Members of the interleukin-17 cytokine family are present in a variety of tissues (1–3), although the founding member, interleukin-17, is expressed exclusively in T cells and B cells (4–8). The cloning and characterization of a novel single-pass transmembrane protein with limited homology to the interleukin-17 receptor is reported. High mRNA levels were detected in prostate, cartilage, kidney, liver, heart, and muscle, whereas transcripts were barely detected in thymus and leukocytes. At least 11 RNA splice variants were found, transcribed from 19 exons on human chromosome 3p25.3–3p24.1. Differential exon usage was found in different tissues by quantitative reverse transcriptase-PCR. Predicted proteins range from 186 to 720 amino acids. Soluble secreted proteins lacking transmembrane and intracellular domains are predicted from several splice isoforms and may function as extracellular antagonists to cytokine signaling by functioning as soluble decoy receptors. Using antibodies directed at the cytoplasmic and extracellular domains of this protein, we investigated its localization and found that it was expressed in a variety of normal human tissues including prostate and in prostate cancer.

Interleukins were historically defined as soluble secreted factors expressed in immune cells that mediate interactions between leukocytes. However, this definition has evolved to include cytokines with a spectrum of pleiotropic actions (reviewed in Refs. 9 and 10). Interleukin-17 is a recently discovered cytokine that exerts its effect on many different tissues and is expressed in human prostate and in prostate cancer. This protein was discovered as a novel secreted protein lacking transmembrane and cytoplasmic domains and may function as a soluble cytokine signaling ligand. The IL-17 signaling pathway is currently being studied. Although it is not a ligand itself, the IL-17 receptor (IL-17R) has been shown to transduce its signal through the activation of ERK, JNK/SAPK, and p38 MAP kinase pathways (25–27). In the presence of IL-17 ligand, these pathways lead to the up-regulation of genes typically associated with inflammation, such as stromelysin, IL-6, and IL-1β, and the activation of NFκB (28–30). One additional receptor was first identified as a receptor for IL-17B and named IL-17BR (3). This receptor was subsequently shown to have greater affinity for IL-17E than for IL-17B and was also named IL-17Rb1. This receptor was shown to activate NFκB in an in vitro luciferase assay (2). However, the signal transduction pathway and the in vivo functions of this receptor are not known.

The existence of several IL-17-related proteins led us to explore the existence of additional members of the IL-17 receptor family. With this in mind, we searched human sequences in the GenBank data base, and in this report, we describe the cloning of a new IL-17R-related mRNA and elucidation of its genomic structure. We characterize its expression in various tissues and demonstrate differential exon usage in different tissues. We present evidence of splice variants that code for single-pass transmembrane proteins as well as secreted proteins that lack the transmembrane and cytoplasmic domains and may function as soluble cytokine receptors. This novel receptor is expressed in human prostate and in prostate cancer.

**EXPERIMENTAL PROCEDURES**

*GenBank Data Base Searching*—A systematic search of the GenBank EST data base was done using the public BLAST search algorithms. A series of ESTs was identified that had limited homology to the interleukin-17 receptor mRNA cytoplasmic domain. These sequences were assembled using AssemblyLign and MacVector (Accelrys Inc., San Diego, CA) to create a consensus sequence. The consensus sequence was used to search for additional overlapping human EST sequences, and this process was repeated until no further ESTs could be identified. The consensus sequence was compared with the human genomic DNA working draft sequences, including BAC clone AC018809 and others. This alignment was used to identify the intron-exon borders and the differentially spliced isoforms, and MacVector was used to identify and translate the open reading frames. Similar methods were used to identify the murine, bovine, and chicken homologs. MacVector, AssemblyLign, and the programs in the public domain (BLAST, PredictProtein) were used to predict the protein sequences, homology searches, and protein analysis. NetPhos2.0 (www.cbs.dtu.dk) was used to identify and score all possible cytoplasmic serine, threonine, and tyrosine phosphorylation sites, and scores greater than 0.90 were considered probable sites of potential phosphorylation.
Northern Blots—Total RNA was isolated from homogenized tissues using RNeasy mini-columns (Qiagen, Valencia, CA) or purchased from CLONTECH (Palo Alto, CA), electrophoresed on 1% agarose gels, transferred to Hybond-N+ membrane (Amer sham Biosciences, Inc.), and UV cross-linked. Two μg of mRNA was isolated from primary human chondrocytes and processed as described above. The Multiple Tissue Northern Filter (CLONTECH) has 1 μg of mRNA from various human tissues in each lane. Probes were made using Random-Primed II (Stratagene, San Diego, CA) using full-length 2402-bp cDNA. Prehybridization was done at 68 °C for 30 min, and the hybridization was performed overnight at 65 °C in 0.2 M sodium acetate, pH 7.2, 7% SDS, 1 mM EDTA, and 0.5% bovine serum albumin. Blots were washed in 2× SSC, 0.5% SDS four times at room temperature and then washed once for 30 min in 0.2× SSC, 0.1% SDS at 60 °C and exposed overnight to a Molecular Dynamics (Amersham Biosciences, Inc.) phosphor-storage screen, and they were finally digitized on a Molecular Dynamics Storm machine at 100-μm resolution.

