

Study on Population Genetics of Invasive Pest *Stictocephala bisonia* (Hemiptera: Membracidae: Smiliinae)

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Abstract: 【 Background 】 *Stictocephala bisonia* Kopp et Yonke, 1977 (Hemiptera: Membracidae: Smiliinae) is native to the United States; it spread to Hungary in 1912. Since then, it has spread to Europe, North Africa and other regions. In 2017, *S. bisonia* was first discovered in Taibai County, Shaanxi Province, and in 2019 it was found in parts of Xinjiang Uyghur Autonomous Region. *S. bisonia* is a potential economic pest that feeds on 60 species of plants from 16 families, especially economic fruit trees such as apple and cherry. While previous studies have focused on the morphology and life history of *S. bisonia*, population genetics research has been limited. **【 Objective 】** This study aimed to determine the previously unknown source of invasion and diffusion path of the population of *S. bisonia* in China. **【 Method 】** Mitochondrial molecular markers (*COI*, *Cytb*, and *ND5*) and mitochondrial whole genome data were used to study the genetic diversity and population genetic structure of *S. bisonia* in 9 different geographical populations located in Treviso (Italy), Pomerania (Poland), Basel (Switzerland), Oregon (USA), Rushka (Serbia), Taibai County (Shaanxi Province, China), Yining County (Xinjiang Uyghur Autonomous Region, China), Xinyuan County (Xinjiang Uyghur Autonomous Region, China), and Wild Apple Reserve (Xinjiang Uyghur Autonomous Region, China). The world transmission history of *S. bisonia* was also summarized, and the population historical dynamics were analyzed. **【 Result 】** The main results are as follows: (1) Analysis of the *COI+Cytb+ND5* tandem gene fragment of 133 individuals from 9 geographic populations of *S. bisonia* revealed a total of 37 haplotypes, with a total haplotype diversity of 0.8909 and a total nucleotide diversity of 0.007. (2) Analysis of the whole mitochondrial genome of 34 individuals from the same 9 geographic populations of *S. bisonia* showed a total of 27 haplotypes, with a total haplotype diversity of 0.9715 and a total nucleotide diversity of 0.01029. These results indicate relatively rich genetic diversity in various groups of *S. bisonia*. Genetic structure analysis revealed that the main source of overall genetic variation of *S. bisonia* was within populations, with frequent gene exchange among different groups and low level of genetic differentiation. The haplotype relationships between the populations in Xinjiang and

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Europe were similar, as were populations in Shaanxi and America. Generally, there was no distinct geographical lineage among various groups. (3) The dynamic analysis of the population history demonstrated that all populations of *S. bisonia* had experienced founder effect population shrinkage, providing further evidence that *S. bisonia* mainly spreads in the form of eggs through seedling transportation. Ancestral distribution area reconstruction results supported the hypothesis that the origin of all invasion areas was the United States, consistent with existing literature records. **【Conclusion】** The present study is the first to investigate the population genetics of *S. bisonia*, revealing the origin and invasion mode of the population in China. The results showed that the population of *S. bisonia* in Taibai County, Shaanxi Province, originated from the United States, while the populations in Yining County, Xinyuan County and Wild Apple Reserve in Xinjiang originated from Europe. The primary transmission route of *S. bisonia* is through eggs and seedling transportation. The transmission history of *S. bisonia* is relatively short, and there is a low level of genetic differentiation among various populations with no distinct geographical lineage formed.