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Microbiological, chemical and technological characterisation of Sardinian sourdoughs from the MBDS-UNISSCC microbial collection

Roberta Coronas (r.coronas3@phd.uniss.it)

Dept. Department of Agricultural Sciences of University of Sassari, Italy

Tutor: Prof.ssa Marilena Budroni Co-Tutor: Dott. Giacomo Zara

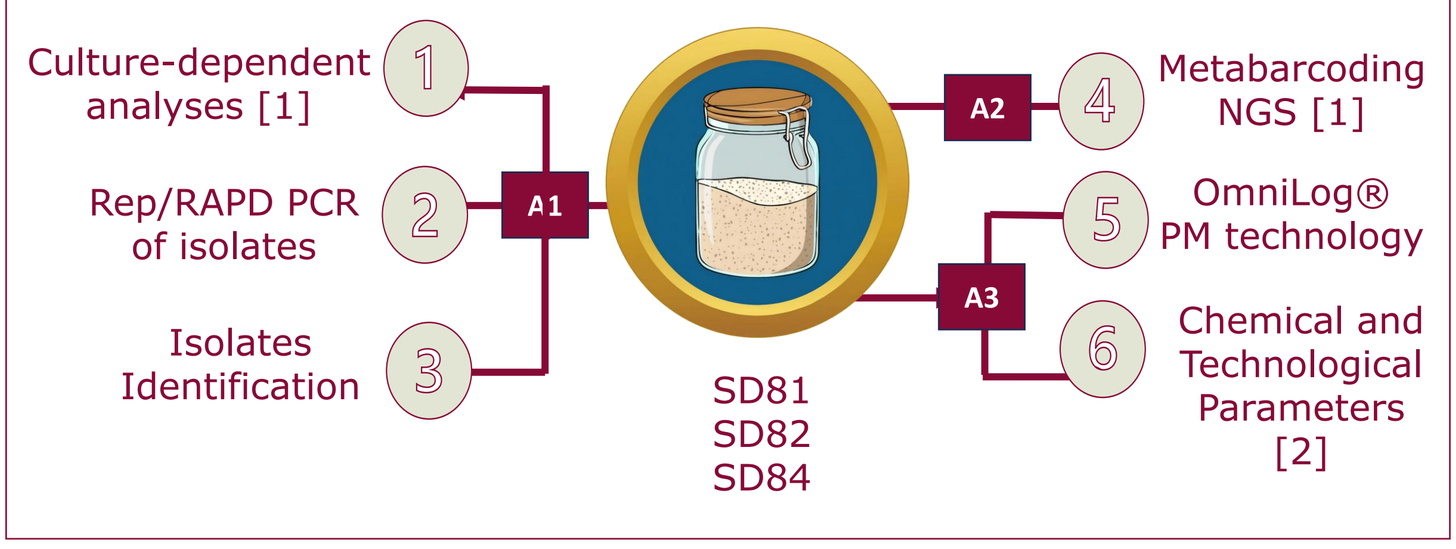
AIMS

A1 Definition and validation of Standard Operation Procedures (SOPs) for the sampling of microbiomes (culture dependent microbiological analyses, molecular identification and characterization of the isolates).

A2 SOPs for genetic characterisation of microbiomes with High-throughput sequencing (HTS) technologies.

A3 Chemical and technological characterisation of sourdoughs and catabolic footprint of sourdough microbiomes using OmniLog® PM technology.

