Qualitative RT-PCR experiments suggest that estrogen may also increase KLK7, 9, 12, and 15 expression in breast cancer cells (71, 389, 444, 445). Notably, the estrogen-responsiveness of each kallikrein differs between breast cancer cell lines that are all ER α - and ER β -positive (223, 446). For example, KLK5 is up-regulated by estrogen in BT-474 and MCF7 cells, but is not expressed in T47D cells. In contrast, KLK8 is estrogen-regulated in T47D and MCF7 cells, but not in BT-474 cells. KLK10, 11, and 14 are produced by all three cell lines, but are only up-regulated by estrogen in BT-474 and MCF7 cells. It has been proposed that the discrepancies between cell lines are due to geLawrence et al.

netic or epigenetic changes at the kallikrein locus or differences in the cross-talk between the ER and other signaling pathways (223). Indeed, it is not clear whether kallikreins are direct or indirect targets of ER in breast cancer cell lines. Using bioinformatics, one study failed to identify any EREs within 6 kb of KLK5, 6, or 8, although another noted that there are several ERE half-sites upstream of KLK5 and 7 (223, 447). The data are more promising for KLK10. An ER α ChIP-on-chip study noted that KLK10 is up-regulated in MCF7 cells within 1 h of estrogen treatment and has a nearby ER α binding site (448).

Although many kallikreins are estrogen-responsive in breast cancer cell lines, few are likely to be estrogen-dependent. KLK5-11 and 15 are all expressed in ER-negative breast cancer cell lines such as BT-20, MDA-MB-231, and MDA-MB-468 (223, 388). Furthermore, there is no correlation between KLK9, 11, 14, and 15 levels and ER status in breast cancer tissue specimens (192, 407, 449, 450). Only KLK3 and KLK13 are more highly expressed in ER-positive tumors (451, 452). For KLK3, this trend may be due to coexpression of other hormone receptors with ER given that estrogen down-regulates KLK3 in vitro (451). Although KLK5, 6, and 10 are estrogen-responsive in breast cancer cell lines, these kallikreins are more highly expressed in ER-negative tumors (453, 454). In addition, KLK10 is an independent predictive marker of tumors that fail to respond to the ER antagonist tamoxifen and may therefore lack the ER (453).

Our analysis of published microarray data from 586 breast cancer specimens confirms the trend where estrogenregulated kallikreins are more highly expressed in ER-negative tumors (Supplemental Fig. 2). We examined other microarray datasets to further investigate this paradox. Data from the Neve et al. study (455) of 51 breast cancer cell lines shows that KLK5, 6, 8, and 10 are more highly expressed in the "Basal A" subset of ER-negative cell lines than the "Luminal" subset of ER-positive cells (Fig. 5A). Indeed, KLK6 and 8 were included in the list of 305 classifier genes that could be used to discriminate between different subtypes of breast cancer (455). KLK5, 6, 8, and 10 are also more highly expressed in patient specimens of ER-negative basal breast cancer compared with ER-positive luminal breast cancer (Fig. 5B). There is little variation in the expression of other kallikreins between cell lines or tumor specimens. These observations are surprising because KLK6 and 10 have long been classed as tumor suppressor genes in breast cancer (134, 198, 456, 457). The association of *KLK6* and 10 with breast cancer may be more complex where they are down-regulated in the luminal, but not basal, subset of tumors. Although in vitro experiments with luminal cell lines show that kallikreins are estrogen-responsive in some contexts, the microarray data also strongly suggest that kallikrein expression in breast is not estrogen-dependent.

