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Research Summaries

Title

Assessing Connectivity of Red Sea Urchin Populations Using New Genetic Tools

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Assessing Connectivity of Red Sea Urchin Populations Using New Genetic Tools

Ronald Burton, UC San Diego

SUMMARY

Using seven microsatellite markers, scientists examined the “connectivity” of red sea urchins (*Strongylocentrotus franciscanus*) along the West Coast of North America and found Canadian and California populations to be genetically differentiated. This is the first research project to find evidence of population structure for this species across its range.

Some genetic structure was also detected among different sizes of urchins (recruits and adults) at a single site off San Diego. California populations overall, however, appear genetically the same, or “homogenized.” It should be emphasized that this apparent lack of genetic structure does not preclude the possibility of significant local recruitment within populations.

METHOD

Red urchin tissue samples analyzed for this project came from four locations in California (Pt. Loma, La Jolla, Malibu and Pt. Arena) and two locations in British Columbia, Canada (Campbell River and Louscoone Inlet). The Canadian samples were collected by Canadian scientists for a previous study and scored by them for five microsatellite markers. The Sea Grant researchers validated the applicability of these markers and two others to California urchins and then scored all California specimens on these seven loci.

RESULTS

Genetic Variation within Samples

All seven microsatellite markers were highly polymorphic with no significant differences in the number of alleles observed within each population. By population, genotype frequencies in La Jolla showed the greatest departure from random mating, with every locus having significantly low heterozygote frequencies.

Genetic Variation among Samples

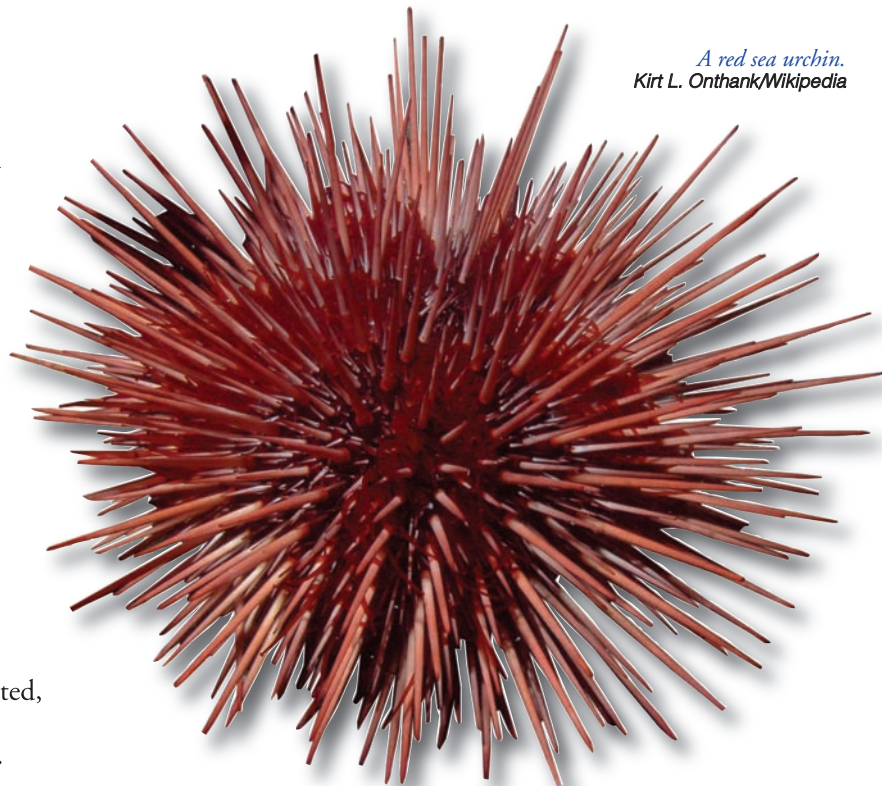
Global genotypic variation across loci was highly significant between Canadian and California populations, and insignificant among the four California samples; however, when California populations were compared at individual loci, some significant differences surfaced. Specifically, Pt. Loma and Pt. Arena urchins appeared genetically differentiated at one locus, while Pt. Loma samples were markedly different from La Jolla and Malibu samples at another locus.

The two British Columbia populations were highly differentiated, when analyzed across the five markers mentioned previously. Across these same five markers, urchins from Pt. Loma and Pt.

Arena – the most geographically separated sites in California – also appeared significantly differentiated. Using all seven loci for California populations, Pt. Loma specimens were found to be significantly different from Malibu and Pt. Arena, but not La Jolla. Malibu and La Jolla samples were also significantly different.

As broadcast-spawning marine organisms with long larval periods, scientists expect urchin populations to be highly connected and hence genetically homogenized. When this is true, the degree of genetic divergence between populations is uncorrelated with the distance separating them. As expected, when only California populations were considered, there was no relationship between divergence and distance; however, when Canadian populations were added to the analysis there was a significant “isolation-by-distance” effect. That is, the most separated populations were the most genetically divergent.

Pt. Loma was the only sampling site with enough recruits for a size-stratified analysis of genetic differentiation. This analysis showed significant genetic differentiation between recruits and adults, but no significant differentiation among the largest and smallest size classes in the sample.



A red sea urchin.
Kirt L. Onthank/Wikipedia

NEW TOOL

Seven microsatellite markers previously used to study Canadian urchins were found to be valuable markers for California urchins, too.

INTERNATIONAL IMPLICATIONS

The red sea urchin fisheries in California and Canada are currently managed as separate stocks. The main finding of this project, that indeed these animals appear genetically differentiated, lends credence to this management approach.

CONCLUSION

The red urchin is a key kelp forest species and a lucrative commercial fishery, worth an estimated \$5.5 million ex-vessel in 2006. This study shows that four populations of urchins in California (both north and south of Pt. Conception) are genetically differentiated from two populations in British Columbia, suggesting that connectivity between the regions is low.

Using currently available genetic tools, California populations appear highly connected. It is possible, however, that the apparent homogeneity is an artifact of the relatively few genes surveyed for the analysis. Continued advances in genetic tests may make it possible to detect population structure in the future. As a way to further investigate whether such structure indeed exists, scientists recommend examining patterns of genetic differentiation across the same year classes of urchins, to more completely track patterns of parentage and larval sources. Such work would add detail to the study described so far and would have meaningful applications in designing marine reserves and/or modifying management practices to prevent overharvesting of the species.



Cracked red sea urchin, showing the edible roe inside.

R.M. Harbo/Fisheries and Oceans Canada

STUDENT

Celeste Benham, Master's

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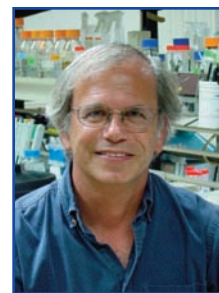
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