

Review

Understanding the roles of negative immune regulator TIPE2 in different diseases and tumourigenesis

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Summary. Tumour necrosis factor (TNF)- α -induced protein 8-like 2 (TIPE2 or TNFAIP8L2) is a novel identified negative regulator of both innate and adaptive immunity, which participates in immune homeostasis. TIPE2 is expressed in both immune tissues and non-immune tissues. It is significantly down-regulated in patients with infectious and autoimmune diseases, and the depletion of TIPE2 causes severe inflammatory disease. In recent years, accumulating evidence has shown that TIPE2 serves as an ideal biomarker and as a tumour suppressor in several tumour types. In this review, we summarized the roles and corresponding mechanisms of TIPE2 in immune regulation and different diseases, especially in tumourigenesis.

Key words: TIPE2, Expression profile, Immune regulator, Inflammatory diseases, Tumourigenesis

Introduction

Tumour necrosis factor (TNF)- α -induced protein 8 (TNFAIP8)-like 2 belongs to the TNFAIP8 family, a novel identified group of proteins that consist of TNFAIP8 (TIPE), TIPE1 (TNFAIP8L1), TIPE2

(TNFAIP8L2), and TIPE3 (TNFAIP8L3). TIPE2 was initially identified as an abnormally expressed gene in the inflamed spinal cord of experimental autoimmune encephalomyelitis (EAE) mice (Freundt et al., 2008; Sun et al., 2008). TIPE2 is significantly down-regulated in patients with infectious or autoimmune diseases and primarily functions as an essential negative immune regulator of vital importance in maintaining immune homeostasis (Li et al., 2009; Xi et al., 2011). A recent study reported that TIPE2 is also involved in the development of a variety of tumours (Cao et al., 2013; Zhang et al., 2013; Li et al., 2016b). According to the most recent studies, we summarized the basic information, expression conditions, functions and

Abbreviations. TIPE2, Tumour necrosis factor (TNF)- α -induced protein 8 (TNFAIP8) like 2; EAE, experimental autoimmune encephalomyelitis; DED, death effector domain; TGF- β , transforming growth factor- β ; IL-10, interleukin-10; TLR, Toll-like receptor; Foxp3, forkhead box P3; ROS, reactive oxygen species; LPS, lipopolysaccharide; TCR, T cell receptor; IFN- γ , interferon- γ ; CTLA4, cytotoxic T-lymphocyte-associated protein 4; PBMCs, peripheral blood mononuclear cells; ALT, alanine aminotransferase; AST, aspartate aminotransferase; Tbil, total bilirubin; ACHBLF, acute-on-chronic hepatitis B liver failure; ox-LDL, oxidized low-density lipoprotein; PRR, pattern-recognition receptor; I/R, ischemia/reperfusion; SLE, systemic lupus erythematosus; SLEDAI, SLE disease activity index; AA-FLSs, adjuvant arthritis-fibroblast-like synoviocytes; DR5, death receptor 5; MG, Myasthenia gravis; CR, chronic rejection; DSS, dextran sodium sulfate; HCC, hepatocellular carcinoma; MMP9, matrix metalloproteinase 9; uPA, urokinase plasminogen activator; NSCLC, non-small cell lung cancer; TAMs, tumour-associated macrophages; SCC, skin squamous carcinoma; EMT, epithelial-mesenchymal transition.

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corresponding mechanisms of *TIPE2* in this review.

The gene location and protein structure of *TIPE2*

By aligning the murine and human *TIPE2* sequences with murine and human genome databases, the chromosome location of *TIPE2* was determined. Murine *TIPE2* was identified on chromosome III (3f1–3f3), while human *TIPE2* was identified on chromosome I (1q21.2–1q21.3) (Sun et al., 2008).

TIPE2 is a cytoplasmic protein that consists of 184 amino acids. Human *TIPE2* shared approximately 53% identity and 78% similarity amino acid sequence with TNFAIP8, and 94% homologous with murine *TIPE2* (Sun et al., 2008). The high-resolution crystal structure of *TIPE2* showed that *TIPE2* consists of six antiparallel α -helices. The helix $\alpha 5$ contains a kink, caused by Pro153, which disassociates the two helices, $\alpha 5a$ and $\alpha 5b$. *TIPE2* has a structure similar to a death effector domain (DED), referred to as a DED-like domain. Interestingly, in the topology of *TIPE2*, the DED-like domain appears as a mirror image of the DED domain of caspase-8 or c-FLIP (Zhang et al., 2009). Strikingly, *TIPE2* contains a large, hydrophobic central cavity, which is proposed as a binding site for cofactors. These structural features are important for understanding the functions of *TIPE2*.