Quantitative RT-PCR—Synthetic oligonucleotide primers were designed to specifically amplify portions of exons 1, 7, 12, 14, and 18 using PrimerExpress-1.7 software (Applied Biosystems, Foster City, CA). cDNA was made from 2 μg of random primed total RNA using TaqMan Reverse Transcription reagent kits (Applied Biosystems) and with ThermoScript Reverse Transcription System (Invitrogen). Real-time quantitative RT-PCR was done on an ABI 7700 Sequence Detector using Sybr-Green and GAPDH TaqMan reagents (Applied Biosystems) following recommended protocols. Reverse transcription reactions were performed several times and analyzed by real-time quantitative PCR in triplicate. Results were normalized to GAPDH levels using the recommended Δ Ct method. For comparison of exon usage across RNA from tissues, a plasmid containing the full-length cDNA was used as a control because each plasmid has exactly one copy of each exon. Student’s t tests were performed to assess statistical significance.

Antibody Production—Rabbit polyclonal antibodies were made against synthetic peptides QRPEKELNHTQGLPDC and DSYFHPGTPAPGRC, corresponding to portions of IL17-RL-translated from exons 6 and 19. These antibodies will be referred to as anti-extracellular domain and anti-cytoplasmic domain, respectively. The peptides were coupled to SulfoLink beads (Pierce) and were used to affinity-purify antibodies from the rabbit serum as recommended by the manufacturer. Purified antibodies were diluted to 2 μg/ml for Western blotting and 30 μg/ml for immunohistochemistry.

Western Blotting—A 50-mg sample from a human prostate was homogenized in reducing SDS-PAGE sample buffer, boiled for 5 min, and then electrophoresed on precast 4–12% gradient gels (Invitrogen). After transfer to Immobilon-P (Millipore, Bedford, MA), the membranes were blocked with 2% bovine serum albumin and then incubated with the anti-ECD or anti-CYTO antibodies at 2 μg/ml. Horseradish peroxidase-conjugated goat anti-rabbit secondary antibodies and ECL chemiluminescence (Amersham Biosciences, Inc.) were used for detection.

Immunohistochemistry—Arrays of various human tissues (Imgenex, San Diego, CA) were incubated with 30 μg/ml of either anti-ECD, anti-CYTO, or normal rabbit IgG followed by fluorescein isothiocyanate-conjugated anti-rabbit. Slides were mounted in VectaShield (Vector Laboratories, Burlingame, CA) containing the nuclear stain propidium iodide. Digital images were acquired on a Zeiss LSM-510 confocal microscope.

