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PROSCIUTTO TOSCANO DOP

Tracing autochthonous pig breeds with meat near-infrared spectra data pig

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Near Infrared spectroscopy (NIRS) offers an easy to use and cost-effective tool for quantitative and qualitative application in animal science. Of special interest could be considered the use of NIRS for tracing meat origin on the basis of breed specification. The aim of this study was to investigate the potential use of meat NIRS as a "fingerprint" of autochthonous pig breeds. The research considered intact and grounded sample of Longissimus Dorsi (n=371) collected from 11 European local pig breeds from the TREASURE project, namely: Alentejana (ALE), Bisara (BIS), Crna Slawonska (CRN), Gascon (GAS), Iberian (IBE), Krskopolje (KRS), Lithuanian Wattle (LIA), Lithuanian White (LIH), Negre Mallorqui (NEG), Schwabish Hallisches (SCH) and Turopolje (TUR). For each muscle sample, two aliquots were scanned using FT-NIRS Antaris II model (Thermo Fisher Scientific) in absorbance mode considering the infrared region (3999 to 9999 cm^{-1}) and averaged.
Discriminant analysis of principal components (DAPC) on meat NIRS was used to assess: i) breed traceability and ii) similarity among breeds. DAPC was applied on standardised (centred and scaled) spectra using the R package. For breed traceability, cross-validation was applied: five samples per breed were sampled at random, without replacement, and used in validation. The procedure was repeated ten times and each breed was analysed separately. In this case, all breeds were present in the training set. Similarity among breeds was assessed by excluding each breed from the training set and assigning the samples in the validation set to the breeds in the training one. Overall correct classification was 68.0 and 77.6% for intact and grounded meat, respectively. Alentejana had 100% correct classification for both intact and grounded meat. For CRN, KRS, LIA, LIH and NEG use of grounded meat spectra resulted in higher classification rates from 44 to 64% for intact and from 66 to 90% for grounded meat), while for GAS the opposite was found (80% for intact vs. 70% for grounded). For the rest of the breeds slight or no differences were observed between intact and grounded samples and classification rates ranged between 66 (CRN and SCH) to 72% (BIS). The lowest classification rates were observed in both cases for CRN. Similarity among breeds was greatly varied upon dataset used (e.g. ALE samples were classified as IBE (40%), TUR (40%) and SCH (10%) using intact meat while 100% were classified as CRN using grounded meat). Our results mark NIRS as a promising tool for traceability of pig breed meat origin and support the use of grounded over intact samples.

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Evolution of the volatile compounds along curing in Semimembranosus muscle of the Toscano ham

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The volatile profile of Toscano hams from 0 to 18 months of ripening was studied. Ten green hams of 15.60 were seasoned according to the 'Toscano' PDO Consortium ripening protocol. *Semimembranosus* muscle was sampled after trimming (0), 1, 3, 6, 12, 14, 16 and 18 months of ripening by means of 5-mm punch corer. The volatile compound profile was obtained by SPME–GC–MS using an Agilent 7890 Chromatograph equipped with a 5975A MSD with EI ionisation and a three-phase DVB/Carboxen/PDMS 75-µm SPME fibre, exposed in the head space of the vials at 60 °C for 30 min. The identification of volatile compounds (VOCs) was done matching the peak spectra with library database and matching Kovat index (KIS) with KIS from literature. VOCs evolution was studied using a linear model and a multivariate approach, which was performed to test the feasibility of using the VOCs profile to predict the seasoning stage of Toscano ham. Ninety-seven VOCs, belonging to 7 chemical families (29 aldehydes, 16 esters, 14 alcohols, 13 hydrocarbons, 12 ketones, 10 acids, 2 furans and 1 nitrogenous compound), were identified. Firstly, the stepwise discriminant analysis (SDA) was applied to selected 26 compounds able to discriminate low maturing class (LMC) from high maturing class (HMC). Then, canonical discriminant analysis (CDA) was applied using the 26 selected compounds. The two maturing classes resulted clear separated ($P < 0.0001$). Among the 26 compounds the most influencing were: the 2,3-dimethyl pentane, acetophenone and 9-decenoic acid for LMC and dodecanoic, benzeneacetaldehyde, 3-octen-2one and pentanoic acid ethylester for HMC. Dodecanoic acid was the most effective in identifying HMC hams, indeed, it increased from 0 to 18th month. The other high-discriminant compounds followed the same trend during ripening, except for 3-octen-2one, whose lower occurrence in HMC than in LMC, acted as the discriminant factor. Secondly, the SDA was applied only to HMC hams (12, 14, 16 and 18 seasoning months), selecting 17 compounds. Samples seasoned for 14 and 18 months resulted separated ($P=0.02$). CAN analysis also differentiated "12 months" seasoning class from the other classes and "18 months" class from "16 months" one. The main VOCs associated to the "12 months" class were nonanal, 1,5-Diphenyl-3-methylthio-1,2,4-triazole and 6-methoxy 2-hexanone. Also 3-nonen-5-yne,4-methyl played an important role in the characterization of 18 months samples respect to 14 and 16 ones. The 26 compounds identified in the first scenario could be a useful tool to determine the ripening status of unknown samples. Despite the loss of accuracy observed in the second scenario, also the 17 compounds identified as discriminating within the HMC samples, turned out to be an interesting way to separate at least 12th months samples from 18th ones.

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