The expression and localization of *TIPE2* in different tissues and cells

The expression of *TIPE2* in humans and murine animals is not precisely the same, and differs in different tissues (Table 1). Zhang et al. generated a specific antibody to *TIPE2* and detected *TIPE2* expression in various murine tissues and a number of human cell lines (Zhang et al., 2010). *TIPE2* has been identified as a cytoplasmic protein. *TIPE2* is mainly expressed in the T cell zone in the spleens of mice. In murine lymphoid tissues, *TIPE2* protein was mainly observed in the paracortical areas and reticular cells in the medullary cords. *TIPE2* expression was negative in B-lymphoid cells in the bone marrow and germinal centre B cells in the spleen and lymph node. Moderate *TIPE2* protein expression can be detected in bone marrow polymorphonuclear cells. Moreover, high *TIPE2* expression can also be detected in monocyte/macrophage-derived human cell line THP1 and mouse cell lines RAW264.7 or J774A.1. Furthermore, *TIPE2* is preferentially expressed in glandular epithelium, such as renal proximal tubules, glucocorticoid-secreting cells of the adrenal medulla, islets of pancreas, and parietal cells of the stomach, suggesting that *TIPE2* may be involved in endocrine functions. *TIPE2* was initially identified as a gene abnormally expressed in the inflamed spinal cord of mice with experimental autoimmune encephalomyelitis (EAE) (Sun et al., 2008). Interestingly, *TIPE2* expression was negative in neuronal cells of the central nervous system. The increased *TIPE2* expression in

inflamed neural tissue may result from leukocyte infiltration. In addition, *TIPE2* could also be detected in somatic and germ cells of both female and male

Table 1. *TIPE2* protein expression profiles in different tissues and organs.

Tissues and Organs	<i>TIPE2</i> expression (C57BL/6 mice) Zhang et al., 2010	<i>TIPE2</i> expression (Human) Zhang et al., 2011
Lymph node		
T cell zone	++	++
Germinal center	-	-
Thymus	-	N.A.
Spleen		N.A.
T cell zone	++	
Germinal center	-	
Bone marrow		N.A.
Megakaryocytes	+	
Erythroid cell	-	
Cerebellum	-	-
Hippocampus	-	N.A.
Heart	-	+
Cardiovascular muscle	-	+
Skeletal muscle	+++	+
Smooth muscle	-	N.A.
Skin	-	+
Trachea	-	+
Lung	-	-
Esophagus	-	+++
Stomach		
Epithelium	-	-
Parietal cell	+	++
Chief cell	-	++
Small intestine		-
Enterocyte	±	
Crypt cell	-	
Granulocyte	++++	
Colon	N.A.	+++
Rectum	N.A.	-
Appendix	N.A.	+++
Liver	-	+
Pancreas		-
Exocrine portion	-	
Pancreatic islet	++	
Kidney		-
Glomerulus	++	
Proximal convoluted tubule	++	
Distal convoluted tubule	-	
Thyroid gland	±	-
Mammary gland	-	N.A.
Adrenal gland		N.A.
Cortex	-	
Medulla	+	
Ovary		N.A.
Primaryocyte	+	
Follicular cell	++	
Granulosa lutein cell	++	
Testis		++
Spermatogonium	-	
Spermatozoon	±	
Leydig cell	++	
Sertoli cell	-	
Epididymis	-	
Prostate	-	-
Bladder	N.A.	++
Uterus	-	++

reproductive organs (Zhang et al., 2010).

To determine the expression profile of human *TIPE2*, Zhang et al. generated a specific anti-human *TIPE2* antibody and examined *TIPE2* expression in various human tissues (Zhang et al., 2011). *TIPE2* was expressed not only in monocytes and T cells but also in B cells, which are different from those in murine animals, as murine *TIPE2* was not expressed in B cells. As to the non-immune tissues and cells, *TIPE2* was preferentially expressed in stratified squamous epithelium, including stratum basal, stratum spinosum, stratum granulosum, stratum lucidum, and stratum corneum, but not in simple epithelium, such as simple lung squamous epithelium, simple small intestine columnar mucous cells, and renal tubule cuboidal epithelium. Moreover, in the human oesophagus and cervix-stratified squamous epithelial tissues, *TIPE2* was differentially expressed in the outer cells rather than in the inner cells. Consistent with that in murine animals, human *TIPE2* was also selectively expressed in glandular epithelial tissues and certain types of cells that have secretory activity, suggesting the relationship of this protein with secretory functions. Unlike the expression conditions in murine animals, human *TIPE2* was expressed in the neurons of the brain and brainstem. Additionally, *TIPE2* was also expressed in liver hepatocytes and trachea chondrocytes (Zhang et al., 2010, 2011).

TIPE2 expression was low or negative in most human carcinoma cell lines but is highly expressed in monocyte/macrophage derived-cell lines, and SK-OV-3 originated from ovarian adenocarcinoma. We also found that *TIPE2* was highly expressed in human endometrial carcinoma cell lines, Ishikawa and HEC-1A (Our unpublished data). In addition, *TIPE2* could also be detected in Treg cells, which plays an important role in regulating the functions of Treg cells (Luan et al., 2011). Collectively, the expression profile of human *TIPE2* and murine *TIPE2* is different. *TIPE2* protein was expressed in both immune and non-immune tissues, indicating that *TIPE2* may have functions other than immune regulation.

