



Development of polymorphic microsatellites for *Sillago sihama* based on next-generation sequencing and transferability to *Sillago japonica*

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ABSTRACT. *Sillago sihama* (Forsskål, 1775), a commercially important marine fishery species in the Indo-West Pacific, is being developed as a target species for aquaculture and stock enhancement in China. However, due to the limitations of traditional isolation methods, the available microsatellite loci, or simple sequence repeats (SSRs), of *S. sihama* lack diversity. We used a stepwise approach including Illumina sequencing, primer screening, and SSR marker validation to develop diverse SSRs for *S. sihama*. A total of 853.48 Mb clean sequences were assembled with high coverage and sequencing depth, and 27,288 potential SSRs were identified. A set of 18 novel SSR markers with four type motifs including 11 di-, 1 tri-, 5 tetra-, and 1 hexanucleotide repeats were successfully isolated. The ranges of number of alleles per locus and observed and expected heterozygosities were 5-24, 0.226-0.968, and 0.319-0.950, respectively. The diversity parameters exhibited high

levels of polymorphism in these 18 loci. Three loci with the presence of both null alleles and inbreeding showed significant deviation from Hardy-Weinberg equilibrium after Bonferroni correction. Moreover, 13 loci developed in *S. sihama* showed high transferability to the closely related species *Sillago japonica*. The polymorphic SSR markers developed in this study may serve as valuable tools for further basic and applied research on the genetic resources of *S. sihama* as well as *S. japonica*. Our results indicate that this approach, based on next-generation sequencing technology, is convenient, cost-effective, and suitable for SSR marker isolation in other sillaginid fishes.

Key words: *Sillago sihama*; *Sillago japonica*; Microsatellite loci; Next-generation sequencing; Loci transferability