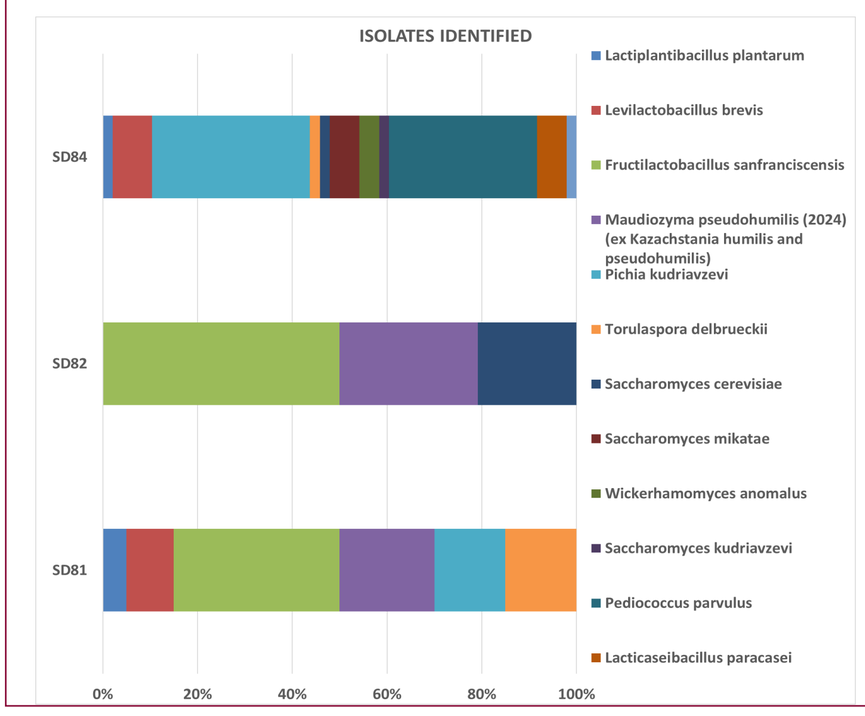
METHODOLOGY



RESULTS

A1 VIABLE COUNT AND YEAST/BACTERIA RATIO

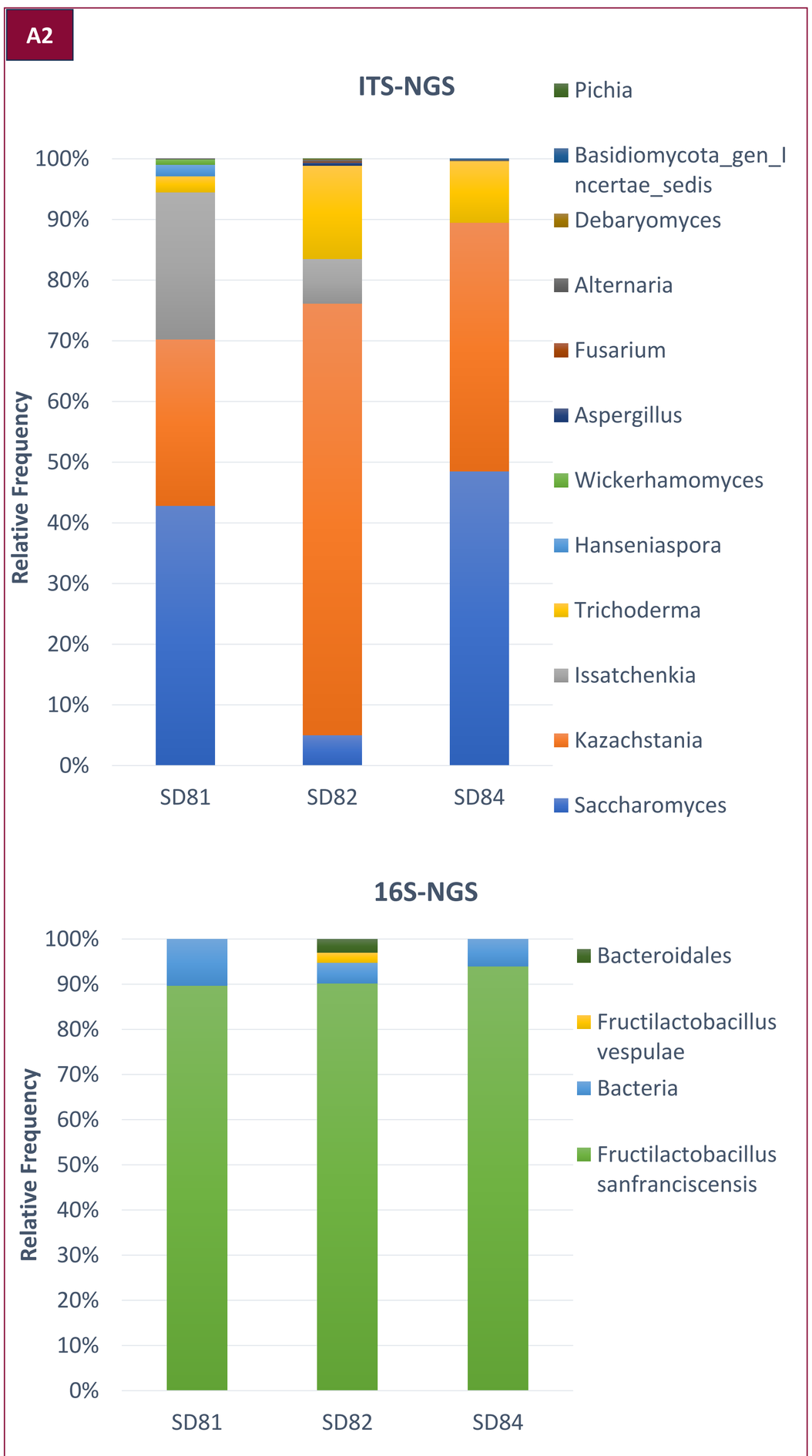
SAMPLE	YEAST (WL)	LAB (MRS)	Y:B
SD81	7.26±0.03	8.88±0.05	1:42.
SD82	7.74±0.02	8.54±0.08	1:6.5.
SD84	7.37±0.09	7.88±0.07	1:3.