RESULTS

Genomic Structure Reveals Alternative Splicing—Data base searches revealed 108 human ESTs with overlapping sequences from which a continuous consensus sequence of 2402 base pairs was assembled. Alignment against the working draft of the human genome indicated that the gene is comprised of 19 exons located on chromosome 3 and spans 16,550 base pairs within the chromosomal region 3p25.3 to 3.24.1 (Fig. 1A). Each exon is flanked by consensus splice acceptor and exon donor sequences with the exception of exon 1, which is not preceded by a splice acceptor, and exon 19, which is not preceded by a splice acceptor, and exon 19.
followed by a splice donor. Extensive use of alternative splicing was revealed by the alignment of the ESTs with the consensus full-length 2402-bp cDNA sequence. Exons 7, 12, 14, 15, and 18 are frequently spliced out. In addition, exons 6, 8, 9, 11, 14, 18, and 19 have alternative splice donor and acceptor sites that are used in several ESTs from different libraries (Fig. 1B). The full-length 2402-bp cDNA consists of exons 1–19 as shown in Fig. 2.

**Full-length Protein Translation Predicts Type I Transmembrane Protein**—The first AUG is at position 205 in exon 1 followed by a 2157-bp open reading frame and a 37-bp 3′ untranslated region with a consensus polyadenylation signal. The translation of this open reading frame yields a 720-amino acid protein, which will be referred to from now on as full-length to distinguish it from the numerous predicted shorter protein sequences from alternatively spliced mRNAs. Computer analysis of the full-length amino acid sequence predicts that the initiation methionine is followed by a stretch of 20 hydrophobic amino acids with a consensus signal peptide cleavage site at position 21. The full-length mature protein consists of a 447-residue N-terminal extracellular domain followed by a single 21-amino acid hydrophilic alpha-helical transmembrane domain encoded by exon 17 and a 232-amino acid domain predicted to be cytoplasmic (Fig. 2). The calculated molecular size of the mature full-length protein is 76,378 daltons. The acidic extracellular domain has a predicted isoelectric point of 4.71 with nine potential sites for N-linked glycosylation. The 22 cysteines, 66 leucines, and 35 prolines in the extracellular domain have the potential for forming extensive secondary structure. The 232-amino acid cytoplasmic domain contains 20 arginines, 6 histidines, and 4 lysines, which contribute to its basic isoelectric point of 10.04. It also contains 16 serines, 5 threonines, and 3 tyrosines. Of these, 4 serines and 2 threonines were predicted by NetPhos software to be in a context in which they may be phosphorylated by intracellular kinases (see “Experimental Procedures”). There are no SH2 or SH3 domains nor is the cytoplasmic domain predicted to have any kinase activity of its own.

**Protein Homology to IL-17 Receptor**—Overall this protein is 22% identical and 34% similar to the human IL-17R (accession number NM_014339). The cytoplasmic domains of these proteins are more conserved, sharing 25% identity and 41% similarity across their membrane-proximal 233 amino acids (Fig. 3A).

**Sequence Conservation**—We identified the murine homolog of the full-length protein by assembly of mouse ESTs. It is 699 amino acids in length and shares 66% identity and 75% similarity to the human protein (Fig. 3B). Two of the potentially phosphorylated serines in the cytoplasmic domain are conserved in the mouse homolog, as are seven of the nine N-linked glycosylation sites in the extracellular domain. In addition, we identified several bovine, rat, and chicken ESTs that, when translated, showed a similar degree of homology to the human protein. However, it is impossible to assemble full-length sequences due to the paucity of sequence data.

**Splice Variants and Predicted Protein Products**—The EST data base contains many ESTs that align to the full-length sequence but are missing certain exons. Exons 7, 12, 14, and 15 are frequently spliced out, and there is evidence that these exons can be spliced out in combinations, leading to a great number of possible protein translations. Because no EST covered the entire 2402-base pair full-length cDNA, there are more possibilities for combining exon usage than we report here. For example, one EST (accession number A1078128) sequence begins at the NotI site in exon 17 and then continues through exons 16, 13, 11, 10, 9, and most of exon 8 of the full-length cDNA, indicating that exons 12, 14, and 15 were spliced out. If we assume that the mRNA from which this was derived contains exons 1–8, then this mRNA would be translated into a protein of 1372 amino acids. Deletion of exons 14 and 15 introduces a frameshift so that the protein would contain the secretion signal peptide and most of the extracellular domain including all nine glycosylation sites but not the transmembrane or cytoplasmic domains. From the existing ESTs in the data base, we predict that at least 12 different proteins can be made from this gene (Fig. 1C). The translated proteins fall into two major categories, each with minor variations. The first category includes full extracellular domain transmembrane proteins with intact phosphorylation sites in the cytoplasmic tail. The second includes soluble secreted proteins without transmembrane or cytoplasmic domains.

