

Origins of type I AFPs

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Type I AFPs are found in four disparate taxa, interspersed with fish that either lack AFPs or produce different types of AFPs. We previously hypothesized that the AFPs of these four taxa arose via convergent evolution by noting that the cDNA sequences were inconsistent with homology (Graham LA et al. (2013) PLoS One 8:e81285), but the origins of the AFPs were not known. We have now identified progenitor genes for three of these AFPs. Here, we focus on the cunner, and have determined that its gene arose from an Ala-rich C-terminal extension of a GTPase (GIMAP) involved in T-cell maturation and apoptosis. Additionally, the rest of the *AFP* gene, including the intron and flanking sequences, is also highly similar to the *GIMAP* gene, excepting the GTPase domain. In addition, the marked Ala codon preference of this AFP for GCT (unique among type I AFPs) is mirrored by the codon bias in the *GIMAP* extension. There are 11 *AFP* genes at a single locus in the cunner genome, and these are interspersed with seven *GIMAP* genes.

We also determined the origins of the flounder AFP and published earlier this year (Graham et al. (2022) Sci Rep 12:8536). Similar to the cunner, the flounder *AFP* shows high similarity to its progenitor gene *Gig2*. The *Gig2* protein is required for viral immunity and it contains a poly (ADP-ribose) polymerase domain. However, the region of *Gig2* that is thought to have given rise to the AFP is much shorter than the Ala-rich region of the *GIMAP* protein. Additionally, the *Gig2* genes were duplicated at a second locus and were replaced by multiple *AFP* genes at the original locus. The origin of the sculpin gene has also been traced, but unlike the cunner and flounder progenitors, the protein is not involved in immunity. Rather, it is involved in the functioning of the endoplasmic reticulum. Therefore, with three of four progenitors identified, and the snailfish AFP gene lacking similarity to these genes, it is clear that the type I AFP has arisen independently in the four lineages.

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