Role of *TIPE2* in immune regulation

The human defence against a number of pathogens primarily depends on the normal functions of the immune system, while immune homeostasis is important to maintain normal immunoreactions. The detailed mechanisms through which immune homeostasis is maintained are not fully understood. Recent studies have indicated the requirement of at least two classes of molecules (Sun et al., 2008). The first class of molecules mainly includes inhibitory cytokines, such as transforming growth factor- β (TGF- β) and interleukin-10 (IL-10), negative regulators of the antigen receptor and Toll-like receptor (TLR) signalling, such as CTLA-4, inhibitor-of-kB and *Socs1*, and repressive transcription factors, such as forkhead box P3 (Foxp3).

These molecules could limit the activation and expansion of immune cells (Van Parijs and Abbas, 1998; Wahl et al., 2006). The second class of molecules includes Fas, Bim, Bax, caspase-8 and caspase-10, which are responsible for controlling cell death (Suda et al., 1995; Van Parijs and Abbas, 1998; Van Parijs et al., 1998). There are still a large number of genes have not yet been characterized. *TIPE2* is a novel characterized negative immune regulator required for maintaining immune homeostasis (Sun et al., 2008).

TIPE2 is involved in regulating innate immunity

Phagocytosis and oxidative burst are two fundamental effector mechanisms of innate immunity (Diebold and Bokoch, 2005; Niedergang and Chavrier, 2005; Mao and Finnemann, 2015). Phagocytosis enables the monocytes and granulocytes of the immune system to engulf and contain infectious microbes in phagosomes. Oxidative burst subsequently results in the release of vacuole reactive oxygen species (ROS) that kill the microbes. Deficiencies in either of these innate immune mechanisms lead to immune deficiency and uncontrolled infections (Roberts et al., 1999; Ambruso et al., 2000; Heyworth et al., 2003; Assari, 2006).

TLR activates both phagocytosis and oxidative burst, and plays an important role in the pathogen recognition and innate immune responses. Sun et al. found that upon stimulation with lipopolysaccharide (LPS), macrophages derived from *TIPE2*^{-/-} bone marrow produced significantly more IL-6 and IL-12 than wild-type cells. *TIPE2* knockdown in RAW 264.7 macrophages significantly increased the expression of IL-6 at both mRNA and protein levels. Moreover, *TIPE2* may regulate innate but not adaptive B cell responses, as *TIPE2*^{-/-} splenic B cells significantly expressed more IL-1 β and TNF- α than wild-type B cells upon stimulation with LPS or CpG (cytosine guanine nucleotides), while the proliferation, apoptosis, and Ig secretion of B cells treated with anti-IgM were not significantly different between wild type and *TIPE2*^{-/-} groups. Wang et al. found that upon stimulation with the TLR4 ligand, TLR3 agonist, and TLR2 ligand, significantly increased the expression of IL-6, TNF- α and IFN- β 1, while *TIPE2* expression was significantly diminished (Sun et al., 2012).

Both phagocytosis and oxidative burst are controlled by the Rac proteins of the Ras small GTPase superfamily (Roberts et al., 1999; Ambruso et al., 2000; Diebold and Bokoch, 2005; Niedergang and Chavrier, 2005). Rac GTPases control phagocytosis by promoting actin polymerization, and these enzymes also mediate ROS production by binding and activating the NADPH oxidase complex (Diebold and Bokoch, 2005). RacGTPase deficiency in mice and humans leads to an immune-deficient syndrome characterized by defective phagocytosis and oxidative burst (Roberts et al., 1999; Ambruso et al., 2000; Heyworth et al., 2003; Assari, 2006). Wang et al. reported that *TIPE2* binds to Rac

GTPases through a C-terminal CAAX motif, resulting in the inhibition of Rac membrane translocation, Rac activation and the downstream effects of Rac signalling (Such as the JNK and the PAK pathways). *TIPE2*-Rac interactions result in the inhibition of basal level phagocytosis, which also contributes to TLR-induced augmentation of phagocytosis. Similarly, *TIPE2* also inhibits oxidative burst via binding with Rac, which subsequently leads to the TLR-induced augmentation of bactericidal activity (Sun et al., 2012; Wang et al., 2012).

The effects of TIPE2 on adaptive immunity

Sun et al. found that *TIPE2*^{-/-} could augment both CD4⁺ and CD8⁺ T cell immune responses. T cells derived from *TIPE2*^{-/-} mice were hyper-reactive to T cell receptor (TCR) ligation and the production of Th17 cytokines, and Th1 cytokines (IFN- γ) and Th2 cytokines (IL-4) were also significantly increased. The expression of CD25, CD44 and CD69 was also significantly increased in *TIPE2*^{-/-} T cells. In addition, *TIPE2* overexpression in haematopoietic cells markedly reduced the expression of CD69 and IFN- γ after stimulation with antigens. This evidence indicates that *TIPE2* suppresses TCR-mediated T cell activation.

