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Review Article

MASP-1

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MASP-1 (mannose/mannan binding lectin associated serine protease-1) is a serum protein (~79kDa poylpeptide) predominantly synthesized by the liver. It is an important player in the innate immune system and is mainly bound to multimeric pathogen recognition receptors such as mannose/mannan-binding lectin (MBL) and the three ficolins (M-ficolin, L-ficolin and H-ficolin). MASP-1 has two CUB, a calcium-binding EGF-like, a trypsin-like serine protease and two complement control protein (CCP) domains. The serine protease domain is auto-activated upon binding of these receptors to their appropriate pathogenic ligands, generally carbohydrate domains or acetylated sugar residues. MASP-1 is therefore a component of the lectin pathway of complement activation. The primary substrate for MASP-1 activity is MASP-2, another serine protease. MASP-2 in turn cleaves and activates complement proteins C4 and C2, thus converging the lectin pathway with the classical pathway of complement activation. MASP-1 activity is negatively regulated by the presence of alternate splice variants, MASP-3 and MAp44. MASP-1 by virtue of its serine protease activity, also plays a role in the coagulation pathway.

KEYWORDS

Complement-activating component of Ra-reactive factor; CRARF; CRARF1; Mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor); Mannanbinding lectin serine protease 1; Mannose-binding lectinassociated serine protease 1; Mannose-binding proteinassociated serine protease; MASP; MASP-1; MASP1; PRSS5; Ra-reactive factor serine protease p100; RaRF; Serine protease 5

IDENTIFIERS

Molecule Page ID:A004274, Species:Human, NCBI Gene ID: 5648, Protein Accession:NP_001870.3, Gene Symbol:MASP1

PROTEIN FUNCTION

Complement activation: The complement pathway is one of the important innate immune mechanisms to counter pathagenic attack. The complement pathway is activated by three different routes: classical, alternative and lectin. The lectin pathways is activated upon binding of host receptors such as, collectins (mannose/mannan- binding lectin (MBL) and collectin kidney 1 (CL-K1 or CL-11) and the three ficolins (M-ficolin, L-ficolin and H-ficolin) to their respective pathogenic ligands. MASP-1 activates the lectin pathway of complement activation by co-operating with MASP-2 in generation of C3 convertase (Møller-Kristensen et al. 2007). Unlike MASP-2, MASP-1 cannot cleave C4 and can only marginally activate C2 and C3 (Sørensen et al. 2005, Héja et al. 2012, Matsushita and Fujita 1995, Matsushita et al. 1998, Matsushita et al. 2000, Chen and Wallis 2004, Rossi et al. 2001, Ambrus et al. 2003). Studies in a MASP-1 deficient patient, use of inhibitors and structural details all reveal that MASP-1 is responsible for cleavage and thereby activation of MASP-2 (Degn et al. 2012, Kocsis et al. 2010, Heja et al. 2012a, Heja et al. 2012b, Megyeri et al. 2013). Studies in knockout mice also show similar results and further suggest a role for MASP-1 in activation of complement factor D (fD) and thereby alternative complement pathway (Takahashi et al. 2008, Takahashi et al. 2010, Banda et al. 2011). Further, MASP-1 has been shown to cleave MASP-3 (Iwaki et al. 2011, Megyeri et al. 2013).

Coagulation pathway: MASP-1 has thrombin-like activity (Presanis *et al.* 2004) and mediates complement cross-talk with the coagulation and the kallikrein (a serine protease) systems, leading to formation of a fibrin clot (Gulla *et al.* 2010, Dobo *et al.* 2011, Takahashi *et al.* 2011, Hess *et al.* 2012). The crystal structure of MASP-1 reveals differences between MASP-1 and other serine proteases such as, MASP-2, C1r and C1s and also specificity for thrombin (Dobo *et al.* 2008, Dobo *et al.* 2009).

