

All TRAFs are not created equal: common and distinct molecular mechanisms of TRAF-mediated signal transduction

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Summary

The tumor necrosis factor (TNF) receptor associated factors (TRAFs) have emerged as the major signal transducers for the TNF receptor superfamily and the interleukin-1 receptor/Toll-like receptor (IL-1R/TLR) superfamily. TRAFs collectively play important functions in both adaptive and innate immunity. Recent functional and structural studies have revealed the individuality of each of the mammalian TRAFs and advanced our understanding of the underlying molecular mechanisms.

Here, we examine this functional divergence among TRAFs from a perspective of both upstream and downstream TRAF signal transduction pathways and of signaling-dependent regulation of TRAF trafficking. We raise additional questions and propose hypotheses regarding the molecular basis of TRAF signaling specificity.

Key words: TRAF, TNF, IL-1R/TLR, NF- κ B, AP-1

Introduction

The tumor necrosis factor (TNF) receptor associated factors (TRAFs) constitute a family of genetically conserved adapter proteins that has been found in mammals (TRAF1-6, see review (Arch et al., 1998)), as well as in other multicellular organisms such as *Drosophila* (Liu et al., 1999; Grech et al., 2000; Medzhitov and Janeway, 2000; Zapata et al., 2000), *Caenorhabditis elegans* (Wajant et al., 1998) and *Dictyostelium discoideum* (Regnier et al., 1995). Mammalian TRAFs have emerged as the major signal transducers for the TNF receptor superfamily and the interleukin-1 receptor/Toll-like receptor (IL-1R/TLR) superfamily (Table 1). A wide range of biological functions, such as adaptive and innate immunity, embryonic development, stress response and bone metabolism, are mediated by TRAFs through the induction of cell survival, proliferation, differentiation and death. TRAFs are also involved in the signal transduction of the Epstein-Barr virus transforming protein LMP-1 (Mosialos et al., 1995). In *Drosophila*, TRAFs are essential for dorsoventral polarization and innate host defense by the signal transduction initiated through the Toll receptor (Imler and Hoffmann, 2001; Preiss et al., 2001).

The TRAF proteins are characterized by the presence of a novel TRAF domain at the C-terminus, which consists of a coiled-coil domain followed by a conserved TRAF-C domain (Rothe et al., 1994) (Fig. 1). The TRAF domain plays an important role in TRAF function by mediating self-association and upstream interactions with receptors and other signaling proteins (Takeuchi et al., 1996). The N-terminal portion of most TRAF proteins contains a RING finger and several zinc finger motifs, which are important for downstream signaling events (Rothe et al., 1995; Takeuchi et al., 1996).

Many of the biological effects of TRAF signaling appear to be mediated through the activation of transcription factors of

the NF- κ B and AP-1 family. NF- κ B promotes the expression of genes involved in inflammatory and anti-apoptotic responses (Baeuerle and Baltimore, 1996; Beg and Baltimore, 1996; Liu et al., 1996). It is activated by the I κ B kinase (IKK), which consists of two kinase subunits, IKK α and IKK β , and a regulatory subunit, IKK γ /NEMO (DiDonato et al., 1997; Regnier et al., 1997; Zandi et al., 1997; Krappmann et al., 2000). Phosphorylation and degradation of I κ B lead to the release and translocation of NF- κ B to the nucleus to activate transcription (Stancovski and Baltimore, 1997). AP-1 activity is stimulated by mitogen-activated protein (MAP) kinases through either direct phosphorylation or transcription of AP-1 components (Karin, 1996). MAP kinases, which include Ser/Thr kinases such as JNKs/SAPKs, ERKs and p38s, are at the downstream end of a three-tiered system that also contains MAP kinase kinase (MAP2K) and MAP kinase kinase kinase (MAP3K). The stimulation of AP-1 activity by MAP kinases may elicit stress responses and promote both cell survival and cell death (Shaulian and Karin, 2001).

As adapter proteins, TRAFs elaborate receptor signal transduction by serving as both a convergent and a divergent platform. Therefore, different TRAFs are created with their own specific biological roles. Their distinct upstream and downstream signaling pathways may determine this specificity. Recent structural and biochemical data have provided us with a much better understanding of the upstream signaling mechanism of TRAFs. Many of the current studies of TRAF downstream signaling focus on the activation of NF- κ B and AP-1 transcription factors. However, accumulating evidence points to the differential regulation of this apparently common downstream pathway as well as to additional TRAF-specific pathways for eliciting different biological functions. We further suggest that signaling-dependent TRAF trafficking may be another crucial regulatory factor. This commentary will focus