**Gene Expression**—Northern blot analysis of 5 μg of total RNA isolated from various human tissues shows that the mRNA is strongly expressed in prostate, kidney, and trachea. Northern blot analysis of 2 μg of mRNA from various human tissues shows one major band with a mobility of ~2.5 kb with some diffuse bands between 2.1 and 3.1 kb (Fig. 4). The highest expression was in prostate, liver, kidney, muscle, and heart. Intermediate expression was in cartilage, brain, colon, intestine, placenta, and lung, and barely detectable expression was in thymus and peripheral blood leukocytes.

**Exon Usage by Quantitative RT-PCR**—Primers were designed to specifically amplify regions of exons 7, 12, 14, 15, 18, and 19. These primers were used in real-time quantitative PCR on cDNA made from various commercially available total RNA or on a plasmid clone of the full-length cDNA, which has exactly one copy of each exon per plasmid. Detection of PCR products corresponding to exons 12, 14, 15, 18, and 19 occurred at almost the same cycle for all tissues, indicating that these exons are transcribed in equal numbers in the tissues examined. However, the PCR products from exon 7 were consistently detected at 1.6–3 cycles later (p = 0.0006), which indicates that only about from 1⁄3 to 1⁄8 of the total RNA or on a plasmid clone of the full-length cDNA, which has exactly one copy of each exon per plasmid. Detection of PCR products corresponding to exons 12, 14, 15, 18, and 19 occurred at almost the same cycle for all tissues, indicating that these exons are transcribed in equal numbers in the tissues examined. However, the PCR products from exon 7 were consistently detected at 1.6–3 cycles later (p = 0.0006), which indicates that only about from 1⁄3 to 1⁄8 of the transcripts that include exons 12–19 also include exon 7. In addition, there is some evidence that in brain tissue, exon 7 is used even less often than in liver (p = 0.05) or heart (p = 0.06) tissues. These experiments were repeated with cDNA made from the same RNA but using a different reverse transcriptase enzyme system at a different temperature to reduce the possibility that the measured differences stemmed from inefficient reverse transcription reactions rather than differential use of exons. Controls with a full-length plasmid template (containing an equal copy number of each exon) returned equal values for each primer set across many dilutions. These controls show that the measured differences in exon usage are indeed real and not artifacts of a specific reverse transcription system nor of the amplification efficiency of the TaqMan detection primers.

**Immunoblotting**—A human prostate biopsy was homogenized, electrophoresed on SDS-PAGE, and analyzed by Western blotting with affinity-purified antibodies directed against the extracellular and cytoplasmic domains of IL17-RL. The anti-ECD antibody, directed against the N terminus of the protein, detected multiple bands ranging in size from ~33 to almost 60 kDa, confirming the predicted presence of multiple isoforms of IL17-RL. The larger of these bands was also detected by anti-CYTO, which is directed against the carboxyl-terminal cytoplasmic domain of IL17-RL (Fig. 5).

**Immunohistochemistry**—Immunohistochemical analysis was performed on arrays of human tissue biopsies using both anti-ECD and anti-CYTO antibodies. We found strong reactivity with anti-ECD, which is directed against the N-terminal extracellular
Interleukin-17 Receptor Like (IL-17RL) nucleotide and peptide sequence

FIG. 2. Annotated nucleotide and deduced amino acid sequences of full-length product. Translated and untranslated regions of the cDNA are capitalized and lowercase, respectively. Exons are indicated in numbers above the cDNA sequence. The signal peptide of the deduced protein is underlined (thin underline). Extracellular N-glycosylation sites are boxed. The transmembrane domain is underlined (thick underline). The potential sites for serine and threonine phosphorylation in the cytoplasmic domain are underlined with dashes and dots, respectively. Peptides with double underlines were used to generate rabbit polyclonal antibodies.
domain of IL17-RL, in skeletal muscle, prostate, kidney, and placenta. Skeletal muscle showed low reactivity with anti-CYTO, which is directed against the C-terminal cytoplasmic domain of IL17-RL. Prostate, kidney, and placenta showed weak, intermediate, and strong reactivity with anti-CYTO, respectively (Fig. 6).

