Genetic and developmental basis of evolutionary pelvic reduction in threespine sticklebacks

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Background

- Adaptive radiation
- Two populations of stickleback: lake and marine
- Rapid pelvic reduction in lake population
- Common morphological change
- Mechanism?
Questions

• What chromosome regions control pelvis development?

• Regulatory changes or protein coding changes?

• Similar genetic basis for pelvic reduction in other populations?
QTL Analysis

- QTL = Quantitative trait locus
- Goal: identify chromosome regions that contribute to pelvic reduction
Conclusion

- *Pitx1* is tightly linked with the major gene controlling pelvic reduction.
DNA Sequence Experiment

Purpose: To determine whether there is a difference in the Pitx1 gene between the populations
Conclusion

The Pitx1 gene produces the same protein in both populations

In situ hybridization experiment

Purpose: to determine differences in Pitx1 expression between populations
Results

Conclusion

While in the marine population Pitx1 is expressed in the hind pelvic region, in the benthic population it is not
In situ hybridization Pt. 2

Measured Pitx1 expression elsewhere in the embryo (thymus and trunk neuroblasts)

Results
Conclusions

• The global regulation of Pitx1 is not responsible for its absence in pelvic region of the benthic population

Complementation Cross

• Goal: to see if pelvic reduction in different populations has a similar genetic basis

• Paxton Lake X Lake Vilfilsstadavatn

• Do hybrid progeny develop pelves?
One possibility:

Another possibility:
Control Cross

Lake V. (reduced pelvis) × Marine (full pelvis)

All progeny have a full pelvis

Conclusion

- Failure to complement → similar genetic basis
- But is Pitx1 responsible?
Broad Conclusion

Pelvic reduction in benthic sticklebacks is associated with the disruption of local Pitx1 expression
**EXPERIMENT**

**Control** | **Gremlin added**
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**CONCLUSION:** Differences in *gremlin* gene expression cause differences in morphology, allowing duck hindlimbs to retain their webbing.