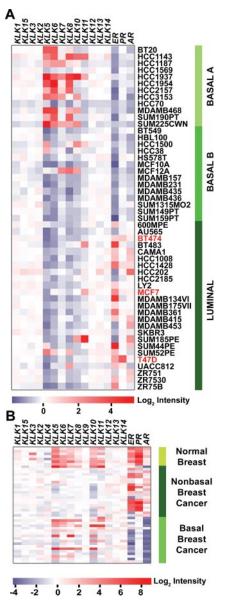


FIG. 5. Median-centered kallikrein and sex hormone receptor expression in breast cancer cell lines and tissues. A, Data from the Neve *et al.* study (455) of 51 breast cancer cell lines shows that *KLK5-8* and *10* tend to be more highly expressed in the Basal subset, whereas the ER, PR, and AR are more highly expressed in the Luminal subset of cells. There is little variation in *KLK1-3* and *12–15* between cell lines. BT-474, MCF7, and T47D cells are labeled in *red* because they are commonly used to study the hormonal regulation of kallikreins in breast. B, Gene expression in breast cancer specimens from the Richardson *et al.* dataset (498). *KLK5-8*, *10*, and *11* are more highly expressed in normal breast and basal breast cancer than luminal breast cancer. In contrast, ER, PR, and AR are lowly expressed in basal breast cancer. There is little variation in *KLK1-4*, *9*, and *12-15* expression between samples.

XV. Nonsteroid Hormone Regulation of Kallikrein Expression

A. Thyroid hormone

Compared with steroid hormone receptors, relatively little is known about the role of other members of the nuclear receptor superfamily in regulating kallikrein expression. Nevertheless, several early studies examined whether

kallikrein genes are responsive to thyroid hormone in animal models. For example, in the rat SMG, thyroid hormone increases the levels of Klk1c2, Klk1c3, Klk1c7, Klk1c8, and Klk1c9, but not Klk1 (458). Little change in kallikrein expression was detected in other organs (458, 459). There is a similar trend in the mouse where thyroid hormone induces Klk1b3, but either does not change or decreases Klk1 expression depending on the experimental model (288, 460). Yet it takes 1 wk for these changes to occur, suggesting that increased expression of classical rat and mouse kallikrein is probably a secondary effect of changes in cellular differentiation (288). Thyroid hormone seems to have a more direct effect on the human KLK3 gene that has a functional thyroid HRE (GGTGCAtccaGGGTGA) at -183 to -198 bp from the TSS (461). Through this element, thyroid hormone synergistically increases the androgen-dependent expression of KLK3 in LNCaP prostate cancer cells (461, 462).

B. Vitamin D

Just as KLK3 is widely used as a prototypical androgenregulated gene, KLK6 has emerged as a reliable marker of vitamin D receptor activity. Vitamin D3 and related analogs rapidly up-regulate KLK6 expression in head and neck, breast, colon, and prostate cancer cell lines as well as normal and transformed human skin keratinocytes (463–466). In addition, a vitamin D response element (AGTTCAacgAGTTCT) has been identified 489 bp upstream of the KLK6 TSS using ChIP assays (467). Significantly, vitamin D also up-regulates KLK5, 7, 8, 10, and 13 in keratinocytes, suggesting that the vitamin D receptor may regulate the expression of the kallikrein cascade in skin (468). In prostate cancer cells, vitamin D indirectly stimulates the androgen-dependent expression of KLK2 and *KLK3* by increasing the expression and nuclear translocation of the AR (378, 469-471). In the absence of androgens, vitamin D has no effect.

C. Retinoic acid

Kallikreins are differentially regulated by retinoic acid: *KLK10* is up-regulated in breast cancer cells, but *KLK3* is down-regulated in prostate cancer cells. *KLK10* has a retinoic acid response element (TGACCTcgTGATCC) 1014 bp upstream of the TSS (472). Reporter assays show that this element is necessary and sufficient for retinoic acid-regulated gene expression. In 76R-30 breast cells, retinoic acid receptor and retinoid X receptor (RXR) both bind the *KLK10* retinoic acid response element in a ligand-independent manner, whereas their coactivator, ADA3, is recruited in response to retinoic acid treatment. RXR also binds the promoter of *KLK3*, but its association with gene expression is more complex (473). In the absence of retinoic acid, RXR acts as a weak coactivator of androgen-

regulated *KLK3* expression in prostate cancer cells. Under these conditions, the RXR and AR bind to each other as well as to *KLK3* AREI and AREIII. In cells treated with both 9-cis retinoic acid and androgens, the RXR and AR still interact; however, their recruitment to AREI and AREIII is reduced. As a result, *KLK3* expression decreases. Because retinoic acid also down-regulates *KLK2* expression in prostate cancer cells (474), it is likely that RXR will repress all androgen-regulated kallikreins through its interaction with the AR.