Table 1. Current members of the TNF receptor and IL-1R/TLR superfamilies

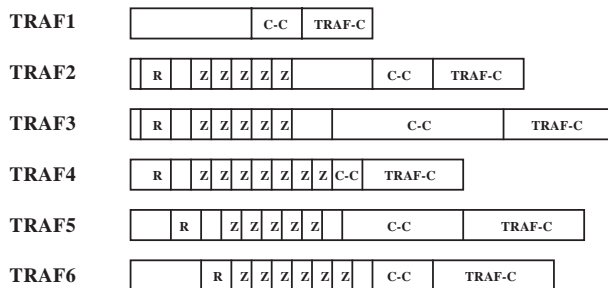
| | |
|---|--|
| TNF receptor superfamily | |
| Receptors with intracellular death domains: TNFR1, Fas, DR3, DR4, DR5, DR6, NGFR | |
| Receptors with no intracellular death domains: TNFR2, LTβR, CD40, CD30, OX40, CD27, 4-1BB, RANK/TRANCE-R, Troy, HveA, EDAR, XEDAR, AITR, TACI, BCMA | |
| IL-1R/TLR superfamily | |
| IL-1 receptor family: IL-1R, IL-1RAcP, IL-18R, IL-18RAcP | |
| Toll-like receptor family: TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10 | |

on the common and distinct molecular mechanisms of TRAF-mediated signal transduction. For complementary information, please refer to other recent reviews on TRAFs and TNF receptors (Wallach et al., 1999; Inoue et al., 2000; Locksley et al., 2001; Wajant et al., 2001).

Specific biological functions of mammalian TRAFs

Mammalian TRAF1 and TRAF2 were originally identified by their association with TNFR2 (Rothe et al., 1994). The other mammalian TRAFs were identified as follows: TRAF3 by its interaction with CD40 and the Epstein-Barr virus transforming protein LMP1 (Cheng et al., 1995; Mosialos et al., 1995; Sato et al., 1995); TRAF4 by its overexpression in breast carcinoma cells (Regnier et al., 1995); TRAF5 by its interaction with CD40 and LTβR (Ishida et al., 1996; Nakano et al., 1996; Mizushima et al., 1998) and TRAF6 by its participation in the signal transduction of CD40 and interleukin-1, a cytokine that is not related to TNF (Cao et al., 1996b; Ishida et al., 1996).

A.



B.

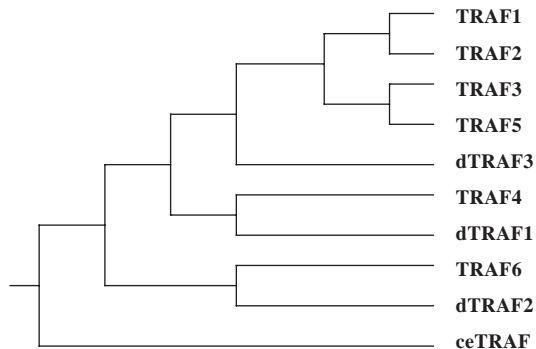


Fig. 1. Sequence characteristics of TRAFs. (A) Domain organization of the mammalian TRAFs. R, RING domain; Z, zinc-finger domain; C-C, coiled-coil domain; TRAF-C, TRAF-C domain. The TRAF domain comprises the coiled-coil domain and the TRAF-C domain. (B) The proposed evolutionary tree for the mammalian, *Drosophila* and *C. elegans* TRAFs. This figure is adapted from Grech et al. (Grech et al., 2000).

However, further extensive studies have shown that the specific biological function of each TRAF protein is not necessarily related to its origin of identification (Table 2, Fig. 2).

Since its discovery, TRAF2 has become the prototypical member of the TRAF family. The paradigm of TRAF-mediated NF-κB and MAP kinase activation was first demonstrated using both TRAF2 overexpression and a dominant-negative phenotype of a TRAF2 derivative lacking the RING domain (Rothe et al., 1995; Hsu et al., 1996b; Takeuchi et al., 1996; Duckett et al., 1997; Reinhard et al., 1997; Arch et al., 1998). TRAF2 transcripts have been detected in almost every tissue (Rothe et al., 1994), making TRAF2 the most widely expressed TRAF family member.

TRAF2 plays a cytoprotective role, which was demonstrated by the premature death of TRAF2-deficient mice owing to severe runting. In addition, TRAF2-deficient cells are highly sensitive to TNF-induced cell death (Yeh et al., 1997). The lack of TRAF2 or the expression of a dominant-negative form of TRAF2 only led to a modest defect in TNF-induced NF-κB activation but resulted in a severe reduction of JNK/SAPK activation (Lee et al., 1997; Yeh et al., 1997; Devin et al., 2000). Recent data suggest that TRAF2 is important for NF-κB activation, but this role may be partially compensated for by the highly related TRAF5 (see below) (Nakano et al., 2000). The sensitization to TNF-induced cell death in the absence of TRAF2 must have been largely due to an NF-κB-independent mechanism (Lee et al., 1997; Yeh et al., 1997; Lee et al., 1998). One possibility may be related to the failure to recruit other proteins such as cellular inhibitors of apoptosis proteins (cIAPs) to the TNFR1 receptor signaling complex in the absence of TRAF2 (Wang et al., 1998; Park et al., 2000). TNF toxicity through TNFR1 appears to contribute significantly to the survival defects in TRAF2-deficient mice because a double

