PROGRAM & BOOK OF ABSTRACTS

FOODINTEGRITY 2017 CONFERENCE

10 -11 MAY 2017

STARHOTEL DU PARC PARMA, ITALY

Assuring the integrity of the food chain: Turning science into solutions

EDITORS

MICHELE SUMAN - ELENA MAESTRI - PAUL BRERETON

Barilla

The Italian Food Company Since 1877

UNIVERSITÀ DI PARMA

SITEIA parma

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TOWARDS HONEY AUTHENTICATION: ASSESSING EUROPEAN HONEY ENTOMOLOGICAL ORIGIN BY A MOLECULAR IDENTIFICATION APPROACH

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Following the European Union (EU) legislation, honey should be produced by the western honey bee, Apis mellifera. Across Europe, 10 different A. mellifera subspecies can be found, comprising 3 different lineages (A, M and C) based on mtDNA [1]. In general, honey bees occupy allopatric geographical ranges according to their evolutionary lineages, allowing to establish an entomological origin for honey produced in different EU countries. Additionally, several honeys with protected designation of origin (PDO) detail the subspecies traditionally used in their production [2]. While numerous works focused on the botanical and/or geographical authenticity of honey, only a few have attempted its entomological authentication. For that purpose, DNA-based methods have been considered as the most suitable tools since they allow the unequivocal species identification. So far, only few works described the use of DNA-based methods to establish the entomological origin of honey [3,4] and those were focused on different species of honey bees, including Meliponini and/or Trigonini stingless bees. To our knowledge, this is the first attempt to distinguish among different European honey bee subspecies commonly used in honey production, with further application to honey authentication.

In this work, DNA markers were developed for the differentiation of A. mellifera subspecies DNA in honey. For this purpose, individuals of A. m. iberiensis lineage A (n=22) from Portugal and Spain (n=5), A. m. iberiensis lineage M from Spain (n=7), A. m. mellifera lineage M from France, Netherlands, Scotland and Norway (n=7), A. m. ligustica lineage C from Italy (n=4), A. m. carnica lineage C from Croacia and Serbia (n=4) and commercial Buckfast lineage C bees (n=10) were tested. Different sets of primers were designed targeting the cytochrome oxidase I gene. The specificity and sensitivity of the designed primers were assayed by qualitative polymerase chain reaction (PCR). Species-specific primers successfully allowed the identification of A. m. iberiensis lineage A by end-point PCR. The use of real-time PCR coupled with High Resolution Melting analysis allowed the separation of A. mellifera honey bee subspecies in

different clusters according to their lineages. The developed methodologies were applied to the analysis of authentic honey samples from Portugal (produced by A. m. iberiensis lineage A), Spain (produced by A. m. iberiensis lineage M), and Italy (produced by A. m. ligustica lineage C), allowing its successful entomological origin identification.

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