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Transcriptional rewiring, post-transcriptional regulation and neo-functionalization: how the master sex-determining gene of medaka was born

The medaka *Oryzias latipes* has genetic sex determination of the XX/XY type. *Dmrt1bY*, the male sex-determining gene, arose through a segmental gene duplication event from an autosomal gene, *dmrt1a*. Both genes are co-orthologs of the highly conserved *dmrt1* gene, which acts downstream in the sex determining cascade of mammals, similar to its *Drosophila* and *C. elegans* homologues. In Medaka, the duplication of the chromosomal fragment that included *dmrt1a* occurred approximately 10 million years ago. After insertion into the proto-Y chromosome a massive degeneration of all genes except *dmrt1bY* occurred. Subsequent loss of *dmrt1bY* in several medaka strains reveals the high degree of plasticity of this sex determining mechanism.

From the molecular evolution point of view the main question is how in medaka *dmrt1bY* could become the master regulator of male development after acquiring an upstream position in the sex-determining cascade. Remarkably, this evolutionary novelty, requiring a rewiring of the regulatory network, was brought about by co-optation of pre-existing cis-regulatory elements contributed by transposable elements. On another level of regulation, differential gene expression of the two *dmrt1* co-orthologs seems to be also mediated by post-transcriptional regulation through a highly conserved cis-regulatory motif that directs differential gonadal synexpression of *dmrt1* transcripts during gonad development. While the autosomal *dmrt1a* medaka gene is essential for testis maintenance, in contrast, *dmrt1bY* was shown to be responsible for male-specific primordial germ cell (PGC) mitotic arrest in the developing gonad at the sex-determination stage, suggesting neo-functionalization.

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Paradigm shift in sex chromosome evolution

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