Armstrong suggest a Bayesian method based on real galaxy morphology distributions [8]; the sFIT method calibrates the shear measurement bias using simulations with a realistic image generation pipeline [9]. It is timely to point out a convenient route in building unbiased shear estimators: through Fourier transformation. It is mainly for the following reasons: (i) linear mappings (e.g. shear) in real space remain linear in Fourier space; (ii) convolutions in real space (e.g. the PSF effect) correspond to multiplications in Fourier space, which is much easier to deal with; (iii) spectral properties of the original source signal and the Poisson noise are distinct, making it straightforward to correct for the bias due to Poisson noise in the Fourier domain; (iv) For images sampled at the Nyquist frequency or higher, multipole moments of the source spectrum defined in Fourier space converge quickly to their right values, without the need for any interpolations of the image in real space. The method of Zhang, Luo, and Foucaud [10] is an example of Fourier-space shear estimator, which indeed enjoys all the above advantages, and performs very well in a recent open test [11]. Several other shear measurement ideas [12,13] are also based in Fourier space.

Despite of our partial success in building shear estimators, we caution that there are a number of other related issues need to be solved, including: PSF reconstruction from star images; determination of source boundaries; treatment of bad pixels; etc. Furthermore, it is recently reported that complex photo electronics may introduce a certain level of inhomogeneous or nonlinear pixel response to light, such as the charge-transfer inefficiency [14] and the brighter-fatter effect [15], which may affect galaxy shape measurement. It is therefore desirable to further develop current shear estimators, making them available for more general assumptions about astronomical images. This is crucial for fully achieving the scientific potential of the large scale galaxy surveys.

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IMMUNOLOGY

Advances in innate immune signaling: new activators and regulators
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The innate immune system can detect the invading microbe components via three major pattern recognition receptors—Toll-like receptors, RIG-I-like receptors and NOD-like receptors as well as a variety of cytoplasmic DNA or RNA sensors. These innate receptors induce a series of intracellular downstream signaling pathways, leading to the efficient innate immune responses to eliminate pathogens (Fig. 1). Meanwhile, a flexible and conditional regulatory network contributes to the fine-tuning of innate immune signaling for the maintenance of immune homeostasis and prevention of immunological disorders. The detailed mechanisms for the initiation and regulation of innate immune signaling are attracting increasing attention in recent years. In this paper, we focus on recent advances in the identification and functional characterization of new activators (in the first two paragraphs) and regulators (in the next two paragraphs) of PRR-triggered innate signaling pathways.

First, novel mechanisms of intracellular DNA and RNA sensing in different cell types or in response to different pathogens are recently proposed. It was previously thought that only dsDNA from DNA virus over 40 bp could induce innate antiviral immunity. But a recent study shows that unpaired guanosines flanking short (12–20 bp)
Figure 1. Activation and regulation of PRR-triggered innate immune signalings. The positive regulators such as GBPs and DRP1/3 and negative regulators such as Tet2, Rhbds3, and Ash1l are respectively shown in red and blue circles.

dsDNA (Y-form DNA) found in HIV-1 could also activate DNA sensor cyclic GMP-AMP synthase (cGAS), leading to production of type I IFN [1]. Besides, transcriptional factor SOX2 could sense pathogenic DNA via the high-mobility-group domain in neutrophils and then trigger transforming growth factor beta-activated kinase1 (TAK1)/TAK1-associated binding protein 2 (TAB2) signaling pathway, leading to activation of NF-κB and AP-1 and initiation of innate immunity against microbial infection [2]. Interestingly, a complex consisting of interleukin-26 (IL-26) released by human Th17 cells and intracellular DNA derived from invading pathogens or injured self-tissues could trigger type I IFN production by plasmacytoid dendritic cells via TLR9 [3]. This study illustrates the novel mechanism how adaptive immune cells (Th17 cells) participate in innate sensing of pathogenic DNA via specific cytokines (IL-26). In addition, retinoic acid-inducible gene 1 (RIG-I), the cytosolic RNA sensor, which could induce type I IFN antiviral responses via sensing RNAs bearing 5′-triphosphates (5′ppp) for antiviral immunity [4]. These studies suggest novel mechanisms for discrimination between self and non-self nucleic acid by the innate immune system.

