Cloning and Sequencing of Protein Kinase cDNA from Harbor Seal (Phoca vitulina) Lymphocytes

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Protein kinases (PKs) play critical roles in signal transduction and activation of lymphocytes. Their identification and cloning provides a tool for understanding mechanisms of immunotoxic xenobiotics. As part of a larger study investigating persistent organic pollutants in the harbor seal and their possible immunomodulatory actions, we sequenced harbor seal cDNA fragments encoding PKs. Using degenerate primers based on conserved motifs of human protein tyrosine kinases (PTKs), we successfully amplified nine phocid PK gene fragments with high homology to human and rodent orthologs. We identified eight PTKs and one dual (serine/threonine and tyrosine) kinase. Among these were several PKs important in early signaling events through the B- and T-cell receptors (FYN, LYN, ITK and SYK) and a MAP kinase involved in downstream signal transduction. V-FGR, RET and DDR2 were also expressed. Sequential activation of protein kinases ultimately induces gene transcription leading to the proliferation and differentiation of lymphocytes critical to adaptive immunity. PKs are potential targets of bioactive xenobiotics, including persistent organic pollutants of the marine environment; characterization of these molecules in the harbor seal provides a foundation for further research illuminating mechanisms of action of contaminants speculated to contribute to large-scale die-offs of marine mammals via immunosuppression.

Keywords: Harbor seal; Phoca vitulina; Protein (tyrosine) kinase; Lymphocyte activation and differentiation

INTRODUCTION

Protein kinases (PKs) play critical roles in cellular functions including signal transduction, cell cycle regulation, cell division and cell differentiation (Hunter et al., 1985; Edelman et al., 1987). Signal transduction controls many critical and complex cellular functions, including activation of lymphocytes in the adaptive immune response. Signal transduction through the B- and T-cell receptors (BCR and TCR, respectively) and cytokine receptors on the surface of lymphocytes occurs largely via tyrosine phosphorylation of intracellular substrates by protein tyrosine kinases (PTKs). Tyrosine kinases (TKs) play a major role in many disorders of cell proliferation, differentiation, survival and migration, which are fundamental to many diseases and abnormalities.

Although research in this area is limited and relatively recent, there is already experimental evidence that certain halogenated aromatic hydrocarbons [HAs such as polychlorinated biphenyls (PCBs) and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD)] and polycyclic aromatic hydrocarbons (PAHs)—affect tyrosine kinases. For example, in vitro exposure of murine B lymphocytes to TCDD increased membrane protein phosphorylation and, in particular, stimulated tyrosine-specific protein phosphorylation (Clark et al., 1991). Similarly, certain PAHs have been shown to activate PTKs in human cell lines—specifically, FYN and LCK in T-cells and LYN and SYK in B cells (Archuleta et al., 1993; Mounho and Burchiel, 1998). These authors also reported that mobilization of intracellular calcium was coupled to increased tyrosine phosphorylation, and suggested that PAH-induced PTK activation and increased cellular Ca\(^{2+}\) may alter antigen receptor signaling in human B cells.

Disruption of immune function associated with tissue accumulation of halogenated aromatic hydrocarbons in the marine environment has been suggested as a factor altering health in several marine mammal species (Addison, 1989; Tanabe et al., 1994). For example, it has been speculated that contaminant-induced immunosuppression may have contributed to the high mortality observed in several marine mammal populations during recent morbillivirus epizootics (Hall et al., 1992; Aguilar and Borrell, 1994). HAs and PAHs are known to elicit a broad spectrum of immunotoxic effects in laboratory animals.
animals (Kerkvliet and Burleson, 1994; White et al., 1994). In marine mammals, PAHs and organochlorines (such as PCBs and DDT) also have been associated with impaired immunological function (Martineau et al., 1994; Lahvis et al., 1995; Ross et al., 1996; Beckmen et al., 2003). Recently, certain PCB and PAH compounds were shown to suppress harbor seal T-cell mitogenesis in vitro (Neale et al., 2002).

