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Development of polymorphic SSR markers in the razor clam (*Sinonovacula constricta*) and cross-species amplification

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ABSTRACT. Next-generation sequencing provides large-scale sequencing data with relative ease and at a reasonable cost, making it possible to identify a large amount of SSR markers in a timely and cost-effective manner. On the basis of the transcriptome database of *Sinonovacula constricta* obtained by Illumina/Solexa pyrosequencing, 60 polymorphic SSR markers were developed and characterized in 30 individuals. The number of alleles per polymorphic locus ranged from 2 to 7 with an average of 3.75 alleles. The observed and expected heterozygosities varied from 0.050 to 1.000 and from 0.050 to 0.836, respectively. Nineteen loci significantly deviated from Hardy-Weinberg equilibrium ($P < 0.01$) after Bonferroni's correction for multiple tests. In addition, interspecific transferability revealed that 20 polymorphic loci in *Solen linearis* were first characterized in this study. To the best of our knowledge, this is the highest number of SSRs in *S. constricta* and the first report of cross-species amplification. These novel polymorphic SSR markers will be particularly useful for conservation

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genetics, evolutionary studies, genetic trait mapping, and marker assisted selection in the species.

Key words: *Sinonovacula constricta*; Expressed sequence tags; Single sequence repeats; Cross-species amplification

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