Interpretation of morphometric data using microsatellite DNA markers

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INTRODUCTION

Features of the forewing of honeybee workers are used for the determination of the three subspecies of bees bred in Poland (A. m. mellifera, A. m. carnica and A. m. caucasica). The wing vein junctions are treated as coordinates and then subjected to canonical analysis; determination of 19 vein junctions and calculation procedures are automated with a computer software [1]. Based on canonical analysis, models for each subspecies have been elaborated. Most of the colonies of a given subspecies lay within a circle of radius 3 the around the mean canonical scores of this subspecies. It could be assumed that if a colony is within the circle it belongs to the subspecies. Nevertheless, it was shown that the range of metric variability of the forewings in A. m. carnica and A. m. caucasica strongly overlap [1, 2]. During the survey we found colonies that did not fit the model of the declared subspecies as well as any other developed models (later called: outside the model).

Here, we aimed to verify identity of these bees on the basis of microsatellite DNA analysis.

MATERIALS AND METHODS

In this study we included samples from commercial Carniolan and Caucasian bee breeds, which were previously examined on the basis of forewing venation. For the DNA analysis we selected samples which were outside the morphometric model (Fig. 1 A) or disqualified due to crossbreeding (Fig. 1 B,C). Altogether, we analysed 34 colonies of Carniolan bees and 24 colonies of Caucasian bees. From each colony, a sample of 16 worker bees were analyzed. Insects were taken directly from hive frames and conserved in 90% ethanol.


In order to assign genotypes to specific subspecies, we used a Bayesian statistical method implemented in the STRUCTURE ver. 3.2.1 [4]. As input data we used queen genotypes inferred from their offspring with MSF [5, 6]. The probability of belonging to the declared subspecies was lower in samples disqualified based on wing venation. In contrast, the highest probability of assignment to the right subspecies was estimated for samples outside the morphometric model (Fig 3).

RESULTS AND DISCUSSION

The probability of belonging to the declared subspecies was lower in samples disqualified based on wing venation. In contrast, the highest probability of assignment to the right subspecies was estimated for samples outside the morphometric model (Fig 3).

CONCLUSION

Morphometric models that are currently used for discrimination of honeybee subspecies should be updated based on samples with the identity verified by DNA analysis.

REFERENCES