Antigen receptor repertoires of one of the smallest known vertebrates

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Abstract

The rules underlying the structure of antigen receptor repertoires are not yet fully defined, despite their enormous importance for the understanding of adaptive immunity. With current technology, the large antigen receptor repertoires of mice and humans cannot be comprehensively studied. To circumvent the problems associated with incomplete sampling, we have studied the immunogenetic features of one of the smallest known vertebrates, the cyprinid fish *Paedocypris* sp. "Singkep" ("minifish"). Despite its small size, minifish has the key genetic facilities characterizing the principal vertebrate lymphocyte lineages. As described for mammals, the frequency distributions of immunoglobulin and T cell receptor clonotypes exhibit the features of fractal systems, demonstrating that self-similarity is a fundamental property of antigen receptor repertoires of vertebrates, irrespective of body size. Hence, minifish achieve immunocompetence via a few thousand lymphocytes organized in robust scale-free networks, thereby ensuring immune reactivity even when cells are lost or clone sizes fluctuate during immune responses.

Figure

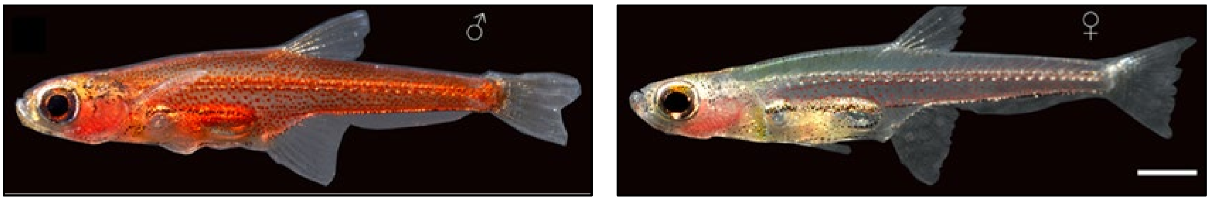
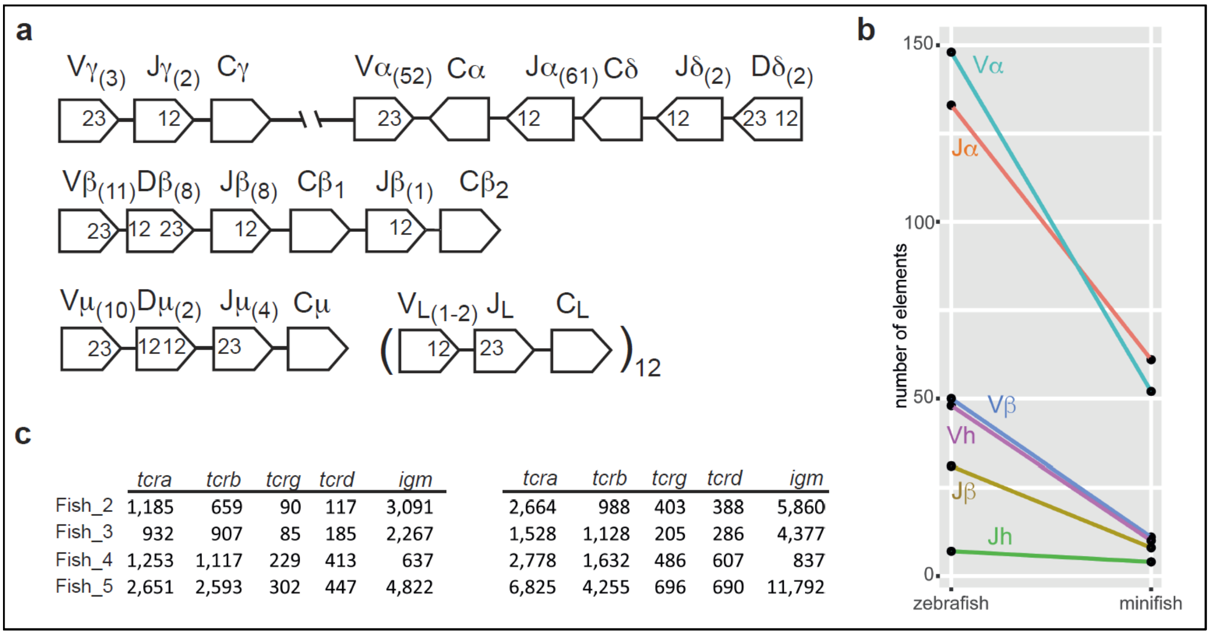


Fig. 1. A male and a female adult minifish (*Paedocypris* sp. "Singkep"). Length of each fish, approximately 0.8 cm.



	tcra	*tcrb*	*tcrg*	*tcrd*	*igm*
Fish_2	1,185	659	90	117	3,091
Fish_3	932	907	85	185	2,267
Fish_4	1,253	1,117	229	413	637
Fish_5	2,651	2,593	302	447	4,822

tcra	*tcrb*	*tcrg*	*tcrd*	*igm*
2,664	988	403	388	5,860
1,528	1,128	205	286	4,377
2,778	1,632	486	607	837
6,825	4,255	696	690	11,792

Fig. 2. Characteristics of germline and rearranged antigen receptors of minifish. (**A**) Germline structure of immune antigen receptor genes. The numbers of elements are indicated in parentheses; the spacer lengths of recombination signal sequences are indicated by numbers inside the cartoons. (**B**) General reduction of genetic elements in minifish compared to zebrafish. (**C**) Numbers of antigen receptor clonotypes (left table) and corresponding cDNA molecules (right table) in four unrelated individuals; these numbers were determined by subjecting one third of total RNA to sequencing.