



66th
Brazilian
Congress of
Genetics

2021

GENÉTICA

13 a 16 | setembro | 2021 ON-LINE

Homenageados: pesquisadores e profissionais da saúde



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SOBRE

Validation of a low-density SNP panel for genetic structure and diversity analysis of Pacific white shrimp (*Litopenaeus vannamei*)

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ABSTRACT

The Pacific white shrimp (*Litopenaeus vannamei*) is the most cultivated penaeid species in the world, with a worldwide production of 4.1 million tons in 2016. The objective of this study was to validate a markers panel with 96 SNP (Single Nucleotide Polymorphism) markers for performing genetic variability and structuring analysis of vannamei shrimp populations from a commercial breeding nucleus and in shrimp samples collected from retail stores in Brazil. For this, 167 samples from four selection lines (SLA, SLB, SLC and SLD) from a producer of shrimp larvae, and 191 samples from seven retail stores (DF1, DF2, DF3, DF4, DF5, DF6 and PB) were genotyped with 96 SNPs in a Fluidigm EP1 platform. Samples and SNPs with Call Rates <0.90 were discarded from the dataset. Additional SNPs were eliminated based on observed MAF <0.10, Hardy-Weinberg deviations ($p < 0.01$) and $r^2 > 0.10$. Data resulting were analyzed with SVS Golden Helix, STRUCTURE 2.3.4, Clumpak and GeneClass 2.0. Principal component analysis (PCA) and population structuring evaluated with STRUCTURE separated the retail store samples into a cluster that diverges from the SLA, SLB, SLC and SLD selection lines. Furthermore, the highest value of ΔK was observed when a model assuming two populations was used. Estimated F_{st} varied between 0.002 to 0.103. The smallest F_{st} estimate (0.002) was observed between DF4 and DF6, while the largest (0.103) was observed between SLB and PB. Mean population H_o varied from 0.319 (DF5) to 0.471 (SLB). Overall H_o mean, considering for all sampled populations was 0.374 and the largest observed difference between H_o and H_e was 0.039 (DF5). Mean estimated F_{is} was 0.022 and ranged from -0.075 (SLC) to 0.109 (DF5). Overall average correct population assignment was 87% and ranged from 98% (SLB) to 75% (DF6). These results indicated: (i) high levels of genetic variability in the samples tested, (ii) limited amount of inbreeding in retailer populations, and (iii) genetic structuring present between commercial samples from retail stores and selection lines. The first and second results indicate that the populations come from breeding programs that control mating between relatives and maintain high levels of genetic variability in the Pacific white shrimp broodstocks. The third result indicates the existence of genetic structuring, however, STRUCTURE demonstrates that a genetic group is present both in commercial samples from retail stores, with an average of 85%, and in lines with 29%. The results indicate, therefore, that the validated panel provides satisfactory information in analyzes of genetic variation and population structuring of Pacific white shrimp.

KEYWORDS: genetic improvement; *pedigree*; shrimp farming