Table 2. Summary of TRAF functions

| TRAFs | Implicated functions |
|-------------|--|
| TRAF1 | Apoptotic protection Feedback regulation of receptor signaling |
| TRAF2 | Anti-apoptotic signaling JNK activation Perinatal survival |
| TRAF3 | T-cell-dependent antigen response Perinatal survival |
| TRAF4 | Tracheal formation |
| TRAF5 | CD27 and CD40 signaling |
| TRAF2 and 5 | NF-κB activation |
| TRAF6 | Bone metabolism CD40 signaling IL-1 signaling LPS signaling Perinatal survival |

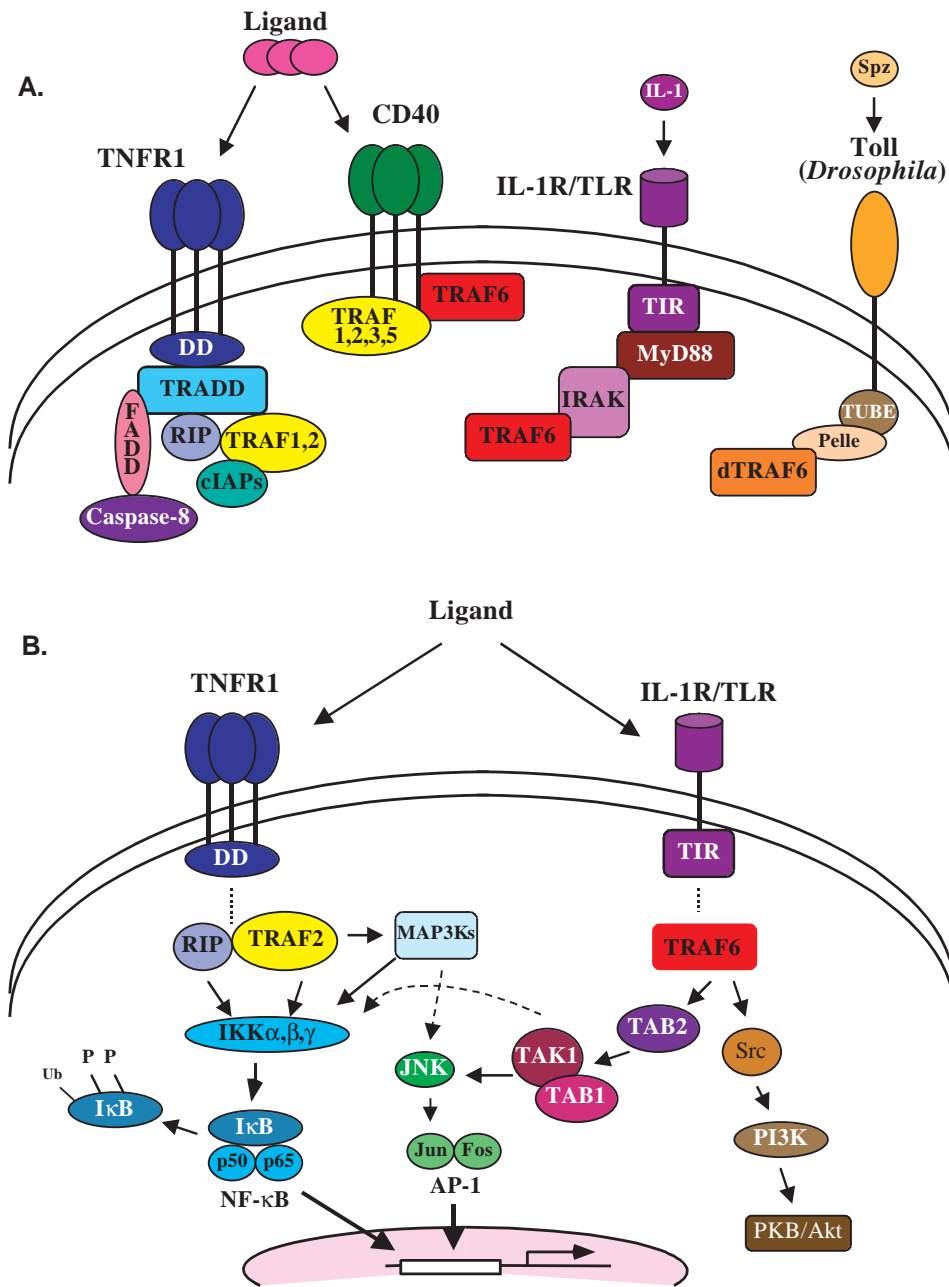


Fig. 2. TRAF signaling pathways. (A) Membrane-proximal events in TRAF signaling, showing direct receptor-TRAF recruitment and indirect receptor-TRAF interactions. (B) Downstream signaling events for TRAFs, shown here for two representative TRAF family members, TRAF2 and TRAF6.

are specifically recruited through TRAF1 and TRAF2 (Wang et al., 1998; Park et al., 2000).

