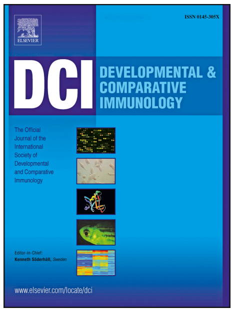

Describing the diversity of Ag specific receptors in vertebrates: Contribution of repertoire deep sequencing

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Abstract :

During the last decades, gene and cDNA cloning identified TCR and Ig genes across vertebrates; genome sequencing of TCR and Ig loci in many species revealed the different organizations selected during evolution under the pressure of generating diverse repertoires of Ag receptors. By detecting clonotypes over a wide range of frequency, deep sequencing of Ig and TCR transcripts provides a new way to compare the structure of expressed repertoires in species of various sizes, at different stages of development, with different physiologies, and displaying multiple adaptations to the environment. In this review, we provide a short overview of the technologies currently used to produce global description of immune repertoires, describe how they have already been used in comparative immunology, and we discuss the future potential of such approaches. The development of these methodologies in new species holds promise for new discoveries concerning particular adaptations. As an example, understanding the development of adaptive immunity across metamorphosis in frogs has been made possible by such approaches. Repertoire sequencing is now widely used, not only in basic research but also in the context of immunotherapy and vaccination. Analysis of fish responses to pathogens and vaccines has already benefited from these methods. Finally, we also discuss potential advances based on repertoire sequencing of multigene families of immune sensors and effectors in invertebrates.