D. Other nuclear receptors

KLK3 expression in prostate cancer cells is modulated by several other members of the nuclear receptor superfamily, mostly through indirect mechanisms. For example, the liver X receptor reduces AR-dependent KLK3 expression by up-regulating SULT2A1, an enzyme that metabolizes androgens (475). In addition, the synthetic liver X receptor agonist T0901317 has been shown to decrease KLK3 expression by acting as an AR antagonist (476). Peroxisome proliferator-activated receptor γ agonists (PPARy) also down-regulate KLK3 expression in prostate cancer cells (477). Intriguingly, this effect is independent of the PPAR γ (478). Low concentrations of PPAR γ agonists reduce AR recruitment to the *KLK3* promoter, whereas higher concentrations cause down-regulation of the AR (479). Estrogen receptor-related receptor α (ERR α) has also been shown to alter KLK3 expression (480). ERR α binds to the *KLK3* enhancer in the presence of the AR and stimulates KLK3 expression. A specific ERR α inverse agonist, XCT790, increases the occupancy of ERR α at the KLK3 enhancer, but transforms the receptor into a repressor, which down-regulates androgen-dependent KLK3 expression. Collectively, these studies show that although the AR is the most important regulator of KLK3 expression, other members of the nuclear receptor superfamily may influence KLK3 levels under some conditions.

XVI. Future Challenges

A. Are kallikreins direct targets of hormone receptors?

Uncertainty about kallikreins being direct or indirect targets of hormone receptors is a recurring theme among studies. This is an important distinction if kallikrein genes are to be used as models of hormone responsiveness. The problem is exemplified by studies with animal models from the 1970s and 1980s. These experiments often involved chronic hormone treatments or complete hormone ablation though castration, ovariectomy, or adrenalectomy. In some cases, these studies generated valuable preliminary data that have since been confirmed and expanded upon. Other results are now considered to be secondary effects of hormone-related changes in cellular dif-

ferentiation and proliferation or feedback from other endocrine pathways. More recent studies have relied on cell lines, which are less complex and more convenient. Yet many of these experiments still fail to distinguish between the direct and indirect effects of hormones. For instance, when cells are treated with hormones for days, not hours, changes in kallikrein levels may reflect differences in proliferation or differentiation rather than hormone receptor activity. Rapid changes in kallikrein expression can also be ambiguous. Most studies use tumor cell lines, some of which have mutated hormone receptors with more promiscuous affinity for ligands. For example, the AR is activated by nonandrogenic steroid hormones in LNCaP prostate cancer cells due to the T877A mutation in the ligand-binding domain (481, 482). Therefore, the increase in KLK2, 3, 4, and 15 expression with progestins in LNCaP cells may be mediated by the AR rather than the PR (384, 388, 390, 481). Another source of ambiguity may be the metabolism of the ligand of interest into other steroid hormones. For example, breast cancer cells can metabolize dihydrotestosterone, an androgen, into 5α androstane- 3β ,17b-diol, an estrogenic hormone that activates ER α and ER β (483). Conversely, prostate cancer cells use steroidogenic enzymes to generate dihydrotestosterone from progesterone (484). Future studies can overcome these problems by using shorter time courses, specific hormone receptor antagonists, and promoter-based assays.