Other roles: MASP-1 can cleave protease activated receptor 4 (PAR4) on endothelial cells due to its thrombin-like activity (Megyeri *et al.* 2009). PAR4 cleavage and thereby activation in turn leads to activation of cytokine release, leukocyte rolling and inflammatory pathways, thus linking MASP-1 activity to these physiological phenomena. MBL-MASPs complex aids phagocytosis of *Staphylococcus aureus* (Neth *et al.* 2002). L-ficolin-MASP complex binds to capsular polysaccharide of group B streptococci and aids its opsonophagocytosis (Aoyagi *et al.* 2005). However, it is not clear if MASP is required or MBL alone is sufficient for this function (Shiratsuchi *et al.* 2008).

REGULATION OF ACTIVITY

C1 inhibitor (C1INH), an inhibitor for C1r and C1s, formed equimolar complexes with MASP-1 and MASP-2 and inhibited their proteolytic activities (Matsushita et al. 2000, Ambrus et al. 2003, Presanis et al. 2004). Alpha 2-macroglobulin was also shown to inhibit MASP-1 proteolytic activity (Ambrus et al. 2003). Among the thrombin inhibitors, boroMpg could inhibit MASP-1, while anti-thrombin III required presence of heparin to inhibit MASP-1 (Presanis et al. 2004). Both the splice variants of MASP1, MASP-3 and MAp44, can compete with MASP-1 to bind to MBL and ficolins and thereby downregulate complement activation (Dahl et al. 2001, Degn et al. 2013, Skjoedt et al. 2010). MASP-1/3 promoter activity was increased in the presence of interleukin (IL)-1β. However, this increase is nullified in the presence of IL-6. Further, promoter activity is also down-regulated by interferon (IFN)y (Endo et al. 2002).

INTERACTIONS

With MBL and ficolins: MASP-1 forms head to tail homo-

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dimers (Thielens *et al.* 2001, Teillet *et al.* 2008). The homodimers then go on to interact with MBL in a Ca²⁺ dependent manner (Matsushita and Fujita 1992, Thiel *et al.* 2000, Thielens *et al.* 2001). Gly54 and Lys55 of MBL (residue numbers correspond to the mature protein) are important in binding to MASP-1 (Matsushita *et al.* 1995, Teillet *et al.* 2007, Teillet *et al.* 2008). MASP-1 interacts with higher forms of MBL (Terai *et al.* 2003) and the oligomerization state of MBL has no influence on the binding affinities for MASPs (K_D values are similar for binding to a trimer or tetramer) (Teillet *et al.* 2005).

MASP-1 can interact with L-ficolin and H-ficolin (Matsushita *et al.* 2002, Ma *et al.* 2004, Matsushita and Fujita 2001, Cseh *et al.* 2002) to activate the complement pathway. Lys57 and Lys47 of L-ficolin and H-ficolin respectively (residue numbers correspond to the mature proteins) are important in binding to MASP-1 (Lacroix *et al.* 2009). MASP-1 also interacts with a novel collectin, collectin kidney 1 (CL-K1 or CL-11), which leads to complement pathway activation (Hansen *et al.* 2010, Ali *et al.* 2013, Ma *et al.* 2013).

With other MASPs: MASP-1 has been shown to interact with MASP-2, which can be disrupted by MAp44 (Degn *et al.* 2013). Complexes such as MBL-MASP and ficolin-MASP, interact with MASP-1, along with other MASPs such as MASP-2, sMAP (a splice variant of *MASP2*) and MASP-3 (Matsushita *et al.* 2000, Takahashi *et al.* 1999, Tateishi *et al.* 2011, Cseh *et al.* 2002, Dahl *et al.* 2001).

The experimental methods used to characterize these interactions are documented in CMAP, a complement map database (Yang *et al.* 2013).

