A Computer Simulation to Evaluate Dispersal by Cloning (Asexual Reproduction) Larvae of Tropical Sea Stars

Tammy Graff  
Illinois Wesleyan University

William Jaeckle, Faculty Advisor  
Illinois Wesleyan University

Follow this and additional works at: https://digitalcommons.iwu.edu/jwprc

https://digitalcommons.iwu.edu/jwprc/2004/oralpres3/2

This is protected by copyright and/or related rights. It has been brought to you by Digital Commons @ IWU with permission from the rights-holder(s). You are free to use this material in any way that is permitted by the copyright and related rights legislation that applies to your use. For other uses you need to obtain permission from the rights-holder(s) directly, unless additional rights are indicated by a Creative Commons license in the record and/or on the work itself. This material has been accepted for inclusion by faculty at Illinois Wesleyan University. For more information, please contact digitalcommons@iwu.edu.

©Copyright is owned by the author of this document.
Larvae of some tropical sea stars are able to produce genetically identical individuals by asexual reproduction (cloning). Each “parental” larva has the potential to produce as many as 6 new individuals. Although cloning by larvae should increase the dispersal potential of each cohort of larvae (and their respective genomes), empirical evidence is absent. To assess the potential of sea star larvae originating off the African coast to be carried over prevailing ocean current (South Equatorial Current, SEC) to South America was studied through the development of a computer simulation. The simulation assumes an initial population size of 100,000 individuals from a single spawning event off the coast of Africa, which enter the SEC (11.3 cm/s) and are carried toward the east coast of South America, distance of 3788 km. Each individual (and subsequent offspring) was followed throughout its entire lifetime or until it reached South America. Although no individual larva that enters the SEC is predicted to travel the entire distance (complete development requires ca. 30 days), each individual’s genes may travel through successive generations of clones. The effect on instantaneous mortality rates and cloning frequency on the number of larvae that survive the complete dispersal to South America was assessed. This simulation will predict the conditions that must occur in order for cloning by larvae to have a significant influence on the potential for transatlantic dispersal.