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Stickleback's view of sex chromosome evolution

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A recent study of the threespine stickleback (*Gasterosteus aculeatus*) brings new light to studies of the early stages of sex chromosome evolution.

The multiple independent evolution of sex chromosomes in different groups of animals and plants has long fascinated evolutionary biologists (eg Bull, 1983). Despite independent origins, sex chromosomes have very similar properties: recombination between the sex chromosomes is suppressed in the heterogametic sex, and the sex-determining chromosome (Y or W with male or female heterogamety, respectively) is usually degenerate. Studying the origins of sex chromosomes in model organisms, such as *Drosophila*, mouse and chicken, is close to impossible though, as they arose many millions of years ago. Many organisms, however, have much younger sex chromosomes. In particular, some plant (eg papaya, Liu *et al*, 2004; and *Silene*, Charlesworth, 2004) and fish species are very convenient for studying the early stages of sex chromosome evolution. In a recent paper in *Current Biology*, Peichel *et al* (2004) publish the results of their studies of the threespine stickleback (*G. aculeatus*), used for just this purpose.

Sex determination varies within the stickleback genus, with some species (eg *G. weatlandi*) having sex chromosomes, while others, like the threespine stickleback (*G. aculeatus*), lack cytologically distinguishable sex chromosomes. Peichel *et al* (2004) used a large panel of previously developed microsatellite markers to genetically map the sex-determining region in threespine stickleback. They analysed these markers for co-segregation with sex in two independent genetic crosses between the subspecies of *G. aculeatus* and demonstrated that a single genomic region at the end of chromosome 19 was responsible for sex determination in the threespine sticklebacks.

The linkage to the Y chromosome of genes advantageous in males and detrimental in females may confer a selective advantage, which may in turn promote suppression of recombination between the X and Y chromosomes (Bull, 1983; Rice, 1987). This would result in the formation of the nonrecombining region on the Y chromosome (NRY). Excitingly, the mapping of the sex-determining region in the threespine stickleback revealed that the genetic distances between the markers adjacent to the sex locus are much shorter in males than in females, which might reflect the evolution of the NRY on the proto-Y-chromosome in threespine stickleback males. If the pairing of the two homologous chromosomes close to the sex locus is suppressed, then chiasmata (and recombination), which could have occurred in this region, form elsewhere on the same chromosome, leading to more frequent recombination in the region beyond the NRY. Indeed, suppression of recombination near the sex-determining region resulted in the doubling of recombination frequency along the rest of chromosome 19 in males. Similar, but much more pronounced, redistribution of recombination occurs in human and mouse sex chromosomes in males, which pair and recombine only in a small region of X/Y homology, the pseudoautosomal region (PAR). So, recombination from the entire X is being squeezed into a small PAR region.

When the authors sequenced a 250 kb region closely linked to the sex locus in threespine sticklebacks, they found five known genes (*Sema4B*, *Idh*, *Znf*, *Rasgrf1* and *Band4.1*). Interestingly, these loci are also adjacent to each other in the human genome, so synteny in this region has been maintained for several hundred million years. Although the overall nucleotide identity between homologous X- and Y-linked sequences was fairly low (63.7%), the divergence was mostly due to multiple insertions and deletions (indels). These indels were probably due to the accumulation of repetitive sequences on the Y chromosome, which is very typical for the Y chromosomes in the other species (Charlesworth *et al*, 1994). In the regions uninterrupted by insertions and deletions, X/Y identity is much higher, over 95%. In particular, the average pairwise nucleotide X/Y divergence in the 3′ untranslated region of the *Idh* gene and in the second exon of the *Znf* gene did not exceed 1.5%, that is, it is approximately the same as divergence between humans and chimpanzees.

Although the X/Y divergence in the *Idh* and *Znf* genes is relatively low, it is still surprising that the X- and the Y-linked copies of these genes diverge at all, given that these genes are not completely linked to the sex locus. As the recombinants between the *Idh* and the sex locus have been detected among a few hundred of F2 progeny of the genetic crosses, due to recombination, the chance of the 'Y-like' *Idh* to end up in a female is quite high in natural populations. Thus, if *Idh* and *Znf* are not completely sex-linked, recombination should mix up the X- and Y-linked copies, and they are not expected to diverge. That is why the evidence for divergence between the X- and Y-linked copies of the *Idh* and *Znf* genes is inconsistent with incomplete sex linkage of the *Idh* gene, reported in the same paper. Accumulation of the repetitive DNA only in the Y-linked sequences is also quite surprising, given recombination between the X and the Y in the studied region. A possible rescue from this paradox is that recombination between the *Idh* and the sex locus observed in the genetic crosses may not occur in nature. For example, recombination between the X and Y chromosomes near the *Idh* and *Znf* genes may occur only in the interspecific crosses used for genetic mapping by Peichel *et al* (2004): one cross between two stickleback species from the Priest Lake in British Columbia (the Priest cross), and the other between a species from the Paxton Lake (British Columbia) and a species from Japan (the Paxton cross). These stickleback (sub-)species have developed some degree of reproductive isolation, but can be artificially crossed in the lab to produce viable and fertile offspring. If the suppression of X/Y recombination in different species occurs via different mechanisms, it may not work in the interspecific hybrids and may result in partial restoration of X/Y recombination in the Paxton and the Priest genetic crosses.

Interestingly, the X- and Y-linked sequences of the *Idh* and *Znf* genes from *G. aculeatus* are more similar to each other than to the sequence of the same region from *G. weatlandi*, which has cytologically distinguishable sex

chromosomes. Thus, the split of the two species about 10 million years ago preceded the evolution of the sex chromosomes in the *G. aculeatus*. Given the low age of the X and Y in *G. aculeatus*, it is not surprising that the sex chromosomes are not distinguishable under the microscope. The origin and age of the cytologically distinguishable sex chromosomes in the *G. weatlandi* are less clear. As the *Idh* gene is sex-linked in *G. aculeatus*, but not in *G. weatlandi*, the sex chromosomes may have evolved completely independently in these two species. The sex chromosomes in *G. weatlandi* may represent an ancestral type of sex chromosome, which could have been lost in *G. aculeatus*, which later evolved a new pair of sex chromosomes. In fact, the evolution of a new sex locus on the chromosome 19 in *G. aculeatus* could be the cause of the loss of the ancestral (*G. weatlandi*-like) sex chromosomes in this species: the new genetic factor could have taken charge of sex determination in threespine sticklebacks, making the old Y chromosome redundant. Such swapping of sex-determining factors is known in the other organisms (eg *Musca domestica*, Schmidt *et al*, 1997), and may be a good illustration of surprising evolutionary dynamism in sex determination systems and sex chromosomes.

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Bull JJ (1983). *Evolution of sex determining mechanisms*. The Benjamin/Cummings Publishing Company: California, USA.
Charlesworth B *et al* (1994). *Nature* **371**: 215–220.
Charlesworth D (2004). *Curr Biol* **14**: R271–R273.
Liu Z *et al* (2004). *Nature* **427**: 348–352.
Peichel CL *et al* (2004). *Curr Biol* **14**: 1416–1424.
Rice WR (1987). *Evolution* **41**: 911–914.
Schmidt R *et al* (1997). *Genetics* **147**: 271–280.