The relationship between muscle fiber characteristics and some meat quality parameters in Turkish native goat breeds

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This study was conducted to determine muscle fiber characteristics and its effect on some meat quality parameters in Longissimus dorsi (LD) and semitendinosus (ST) muscles from kids of some Turkish native goat breeds. A total of 24 male kids were used as experimental pure breed goat of Hair ($n=6$), Angora ($n=6$), Kilis ($n=6$) and Honamli ($n=6$) breeds. All kids were slaughtered at 3 m of weaning age. Following slaughtered, LD and ST muscle samples were collected for determination of type I, IIA and IIB muscle fibers composition and cooking loss, intra muscular fat, tenderness, water holding capacity, pH and color of muscle samples. Type IIA muscle fiber numbers of Hair and Honamli kids were higher than those of other breeds in LD muscle ($P<0.05$). Similarly, Hair kids had higher number of ($P<0.05$) type IIA fibers in ST muscle compared to other breeds. There were positive and negative correlations between some muscle fiber compositions, cross-sectional area and meat quality parameters ($P<0.05$). In conclusion, kids of Turkish native goat breeds had different muscle fiber characteristics and these differences can affect instrumental meat quality parameters.

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Biocatalysis/Biotransformation

Laccase activity as a key factor in the oligomerization of rutin

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The polymerization of natural flavonoids, such as rutin, catalysed by laccase from *Trametes versicolor*, has gained interest due to the enhanced properties of its products. This work aims to provide insight on the influence of enzymatic activity in rutin oligomerization by evaluating products from reactions using low and high initial laccase activities (1000–10,000 U/L). Products obtained using low laccase activity showed thermal stability and antioxidant capacity similar to control reaction but led to higher aqueous solubility and better xanthine oxidase inhibitory activity. Oligomers produced with 10,000 U/L exhibited better aqueous solubility but poor biological activities and stability. Low antioxidant activity was related to low phenolic content, which could be attributed to the formation of several intermolecular bonds. MALDI-TOF analysis allowed to confirm that rutin oligomerization took place and the average molecular mass of the oligomers was determined by HPSEC. High molecular weight oligomers showed better properties compared to lower weight oligomers.

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Intensification of biocatalytic processes by reactor miniaturization

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Integration of biocatalysis with micro-flow devices offers huge potential for bridging the “valley of death” between academia and industry. Micro-flow devices were found as extremely efficient tools for biocatalytic process development and for the intensification of these processes in multiphase systems. The inherent feature of microfluidic devices to operate in a continuous mode brings additional interest for their use in biocatalytic reaction systems and in connection with downstream processing units. Various biotransformations with dissolved and immobilized biocatalysts, namely lipases and amine transferases, recently studied within the Microprocess Engineering Research Laboratory established at the University of Ljubljana, will be discussed. Comparisons made with classical laboratory reactors indicated a pronounced intensification of processes. Very efficient scale-up of micro- towards meso-scale reactors enabling high productivities was developed.

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Bioinformatics/system biology

Genomic analysis of the endosymbiotic bacterium *Candidatus Erwinia dacicola* provides insights for the management of the olive pest *Bactrocera oleae*

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The olive fruit fly, *Bactrocera oleae*, is a widespread pest whose impact is devastating on olive production. To date, there is no specific pesticide nor agent to control it. Herein, we propose a novel strategy to manage this pest via identifying novel pharmacological targets on the genome of its obligate endosymbiotic bacterium *Candidatus Erwinia dacicola*. Our bioinformatics study revealed almost 1500 fewer genes in the *Candidatus Erwinia dacicola* bacterial strain compared to closely related non-symbiotic strains. Three genes were selected as pharmacological targets based on the *in silico* study. In this direction, the 3D models of the L-asparaginase, glutathione S-transferase and protease-C genes were designed and subsequently optimized by means of molecular dynamics simulations. Successively, a series of structure-based pharmacophore models were elucidated in an effort to pave the way for the efficient high throughput virtual screening of libraries of low-molecular weight compounds and thus the discovery of novel modulating agents. Our methodology provides the means to design, test and identify highly specific pest control substances that minimize the impact of toxic chemicals on health, economy and the environment.

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