Although TRAF3 possesses a putative domain organization similar to TRAF2 and TRAF5, overexpression of TRAF3 did not activate NF- κ B (Rothe et al., 1995). In contrast, it was reported that TRAF3 recruitment to LT β R led to cell death (Force et al., 1997), and that both N- and C-terminal domains of TRAF3 negatively regulate NF- κ B activation induced by Ox40 (Takaori-Kondo et al., 2000). However, it has also been shown that there are a variety of mRNA species of TRAF3 and that some splice variants do induce NF- κ B activation (van Eyndhoven et al., 1999). Similar to TRAF2-deficient mice, TRAF3-deficient mice have poor perinatal and neonatal survival (Xu et al., 1996). However, despite the runting phenotype and the hypotrophy of the spleen and thymus, which is similar to the phenotype displayed by TRAF2-deficient mice, the immune system is fairly normal except in the T-cell-dependent antigen responses (Xu et al., 1996).

The biological importance of TRAF4 was revealed by the gross tracheal malformation displayed by TRAF4-deficient mice (Shiels et al., 2000), which suggested a parallel

function of TRAF4 with the *Drosophila* Toll pathway in body organization. Analysis of TRAF4 expression has also implicated TRAF4 in the function of neural multipotent cells and epithelial stem cells in adult mammals (Krajewska et al., 1998; Masson et al., 1998). Even though there is evidence that TRAF4 may interact with several receptors in the TNF receptor superfamily (Krajewska et al., 1998; Ye et al., 1999), further studies are required to elucidate the molecular pathway of TRAF4 signaling.

TRAF5 is considered to be a close functional and structural homologue of TRAF2, and overexpression of TRAF5 can also activate NF- κ B and AP-1 transcription factors (Ishida et al., 1996; Nakano et al., 1996). However, deletion of TRAF5 did not cause perinatal lethality, perhaps owing to the more restricted expression pattern of TRAF5 compared with TRAF2 (Ishida et al., 1996; Nakano et al., 1996). TRAF5 deficiency

deficiency in TRAF2 and TNFR1 resulted in increased survival (Yeh et al., 1999).

TRAF1, unlike TRAF2 and other TRAFs, does not have the N-terminal RING and zinc-finger domains (Rothe et al., 1994). TRAF1 expression is fairly restricted (Rothe et al., 1994; Mosialos et al., 1995) and can be upregulated in lymphoid tumors and transformed lymphoid cells (Durkop et al., 1999; Zapata et al., 2000). The current data are consistent with the idea that TRAF1 is an NF- κ B inducible protein that protects cells from apoptosis and plays a role in the feedback regulation of receptor signaling (Speiser et al., 1997; Wang et al., 1998; Carpentier and Beyaert, 1999; Schwenzer et al., 1999; Nolan et al., 2000). It appears that TRAF1 works in conjunction with TRAF2 and cIAPs to fully suppress TNF-induced apoptosis. This may be achieved through the direct suppression of caspase activation in the TNFR1 signaling complex by cIAPs, which

led to more specific defects in CD40- and CD27-mediated lymphocyte activation, whereas TNF-mediated NF- κ B activation was not severely affected (Nakano et al., 1999). Interestingly, TRAF2 and 5 double knockout animals did exhibit a severe reduction in TNF-induced NF- κ B activation, which suggests that TRAF5 and TRAF2 are partially functionally redundant (Nakano et al., 2000).

TRAF6 possesses a unique receptor-binding specificity that results in its crucial role as the signaling mediator for both the TNF receptor superfamily and the IL-1R/TLR superfamily. As shown by targeted gene ablation, TRAF6 is functionally important for both TRANCE-R-mediated osteoclast activation and CD40 signaling (Lomaga et al., 1999; Naito et al., 1999; Wong et al., 1999b), even though both CD40 and TRANCE-R can also signal through TRAF2 (Pullen et al., 1998; Wong et al., 1998). In the IL-1R/TLR superfamily, lack of TRAF6 leads to defective signaling by IL-1 and IL-18 as well as hyporesponsiveness to bacterial lipopolysaccharides (LPS), the cell wall component of Gram-negative bacteria, which signals through TLR4 (Lomaga et al., 1999; Naito et al., 1999). These observations place TRAF6 as an important player in innate immunity against pathogens.

The functional divergence of TRAFs appears to correlate well with a proposed evolutionary relationship among TRAFs in mammals and other organisms on the basis of sequence conservation in the TRAF domain and gene structure analysis (Grech et al., 2000) (Fig. 1). In this hypothesis, TRAF4 and TRAF6 precursors appear to have arisen earlier in evolution. We propose that TRAF4 and TRAF6 may be functional descendants of dTRAF1 and dTRAF2, which have been implicated in Toll signal transduction (Zapata et al., 2000; Shen et al., 2001). This argument points to the existence of a yet to be identified TRAF4-interacting receptor. On the other hand, TRAF1, 2, 3 and 5 appear to be more recent siblings in the TRAF family (Grech et al., 2000). This observation is supported by the similar receptor-binding specificity of these four TRAFs towards the TNF receptor superfamily (see below) and the lack of known homologues of these receptors beyond mammals.