Further investigation revealed that *TIPE2* is a negative regulator of NF- κ B, JNK and p38 pathways. Caspase-8 is an apoptosis initiator that plays important roles in lymphocyte and myeloid cell activation and inducing apoptosis. Caspase-8-deficient immune cells are defective in response to both TLR and antigen receptor stimulations (Chun et al., 2002; Salmena and Hakem, 2005; Su et al., 2005; Tang et al., 2005; Bidere et al., 2006; Lemmers et al., 2007). *TIPE2* regulates the NF- κ B pathway by binding to caspase-8. However, the effect of *TIPE2* on MAPK might be independent of caspase-8. Moreover, *TIPE2* is involved in the regulation of Fas-mediated apoptosis and activation-induced cell death of T cells. By regulating the expression of cytotoxic T-lymphocyte-associated protein 4 (CTLA4), Foxp3, TGF- β and IL-10, *TIPE2* can maintain the immunosuppressive properties of CD4⁺CD25⁺ regulatory T cells (Luan et al., 2011). In addition, *TIPE2* inhibits inducible nitric oxide synthase and nitric oxide generation, which consequently suppresses inflammation by switching arginine metabolism from nitric oxide synthase to arginase (Lou et al., 2014).

Roles of *TIPE2* in different diseases

TIPE2 was initially identified as an abnormally expressed gene in the inflamed spinal cord of EAE mice. Since then, a number of studies have been focused on the roles of *TIPE2* in different diseases. Accumulating evidence has shown that immunological factors are the key points for numerous diseases, indicating that the functions of *TIPE2* are ubiquitous. Table 2 summarizes the recent advances on the expression conditions and roles of *TIPE2* in different diseases.

TIPE2 in infectious diseases

TIPE2 has been demonstrated as a key molecule in regulating both innate and adaptive immunity, which determined its role in infectious diseases. Sun et al. reported that *TIPE2*-deficient mice are hypersensitive to septic shock, and consistently undergo fatal inflammatory diseases (Sun et al., 2008). By using a mouse sepsis model, Liu et al found that down-regulated *TIPE2* expression was associated with decreased apoptosis and increased Th1 cytokines, which enhances the immune capacity of the host against sepsis (Liu et al., 2015a).

A number of studies have focused on the effect of *TIPE2* in hepatitis. *TIPE2* expression was down-regulated in the peripheral blood mononuclear cells (PBMCs) of hepatitis B patients, and *TIPE2* expression was negatively correlated with the blood levels of alanine aminotransferase (ALT), aspartate aminotransferase (AST), and total bilirubin (Tbil) as well as the HBV load of the patients. *TIPE2*-deficient mice developed more severe hepatic inflammation than wild-type mice. Moreover, *TIPE2* down-regulation preferentially occurred in cytotoxic CD8⁺ T cells, with increased expression of perforin, granzyme B and IFN- γ , indicating that *TIPE2* is involved in regulating the functions of HBV-specific CD8⁺T lymphocytes (Xi et al., 2011; Wang et al., 2015).

TIPE2 was demonstrated as a biomarker in predicting the prognosis of patients with hepatitis B infections. Wang et al. reported that *TIPE2* might be involved in the pathogenesis of acute-on-chronic hepatitis B liver failure (ACHBLF) by negatively regulating immune responses, as *TIPE2* mRNA expression was higher in patients with ACHBLF, and *TIPE2* expression serves as a potential indicator for the prognosis of patients with ACHBLF (Wang et al., 2014). By a prospective single-centre study, Fan et al demonstrated that *TIPE2* mRNA level in PBMCs serves as a novel biomarker in predicting 3-month mortality of ACHBLF (Fan et al., 2015). In addition, *TIPE2* expression was significantly decreased in the PBMCs of chronic hepatitis C patients. *TIPE2* was also negatively correlated with serum ALT, AST and HCV RNA levels. Moreover, the expression of *TIPE2* increased after anti-virus treatment, suggesting that *TIPE2* is also involved in hepatitis C infection, and its expression may serve as a marker of the viral load (Kong et al., 2013).

TIPE2 in cardiovascular disease

Atherosclerosis is a key aetiology of several cardiovascular diseases, and this condition has been widely recognized as an inflammatory disease of the arterial wall. As an anti-inflammatory protein, *TIPE2* is also involved in the development of atherosclerosis. Macrophages are considered essential for the development of atherosclerosis. Lou et al. found that macrophages from *TIPE2*^{-/-} mice produced more

oxidative stress and pro-inflammatory cytokines after treatment with oxidized low-density lipoprotein (ox-LDL), which resulted in exacerbated atherosclerosis development, indicating that *TIPE2* expression in macrophages may play an atheroprotective role by negatively regulating ox-LDL-induced inflammatory responses (Lou et al., 2013).

Yi et al found that genetic ablation of *TIPE2* significantly increased the cerebral volume of infarction and neurological dysfunction in mice after cerebral ischaemia reperfusion induced by middle cerebral artery occlusion, suggesting that *TIPE2* is involved in the signal transduction pathway linking the inflammatory immune response to specific conditions after cerebral ischaemia (Zhang et al., 2012). *TIPE2* also acts as a negative regulator linking NOD2, an intracellular pattern-recognition receptor (PRR), and inflammatory responses. The *TIPE2*-NOD2 interaction plays an important role in the pathogenesis of myocardial ischaemia/reperfusion (I/R) injury (Zhang et al., 2015a). These studies suggest that *TIPE2* is an important regulator in the progression of cardiovascular diseases.

