

Toll-like receptor and silk sericin for tissue engineering

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Abstract

Toll-like receptor (TLR) is responsible for the recognition of foreign protein. Accordingly, TLR is mainly expressed in the immune associated cells. When foreign protein such as silk sericin is considered for the graft, the response of TLR should be considered. TLR is not all or none responsive receptor. TLR can be activated differently by the intensity of the input. Silk sericin is easily fragmented. The protein conformation of silk sericin is different to the degumming method. TLR response to silk sericin may be different to the degumming method. Consequently, objective tailored extraction method should be investigated and developed.

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Introduction

Graft has been developed to restore the defect in the body (Kang *et al.*, 2019). If graft is taken from recipient body, it is called autograft. Autograft has the same genetic background to the recipient. Accordingly, there is no serious immune reaction. If graft is from the outside, it is foreign. When foreign material is implanted into the body, foreign body reaction is unavoidable (Kim *et al.*, 2018). When we differentiate the different kind of materials, each one is characterized by its own features and has a name. This name is a main tool for categorization. However, immune cells don't have sensitizing organs such as eye, ear, or nose. In addition, many types of antigen look similar and there are too many antigens. Accordingly, immune cells recognize the pattern of foreign material. For their recognition, pattern recognition receptors are important (Kulkarni *et al.*, 2020). Pattern recognition receptors can be classified as complement

system, formylated peptide receptor, scavenger receptor, and toll-like receptor (TLR) (Kulkarni *et al.*, 2020).

To modulate immune reaction to the graft as favorable, the understanding of these pattern recognition receptors are important (Kim, 2020). Silk sericin is collective term for the degumming product of silkworm cocoon (Park *et al.*, 2019). Except for silk fibroin, silk sericin is bonding protein between fibroin fibers. In silk sericin, there are sericin 1, sericin 3, seroin, and many protease inhibitors (Zhang *et al.*, 2015). Sericin 1 and sericin 3 are approximately 110 kDa each based on protein database (<https://www.ncbi.nlm.nih.gov/protein>). Inner layer has more sericin 3 and outer layer more sericin 1 (Kaur *et al.*, 2013; Zhang *et al.*, 2015). In boiling condition, small sized proteins are degraded. Only sericin 1 and 3 combination are detected as fragmented forms in this condition (Jo *et al.*, 2020).

When silk sericin is grafted into the body, immune cells will respond to it. As the protein conformation of silk sericin will be

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different to the degumming condition, the activation of pattern recognition receptors will be different. To modulate host response to silk sericin as favorable, optimization of sericin extraction condition is important. Pattern recognition receptors recognize pattern of protein (Rapsinski *et al.*, 2015). Silk sericin has many β -sheet structures and random coil structures (Oh *et al.*, 2011). The content of β -sheet structures may influence the response of pattern recognition receptors (Tukel *et al.*, 2009).

The purpose of this review was to investigate current knowledge of TLR and protein pattern of sericin from different type of degumming process.

Toll-like receptors (TLR)

Classification

TLR was found in *Drosophila fliea* in 1988, first (Hashimoto *et al.*, 1988). Its association with innate immunity was found later (Belvin and Anderson, 1996). In human, TLR4 was identified in 1997 and its activation produces inflammatory cytokines (Medzhitov *et al.*, 1997). Until now, 11 human TLRs have been reported (Kulkarni *et al.*, 2020). The phylogenetic analysis of TLR is shown in Fig. 1. Different kinds of molecules can bind to TLRs. They can be microbial products, synthetic analogs of natural products, and damage-associated molecules from self. The preference to ligand is different to TLR type. For example, double strand RNA is bound to TLR3 and unmethylated CpG-DNA is bound to TLR9 (Dembic, 2005). TLRs are mainly expressed in immune cells such as macrophages (O'Neill *et al.*, 2013). TLRs are also expressed in non-immune cells such as epithelial cells and fibroblast (Kawasaki and Kawai, 2014).

