

USING MICROSATELLITES TO TRACK HATCHERY RELEASED BLUE CRABS

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The main goal of the blue crab project at the Center of Marine Biotechnology (COMB) has been to increase the spawning stock in the Chesapeake Bay by releasing hatchery-raised crabs into the wild. Thousands of crabs have been released every summer since the inception of this program in 2002. To evaluate the effectiveness of these releases, hatchery crabs were tagged using elastomer tags, coded wire tags, or a combination of both types. The difficulty with using these types of tags is that each crab has to be tagged individually which is time consuming and labor intensive.

At COMB we have developed genetic markers as an alternative approach to these tagging methods. A combination of mitochondrial and nuclear markers appears to give us the best advantage in distinguishing hatchery crabs from wild crabs. In 2004 and 2005, blue crab samples were collected by researchers at the Smithsonian Environmental Research Center (Edgewater, MD) and the Virginia Institute of Marine Science (Gloucester Point, VA). These samples were already known to be either wild or hatchery crabs based on the presence of coded wire or elastomer tags. All individuals (n=99 in 2004 and n=349 in 2005) were genotyped at 6 microsatellite loci.

The microsatellite results are currently being analyzed using two methods. The first approach is an assignment test using GeneClass2 ver.2.0.d (Piry et al. 2004). This program calculates the likelihood for the assignment of each multilocus genotype tested against a reference sample and, for our purposes, requires knowledge of the genotypes of hatchery released offspring. The second approach is a Bayesian approach developed by Michael Tringali (2005) of the Florida Fish and Wildlife Conservation Commission. This method incorporates allele-frequency data from the recipient stock and genotype data from the parents to determine the likelihood of individuals being related to a female that produced a batch of hatchery crabs.

Using GeneClass2 we have been able to successfully identify 93% of hatchery crabs in the 2005 samples. The Bayesian method is still being customized for blue crab microsatellites and the results should be available soon.

References

- Piry S., Alapetite A., Cornuet J-M., et al. (2004) GENECLASS2: A software for genetic assignment and first generation migrant detection. *Journal of Heredity* 95:536-539.
- Tringali, M.D. (2005) A Bayesian approach for the genetic tracking of cultured and released individuals. *Fisheries Research* 77:159-172.