Common and distinct signal transduction mechanisms up-stream of TRAFs

Each TRAF protein interacts with and mediates the signal transduction of multiple receptors, and in turn each receptor utilizes multiple TRAFs for specific functions (Arch et al., 1998). There are at least three distinct ways that TRAF proteins can be recruited to and activated by ligand-engaged receptors (Fig. 2A). Members of the TNF receptor superfamily that do not contain intracellular death domains, such as TNFR2 and CD40, recruit TRAFs directly via short sequences in their intracellular tails (Rothe et al., 1994; Cheng et al., 1995; Pullen et al., 1998). Those that contain an intracellular death domain, such as TNFR1, first recruit an adapter protein, TRADD, via a death-domain-death-domain interaction (Hsu et al., 1995). TRADD then serves as a central platform of the TNFR1 signaling complex, which assembles TRAF2 (Hsu et al., 1996b) and RIP (Stanger et al., 1995; Hsu et al., 1996a) for survival signaling, and FADD and caspase-8 for the induction of apoptosis (Hsu et al., 1996b). Members of the IL-1R/TLR superfamily contain a protein interaction module known as the TIR domain (Xu et al.,

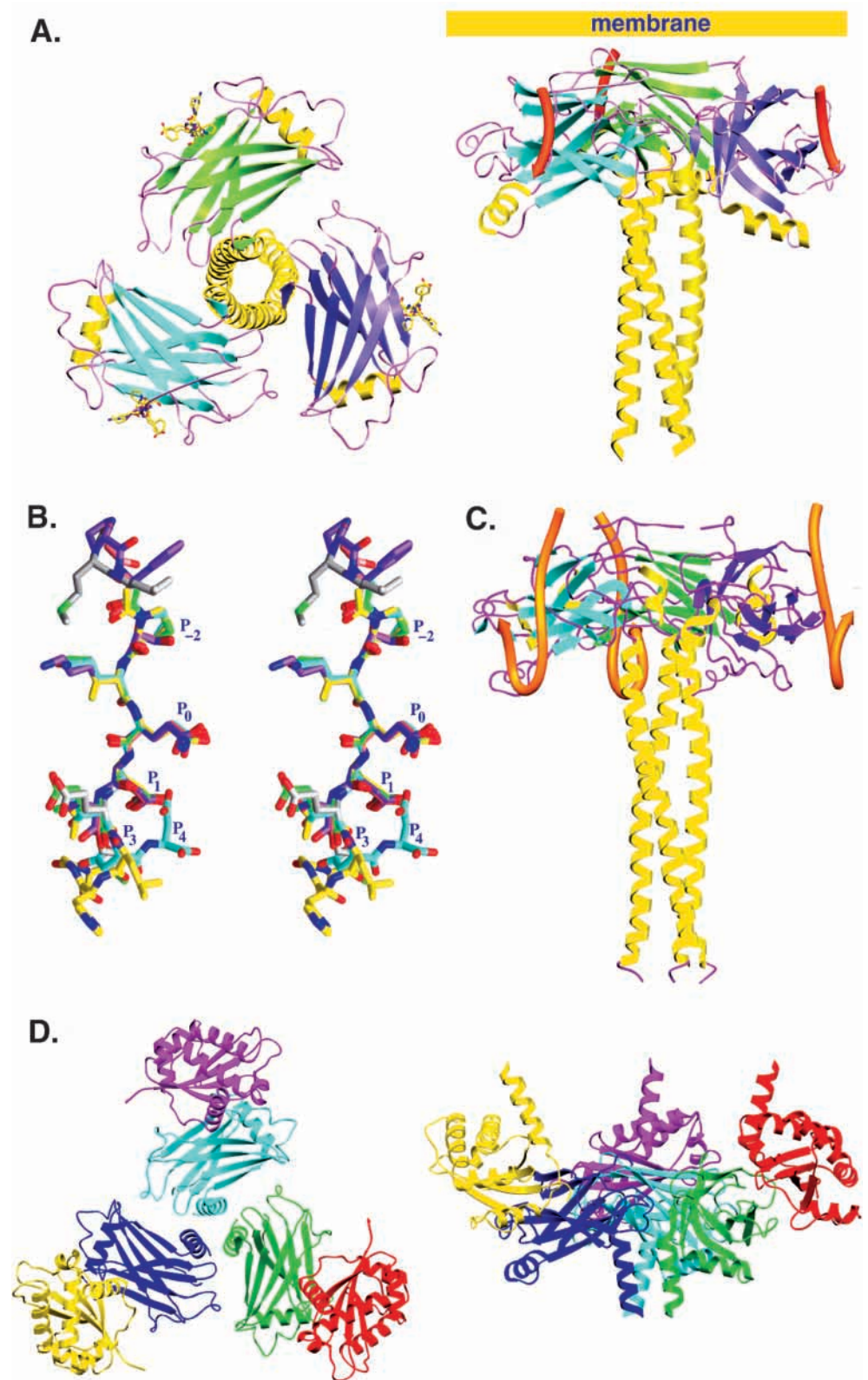
2000), which recruits, sequentially, MyD88 (Wesche et al., 1997), a TIR domain and death domain containing protein, and IRAKs (Cao et al., 1996a; Muzio et al., 1997; Wesche et al., 1999), adapter Ser/Thr kinases with death domains. IRAKs in turn associate with TRAF6 to elicit signaling by IL-1 and pathogenic components such as LPS (Cao et al., 1996b; Zhang et al., 1999; Hacker et al., 2000; Wang et al., 2001).