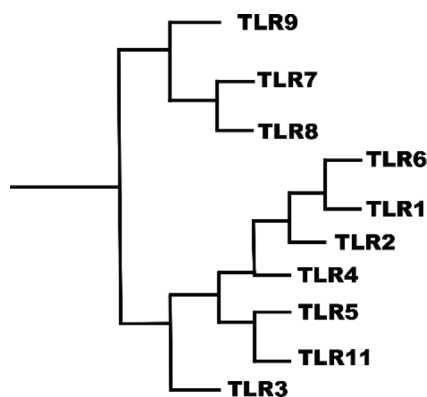


Fig. 1. Phylogenetic analysis of toll-like receptor (TLR). This figure was re-drawn from previous publication (Zhang *et al.*, 2004).

TLR1, TLR2, TLR4, TLR5, TLR6, and TLR10 are found in cellular surface. However, other TLRs are localized in the endosome (Kawai and Akira, 2010; Celhar *et al.*, 2012).

Signal transmission

All signaling from TLRs except for TLR3 is transmitted through myeloid differentiation primary response 88 (MyD88) (Kulkarni *et al.*, 2020). toll/interleukin-1 receptor (TIR)-domain-containing adaptor-inducing interferon- β (TRIF) is another adaptor molecule. TLR3 transmits its signal through TRIF. TLR4 uses both MyD88 and TRIF (Zhao *et al.*, 2014). Schematic drawings for signal transduction is shown in Fig. 2. When TLR is bound to ligand, MyD88 forms complex with interleukin-1 receptor associated kinases (IRAKs). Phosphorylated IRAK1 activates tumor necrosis factor (TNF) receptor associated factor (TRAF6). TRAF6 induces transforming growth factor beta-activated kinase 1 (TAK1) activation (Chen, 2012). TAK1 activates mitogen-activated protein kinases (MAPKs) and nuclear factor- κ B (NF- κ B), subsequently (Ajibade *et al.*, 2012). Among MAPK family, extracellular signal-regulated kinase 1/2 (ERK1/2), p38, and c-Jun N-terminal kinase (JNK) activates activator protein-1 (AP-1), transcription factors (Kawai and Akira, 2010).

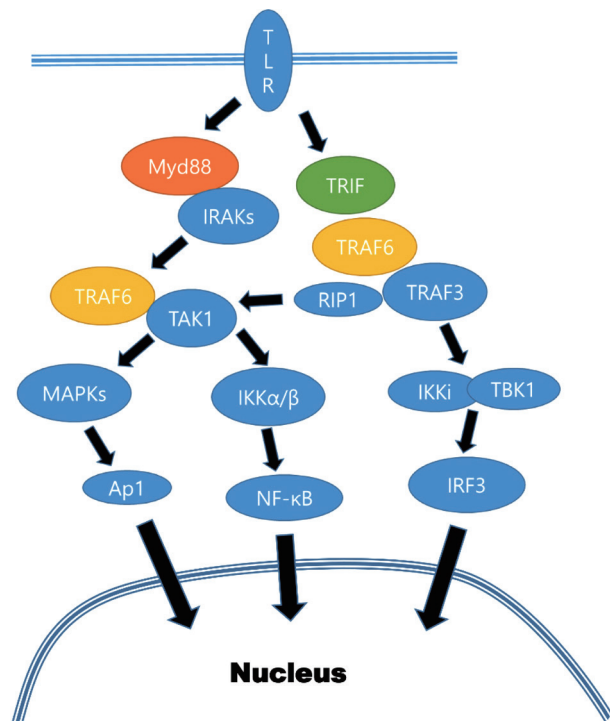


Fig. 2. Summarized signaling pathway of toll-like receptor. The definition of each abbreviation was shown in the main text.

TRIF transduces signal via TRAF3 and TRAF6 (Kawasaki and Kawai, 2014). Receptor-interacting serine/threonine-protein kinase 1 (RIP1) is TRAF6 associated kinase and activates TAK1. RIP1 increases NF- κ B transcription and MAPK activation via TAK1 (Kawasaki and Kawai, 2014). However, TRAF3 recruits I κ B kinase-i (IKKi) and TRAF family member-associated NF- κ B activator (TANK)-binding kinase 1 (TBK1). They phosphorylate interferon regulatory transcription factor 3 (IRF3) and it induces interferon genes (Kawai and Akira, 2010).