PHENOTYPES

MBL-MASP-1 activity can result in glomerular deposition of fibrinogen, which in turn may contribute to the development of advanced glomerular injuries, such as post-streptococcal acute glomerulonephritis (PSAGN) (Hisano et al. 2007) and prolonged urinary abnormalities in patients with Henoch-Schonlein purpura nephritis (HSPN) (Hisano et al. 2005). Increased activity of MBL-MASP-1 complex is also associated with severe fibrosis in hepatitis C virus-infected patients (Brown et al. 2007). A non-sense mutation (W290X) results in a phenotype resembling 3MC (Carnevale, Mingarelli, Malpuech, and Michels) syndrome (Sirmaci et al. 2010). An allele found in some Caucasians, resulting in G54A substitution, is unable to activate the complement pathway (Matsushita et al. 1995). One single nucleotide polymorphism (SNP) for MASP-1 has been documented at position +50074 (relative to the transcription start site, in the second complement control protein (CCP) domain), which results in substitution of glycine with glutamic acid residue (Weiss et al. 2007).

MAJOR SITES OF EXPRESSION

MASP-1 is mainly expressed in the liver (Endo *et al.* 2002), with smaller amounts (~100 fold less compared to liver) found in the small intestine and kidney (Seyfarth *et al.* 2006).

SPLICE VARIANTS

MASP1 has two known splice variants, MASP-3 (Dahl *et al.* 2001) and MAp44 (Degn *et al.* 2009). *MASP1* encodes for six domains: two C1r/C1s/Uegf/bmp1 (CUB) domains, an epidermal growth factor (EGF)-like, two complement control proteins (CCPs) and a serine protease domain. The first five

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domains together form the heavy (or 'A') chain (encoded by exons 1-11), while the serine protease domain forms the light (or 'B') chain (Sato *et al.* 1994, Fujita *et al.* 2002). *MASP1* is alternatively spliced after exon 11 to result in MASP-3. Thus, the heavy chain sequence is similar between MASP-1 and MASP-3. However, the serine protease domain sequences are different, as exons 13-18 encode this domain in MASP-1, while exon 12 encodes the protease domain in MASP-3 (Dahl *et al.* 2001). MAp44 is formed by alternative splicing in the ninth exon of *MASP1*. MAp44 has two CUB domains, EGF and one CCP domain and an unique C-terminal domain of 17 a.a (Degn *et al.* 2009, Skjoedt *et al.* 2010). Please refer to MASP-3 and MAp44 Molecule Pages at www.signalinggateway.org for more information.

REGULATION OF CONCENTRATION

MASP-1 concentration in serum was found to be ~ 11 µg/ml (range 4-30 µg/ml) (Thiel *et al.* 2012) and is present in excess molar amounts over MBL (Vorup-Jensen *et al.* 1998). Further, over 95% of the total MASP-1 in serum is not in complex with MBL (Thiel *et al.* 2000). MASP-1 concentration is highest in the cord blood and in 3-9 year-olds and is fairly stable in adults (Terai *et al.* 1997).

ANTIBODIES

MASP-1 antibodies are available from: Santa Cruz Biotechnology, Abcam, Novus Biologicals, Sigma Aldrich, Hycult Biotech and Abnova.

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Table 1: Functional States

LOCATION	REFERENCES
extracellular region	
extracellular region	Rossi V et al. 2001; Matsushita M et al. 2000
extracellular region	Teillet F et al. 2008; Thielens NM et al. 2001
extracellular region	
extracellular region	Tateishi K et al. 2011
extracellular region	Thielens NM et al. 2001; Teillet F et al. 2005
extracellular region	Teillet F et al. 2008; Teillet F et al. 2005
extracellular region	Teillet F et al. 2005; Teillet F et al. 2008
extracellular region	Lacroix M et al. 2009; Cseh S et al. 2002
extracellular region	Cseh S et al. 2002; Lacroix M et al. 2009
extracellular region	Ma YJ et al.
extracellular region	Csuka D et al. 2013; Lacroix M et al. 2009; Zacho RM et al. 2012
extracellular region	Ambrus G et al. 2003
extracellular region	Fujita T et al. 2002
extracellular region	Héja D et al. 2012; Héja D et al. 2012
	extracellular region extracellular region

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SUPPLEMENTARY

Supplementary information is available online.

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This molecule exists in 15 states , has 20 transitions between these states and has 3 enzyme functions.(Please zoom in the pdf file to view details.)