TIPE2 in autoimmune diseases

As an essential negative regulator of inflammation and immune homeostasis, *TIPE2* is involved in a variety of immune related diseases. Both *TIPE2* mRNA and protein expression were decreased in asthmatic children. The levels of IgE, EO and IL-4 in the children with asthma were obviously higher than those in normal controls. While the expression level of *TIPE2* mRNA was negatively correlated with IgE, EO and IL-4 (Ma et al., 2013). *TIPE2* mRNA expression in the PBMCs of systemic lupus erythematosis (SLE) patients was also significantly decreased, and the *TIPE2* mRNA expression level was negatively correlated with the SLE disease activity index (SLEDAI). Moreover, *TIPE2* alleviates experimental SLE by inducing macrophage polarization to a M2 phenotype (Li et al., 2009, 2016a). *TIPE2* may also be involved in the pathogenesis of rheumatoid arthritis, as *TIPE2* increased the apoptosis of adjuvant arthritis-fibroblast-like synoviocytes (AA-FLSs) by enhancing death receptor 5 (DR5) expression levels, which subsequently promoted the activation of

Table 2. Expression, functions and related mechanisms of *TIPE2* in different diseases.

Disease	Source	<i>TIPE2</i> expression	Experimental data	Mechanisms	References
Hepatitis B	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with hepatic enzymes and HBV load	Regulating the functions of CD8 ⁺ T lymphocytes	Xi et al., 2011; Wang et al., 2015
ACHBLF	PBMCs (Human)	Decreased	<i>TIPE2</i> is a prognostic biomarker	Negatively regulates immune reactions such as IL-6 and TNF- α expression	Wang et al., 2014; Fan et al., 2015
Hepatitis C	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with ALT, AST and HCV RNA levels	N.A.	Kong et al., 2013
Atherosclerosis	Macrophages (Mice)	High	Inhibits the development of atherosclerosis	Inhibits oxidative stress and expression of inflammatory cytokines, regulates the functions of macrophage	Lou et al., 2013
Stroke	Brain (Mice)	Deficiency	<i>TIPE2</i> deficiency exacerbates stroke outcomes	<i>TIPE2</i> deficiency increases inflammatory cytokine expression and alters cerebral inflammatory cell infiltration	Zhang et al., 2012
I/R injury	N.A.	N.A.	<i>TIPE2</i> is negatively mediated by NOD2, and <i>TIPE2</i> silencing counteracted the reduced inflammation and myocardial injury in ischemic mice	Inhibits NOD2-induced activation of MAPK and NF- κ B signaling pathways, thus reducing the production of proinflammatory cytokines in macrophages	Zhang et al., 2015a
Asthma	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with IgE, EO and IL-4	N.A.	Ma et al., 2013
SLE	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with the SLE disease activity index	<i>TIPE2</i> alleviates experimental SLE by inducing macrophage polarization to a M2 phenotype	Li et al., 2009; Li et al., 2016a
Rheumatoid arthritis	FLSs (Rats)	Decreased	Promotes AA-FLS apoptosis	Regulates the DR5-caspase-NF- κ B pathway	Shi et al., 2016
Myasthenia gravis	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with IL-6, IL-17 and IL-21, TLR4 activation could down-regulate <i>TIPE2</i> expression	Negatively regulates TLR4-mediated autoimmune T helper 17 cell responses	Zhang et al., 2015b
Primary biliary cirrhosis	PBMCs (Human)	Decreased	<i>TIPE2</i> expression is negatively correlated with ALT, ALP, GGT, TNF- α , IL-1 β , IL-8 levels	Suppresses NF- κ B pathways	Quin et al., 2016
Chronic kidney allograft rejection	PBMCs and renal tissues (Human)	Increased (PBMCs) Decreased (Renal tissues)	<i>TIPE2</i> in the blood samples could serve as a diagnostic marker in clinical monitoring kidney chronic rejection	N.A.	Jia et al. 2013
Colitis	Colon (Mice)	Deficiency	Promotes colitis	Inhibits mucosal immunity to commensal bacteria	Lou et al., 2014a

Abbreviations: PBMCs, peripheral blood mononuclear cells; ACHBLF, acute-on-chronic hepatitis B liver failure; I/R injury, ischemia/reperfusion injury; SLE, systemic lupus erythematosis; FLSs, fibroblast-like synoviocytes.

caspase and inhibited the activation of NF- κ B in AA-FLSs (Shi et al., 2016).

Myasthenia gravis (MG) is an autoimmune-mediated neuromuscular disease (Heldal et al., 2009). Recently, Zhang et al. reported that TIPE2 mRNA expression was significantly reduced in MG patients, and TIPE2 expression was closely related to the clinical manifestations of this disease. TIPE2 may be involved in the pathogenesis of MG via negatively regulating TLR-mediated autoimmune T helper 17 cell responses (Zhang et al., 2015b).