A common mechanism for the membrane-proximal event in TRAF signaling has been revealed by the conserved trimeric association in the crystal structure of the TRAF domain of TRAF2 (Park et al., 1999; McWhirter et al., 1999). The structure contains a stalk of a trimeric coiled-coil and a cap of trimerized TRAF-C domain with a novel anti-parallel β -sandwich fold, leading to a prominent mushroom shaped structure (Fig. 3A). This trimeric stoichiometry of TRAFs provides a structural basis for signal transduction across the cellular membrane after receptor trimerization by trimeric extracellular ligands in the TNF superfamily (Banner et al., 1993). Interestingly, recent studies suggest that specific ligand-induced receptor trimerization may be primed by non-signaling receptor pre-association prior to ligand binding (Chan et al., 2000; Siegel et al., 2000). Thermodynamic characterization revealed the low affinity nature of monomeric TRAF2-receptor interactions, which confirms the importance of oligomerization-based affinity enhancement or avidity in receptor-mediated TRAF recruitment (Ye and Wu, 2000).

Structural and biochemical studies have shown that a single TRAF protein recognizes diverse receptor sequences via a conserved mode of interaction but with a range of different affinities. In several different TRAF2 complexes, receptor sequences bind invariably to the surface groove on the TRAF-C domain of TRAF2 in an extended conformation, making main chain hydrogen bonding interactions with the edge of the β -sandwich structure (Park et al., 1999; McWhirter et al., 1999; Ye et al., 1999). The chain direction of the receptor peptides allows the receptors to immediately latch on to the TRAF-C domain after exiting from their transmembrane regions. Although TRAF2-binding sequences from different receptors bear limited sequence homology, their interactions with TRAF2 are preserved by a few conserved structural contacts, as shown in the consensus (P/S/T/A)_x(Q/E)E (Ye et al., 1999) (Fig. 3B). A deviation from this consensus, which bears the sequence of PxQxxD, is present in the human Epstein-Barr virus LMP-1 protein and binds to the same surface of TRAF2 via both similar and distinct features (Ye et al., 1999). Thermodynamic characterization further showed variable affinities of TRAF2 with different receptor sequences, which are probably a consequence of affinity modulations by non-conserved residues within and beyond the core binding motif (Ye and Wu, 2000) (Table 3).

Further structural analyses have also revealed how several different TRAFs can recognize a single receptor. The amino-acid residues on the TRAF2 surface used for receptor interactions are conserved among TRAF1, 2, 3 and 5, explaining the overlapping specificity of these TRAFs for different receptors (Park et al., 1999; Ye et al., 1999). However, an identical sequence from CD40 exhibits alternative binding modes to TRAF2 and TRAF3, suggesting that this conserved interaction may vary to some extent in different TRAFs, which modulates the strengths of the interactions (Fig. 3C). In the TRAF3 complex, receptor residues distal to the central core

Fig. 3. Structural studies of upstream interactions of TRAFs. (A) The mushroom-shaped trimeric structure of the TRAF domain of human TRAF2 (left: three-fold axis into the page; right: three-fold axis vertical) is shown here in complex with TNFR2. The coiled-coil region (stalk) is shown as yellow helices. The β -sheet regions of the three TRAF-C domains are shown respectively in blue, green and purple. Bound peptides from TNFR2 are shown as orange arrows, indicating the direction of the peptide chains. The proposed location of the cellular membrane is shown. This figure is modified from (Park et al., 1999). (B) The structural superposition of several TRAF2-interacting receptor peptides is shown using stereo stick models. Nitrogen atoms, blue; oxygen atoms, red; sulfur atoms, green; carbon atoms, yellow (CD40), gray (CD30), green (Ox40), pink (4-1BB), cyan (LMP1) and purple (TNFR2). This figure is adapted from (Ye et al., 1999). (C) The crystal structure of the trimeric complex between the TRAF domain of TRAF3 and a CD40 peptide bound in a hairpin configuration (Ni et al., 2000). The color-coding of the TRAF domain follows that of (A) and the CD40 peptides are shown as orange arrows. (D) A ribbon diagram of the complex between TRADD and TRAF2 (left, three-fold axis into the page; right, three-fold axis vertical). TRAF2, blue, green and purple; TRADD, magenta, red and yellow. The TRAF2-TRADD interface is more extensive and exhibits higher affinity than TRAF2-receptor-peptide interactions. This figure was adapted from Park et al. (Park et al., 2000).



sequence also interact with TRAF3, leading to the formation of a hairpin on the TRAF3 surface, which contributes strongly to TRAF3 interaction (Ni et al., 2000).

