Sequencing a Shrimp Diversity Panel

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Summary and Implications

Eighty-six shrimp (eighty Pacific White, six Tiger shrimp) from ten different geographic regions were sequenced with a twofold goal: first, to better understand and document the genetic makeup of the species, and second, to discover genetic differences between shrimp lines that may facilitate the breeding of shrimp with better performance traits.

Introduction

The Pacific White Shrimp (*Litopenaeus vannamei*) is the common shrimp species captured, farmed and eaten worldwide. However, when farmed they are particularly susceptible to many diseases, such as Taura syndrome (TSV) and White spot syndrome, which can vastly reduce farm output. Certain populations of Pacific White Shrimp display resistance to these diseases. Discovering genetic bases for this resistance would lead to the creation of more robust broodstocks.

Before comparing shrimp genomes, it is necessary to first determine the genetic makeup of the shrimp in general. Currently, there is no reference genome for the Pacific White Shrimp, so the initial focus of this project is to either build that reference genome or to assemble a collection of large segments of the genome that can act as a basis for comparison. When that is done, the next step is to compare known disease-resistant populations to normal populations with the goal of discovering genetic links to evidence of disease resistance. Similar techniques can also be used to identify the genetic basis for other desirable shrimp traits.

Materials and Methods

A total of eighty Pacific White Shrimp were obtained from nine geographic regions – Ecuador, Honduras, Venezuela, Hawaii, continental United States, Mexico, Thailand, Vietnam, and Indonesia. For comparison, six tiger shrimp (*Penaeus monodon*) from India were also used for sequencing. Each sample was sequenced at the Iowa State DNA facility on the Illumina HiSeq 2000, using standard procedures.

Sequencing results, each consisting of over a million DNA segments of 200 base pairs in length, were filtered for quality and then reassembled using a pipeline of state-of-the-art algorithms. This produced large contiguous segments of DNA, which can be compared between shrimp lines to observe regional differences or further assembled to create a more accurate approximation of the shrimp genome.

Results and Discussion

The assembly of parts of the genome is currently in progress. In order to ensure that all areas of the genome were represented, some shrimp lines were pooled according to geographic region; specifically, the samples were placed into Asian, South American and North American groups. As of now, roughly 10% of the total shrimp genome has been assembled in the group with the highest coverage (North America). Given that we did not sequence the genome at a very high rate, it may be difficult to get all the pieces together into individual chromosomes but the contigs produced should be sufficient to perform a reasonable diversity analysis.

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