TIPE2 might be involved in the hyper-reactivity of

monocytes to TLR ligands in primary biliary cirrhosis, a typical organ-specific autoimmune disease characterized by the immune-mediated destruction of small intrahepatic bile-duct, cholestasis, fibrosis and cirrhosis (Selmi et al., 2011). The expression of TIPE2 was significantly decreased in primary biliary cirrhosis, and TIPE2 expression is negatively correlated with the expression levels of ALT, ALP, GGT, TNF- α , IL-1 β , and IL-8. Moreover, TIPE2 expression is significantly increased after ursodeoxycholic acid treatment (Qin et al., 2016).

Jia et al. detected the expression of TIPE2 in the

Table 3. Expression, functions and corresponding signaling pathways of TIPE2 in human cancers.

Cancer types	TIPE2 level	Sample size	Detection methods	Functions	Signaling pathways	Ref.
Gastric cancer	Decreased	Tumour (n=15) v.s. adjacent paraneoplastic tissue (n=15)	IHC and qRT-PCR	Suppresses tumour cell proliferation	Upregulates p27	Zhao et al., 2015
Gastric cancer	Decreased	Gastric cancer cell lines (n=3) v.s. normal gastric mucous epithelial cells (n=1)	qRT-PCR	Inhibits tumour cell growth and induces tumour cell apoptosis	Upregulation of Bax, cleaved Caspase-9, cleaved Caspase-3, cleaved poly ADP ribose polymerase as well as downregulation of Bcl-XL, p-PKB/AKT and p-ERK1/2	Zhu et al., 2016
Gastric cancer	Decreased	Gastric cancer cell lines (n=3) v.s. normal gastric mucous epithelial cells (n=1)	RT-PCR	Suppresses tumour cell migration and invasion	Downregulation of β -catenin signaling through inhibiting AKT and activating GSK3 β	Wu et al., 2016
Hepatocellular carcinoma	Decreased	Tumour tissues (n=115)	IHC	Inhibits tumour cell proliferation, migration and invasion	Targeting Rac1 and then reduces F-actin polymerization and expression of MMP-9 and uPA	Cao et al., 2013
Hepatocellular carcinoma	N.A.	N.A.	N.A.	Suppresses TNF- α induced hepatocellular carcinoma metastasis	Decreasing the expression of MMP-13/MMP-3 through inhibiting ERK1/2 and NF- κ B activation	Zhang et al., 2015c
Hepatocellular carcinoma	Decreased	Tumour tissues (n=10) and pericarcinomatous liver tissues (n=10)	IHC and Western blot	Maintains genomic DNA stability and suppresses tumour development	N.A.	Wang et al., 2016
Colon cancer	Increased	Tumour tissues (n=52) v.s. healthy controls (n=30), colon cancer cell line (HT-29)	IHC and qRT-PCR	Serves as tumour suppressor	Inhibits TLR4-mediated tumorigenesis via caspase-8	Li et al., 2014
Non-small cell lung cancer	Increased	Tumour tissues (n=85) v.s. adjacent normal tissues (n=85)	IHC, qRT-PCR and Western blot	Suppresses tumour invasiveness and angiogenesis	Inhibits the activation of Rac1 and subsequently weakening its downstream effects, including F-actin polymerization and VEGF expression	Li et al., 2016b
Glioma cancer	Decreased	Glioma cell lines (n=3) and normal human astrocytes	qRT-PCR and Western blot	Inhibits hypoxia-induced migration, invasion and the EMT process	Inhibits hypoxia-induced activation of Wnt/beta-catenin pathway	Liu et al., 2016
Renal cell carcinoma	Increased	Tumour tissues (n=46) v.s. control (n=39)	qRT-PCR	N.A.	N.A.	Zhang et al., 2013
Prostate cancer	Decreased	Tumour tissues, prostate cancer cell lines (n=3) and the normal prostate cell line (n=1)	qRT-PCR and Western blot	Suppresses the proliferation, migration, invasion and the EMT process	Inhibits the PI3K/AKT signaling pathway	Lu et al., 2016
Skin squamous carcinoma	Increased	Tumour tissues (n=40)	qRT-PCR	Induces polarization of macrophages to a M2 phenotype	N.A.	Li, 2016
Osteosarcoma	Decreased	Tumour tissues (n=36) v.s. adjacent non-cancer bone tissues (n=36) and osteosarcoma cell lines (n=2)	qRT-PCR and Western blot	Suppresses tumour cell invasiveness	Decreasing the expression of MMP-13	Deng et al., 2015

PBMCs and kidney biopsy samples from 96 recipients of kidney transplants. TIPE2 expression in the PBMCs of patients with chronic rejection (CR) was significantly higher than that of the healthy controls, indicating that the detection of TIPE2 in the blood samples may serve as a diagnostic marker in clinical monitoring chronic kidney rejection (Jia et al., 2013). In addition, using an experimental colitis model induced by dextran sodium sulfate (DSS), Lou et al. found that TIPE2 promotes colitis by inhibiting mucosal immunity to commensal bacteria (Lou et al., 2014b).

