

# Study on genetic structure and phylogeny in Chihsin duck using microsatellite markers <sup>(1)</sup>

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## Abstract

Pekin duck was first introduced into the Livestock Research Institute in Taiwan in the 1950s and 1960s and continuously selected for feather color, weight, and duration of fertility. The novel line was named Chihsin Duck (CH) in 2021. However, because CH are a closed population with a small population size, their allele frequencies and genetic diversity were easily affected by selection and breeding strategies, and should be monitored regularly. Therefore, the purposes of this study were to establish the genetic variation information of CH and to investigate the phylogeny with other duck species. In this study, a total of 11 microsatellite markers selected from the brown Tsaiya duck were used for analysis. The results showed the genetic variations in CH were slightly lower than that of the industrial Pekin duck lines (BPs). The average number of alleles in CH was slightly lower than that of germplasm-persevered Tsaiya ducks and the synthetic line between Pekin duck and brown Tsaiya duck, but higher than the selected white Tsaiya duck. The number of effective alleles was roughly in the same level as that of the aforementioned lines. It may be due to the small population of CH and the long-term selection, resulting in the aforementioned results. However, the values of within-population inbreeding coefficient in different markers were very different, so there should be no serious inbreeding depression in CH at present. The results of the phylogenetic tree showed that CH had the shortest genetic distance with BPs, but it did not form any robust branch between CH with any other breeds (lines), including the BPs. In this study, the pairwise  $F_{ST}$  of CH and BPs were 0.1582 and 0.1873, respectively, which were close to the pairwise  $F_{ST}$  at the lowest breed level. However, the genetic differentiation relationship between CH and BPs should still be close to the line level based on the results of the phylogenetic tree and STRUCTURE. In the future, the genetic variation results analyzed in this study would be used as a reference to regular genetic monitoring. In addition, the results of genetic structure analysis could also be applied to mating and breeding programs when this line was promoted to industry.

Key words: Genetic polymorphism, Genetic structure, Microsatellite markers, Pekin duck.

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