

Emerging roles of microRNAs in the regulation of Toll-like receptor (TLR)-signaling

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1. ABSTRACT

Toll-like receptors (TLRs) are evolutionarily conserved molecules that detect exogenous and endogenous molecular patterns and trigger both the innate and adaptive immune systems to initiate a pathogen-specific immune response and eliminate the threat. However, sustained, or prolonged activation of the immune system disrupts immunological homeostasis and leads to chronic or acute inflammatory diseases. MicroRNAs (miRNAs) can intervene in the initiation and modulation of the complex immunoregulatory networks via regulating the expression of TLRs and multiple components of TLR-signaling pathways including signaling proteins, transcription factors, and cytokines. Moreover, the aberrant expression of TLRs can induce the expression of several miRNAs which in turn regulate the expression of TLR signaling components and TLR-induced cytokines. The present review aims to highlight the emerging roles of miRNA in the regulation of TLR signaling, the interaction between the

miRNAs and TLRs, and their implication in inflammatory diseases.

2. INTRODUCTION

The immune system is a complex network of immune organs, cells, and soluble factors (cytokines) that act locally or systemically through an immediate (innate) inflammatory response by cytokines and phagocytes, and a specific tailored immune response through adaptive immune cells, or a regulated immune-tolerant response. The differing, and sometimes opposing, roles of the immune system are mediated by a complex interplay of intracellular and extracellular signaling pathways. Cells of the immune system participate in the protection of the host from invading pathogens, foreign antigens, and incipient tumor cells, and in development, maintenance of homeostasis, tissue repair and regeneration processes for wound healing (1). The innate immune system depends on the pattern recognizing receptors (PRRs), includes

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components of the complement system and Toll-like receptors (TLRs) family. TLRs are membrane-associated innate-immune sensors that detect the external pathogen-associated molecular patterns (PAMPs) or the internal damage-associated molecular patterns (DAMPs) and execute subsequent immune cell response (2-4). TLRs, the most extensively studied PRRs, are type-I transmembrane glycoprotein receptors. TLRs consist of three structurally important domains namely an ectodomain consisting of hydrophobic leucine-rich repeat region (LRR) for ligand recognition/binding at N-terminus and formation of functional dimers to initiate the signaling cascade, a single transmembrane helix, and a conserved cytoplasmic Toll/Interleukin-1 (IL-1) receptor (TIR) domain at C-terminus required for the activation of downstream intracellular signal transduction pathways (5, 6). Interestingly, the extracellular ligand-binding domains of TLRs contain hydrophobic leucine-rich repeat motifs that form horseshoe-shaped solenoid structures and contain an extensive β -sheet on its concave surface, and numerous ligand-binding insertions (7). TLRs are distinguished based on their ligand specificity, signal transduction pathways, and subcellular localization (8). In mammals, ten human (TLR1-10), and 13 murine TLR protein subfamily (TLR1-9, TLR11-13) have been identified with a functional difference among humans and mice (5, 9-11). TLRs are functionally classified into two categories. The group I TLRs include TLR1, TLR2, TLR4, TLR5, TLR6, and TLR10, and are expressed on the cell membrane and recognize microbially derived lipopolysaccharide (LPS) and lipopeptide ligands (12). The group II TLRs include TLR3, TLR7, TLR8, and TLR9, and are primarily expressed on vesicles and located intracellularly in the endoplasmic reticulum (ER), endosomes, and lysosomes compartments and recognize microbial nucleic acids released from stressed or dying cells (13-15). Unlike the other TLRs, TLR3 is expressed both on the cell surface and in intracellular vesicles and recognize viral dsRNA (16). Thus, TLRs are expressed in all tissues including macrophages, NK cells, DCs, circulating monocytes and neutrophils of the innate immune system; the adaptive immune cells (T and B lymphocytes), as well as non-immune cells and organs, e.g. epithelial and endothelial cells,

fibroblasts, brain, skeletal muscle, heart, lung, small intestine, liver, pancreas, colon, kidney, ovary, placenta, testis and prostate (17, 18).

MicroRNAs (miRNAs) have received considerable attention due to their involvement in the post-transcriptional regulatory mechanisms in almost all known cellular processes including development, differentiation, apoptosis, and the innate and adaptive immune responses to pathogen infections (19-26). Besides, extracellular miRNAs secreted from the donor cells could be delivered into recipient cells via extracellular vesicles and exosomes to establish a cell-cell communication system during various physiological and pathological processes (27-32). Selective miRNA studies in context to the regulation of TLRs suggest that miRNAs can modulate TLR signaling either through their involvement via transcriptional regulation or serving as physiological ligands of TLRs. Moreover, studies suggest that miRNA expression can be directly regulated by TLRs pathway (33). Interestingly, TLR activation modulates the expression of miRNAs that regulate TLR signaling either by the direct targeting of the molecules in the TLR pathway or indirectly through altering the activity of other cellular pathways that participate in crosstalk. The present review is highlighting the implication of TLRs in diseases and the emerging roles of microRNA (miRNA) in regulation of TLRs signaling.

3. PATHOPHYSIOLOGY OF TLR-SIGNALING

TLRs are the cell-surface initiators that trigger the inflammatory process. TLRs recognize conserved microbial-associated molecular patterns including LPS (TLR4), diacyl and triacyl lipopeptides, and zymosan (TLR2 associated with TLR1 or TLR6), peptidoglycan and lipoarabinomannan (TLR2), bacterial flagellin (TLR5), viral dsRNA (TLR3), viral or bacterial ssRNA (TLRs 7 and 8), HMGB1 (TLR2 and TLR4), and CpG-rich unmethylated DNA (TLR9) among others (34-36) (Figure 1). Several TLRs require to

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MAPK: mitogen-associated protein kinase; MyD88: Myeloid differentiation primary response gene 88; NF- κ B: nuclear factor kappa-light-chain-enhancer of activated B cells; PAMPs: pathogen-associated molecular patterns; pri-miRNAs: primary miRNAs; RA: rheumatoid arthritis; SHIP1: Src homology 2 domain-containing inositol polyphosphate-5-phosphatase 1; SARM: Sterile α - and armadillo-motif-containing protein; SLE: systemic lupus erythematosus; TH1: T helper 1; TIRAP or MAL: TIR domain-containing adaptor protein; TRIF: TIR domain-containing adaptor protein inducing IFN- β ; TIR: Toll/Interleukin-1 (IL-1) receptor; TLRs: Toll-like receptors; TRAM: TRIF-related adaptor molecule; TNF- α : tumor necrosis factor-alpha; TAMs: tumor-associated macrophages; TIDCs: tumor-infiltrating dendritic cells; UTR: untranslated region.

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Abbreviations: AP1: activator protein-1; AGO: argonaute; BLP: bacterial lipoprotein; CSF: cerebrospinal fluid; DAMPs: damage-associated molecular patterns; DGCR8: Drosha and the DiGeorge critical region 8 protein; HBV: hepatitis B virus; IL: interleukin; IRAK-1: interleukin-1 receptor-associated kinase 1; LRR: leucine-rich repeat region; LPS: lipopolysaccharide; MMP3: matrix metalloproteinase 3; miRNAs: MicroRNAs; miRISC: miRNA-induced silencing complex;