BOOK OF ABSTRACTS

6th International Symposium on

RECENT ADVANCES IN FOOD ANALYSIS

November 5–8, 2013
Prague, Czech Republic

Jana Pulkrabová, Monika Tomaniová, Michel Nielen and Jana Hajšlová
Editors




INSTITUTE OF CHEMICAL TECHNOLOGY PRAGUE

RIKILT WAGENINGEN UR

B-49
IDENTIFICATION AND QUANTIFICATION OF ROE DEER (*CAPREOLUS CAPREOLUS*) IN FOOD FOR DETECTION OF FOOD ADULTERATION

Barbara Druml[1], Walter Mayer[2], Rupert Hochegger[3], Margit Cichna-Markl[4]*

[1] Department of Analytical Chemistry, University of Vienna, Vienna, Austria and Austrian Agency for Health and Food Safety, Department of Molecular Biology and Microbiology, Vienna, Austria
[2 3] Austrian Agency for Health and Food Safety, Department of Molecular Biology and Microbiology, Vienna, Austria
[4] Department of Analytical Chemistry, University of Vienna, Vienna, Austria
**Corresponding author – E-mail: margit.cichna@univie.ac.at, Phone: +43 1 4277 52374*

According to legal regulations, food manufacturers have to ensure not only the safety but also the authenticity of food products. However, to increase their profit, manufacturers may be tempted to incorrectly label their products and to use lower priced ingredients of inferior quality instead of more expensive ones. In the meat industry, game meat is particularly susceptible for fraudulent labelling since game meat has always been especially appreciated due to its distinctive flavour and its low fat and cholesterol content. According to the Codex Alimentarius Austriacus, in sausages declared as "game sausages" at least 38% of the total meat content has to be game meat. Analytical methods have to be specific and sensitive in order to be applicable for the detection of food adulteration. The real-time polymerase chain reaction (PCR) is a DNA based method that does not only allow the identification but also the quantification of species, e.g. meat species in foods. Quantification of meat species is, however, known to be a difficult task. The quantification strategy is usually based on a reference gene that is found in all animal species. The aim was the development of a real-time PCR method targeting genomic DNA sequences to identify roe deer (Capreolus capreolus) and to quantify its meat content in commercial food products. The challenge for the development of the method was the design of specific primers and probes. No cross-reactivities with other animal species, especially closely related game species, and spices that are often found in processed foods, should be achieved. In the present study, a TaqMan real-time PCR method for the identification and quantification of roe deer in game meat products was developed and validated. The PCR method was found to be specific for roe deer and does not show any cross-reactivities with other game species (e.g.: red deer, sika deer, fallow deer, wild boar and reindeer), other animal species (e.g.: pork, cattle, chicken and horse) and spices. The analysis of meat mixtures from roe deer and pork showed that the real-time PCR method is applicable to quantify the game mea t content in foodstuffs.

[1] Fajardo V, Gonzalez I, Rojas M, Garcia T, Martin R (2010) A review of current PCR-based methodologies for the authentication of meats from game animal species. Trends Food Sci Technol 21:408-421.
[2] Fajardo V, Gonzalez I, Martin I, Rojas M, Hernandez PE, Garcia T, Martin R (2008) Real-time PCR for quantitative detection of chamois (Rupicapra rupicapra) and pyrenean ibex (Capra pyrenaica) in meat mixtures. J AOAC Int 91:103-111.
[3] Laube I, Zagon J, Spiegelberg A, Butschke A, Kroh LW, Broll H (2006) Development and design of a 'ready-to-use' reaction plate for a PCR-based simultaneous detection of animal species used in foods. Int J Food Sci Technol 42:9-17.
[4] Mafra I, Ferreira IMPLVO, Oliveira MBPP (2008) Food authentication by PCR-based methods. Eur Food Res Technol 227:649-665.

Keywords: *food authentication, game meat, capreolus capreolus, real-time PCR, quantification*

B-50
EXPLOITING DNA MARKERS FOR THE BOTANICAL ORIGIN IDENTIFICATION OF HONEY

Sónia Soares[1], Joana Amaral[2], Maria Beatriz Oliveira[3], Isabel Mafra[4]*

[1 2 3 4] Requimte
**Corresponding author – E-mail: isabel.mafra@ff.up.pt, Phone: 220428640*

Honey is a natural product highly consumed due its known association with health benefits. Monofloral and Protected Designation of Origin (PDO) honeys have generally higher economic value since they are considered to have higher quality due to its specific and well-defined flavor and aroma. Thus, these products are susceptible to misleading labeling and fraudulent practices, making their assessment of botanical origin and authentication a task of utmost importance. For this purpose, traditional methods based on pollen identification by microscopic analysis are presently used. However, this is time consuming and greatly depends on the experience and skill of trained analysts [1]. Recently, due to its high specificity and sensitivity, DNA-based methods are emerging as alternative tools for food authentication since they allow the unequivocal species identification. In this sense, the aim of this work is to extract amplifiable pollen DNA from honey for further exploiting molecular markers for botanical authentication. Considering the complexity of honey matrix, four extraction methods were tested and optimized: the commercial kits NucleoSpin® Plant II and DNeasy® Plant Mini Kit; and the in-house CTAB-based and Wizard methods as described by Mafra et al. [2] with modifications. Prior to DNA extraction, three different pretreatments were tested, accounting for a total of twelve protocols, which were applied to four different honey samples (Ericaceae, Rosmarinus officinalis and Eucalyptus spp. and multifloral). DNA extracts were evaluated by UV spectrophotometry to determine yield and purity. The amplifiability was tested by polymerase chain reaction (PCR) targeting rbcL gene, as a candidate locus for DNA barcoding. The obtained honey extracts revealed low DNA yields for all the extraction protocols, but adequate purity for PCR was achieved using the Wizard method. The amplifications were successfully attained with the Wizard metho d with one of the pretreatments when applied to all honey samples, while the other three methods exhibited lower reproducibility of results and low DNA yields regardless the applied pretreatment. The obtained results suggest the high potentiality of DNA-based methods to assess honey authenticity and the possibility to propose more robust, reliable, simple and sensitive assays alternative to the classical method for analyzing the botanical origin of honey.

[1] Laube, I, Hird, H, Brodmann, P, Ullmann, S et al. (2010). Food Chem, 118, 979-986.
[2] Mafra, I, Silva, SA, Moreira, EJMO, Silva, CSF, Oliveira, MBPP (2008). Food Control, 19, 1183-1190.

Keywords: *Honey, authenticity, DNA markers, PCR*

Acknowledgement: *This work has been supported by FCT through grant no. PEst-C/EQB/LA0006/2011. S. Soares is grateful to FCT PhD grant (SFRH/BD/75091/2010) financed by POPH-QREN (subsidized by FSE and MCTES).*