Protein structures and TLR activation

The consequence of TLRs activation is the production of inflammatory cytokines such as interleukin-1 β (IL-1 β) and TNF α (Tu *et al.*, 2016). Interestingly, the consequence of TLR2 and TLR4 activation is the increased expression level of bone morphogenic protein-2 (BMP-2) (Yang *et al.*, 2009; Meng *et al.*, 2008, Su *et al.*, 2011). BMP-2 overexpression is pro-inflammatory response in valve interstitial cells and may result in aortic valve calcification (Yang *et al.*, 2009). Peptidoglycan and lipopolysaccharide (LPS) are the ligand for TLR2 and TLR4. The application of peptidoglycan and LPS to human aortic valve interstitial cells can induce BMP-2 (Meng *et al.*, 2008). Oxidized low density lipoprotein also induces similar BMP-2 expression via TLR2 and TLR4 (Su *et al.*, 2011).

Amyloid proteins induce several diseases such as Parkinson's disease and type II diabetes. Amyloid proteins are produced by both human and micro-organisms (Mok *et al.*, 2007). However, there is no amino acid homology between human and micro-organism. Interestingly, all amyloids have cross- β -sheet quaternary structure (Rapsinski *et al.*, 2015). TLR2 recognizes these cross- β -sheet quaternary structure and TLR2 can't recognize amyloids upon the destruction of cross- β -sheet quaternary structure (Tukel *et al.*, 2009). Cross- β -sheet quaternary structure has been interested in the field of vaccine development. Ten amino acid sized self-assembling peptide originated from amyloid activates TLR2/6 (Al-Halifa *et al.*, 2020). This peptide is used for the development of long-lasting and safe vaccine (Al-Halifa *et al.*, 2020). A peptide from β -sheet structure of TIR domain-containing adaptor protein (TIRAP) inhibits TLR4 signaling (Acheh *et al.*, 2020). Based on these findings, β -sheet structure of proteins seems to be important in the activation of TLR2/4.

Silk sericin structure from different type of degumming process

Silk sericin is the second large component of silkworm cocoon (Oh *et al.*, 2011). Annually 150,000 tons of sericin are trashed as an industrial waste (Oh *et al.*, 2011). Accordingly, recycling of silk sericin is important for reducing an industrial waste. Silk sericin is degraded during the extraction procedure (Oh *et al.*, 2011). High molecular weight fraction is used for biological and medical application (Zhang, 2002; Aramwit and Sangcakul, 2007). Low molecular weight fraction is used for anti-oxidant and anti-tyrosinase (Chlapanidas *et al.*, 2013).

Main gene is sericin 1 and its product has different sizes by alternative splicing (Okamoto *et al.*, 1982; Michaille *et al.*, 1990). Based on sericin1 gene splicing information, the protein size will be 76, 123, 284, and 331 kDa (Garel *et al.*, 1997). However, this size is not maintained during extraction because of fragmentation. There have been several methods for the extraction of sericin from silkworm cocoon. Biochemical properties of silk sericin are influenced by its extraction method (Kurioka *et al.*, 2004; Kweon *et al.*, 2009). Using soap in the alkaline condition is not used for the biomedical application because separation of soap from silk sericin is difficult (Oh *et al.*, 2011). Sericin extraction using urea minimizes sericin degradation (Takasu *et al.*, 2002). However, dialysis procedure is required for removing urea and it is expensive and time-consuming (Oh *et al.*, 2011). Accordingly, sericin extraction using boiling water is widely used for its biomedical application.