B. Where are the hormone response elements?

Hormone receptors may trigger rapid and specific changes in kallikrein expression through genomic or nongenomic actions. The classical model of a ligand-bound hormone receptor activating gene expression by binding to a HRE is well established for AR-mediated expression of KLK2 and KLK3. Other kallikreins may also have functional HREs, but they could be difficult to find given that recent genome-wide ChIP studies have shown that few HREs are located within proximal promoters. The prevalence of hormone receptor binding sites that differ from the classical HRE motif adds further complexity. If kallikrein HREs are nonconsensus and far removed from the locus, they will be challenging to identify using binding site prediction software and promoter deletion constructs. Alternative approaches would be to mine genome-wide ChIP data for putative hormone receptor binding sites, or use chromosome conformation capture assays to investigate long-range genomic interactions. Because many kallikreins have conserved tissue-specific expression profiles between species, novel HREs might also be identified by focusing on the conserved regions of kallikrein promoters.

In addition to binding to HREs, hormone receptors can also modulate gene expression by interacting with other transcription factors, including AP-1 and nuclear factor κB, and activating extranuclear signaling cascades, such as the phosphatidylinositol-3-kinase and Src pathways (485, 486). Therefore, some kallikreins might not have HREs. Instead, they may be specific, but indirect, targets of hormone receptor signaling. One factor that could mediate the nongenomic actions of hormone receptors is cFos because it is associated with hormone-dependent as well as hormone-independent kallikrein expression (400, 487). A more detailed understanding of the structure of kallikrein promoters would help resolve whether they are direct targets of hormone receptors.

C. Do kallikreins have shared enhancers?

Given that kallikreins are colocalized in the genome and coexpressed in some tissues, there has been much speculation that they are jointly regulated by shared enhancer elements. The kallikrein field has referred to shared enhancers as "locus control regions," but this misconstrues the use of this term by other researchers. The term locus control region arose from studies with transgenic mice to describe a potent enhancer that stimulates correct tissuespecific expression of a transgene (488). Rather than coordinately up-regulating several genes, many locus control regions near multigene families only activate one gene at a time. For example, the β -globin locus control region stimulates sequential, not simultaneous, expression of β-globin genes throughout development (489). The human KLK3 enhancer actually fits the criteria of a locus control region because it drives high levels of KLK3 or LacZ expression in the prostate of transgenic mice (490, 491). Interestingly, one study found that maximal KLK3 expression in transgenic mice requires both the KLK2 and KLK3 enhancers (380). This suggests that KLK2 AREII may act as a shared enhancer for KLK2 and KLK3. Further experiments, such as chromatin conformation capture assays, are needed to confirm this observation. It would also be interesting to investigate whether the *KLK2* and KLK3 enhancers influence the expression of other kallikreins, especially KLK4, KLK15, and KLKP1, which are clustered around KLK2 and KLK3 and are also androgen-regulated in the prostate. Given the location and orientation of these genes in the kallikrein locus, interactions between the promoters of KLK4, KLK15, and KLKP1 and the enhancers of KLK2 and KLK3 would require complex patterns of chromatin looping. Because the kallikrein locus probably evolved through a series of gene duplications, it is also possible that the expression of each kallikrein is independently controlled by conserved regulatory elements. Indeed, Kroon et al. (492) showed that the coexpression of rat classical kallikreins in the SMG is due to autonomous rather than shared enhancers. When separate fragments of the kallikrein locus were introduced into mice, all rat kallikreins were still expressed in the SMG at physiological levels. Overall, the evidence for shared enhancers in the kallikrein locus is fairly circumstantial. In future studies, the use of novel techniques like chromatin conformation capture assays may help identify distal regulatory elements, some of which may be shared enhancers.