TIPE2 and tumourigenesis

Subsequent studies further found that unlike murine TIPE2, which is preferentially expressed in haematopoietic cells, human TIPE2 is expressed in a wide variety of nonhaematopoietic cell types, implying a new function in addition to immune modulation (Zhang et al., 2010, 2011). TIPE2 is not detectable or weakly expressed in most human cancer cells, suggesting that TIPE2 alteration may be involved in human cancer progression. Accumulating evidence has demonstrated that TIPE2 exhibits effects not only in inflammation but also in cancer. We previously investigated the expression of TIPE2 in 112 primary hepatocellular carcinoma (HCC) tissues and found that TIPE2 expression was significantly decreased in HCC tissues, and TIPE2 expression was significantly associated with tumour

metastasis. Mechanically, TIPE2 inhibits the migration and invasion of HCC cells through targeting Rac1 and then reduces F-actin polymerization and expression of matrix metalloproteinase 9 (MMP9) and urokinase plasminogen activator (uPA) (Cao et al., 2013). Additionally, Zhang et al found that TIPE2 could significantly suppress the TNF- α -induced HCC metastasis via inhibiting ERK1/2 and NF- κ B activation (Zhang et al., 2015c). A recent study also demonstrated that TIPE2 down-regulation was associated with genomic DNA instability and HCV-induced HCC development (Wang et al., 2016).

Interestingly, although TIPE2 expression is increased in non-small cell lung cancer (NSCLC), this protein was negatively associated with the primary tumour size, lymph node metastasis, and advanced clinical stage, which can be used to predict lymph node metastasis. TIPE2 also serves as a tumour suppressor, as TIPE2 significantly suppresses the migration, invasion and colony formation of NSCLC cells (Li et al., 2016b). Li et al. reported that TIPE2 functions through reducing the expression of Bcl-XL and N-cadherin and increasing the expression of cleaved caspase-9, cleaved caspase-3 and E-cadherin (Li et al., 2015). Liu et al demonstrated that TIPE2 promoted lung cancer cell apoptosis by regulating caspase-3, caspase-9, Bcl-2 and Bax (Liu et al., 2015a,b). Additionally, we demonstrated that TIPE2 serves as a tumour suppressor via inhibiting Rac1 activity in NSCLC. Moreover, TIPE2 suppressed the

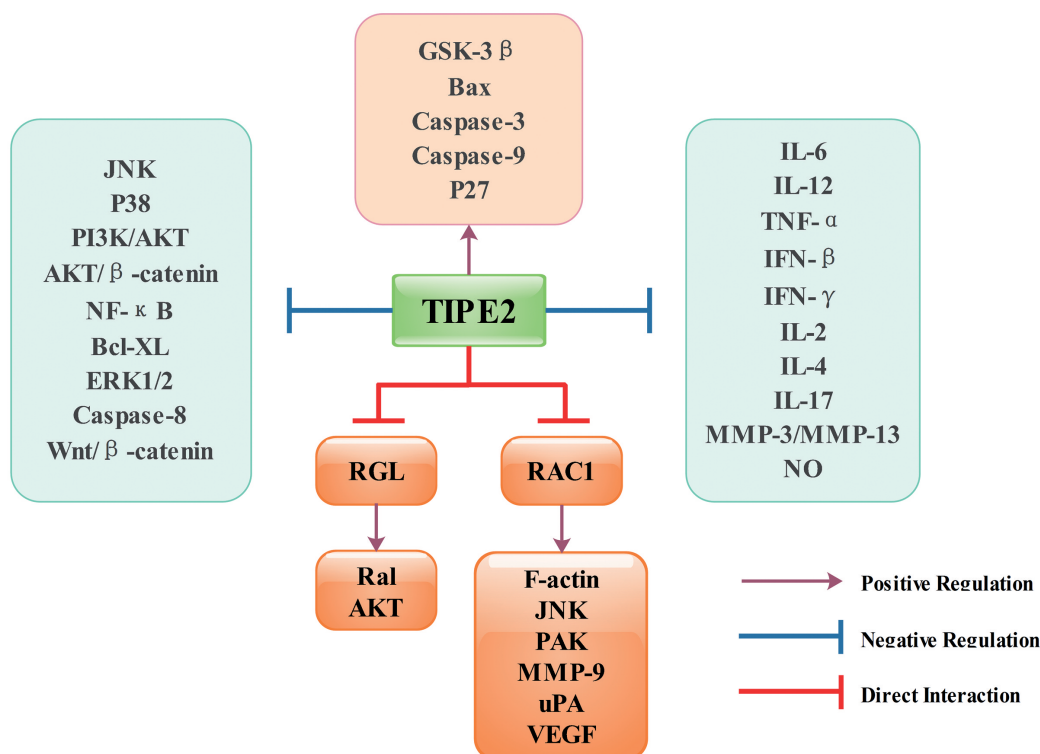


Fig. 1. Proposed molecular mechanism for TIPE2 mediated effects in immune regulation and tumourigenesis. TIPE2 primarily serves as a negative immune regulator by suppressing the expression of a number of inflammatory and pro-inflammatory cytokines. TIPE2 is also involved in apoptosis via regulating several related molecules, such as Bcl-2, Bax and caspases. By interacting with RGL and RAC1, TIPE2 regulates various classical signalling pathways that contribute to inflammation and tumourigenesis.

proliferation, migration, and tube formation of vascular endothelial cells, primarily due to its inhibitory effect on the secretion and expression of VEGF (Li et al., 2016b). This anti-angiogenesis property may account for the suppressive effect of TIPE2 on tumour metastasis.