When sericin is extracted by 100-120°C distilled water, sericin is degraded in the aspartic acid residue (Teramoto *et al.*, 2006). The spectrum of molecular weight from hot-water extracted sericin is between 17 and 250 kDa (Takeuchi *et al.*, 2005). Silk sericin is precipitated in the ethanol (Tsukada, 1979). When ethanol is mixed with water, much narrow molecular weight spectrum is observed compared to water only extraction (Oh *et al.*, 2011). In terms of silk sericin structure, silk sericin from hot water extraction shows random coil structure, but 75 vol.% ethanol shows β -sheet structure (Oh *et al.*, 2011). Unfortunately, β -sheet structure of sericin is not maintained after removal of residual ethanol (Oh *et al.*, 2011). The development of β -sheet structure can be achieved by adding glycerol to silk sericin (Yun *et al.*, 2013). Glycerol mediated β -sheet structure formation has been explained by protein compaction effect (Vagenende *et al.*, 2009). In the glycerol conjugated silk sericin, water is also

important for the development of β -sheet structure (Yun *et al.*, 2016). When sericin is extracted at 50°C for 4 weeks, minimum degradation of silk sericin is found (Chirila *et al.*, 2016). When combined with stirring, authors recommend that the duration should be less than 3 weeks (Chirila *et al.*, 2016).

Prospective of silk sericin for bone tissue engineering

Silk protein has been widely studied for bone tissue engineering. Silk fibroin has been studied in advance and it has been considered as biocompatible scaffold. Unlike silk fibroin, silk sericin is brittle and degraded rapidly. Though sericin coated implant shows improved osteogenicity, its findings are stayed in the cellular level. Recently, natural silk mat has been approved for bone regeneration in clinical trials compared to untreated control (Kim *et al.*, 2019). Silk sericin induced osteogenesis is explained by its macrophage activation (Kim, 2020). Sericin increases the gene expression of BMP-2 and BMP-4 in RAW264.7 cells (Kim *et al.*, 2020a). When sericin is separated by its molecular weight, high molecular weight fraction shows higher TNF α expression (Kim *et al.*, 2020b).

For the application of silk sericin for bone tissue engineering, silk sericin should have an osteoinductive property. BMP and vascular endothelial growth factor (VEGF) are representative proteins for osteoinduction. Sericin induces VEGF expression via hypoxia inducible factor (HIF)-dependent pathway (Jo *et al.*, 2019). Sericin looks like inducing BMP-2 and BMP-4 expression in macrophages (Kim *et al.*, 2020a). However, its detailed mechanism is unclear until now (Fig. 3). As sericin is a foreign protein for human, its pattern can be detected by TLR2/4. Thus, sericin based graft should induce immune reaction via TLR. TLR mediated cytokines are TNF α and BMP-2. All of them can be produced by sericin administration (Kim *et al.*, 2020a; Kim *et al.*, 2020b). For safe and long activation of TLR2/4, β -sheet structured protein is required. There have been introduced several extraction methods for collecting more β -sheet structured silk sericin. Among these methods, the method requires toxic chemicals should be avoided for biomedical application. As a consequence, limited number of extraction method can be considered for sericin extraction. This field is just beginning and should have much more investigation for reliable mass production of silk sericin in the bone tissue engineering.

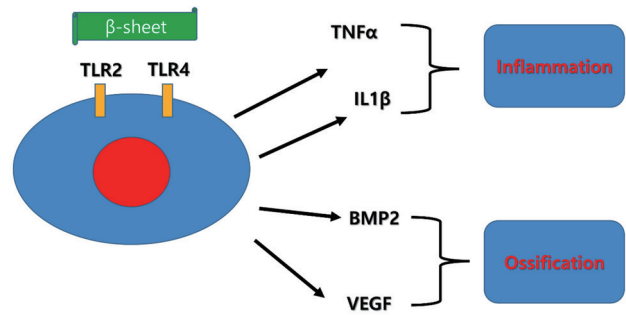


Fig. 3. Protein having β -sheet structure activates toll-like receptor-2/4 (TLR2/4). As a consequence, the expression level of tumor necrosis factor- α (TNF α), interleukin-1 β (IL1 β), bone morphogenic protein-2 (BMP2), and vascular endothelial growth factor (VEGF) can be increased. Detailed pattern of their expression can be different to the type of antigen and recipient cells.

Conclusion

Silk sericin is biocompatible and can be used for biomedical application. As silk sericin is foreign protein, its activation is mediated by TLR pathway. To optimize the quality of silk sericin for bone tissue engineering, the fraction of β -sheet structure in silk sericin should be increased. As the extraction method is important for the structure of silk sericin, it should be developed and optimized through in-depth investigation.

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