Immunohistochemistry was performed on arrays of human prostate cancers using anti-ECD antibodies. Higher grade cancers tended to show decreased reactivity in epithelial cells and an increased reactivity in stromal regions relative to normal prostate (Fig. 7).

**DISCUSSION**

Previous work from our laboratory and others (1–3) has identified new members of the IL-17 family of cytokines and implicated them in a variety of normal and disease-related

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**FIG. 3.** Alignment of human and mouse homologs of novel IL-17 receptor family member. A, alignment with human IL-17 receptor cytoplasmic domain. B, alignment with mouse homolog. The shaded and unshaded areas in the boxes represent identity and similarity, respectively.

**FIG. 4.** Expression of mRNA for the novel IL-17 receptor family member in adult human tissues. Northern blot analysis of 1 μg of mRNA isolated from primary human chondrocytes, and 5 μg of total RNA isolated from either normal adult prostate or benign prostatic hyperplasia surgical specimens (BPH). Blots were hybridized with random prime [32P]dCTP-labeled full-length cDNA, washed, exposed to a phosphor-storage screen, and then digitized on a Molecular Dynamics Storm system at 100-μm resolution. The 2.4-kb mRNA is indicated by the arrow. SK, skeletal.

**FIG. 5.** Immunoblot of homogenized human prostate electrophoresed under reducing conditions. Lane 1 was reacted with anti-ECD antibody directed against the N-terminal extracellular domain of IL17-RL. Lane 2 was reacted with anti-CYTO antibody directed against the cytoplasmic C-terminal domain of IL17-RL.

GenBank—The protein sequences described in this study have recently been annotated in the GenBank data base as hypothetical protein MGC:10763 (human) and MGC:6973 (mouse).
Isoforms of IL17 Receptor-like Protein by RNA Splicing

conditions. The number of newly identified IL-17 family cytokines provided an impetus to explore the existence of additional receptors. The aim of the present study was to identify new receptors based on homology to the published IL-17 receptor. To this end, we have searched the public EST database and identified a cDNA coding for a novel protein related to IL-17R.

**Fig. 6.** Immunohistochemistry of human tissues. Fluorescein-conjugated secondary antibody was used to detect anti-ECD and anti-CYTO antibodies directed against the cytoplasmic and extracellular domain of IL17-RL, shown in green. Propidium iodide staining shows the cell nuclei in red. Note the reactivity with both antibodies in placenta but primarily with the extracellular antibody in other tissues. Bar, 200 μm. All micrographs were taken at the same microscope settings.

**Fig. 7.** Immunohistochemistry of human prostate. Fluorescein-conjugated secondary antibody was used to detect anti-ECD antibodies, shown in green. Propidium iodide staining shows the cell nuclei in red. Note the decreased epithelial reactivity and increased stromal reactivity in samples with a higher Gleason grade. Bar, 50 μm. All micrographs were taken at the same microscope settings.
We named this protein IL17-RL (receptor-like) based on its homology to IL-17R. Its primary sequence suggests that, like IL-17R, it is a single-pass transmembrane protein with an extracellular N terminus. We characterized its expression in a variety of human tissues at the mRNA level, as well as on tissue extracts and histological sections at the protein level. We determined its genomic structure and found evidence of alternative splicing even in the limited number of EST sequences available in the public data bases.