PKs provide the machinery for the differentiation and activation of lymphocytes, processes critical to cell-mediated immunity and host resistance to pathogens. As part of a larger investigation of potential contaminant-induced immune alterations in the harbor seal, we wished to identify key signal transduction molecules in seal immune alterations in the harbor seal, we wished to identify key signal transduction molecules in seal. For this reason, we isolated RNA from PBMC of harbor seals and primed RT-PCR with degenerate primers designed to encode the catalytic domains of (human) PTK. These have been described in detail previously (Robinson et al., 1996; Kung et al., 1998; Lin et al., 1998). Briefly, DFG is present in virtually all tyrosine kinases, whereas DVW is primarily encoded by tyrosine kinases, although a small number of serine kinases can also be primed. These two motifs bound a conserved area of approximately 30 aa which, in phosphorylated tyrosine kinases, interact only with target molecules that contain SH2 domains. The 5' primer used to encode the amino acid sequence K[V/I][S/C/G]DFG is represented by: 5'-AAR RTT DCN GAY TTY GG. The 3' primer used to encode the amino acid sequence DVW[S/A][F/Y] is represented by: 5'-RHA IGM CCA IAC RTC. The mixed bases were defined as follows: N = A/C/T/G, D = A/T/G, R = A/G, Y = C/T, M = A/C and I = deoxyinosine.

RT-PCR

For reverse transcription, approximately 5 μg RNA (in 5 μl water) was added to a mixture of 1 μl (0.5 μg) oligo(dT) primers, 1 μl dNTP Mix (10 mM), and 5 μl water. This mixture was incubated at 70°C for 10 min then cooled on ice. Next, 4 μl of 5 × First Strand Buffer, 2 μl of DTT (0.1 M) and 1 μl (10 units) RNase inhibitor were added to the first mixture and incubated at 42°C for 2 min. Lastly, 1 μl (200 units) Superscript II reverse transcriptase was added for a total volume of 20 μl. This was incubated for 42°C for 50 min. The reverse transcriptase enzyme was heat-killed at 70°C for 15 min. All reagents supplied from Invitrogen (Carlsbad, CA, USA).

Various protein kinase transcripts were PCR-amplified using degenerate primers derived from the conserved motifs DFG (5') and DVW (3') within the catalytic domains of (human) PTK. These have been described in detail previously (Robinson et al., 1996; Kung et al., 1998; Lin et al., 1998). Briefly, DFG is present in virtually all kinases, whereas DVW is primarily encoded by tyrosine kinases, although a small number of serine kinases can also be primed. These two motifs bound a conserved area of approximately 30 aa which, in phosphorylated tyrosine kinases, interact only with target molecules that contain SH2 domains. The 5' primer used to encode the amino acid sequence K[V/I][S/C/G]DFG is represented by: 5'-AAR RTT DCN GAY TTY GG. The 3' primer used to encode the amino acid sequence DVW[S/A][F/Y] is represented by: 5'-RHA IGM CCA IAC RTC. The mixed bases were defined as follows: N = A/C/T/G, D = A/T/G, R = A/G, Y = C/T, M = A/C and I = deoxyinosine.

PCR reactions (25 μl) contained 1 μl cDNA, 2.5 μl 10 × buffer, 0.5 μl each of 3', 5', and dNTP Mix (10 mM), 1.5 μl MgCl₂ (25 mM), 0.5 μl (2.5 units) Taq polymerase, and 18 μl water (PCR profile: 94°C, 11 min; 52°C, 1 min; 72°C, 1.5 min; 31 cycles; 72°C, 10 min). PCR products were electrophoresed in an agarose gel. Due to the roughly even spacing between DFG and DVW in all kinases, we expected and obtained a relatively homogeneous PCR product of ~170 bp. This band was excised and DNA purified using the QIAEX II gel extraction kit (Qiagen, Valencia, CA, USA).

Cloning, Transformation, and Sequencing

Purified fragments were cloned into a plasmid vector using the TOPO TA Cloning Kit for Sequencing (Version H, Invitrogen) and the resulting recombinants were used to electro-transform E. coli, according to the manufacturer’s instructions. Plasmid DNA was isolated using the Qiagen Plasmid Mini Kit (Qiagen, Valencia, CA, USA). PCR and
FIGURE 1  Nucleotide sequence alignment of harbor seal PK cDNA. DFG (5') and DVW (3') domains are bolded and underlined. Sequences have been submitted to Genbank with the following accession numbers: LYN+, #AY611615; LYN, #AY611614; FYN, #AY611616; V-FGR, #AY611622; ITK, #AY611617; SYK, #AY611618; DDR2, #AY611620; MAPK3, #AY611619; RET, #AY611621.

FIGURE 2  Deduced amino acid sequences corresponding to nucleotide sequences of nine harbor seal PK genes. DFG and DVW motifs underlined. Reading frame starting base and total length (amino acids) given.