The distinct mode of TRAF2 recruitment by TRADD was revealed by the crystal structure of the TRAF2-TRADD

complex (Park et al., 2000) (Fig. 3D). The more extensive TRAF2-TRADD interface overlaps spatially and therefore potentially competes with TRAF2-receptor interactions. Biochemical characterization using surface plasmon resonance has shown that the TRAF2-TRADD interaction is

Table 3. Affinity characterization of the interactions of TRAF2 with various receptor peptides and with TRADD

| Receptor peptide | Sequence | K _D (μM) |
|-------------------|-------------------------------------|---------------------|
| hCD30 (573-583) | SDVMLS SV EEEG | 40 |
| hCD40 (250-266) | PV Q ETLHGCGPVT Q EDG | 60 |
| hOX40 (262-266) | PI Q EE | 50 |
| hTNF-R2 (420-428) | QVPF SK EEC | 500 |
| m4-1BB (231-236) | GAA Q EE | 1000 |
| hLMP1 (204-210) | P Q QATDD | 1900 |
| TRADD | | 8 |

The data are from Park et al. (Park et al., 2000) and Ye and Wu (Ye and Wu, 2000). The core sequences are shown in bold and aligned.

unique in two distinct ways. First, TRAF2 has a significantly higher affinity for TRADD than for peptide motifs in direct receptor interactions (Table 3), which leads to more efficient initiation of TRAF2 signaling by TRADD. Second, TRADD has specificity for only TRAF1 and TRAF2, but not other TRAF family members (Fig. 2A). It appears that TRAF1 and TRAF2 work in conjunction with associated caspase inhibitors cIAPs to fully suppress TNF-induced apoptosis in the TNFR1 signaling complex (Wang et al., 1998; Park et al., 2000), leading to dominance of survival signaling for this receptor under most circumstances.

TRAF6 directly interacts with CD40 and TRANCE-R, which are members of the TNF receptor superfamily (Ishida et al., 1996; Pullen et al., 1998; Darnay et al., 1999). For the signal transduction of the IL-1R/TLR superfamily, TRAF6 is indirectly coupled to receptor activation via IRAK and the IRAK-TRAF6 pathway is evolutionarily analogous to the Pelle-dTRAF pathway in *Drosophila* (Liu et al., 1999; Zapata et al., 2000; Shen et al., 2001). Even though biochemical characterizations suggest that TRAF6-receptor and TRAF6-IRAK interactions differ from receptor recognition by other TRAFs (Pullen et al., 1998; Darnay et al., 1999), elucidation of the molecular mechanism of TRAF6 upstream interactions awaits further structural information.

TRAF downstream signal transduction and regulation

TRAF-mediated NF-κB and AP-1 activation has been extensively studied for the representative TRAF family members TRAF2 and TRAF6, which apparently utilize different molecular pathways (Fig. 2B). Two models of TRAF2 downstream signaling pathways have been proposed. The TRAF2-mediated NF-κB activation may involve the direct recruitment of the IKK complex in cooperation with RIP (Yeh et al., 1997; Kelliher et al., 1998; Devin et al., 2000; Nakano et al., 2000; Zhang et al., 2000). Furthermore, artificial oligomerization of either TRAF2 or RIP was sufficient for NF-κB activation (Baud et al., 1999; Poyet et al., 2000). Alternatively, TRAF2 can associate with several upstream MAP kinases to induce NF-κB and AP-1 activation. These include NIK (Malinin et al., 1997; Song et al., 1997), MEKK1 and MEKK3 (Baud et al., 1999; Yang et al., 2001) for IKK activation and ASK1, MEKK1 and GCKR for initiating MAP kinase pathways and AP-1 activation (Nishitoh et al., 1998; Baud et al., 1999; Hoefflich et al., 1999; Shi et al., 1999).

The activation of both NF-κB and AP-1 by TRAF6 in the IL-1 signaling pathway appears to involve a MAP3K known as TAK1 (Yamaguchi et al., 1995; Ninomiya-Tsuji et al., 1999) and two adapter proteins TAB1 (Shibuya et al., 1996) and TAB2 (Takaesu et al., 2000). Upon stimulation, TRAF6 associates with endogenous TAK1 and TAB1 (Ninomiya-Tsuji et al., 1999) and interacts with TAB2 following the translocation of TAB2 from the membrane to the cytosol (Takaesu et al., 2001). Activated TAK1 appears to phosphorylate NIK, which in turn activates IKK (Shirakabe et al., 1997; Ninomiya-Tsuji et al., 1999) and initiates the MAP kinase pathway. Surprisingly, it has been shown recently that ubiquitination plays an important role in TAK1 activation (Deng et al., 2000; Wang et al., 2001). It appears that as a RING-domain-containing protein, TRAF6 operates together with a ubiquitin-conjugating enzyme system to catalyze the synthesis of unique polyubiquitin chains essential for TRAF6 downstream signaling.