D. Is the kallikrein locus relevant in the era of genome-wide analyses?

The kallikrein locus, in particular *KLK3*, has served as a model of hormonal regulation for more than 15 yr. Studies with the KLK3 promoter have provided important insights into AR-mediated gene expression and steroid hormone receptor biology in general (278, 336). Some of these findings, such as the importance of coactivators and chromatin looping, presaged similar observations from genome-wide ChIP studies that have since confirmed their broader significance. Yet, with the increasing use of genome-wide ChIP techniques, it is pertinent to consider whether KLK3 and the kallikrein locus are still relevant. The main advantage of ChIP-on-chip, ChIP-sequencing, and related methods is their breadth, which is the main disadvantage of gene- and locus-centric experiments. Unbiased global ChIP techniques can be used to study many transcription factor binding sites under different contexts, whereas kallikreins represent a subset of target genes in specific contexts. KLK2 and KLK3 for example, are useful androgen-responsive genes for studies of luminal epithelial prostate cells, but not prostatic stroma or other androgen-regulated cell types such as skeletal muscle. Conversely, the major downside of genome-wide ChIP techniques is their cost and complexity compared with experiments with candidate genes that are relatively simple and inexpensive. This suggests that model genes like *KLK3* will continue to be widely used, especially for studies on generic rather than gene-specific mechanisms of transcriptional regulation. Overall, it seems that genomewide and gene-centric experiments are complementary approaches. The advantages of each technique compensate for the disadvantages of the other, so they can be used separately or in conjunction depending on the hypotheses being tested. The most compelling reason for the ongoing use of KLK3 as a model of hormonal regulation is that it is among the most well-characterized genes in the human genome. Indeed, genome-wide AR ChIP studies have often used *KLK3* to test their new hypotheses (272, 279). Therefore, as a model gene, *KLK3* can be used to compare results between laboratories and will continue to provide a link between past and future studies on AR-mediated gene expression.

XVII. Conclusion

The kallikrein family holds great promise, not just as a panel of biomarkers and potential therapeutic targets, but also as an important model of hormonal regulation. Indeed, KLK3 has been extensively used as a prototypical androgen-regulated gene to investigate the mechanisms of AR-mediated gene expression. Yet, it is unlikely that KLK3 will always represent the spectrum of androgenregulated genes in the normal or diseased prostate. For example, KLK2, KLK3, prostatic acid phosphatase, and TMPRSS2 are all well-characterized androgen-dependent genes, but KLK3 and prostatic acid phosphatase are down-regulated during prostate cancer progression, whereas KLK2 and TMPRSS2 are up-regulated (493–497). By analyzing a range of prostatic kallikreins, including KLK2, 3, 4, 15, and KLKP1, and other androgen-regulated genes, studies would be able to distinguish between generic changes in AR signaling and gene- or locus-specific effects. Other kallikreins may also be useful models to study the actions of other nuclear receptors. For instance, KLK6 has emerged as a reliable marker of vitamin D receptor activity, and KLK5 and KLK6 are promising markers of PR signaling in the uterus. Although all kallikrein genes have been shown to be hormone-responsive, it is not yet clear which genes are specific and direct targets of each hormone receptor. Some changes in kallikrein expression may be secondary effects of differences in proliferation or cellular differentiation. Future studies on the hormonal regulation of kallikreins should clarify this point and distinguish between hormone-related and hormone-regulated kallikrein expression. Thus, the kallikrein-related peptidase gene family locus will continue to be a powerful tool for testing hypotheses of hormonal regulation.

Acknowledgments

We gratefully acknowledge the Australian Prostate Cancer Bio-Resource for providing tissue specimens and Dr. Preston Alexander, Triple Point Biologics, for providing primary antibodies. We also thank Ms. Pak Ling Leung, Ms. Satomi Okano, and Dr. Scott Stansfield for their assistance in preparing the figures in this manuscript.

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This work was supported by grants and fellowships from the Queensland Government Growing the Smart State Fund (to M.G.L.), the Cancer Australia and Prostate Cancer Foundation of Australia (to J.L. and J.A.C.), The Cancer Council Queensland (to J.A.C.), the National Breast Cancer Foundation (to J.A.C.), and the National Health and Medical Research Council (to J.A.C. and the Australian Prostate Cancer BioResource).

Disclosure Summary: The authors have nothing to disclose.

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