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Gene Structure Analysis of Chemokines and Their Receptors in Allotetraploid Frog, *Xenopus laevis*

Akimasa Fukui and Masatoshi Matsunami

Abstract

Chemokines, relatively small secreted proteins, are involved in cell migration and function in various biological events, including immunity, morphogenesis, and disease. Due to their nature, chemokines tend to be a target of hijacking of immunity by virus and therefore show an exceptionally high mutation rate. *Xenopus laevis* is considered an excellent model to investigate the effect of whole-genome duplication for gene family evolution. Because its allotetraploidization occurred around 17–18 million years ago, ancestral subgenomes L and S were well conserved. Based on the gene model of human and diploid frog *Xenopus tropicalis*, we identified 52 chemokine genes and 26 chemokine receptors in *X. laevis*. The retention rate of the gene in the *X. laevis* L and S subgenomes was 96% (45/47) and 68% (32/47), respectively. We conducted molecular phylogenetic analysis and found clear orthologies in all receptor genes but not in the ligand genes, suggesting rapid divergences of the ligand. dN/dS calculation demonstrated that dN/dS ratio greater than one was observed in the four ligand genes, *cxcl8b.1.S*, *cxcl18.S*, *ccl21.S*, and *xcl1.L*, but nothing in receptor genes. These results revealed that the whole-genome duplication promotes diversification of chemokine ligands in *X. laevis* while conserving the genes necessary for homeostasis, suggesting that selective pressure also supports a rapid divergence of the chemokines in amphibians.

■理工学研究所との関連

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