The RNA splicing of this gene is of particular interest because a number of the observed splice variants introduce frameshifts and stop codons before the C-terminal transmembrane domain, resulting in the translation of secreted rather than transmembrane protein. We found 12 different splice variants in the 108 ESTs currently in the data base. Exons 7, 12, 14, and 15 were spliced out in several ESTs, and exons 6, 8, 9, 11, 14, 18, and 19 have alternate splice donor or acceptor sites. Some ESTs have combinations of two or more nearby exons spliced out. Additional splice variants with combinations of distant exons are possible, but due to the limited length of sequence available from each EST, we have no direct evidence for this. Also, further splice variations in the 5’ end of the mRNA may have been missed because of the inherent bias toward 3’ ends in the EST data base. The extent of alternative splicing is not immediately evident from Northern blot analysis because many of the exons are of similar size and are relatively small when compared with the overall length of the mRNA. However, we have confirmed the presence of multiple transcripts from single tissues and cell lines using RT-PCR (data not shown).

We have demonstrated by quantitative RT-PCR that most of the mRNA does not contain exon 7. Moreover, there is some evidence that exon 7 usage is tissue-specific because it is present less frequently in RNA isolated from the brain than from the liver or heart. This implies that there may be tissue-specific regulatory factors that control the RNA splicing of this gene and also that there may be a functional difference between proteins made from mRNA with and without exon 7. This raises the additional possibility that regulation of splicing may occur in response to the activation of growth factor signaling pathways.

The assembled full-length cDNA has a single large open reading frame that is predicted to encode a 720-amino acid single-pass transmembrane protein. Translation of the alternatively spliced mRNAs results in at least eleven additional proteins. Although the open reading frame of downstream exons is not affected by the removal of exons 7, 12, or 15, the removal of most other exons causes a frameshift that introduces in-frame stop codons. An in-frame stop codon before exon 17, which codes for the transmembrane domain, will result in translation of a secreted protein. Therefore, the translation products can be classified into two general categories. Both categories contain the presumed ligand binding extracellular domain. The first category is full-length proteins, which have the ligand binding extracellular domain along with transmembrane and cytoplasmic domains. Since the cytoplasmic domain is predicted to contain several phosphorylation sites, this first category of proteins has the potential both for ligand binding and for subsequent activation of cytosolic signal transduction pathways. The second category is truncated proteins, which contain the extracellular domain but in which a stop codon occurs in or before the transmembrane domain. This category consists of either membrane-associated or soluble secreted proteins. Presumably these proteins retain the ligand binding activity but without the capacity for activation of signal transduction pathways. It is likely that the soluble receptor isoforms may thus function as signaling antagonists or decoy receptors.

Analysis by immunoblotting confirms that multiple proteins with different molecular weights are detected in homogenates of a single tissue, presumably from translations of alternatively spliced mRNA. Immunohistochemical analysis also indicates that multiple isoforms of the proteins can exist because some tissues bind strongly to antibodies directed against both the extracellular and the cytoplasmic domain, whereas other tissues only bind strongly to antibodies directed against the extracellular domain. Especially noteworthy is the localization in the prostate and prostate cancers. This differential localization of soluble and membrane-bound receptor implies that certain tissues expressing primarily soluble receptor may not respond to the ligand.

As there was a strong immunohistochemical localization of the novel IL17-RL in prostate by the antibody directed against the extracellular domain (anti-ECD), it was of interest to also compare the localization in prostate cancers. The results are depicted in Fig. 7. In the normal prostate, IL17-RL was localized in both the epithelial and stromal compartments. In prostate cancers with increasing Gleason grade, there was a progressive loss of staining in the epithelium and increased staining in the stroma. The antibody used is directed against the N-terminal extracellular domain, which is present in both the transmembrane and the soluble decoy isoforms of IL17-RL. Thus, it is possible that in prostate cancer, the redistribution of the receptor from epithelial to stromal compartments signifies a dysregulation of expression or signaling of IL17-RL.

With the completion of the human genome project came the realization that the human genome contains far fewer genes than originally predicted (31, 32). The complexity of the gene we have identified, which has 19 exons and codes for at least 12 different mRNAs and therefore can be translated into several functional isoforms, demonstrates the intricate regulation of function by the transcription and translation of multiple RNAs by RNA splicing. The precise function of the novel receptor IL17-RL and its splice isoforms remains unknown, and understanding its function and regulation are the focus of our laboratory.

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Soluble and Transmembrane Isoforms of Novel Interleukin-17 Receptor-like Protein by RNA Splicing and Expression in Prostate Cancer
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