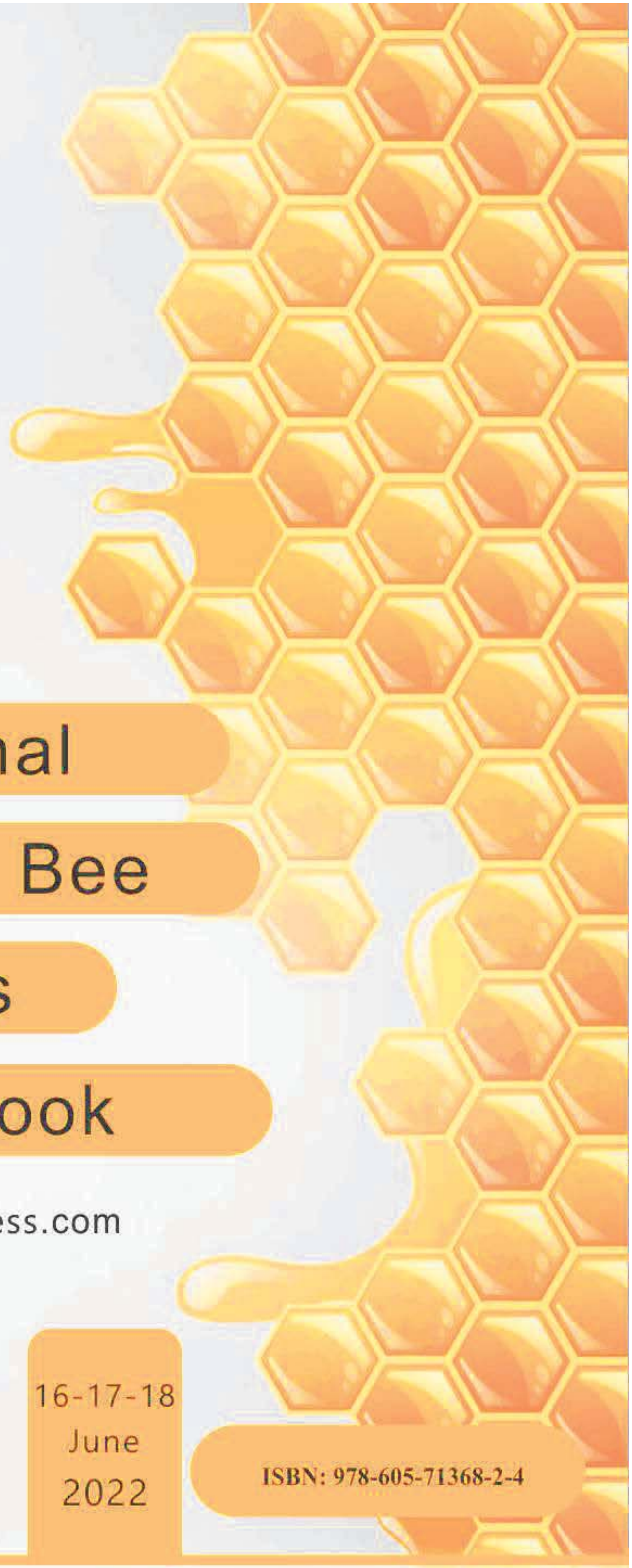

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Oral Presentation

Invasion Patterns Of *Vespa velutina nigrithorax* In Southern Europe: A Genetic Perspective

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Abstract:
Vespa velutina was seen for the first time in Europe in 2004, in pots imported from China into France. Since then, the population rapidly build up and expanded within France and, in 2010, started spreading across other countries, giving rise to one of the most phenomenal insect invasions ever seen in the European continent. Early studies suggested that the invasion originated from a single multi-mated queen introduced from China. However, little was known, until this study, about the genetics underlying the expansion towards south and east of the introduction point in France. Our aim was to further understand *V. velutina* invasion in Europe by surveying the Iberian and Italian peninsulas using microsatellites and mitochondrial DNA. Our results show that the French population was the source of the colonies expanding in Spain, Portugal and Italy, therefore leading to rejection of the hypothesis of multiple introductions from the native habitats. While Spain and Italy were invaded by leading-edge expansions from the French core population, in Portugal this invasion started from a long-distance jump. Both types of expansion were accompanied by a significant reduction in the population genetic diversity, with Portugal presenting the highest loss values (Ar = 17.4%; uHe = 42.3%) than Spain (Ar = 9.0%; uHe = 20.6%) or Italy (Ar = 16.3%; uHe = 26.8%). Population structure results and signatures of differentiation show that a secondary contact occurred between the front derived from the primary propagule introduced in France and the front derived from the secondary propagule introduced in Portugal. First-generation migrants were detected in Iberia and Italy, suggesting that a continuous gene flow is bringing in new alleles in the three invaded countries. This effect is more prominent in Portugal, as it is reflected by a 20.3% increase in allelic richness. Overall, this study provides new insights into the invasion genetics of the honey bee predator *V. velutina* in Europe, which can help developing strategies to manage this major threat to beekeeping.

Keywords: *Vespa velutina*, alien species, biological invasion, genetic diversity, molecular markers

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