LYN+  Start codon: 2  Total length: 64
QVTKVCDFGLARVIEDNEYTAREQAKQKKTKRDLVPNSPLSGQLQKQSTDSVSRSLMCGLLVT

LYN  Start codon: 2  Total length: 54
QVTKVGDFGLARVIEDNEYTAREQAKAFKPKWTAEFINFGCFTIKSDVWSF

FYN  Start codon: 2  Total length: 54
QVTKVADFGLARVIEDNEYTAREQAKAFKPKWTAEALYGRFTIKSVDWSFGN

V-FGR  Start codon: 2  Total length: 54
QVTKVCDFGLARLIEDDEYNPOQAGKPKWTAEALFGRFTIKSDVWSF

ITK  Start codon: 2  Total length: 54
QVTKVADEGMRFVLDDQYRTSSGTKFPKVASPEVFSRSYSSKSDVWACGN

SYK  Start codon: 2  Total length: 56
QVTKJCDFLSKALRANDEYKQATHGKWPKWYAPECINYYKFSKSDVWSGN

DDR2  Start codon: 2  Total length: 55
QVTKVADEGMRSLNLYSGDYRRQGRAVLPFIRWMSWESILGKFTTASDVSFGN

MAPK3  Start codon: 2  Total length: 56
QVTKVSDFGLSVGYLDVSVAKTLDSAGCYPAMPERINPELNQKGNVKSVDWAFGN

RET  Start codon: 1  Total length: 55
PVTKGDGLSLRVDYEDSYVKRSKGRPVKWMESLDFHITYTTQSDVWAFGN

FIGURE 2  Deduced amino acid sequences corresponding to nucleotide sequences of nine harbor seal PK genes. DFG and DVW motifs underlined. Reading frame starting base and total length (amino acids) given.
gel electrophoresis were used at several steps to screen and select positive clones. In addition, because half (8/16) of the clones initially analyzed were identified as ITK, colonies were also screened using restriction endonuclease digestion, in this way we were able to selectively analyze non-ITK clones. Diversity of selection was further enhanced by visualization of slight size variations among positive clones using acrylamide gel electrophoresis. Inserts were sequenced at the DNA sequencing facility (University of California, Davis) using the M13 Reverse universal primer. We used the BLAST program (Altschul et al., 1997) to search protein and DNA databases for sequence similarities.

RESULTS

Clones positive for PK transcripts were generated from all three seals, and multiple clones were identified for most kinases. In all cases, replicate sequences were identical between the DFG and DVW domains. Because the greatest volume of blood (and thus lymphocyte RNA) was obtained from the yearling male, the majority (and greatest diversity) of PK sequences came from this individual.

We obtained nucleotide sequences encoding nine distinct protein kinases, including eight PTK—FYN, LYN and LYN+, ITK, SYK, v-FGR, DDR2 and RET—and one dual kinase (i.e. having both tyrosine and serine/threonine kinase activities), MAPKK3 (Fig. 1). LYN+, a variant of LYN tyrosine kinase, contained an insert of 29 bases beginning at 72, but was otherwise identical in nucleotide sequence to LYN. All other sequences were of the expected length (165–171 nucleotides).

Deduced protein sequences corresponding to the nine harbor seal PK nucleotide sequences are presented in Fig. 2. The 29-base insert of Lyn+ causes a shift in reading frame; consequently, the DVW motif is not encoded, but an open reading frame is maintained.

Identification was based on homology with published cDNA sequences. Nucleotide and deduced amino acid sequences were highly similar to human and rodent orthologs (Table I). Additional information based on the corresponding human proteins is provided in Table II.

DISCUSSION

Here, we demonstrated the ability to prime phocid PK cDNA using a human-based degenerate PCR primer mix and we identified, for the first time, protein kinases in an organism within the order Carnivora. Among the kinases identified were several key players involved in signal transduction through the BCR/TCR and activation of B- and T-cells—namely, FYN, LYN, SYK and MAPKK3.

The Src-family kinases FYN and LYN (together with BLK in B cells and LCK in T cells) are responsible for early events in BCR and TCR signaling (Qian and Weiss, 1997; Tsubata and Wienands, 2001). BCR proximal signaling occurs within “lipid rafts” and depends on the tyrosine kinase activity of LYN.
PKS IN HARBOR SEAL LYMPHOCYTES

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(Tsukata and Wienands, 2001; Chakravarty et al., 2002). Likewise, FYN is critical for initiating TCR signaling and plays an important role in T-cell development as well (Howe and Weiss, 1995). Specifically, phosphorylation of the tyrosines in immunoreceptor tyrosine-based activation motifs (ITAMs) by Src-family PTKs serves as the initial intracellular signal indicating that the lymphocyte has detected its specific antigen (Janeway et al., 1999).

