

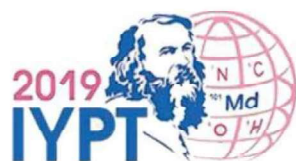


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AMINO ACIDS PROFILE FOR ASSESSING SERRA DA ESTRELA CHEESE PRODUCERS



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OBJECTIVES

Serra da Estrela cheeses collected from 6 producers have typical chemical characteristics that allows its discrimination?

Samples VARIABILITY:

produced during different time periods; the raw milk from different animals; cheese processing may slightly differ between cheesemaking producers.

Cheeses' amino acids profile

ANALYSIS

Characterization of individual amino acids constituents by UHPLC-MS/MS (Dionex Ultimate 3000 UPLC instrument from Thermo Scientific, USA)

diode-array detector and mass detector Linear Ion Trap LTQ XL mass spectrometer (ThermoFinnigan, San Jose, CA, USA) with an ESI source
chromatographic separation with a U-VDSpher PUR C18-E 100mmx2.0 mm id, 1.8 μm column (VDS optilab, Germany) at 40 °C

mobile phase: (A) 0.1% (v/v) formic acid in water and (B) 0.1% (v/v) formic acid in acetonitrile/water (50:50, v/v)

multistep gradient program with flow rate of 0.40 mL/min and an injection volume of 5 μL

data acquisition with Xcalibur@data system (ThermoFinnigan, San Jose, CA, USA).

SAMPLING

6 cheese certified producers located in different municipalities of the region of Serra da Estrela

24 cheeses were collected and samples stored -20°C until analysis

Cheeses with 45 maturation days

5,0 g of cheese + 10 mL of water:acetonitrile (50:50) (v/v) with 3,0 mM N-Acetyl-L-Tyrosine (internal standard) solution

Sonicated for 10 min at room temperature (20 °C)

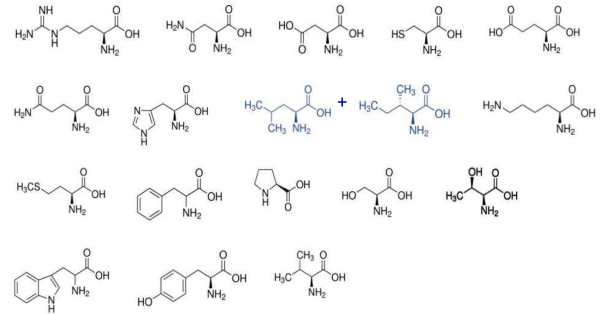
Centrifuged at 4°C at 10.000 rpm for 10 min (Heraeus Multifuge X1R – Thermo Fisher Scientific)

Filtered through 0.2 μm nylon membrane filter (Whatman PURADISC 25 NYL) and stored at -4 °C.

RESULTS

Quantitative amino acid profile in cheese → 17 amino acids

arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, leucine+isoleucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, valine



Correctly classify cheese samples according to their producer (dependent variable)

Amino acids quantification → 10 nmol/μL standard solutions

Calibration of each amino acid within the range of 0–7 nmol/μL → R² > 0.98

Independent variables → amino acids matrix data (centered and scaled)

Linear discriminant analysis → supervised pattern recognition method

Internal evaluation was considered using k-folds (10 folds) (minimize model over-fitting reducing the risk of over-optimistic results)

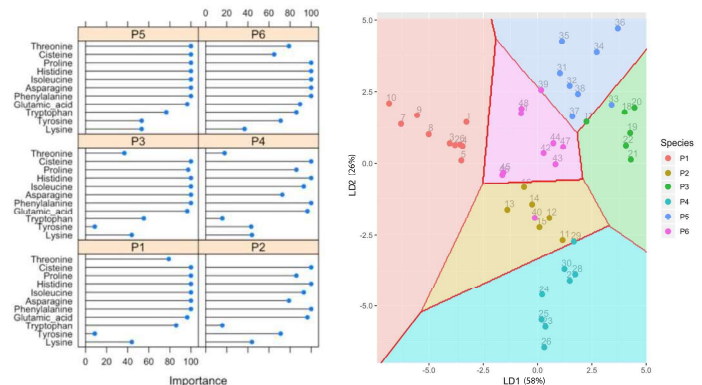
Meta-heuristic simulated annealing variable selection algorithm (selection of amino acids with the optimal discrimination performance)

11 amino acids selected

asparagine, cysteine, glutamic acid, histidine, leucine+isoleucine, lysine, phenylalanine, proline, threonine, tryptophan, tyrosine

CONCLUSION

The obtained models in the cross-validation allowed an average classification accuracy of 90%, while the best model allowed correct classifications with a predictive sensitivity (proportion of positive correct classifications) and specificity (proportion of negatives correct classifications) greater than 95%.



Acknowledgements:

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