By upregulating p27, TIPE2 could significantly suppress the proliferation of gastric cancer cells (Zhao et al., 2015). TIPE2 overexpression also increased the expression of Bax, cleaved caspase-9, cleaved caspase-3, cleaved poly ADP ribose polymerase, activated GSK3 β and decreased the expression of Bcl-XL, p-PKB/AKT, p-ERK1/2 in gastric cancer cells (Wu et al., 2016; Zhu et al., 2016).

TIPE2 is also involved several other types of tumours, such as colon cancer, skin squamous cell carcinoma and osteosarcoma. Li et al. demonstrated that TIPE2 expression is upregulated and related to lymph node metastasis and Dukes stage in colon cancer. In colon cancer cells, TIPE2 binds to caspase-8 and regulates the TLR4 inflammatory effect (Li et al., 2014). Also, Li found that TIPE2 regulates tumour-associated macrophages (TAMs) in skin squamous carcinoma (SCC), and patients with high-TIPE2 TAMs had a poor 5-year survival, indicating that the roles of TIPE2 may differ among different tumours (Li, 2016). Another study showed that TIPE2 expression was significantly decreased in osteosarcoma specimens, and TIPE2 could effectively mediate the suppressive effects of Shikonin on the invasiveness of osteosarcoma cells by decreasing MMP-13 expression (Deng et al., 2015). Recent studies have demonstrated that TIPE2 suppressed the epithelial-mesenchymal transition (EMT) process of glioma cells and also acts as a tumour suppressor by inhibiting the PI3K-AKT signalling pathway in prostate cancer cells (Liu et al., 2016; Lu et al., 2016). The expression, functions and mechanisms of TIPE2 in different tumours are summarized in Table 3.

Conclusions and perspectives

In this review, we briefly summarized the expression and functions of TIPE2, and the related mechanisms are summarized in Fig. 1. We conclude that TIPE2 is a key molecule in regulating immune homeostasis, as TIPE2 is involved in both innate and adaptive immune reactions, which determined the role of TIPE2 in infectious diseases and inflammatory diseases, such as in hepatitis, SLE and MG (Zhang et al., 2009; Xi et al., 2011; Sun et al., 2012; Zhang et al., 2015b; Li et al., 2016a). Currently, an increasing number of diseases have been considered as immune-related diseases. For example, inflammatory reactions and immune cells are essential for the development of atherosclerosis, while TIPE2 has been implicated as important in regulating the differentiation of immune cells and secretion of related cytokines (Lou et al., 2013). Indeed, TIPE2 is tightly associated with a number of immune related diseases, which deserves further investigation.

Inflammation is tightly correlated with tumouri-

genesis. In recent years, there has been a marked increase in understanding its wealth of correlations and potential roles in cancer (Gus-Brautbar et al., 2012; Cao et al., 2013; Li et al., 2016a,b; Liu et al., 2016; Lu et al., 2016). TIPE2 expression is typically decreased in tumour tissues, and TIPE2 regulates various classical signalling pathways that are essential for tumourigenesis. Given its critical roles in the development and progression of a number of tumours, TIPE2 may be considered a novel therapeutic target in cancer treatment. However, studies of TIPE2 in tumour are in the initial stages, and the different roles of TIPE2 in different tumours need further investigation. Moreover, as an immune regulator, the roles of TIPE2 in inflammation-associated cancer initiation and progression and in the immune therapy value of TIPE2 are not clear. To translate the laboratory findings into clinical applications, additional research is warranted to identify the precise mechanism of TIPE2 in cancer development.

We have to focus on the relationship between the structure and functions of TIPE2, as TIPE2 has a DED-like domain, of which the functions are still unknown. Moreover, the role of the large hydrophobic central cavity should also be further investigated (Zhang et al., 2009). In addition, there are four members of the TIPE family, and these members show high homology. However, the functions of these members are completely different (Cui et al., 2011, 2015; Lou and Liu, 2011; Fayngerts et al., 2014; Zhang et al., 2015d; Hu et al., 2016). Exploring the key structural factors and other factors that may affect the functions of the TIPE family is of high research value.

Except for immune regulation and tumour development, studies have focused on the other aspects of TIPE2 in recent years. In a recent study, we showed that TIPE2 is also involved in autophagy and lipid metabolism. Moreover, it seems that TIPE2 may function through different signalling pathways, which deserves further investigation.

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