SYK is a critical PTK in B-cell antigen receptor signaling and B-cell development (Cheng et al., 1995; Turner et al., 1995). Once the ITAMs in the receptor cytoplasmic tails have been phosphorylated, ITAMs in B cells bind SYK (ZAP-70 in T cells). Until SYK has been bound, it is inactive enzymatically. To be activated, it also must be phosphorylated; for this reason, SYK is thought to be important in the negative regulation of receptor TK-coupled signaling processes as well. Once activated, SYK phosphorylates target proteins to initiate a cascade of intracellular signaling molecules (Janeway et al., 1999).

MAPKK3 (mitogen-activated protein kinase kinase 3) is integral to the MAP kinase signaling cascade, one of several pathways leading to activation of transcription factors in the nucleus. The MAP kinase pathway is of great importance in both BCR/TCR signaling and T-cell development (Alberola-Ila et al., 1995; Li et al., 1996; Abbas and Lichtman, 2003). Activated kinase SYK (or ZAP-70 in T cells) activates phospholipase C-γ (leading to the diacylglycerol and inositol trisphosphate pathways) and guanine-nucleotide exchange factors (GEFs). GEFs activate small G proteins, which in turn activate MAP kinase cascades. The role of the dual kinase MAPKK3 is to activate, via phosphorylation of a threonine and a tyrosine residue, particular MAP kinases, which then activate transcription factors to induce specific gene transcription leading to cell proliferation and differentiation.

ITK (murine IL-2 inducible T-cell kinase) is expressed in T lymphocytes (and NK cells) and is required for normal T-cell development (Janeway et al., 1999). There is strong evidence that ITK regulates TCR signaling, but the mechanism underlying this role has not been determined (Liao and Littman, 1995). The Tec family PTK preferentially expressed in T cells is ITK (Qian and Weiss, 1997). ITK was disproportionately represented (50%) in our clones, suggesting that ITK may be highly expressed in harbor seal lymphocytes, although the small scale of this preliminary study prevents quantitative assessment of gene expression.

The relevance to signal transduction and lymphocyte activation of the lesser-known TKs DDR2, v-FGR and RET is not clear, although all three appear to be involved in various disease processes. The recently identified receptor tyrosine kinase DDR2 (discoidin domain receptor family, member 2) is unusual in that it is activated by fibrillar collagens (types I and III) rather than a growth factor-like peptide (Vogel et al., 1997; Leitinger, 2003). In addition to its role as a DDR2 ligand, fibrillar collagen matrix can sequester and provide binding sites for immune mediators such as cytokines and chemokines which may lead to local tissue damage (Somassundaram et al., 2002). The activation of DDR2 also mediates the over-expression of matrix metalloproteinase 1 in cells, which is thought to be involved in the metastasis of some tumors (Wang et al., 2001).

V-FGR and RET were identified as (proto-) oncoproteins. V-FGR (feline sarcoma viral oncogene for fibroblast growth factor) arises from a recombination of a cellular structural gene (gamma actin) with a tyrosine kinase gene (c-fgr) (Baker et al., 1998). The transforming activity of v-FGR appears to lie in its TK, which may activate substrates not normally exposed to tyrosine phosphorylation (Sugita et al., 1989). Certain gene rearrangements of the RET receptor TK kinase proto-oncogene are responsible for cancer pathogenesis (Bongarzone et al., 2003). Activating mutations lead to the expression of deregulated products characterized by ligand-independent activation of the intrinsic tyrosine kinase of RET (Lanzi et al., 2003).

Because of their critical role in adaptive immunity, protein kinases (especially PTK) may represent important targets of immunomodulation by xenobiotics in marine mammals. Harbor seal sequences for PTK could serve as molecular biomarkers in semi-quantitative profiling of kinase gene expression. For example, differential expression of specific PTK, following in vitro exposures
of seal lymphocytes to model compounds, could be identified via RT-PCR and restriction enzyme digest analysis. This technique has been applied previously to human samples to characterize kinase expression in disease (Robinson et al., 1996; Kung et al., 1998; Mao et al., 2002). In this approach, subsamples of labeled DNA (i.e. radioactive or fluorescent tags) are digested with multiple restriction enzymes, after which digested products are resolved via acrylamide gel electrophoresis. Nucleotide sequences of PK and known restriction sites of endonucleases are utilized to identify kinases and assess differential expression, e.g. for treated vs. control samples. Table III shows an optimized digest for the nine harbor seal PK presented here.

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