Second, novel mechanisms of inflammasome activation are newly reported. Inflammasomes are large protein complexes triggered by various NLR members, and cytoplasmic dsDNA sensor AIM2 to promote the activation of caspase-1 and processing and maturation of IL-1β and IL-18 for establishment of innate inflammatory response. More recently, two groups independently reported that detection of Francisella novicida by cytoplasmic DNA sensor cGAS leads to expression of interferon-stimulated genes encoding guanylate-binding proteins GBP2 and GBP5. These GBPs feedback kill cytoplasmic bacterium for release of pathogenic DNA to induce AIM2 inflammasome and subsequent activation of caspase-1 and pyroptosis [5, 6] (Fig. 1). Besides, RNA virus could also induce activation of NLRP3 inflammasome via the signaling pathway mediated by RIP1-RIP3 complex and the GTP enzyme dynamin-related protein1 (DRP1) [7] (Fig. 1). These studies outline new mechanisms of inflammasome activation and also suggest possible targets for intervention of innate inflammatory diseases.

Then, multiple epigenetic modifications including DNA methylation, histone methylation and non-coding RNA are increasingly shown to modulate the innate signaling pathways at transcriptional levels. It’s recently shown that during the late phase of the LPS response, Tet2, an enzyme catalyzing 5-hydroxymethylcytosine (5hmC), recruits HDAC2 to the Il6 promoter to specifically suppress Il6 transcription via histone deacetylation, thus preventing aberrant activation of inflammatory responses [8] (Fig. 1). That Tet2 resolves innate inflammatory responses independently of DNA methylation and hydroxymethylation provides a previously unknown pattern of how DNA methylation enzymes regulate gene transcription. Besides, H3K4 methyltransferase Ash1l selectively accumulates at the promoter region of genes encoding ubiquitinating enzyme A20 to induce its H3K4 methylation, finally contributing to
regulation of TLR-triggered production of proinflammatory cytokines [9] (Fig. 1). Thus, epigenetic modifiers play potent roles in regulating innate immune responses through complex molecular interactions.

Finally, post-translational modification (PTM), including the conventional PTM such as ubiquitination and phosphorylation, and unconventional PTM such as methylation and acetylation of existing proteins, emerge as key mechanisms of altering innate signaling pathway via affecting the function of innate sensors, adapters, modulators, enzymes, transcriptional factors and so on. Protein polyubiquitination of NF-κB essential modifier (NEMO, also known as IkB kinase γ, IKKγ) including lysine 63 (K63)-linked and head-to-tail linked polyubiquitination are essential for IKK complex activation and NF-κB activation. A recent study suggests K27-linked polyubiquitination of IKKγ, in conjunction with Rhomboid protein rhomboid domain containing 3 (Rhbdd3) and ubiquitin-editing enzyme A20 provide an essential protein platform for negative regulation of NF-κB activation and IL-6 production in dendritic cells [10] (Fig. 1). Besides, the methyltransferase Ezh2 could interact with extranuclear regulatory protein Talin to directly methylate Talin, promoting the turnover of adhesion structures and adhesion and migration of innate immune cells like neutrophils and dendritic cells [11]. This study reveals an important role of non-histone methylation by EzH2 in regulation of leukocyte invasion and innate immune responses.

In sum, these studies elucidate the molecular basis for the activation and regulation of PRR signaling and also provide important clues for the pathogenesis and treatment of immunological diseases. Future investigations are required to further uncover the mechanisms of self-regulation and cross-regulation of PRR signaling pathways in different physiological and pathological processes. In especial, the rapid advances in genomic, epigenomic, transcriptomic and proteomic studies will significantly promote the large-scale and in-depth analysis of the complicated innate immune signaling networks. More importantly, a better understanding of innate immune signaling will greatly facilitate the translational study of targeting PRR signaling activation or promoting its regulation to treat immunological diseases.

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**GEOSCIENCES**

Developing policy for the Yellow River sediment sustainable control

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The Yellow River of China is one exception where erosion and sediment delivery have successfully been reduced [1]. This river was once the world’s largest carrier of fluvial sediment load and peaked at about 1.6 Gt yr⁻¹ in the middle of the last century [1–3]. The Yellow River is the birthplace of Chinese civilization, but throughout history it has produced frequent and catastrophic floods and droughts [3,4]. Over thousands of years, a diverse range of strategies and methods have been applied in attempts to control the sediment transport of the Yellow River, but none have succeeded in completely eradicating this scourge [2]. Fortunately, since the 1970s, the sediment transport by the Yellow River has significantly declined [1–5]. Nearly 90% of the sediment load is originated and transported from the Loess Plateau in the...