

Mapping Chromosome Evolution between Species

January 23, 2012

EM Scherer

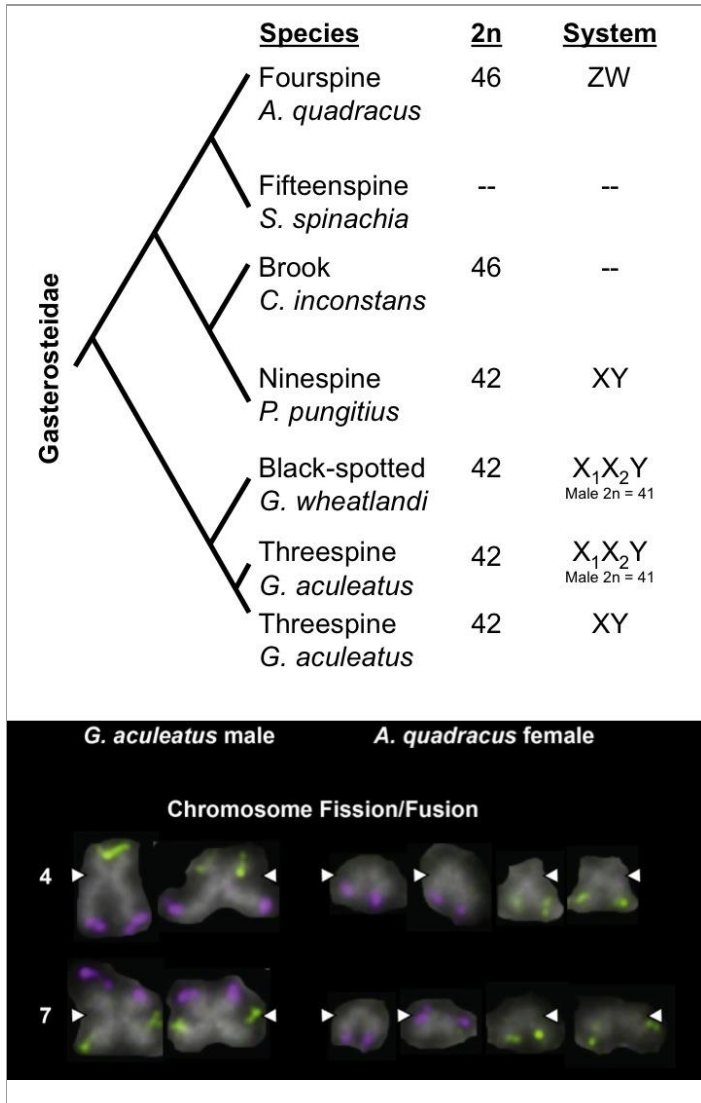
Sticklebacks are small fish that inhabit fresh water and marine environments throughout the Northern Hemisphere. They are established models for the study of species evolution (speciation) and are more recent subjects for the study of chromosome rearrangements, as the chromosomes of the six species within the stickleback family differ in both number and morphology (shape/size). These differences in genome architecture among sticklebacks also include sex chromosome systems. Sex chromosomes are chromosome pairs that genetically determine the sex of an individual. The XX/XY sex chromosome is called a “male heterogametic” system, in which males are XY (one X chromosome and one Y chromosome), females are XX (two X chromosomes), and the presence of the Y chromosome is required for male development. In contrast, the ZZ/ZW sex chromosome is called a “female heterogametic” system, in which females are ZW, males are ZZ, and the W chromosome is required for female development. For both XX/XY and ZZ/ZW sex chromosome systems, the X and Y or Z and W may differ in morphology; these systems are known as heteromorphic sex chromosomes. Two different XX/XY sex chromosome systems have evolved independently in threespine and ninespine sticklebacks, and fourspine sticklebacks have evolved ZZ/ZW sex chromosomes.

In contrast to some organisms whose sex chromosomes have been maintained for hundreds of millions of years (e.g., fruit flies, mice, and humans), the sex chromosomes of other organisms, fish in particular, evolve much more rapidly. For example, two populations of threespine sticklebacks (Japan Sea and Pacific Ocean) evolved different sex chromosome systems as recently as two million years ago when the two populations became geographically isolated. Although it is not understood why some organisms’ sex chromosomes evolve more rapidly than others, it has been shown that sex chromosomes can evolve as a result of sexually antagonistic selection. Explicitly, genes that improve the fitness of one sex or reduce the fitness of the other become linked with sex determination genes, and recombination between sex chromosomes is reduced. Even less is known about why the total numbers of chromosome pairs between closely related species diverge, but sticklebacks provide an excellent model for investigating how and why these types of chromosome rearrangements occur.

Although threespine and fourspine sticklebacks possess different sex chromosome systems and different numbers of chromosome pairs (21 versus 23 pairs, respectively), a recent phylogenetic analysis confirmed that these species share a recent common ancestor. Therefore, former graduate student, Dr. James Urton, and colleagues in the Human Biology Division sought to reveal the chromosome rearrangements that are responsible for this marked divergence in genome architecture. They used fluorescently-labeled DNA fragments from the threespine stickleback genome to identify regions of genetic homology on the chromosomes of the fourspine stickleback, as homologous DNA fragments bind one another like molecular magnets. This technique, called fluorescence *in situ* hybridization (FISH), is used to visualize the physical location of a DNA fragment within an organized profile of chromosome pairs (also known as a karyotype). The authors also measured chromosome length for each pair. They found that two larger chromosome pairs from the threespine stickleback each correspond to two pairs of smaller chromosomes in the fourspine stickleback. There also appears to have been inversions of genetic material between the threespine and fourspine stickleback in eight chromosome pairs. Five of these inversions are found on chromosomes with significantly different morphologies. Lastly, although fourspine sticklebacks from Massachusetts and Maine have ZZ/ZW heteromorphic sex chromosomes, the fourspine stickleback population used in this study (from Connecticut) does not have morphologically distinct sex chromosomes. The authors suggest that this disparity may be due to differences in sex chromosome content between fourspine stickleback populations, and/or the Connecticut population of fourspine sticklebacks simply may not have ZZ/ZW chromosomes that differ in size or shape. Alternatively, the Connecticut fourspine stickleback population may possess an environmental mechanism of sex determination, as opposed to the more widely recognized genetic basis of sex determination.

Additional studies are needed to understand whether the corresponding two chromosome pairs from the threespine stickleback and four chromosome pairs from the fourspine stickleback are the result of chromosome fusion or fission events in the common stickleback ancestor, and how the sex chromosome systems of the threespine and fourspine sticklebacks evolved.

[Urton JR, McCann SR, Peichel CL](#). 2011. Karyotype differentiation between two stickleback species (Gasterosteidae). *Cytogenetic and Genome Research* 135:150-9.



James Urton

Top: The phylogenetic relationship between different species of the stickleback family (Gasterosteidae). Columns denote the number of chromosomes pairs (n) and sex chromosome system for each species. Bottom: A section of chromosome profiles from threespine (*G. aculeatus*) and fourspine (*A. quadracus*) sticklebacks shows regions of DNA homology (purple and green) in divergent genome architectures.