The ability of multiple TRAFs to activate NF-κB and AP-1 transcription factors raises the question of how are the specific biological functions of different TRAFs realized. We propose that the different signaling pathways, such as those utilized by TRAF2 and TRAF6, may lead to preferential activation of specific NF-κB and AP-1 components and therefore the transcription of an overlapping but non-identical set of genes. In addition, many TRAF-interacting proteins have been identified and shown to regulate the activation of NF-κB and AP-1 in a TRAF-specific manner. For example, A20 is a TRAF1- and TRAF2-interacting protein (Song et al., 1996) that inhibits NF-κB activation and regulates TNF-induced cell death responses (Lee et al., 2000). A complete review of these regulatory proteins is beyond the scope of this commentary; however, their potential functions should not be overlooked.

A different level of regulation was revealed by several recent gene knockout studies in which certain proteins were shown to regulate NF-κB transcriptional activity without affecting its DNA-binding activity. For example, in mice deficient in the MAP3K NIK, normal NF-κB DNA-binding activity was observed upon treatment by a variety of cytokines, including TNF, IL-1 and LTβ. However, gene transcription upon LTβR activation was selectively affected by the absence of NIK (Yin et al., 2001). Therefore, as different TRAFs may recruit a different set of these regulatory proteins, their biological functions may be modulated by them.

In addition to NF-κB and AP-1 activation, TRAF proteins have been implicated in the crossover to additional signaling pathways. One such example is TRAF6-mediated activation of Src family kinases. In osteoclasts at least, TRAF6 plays an indispensable role in the activation of c-Src and subsequently the anti-apoptotic kinase PKB/Akt (Coffer et al., 1998; Wong et al., 1999a). Similarly, TRAF6-dependent activation of another protein tyrosine kinase Syk has been shown to mediate IL-1-induced chemokine production (Yamada et al., 2001). Therefore, the differential regulation of NF-κB and AP-1, as well as the specific activation of other signaling pathways, may collectively contribute to the specific functions of TRAFs.

Signaling-dependent TRAF trafficking

Accumulating evidence started to identify the intracellular

localization of TRAFs prior to, during and after receptor activation as an important regulatory mechanism for TRAF-mediated signal transduction. In resting cells, several TRAFs have been shown to localize throughout the cytoplasm or to intracellular punctate structures (Mosialos et al., 1995; Hostager et al., 2000). Upon receptor stimulation, TRAFs are redistributed to the cytoplasmic membrane or to plasma membrane patches or caps (Mosialos et al., 1995; Kuhne et al., 1997). More specifically, receptor recruitment of TRAFs during CD40 signaling could lead to the partitioning of these TRAFs into membrane rafts, which are specific regions of the plasma membrane that are rich in sphingolipid and cholesterol (Hostager et al., 2000; Vidalain et al., 2000). This partitioning could be crucial for TRAF signaling as it physically stabilizes the receptor signaling complexes and places TRAFs in the vicinity of a number of signaling proteins including the Src family kinases, which are preferentially localized in these membrane rafts. In fact, it has been found that among the known TRAFs, the ability to redistribute to insoluble membrane fractions consistently correlated with JNK activation. In addition, the forced localization of TRAF3 to the cell membrane was sufficient to convert this molecule into an activator of JNK (Dadgostar and Cheng, 2000).

Although the redistribution of TRAFs into membrane fractions may lead to a more sustained signaling of the activated receptor, it could also lead to a depletion of cytoplasmic TRAFs and therefore downregulate subsequent TRAF-dependent signal transduction (Arch et al., 2000). Some TRAFs can accumulate in perinuclear compartments after a particular signaling event (Arch et al., 2000; Force et al., 2000) but the eventual fate of these TRAFs is not clear. One possibility is proteasome-dependent TRAF degradation (Duckett and Thompson, 1997; Brown et al., 2001), which would limit the recycling of TRAFs for further signal transduction. Interestingly, several TRAFs have been shown to interact with proteins of the cytoskeleton and/or of particular membranes. These include the p62 nucleoporin, a component of the nuclear pore central plug (Gamper et al., 2000), the membrane-organizing protein caveolin-1 (Feng et al., 2001), the microtubule-binding protein MIP-T3 (Ling and Goeddel, 2000) and filamin (Leonardi et al., 2000). Clearly, this is an important field that requires further exploration and may hold many of the clues to the specificity of TRAF-mediated signal transduction.

Perspectives

Since the identification of the first two TRAF family members in 1994, it has become clear that different TRAFs exhibit specific biological functions. The membrane-proximal events for initiating differential TRAF signal transduction have been relatively well established from the wealth of structural and functional studies. The biggest challenge ahead is to further elucidate the molecular mechanisms of specific TRAF downstream signal transduction by differential TRAF localization and interactions with various intracellular proteins.

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