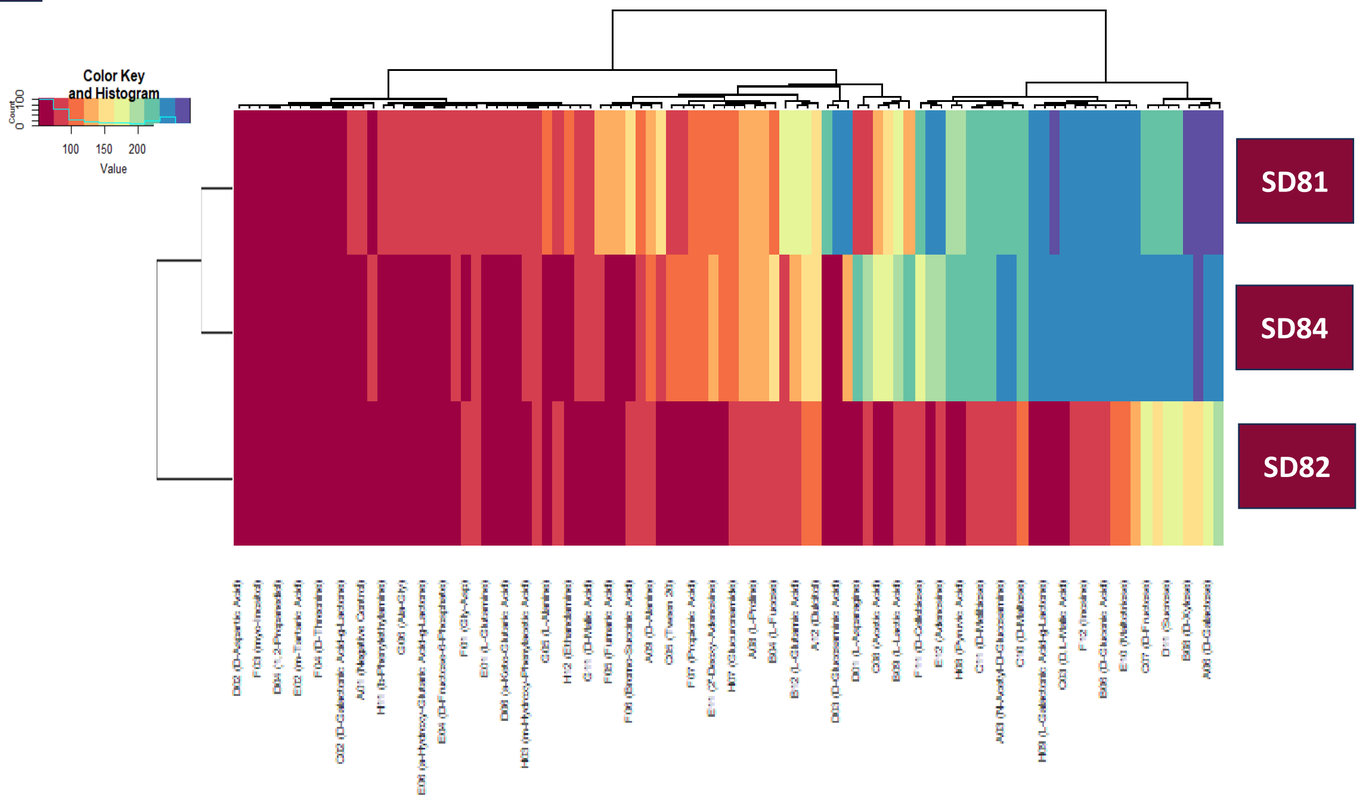
In the **SD81** sourdough, 11 and 10 different Rep/RAPD clusters were identified for bacteria and yeast, respectively.
For **SD82**, 5 different bacterial and yeast clusters were identified.
Similarly, in the **SD84** 6 cluster for bacteria and 6 for yeasts were identified

(Pearson's coefficient 90% for bacteria and 80% for yeasts).

A2



A3 CATABOLIC FOOTPRINT_PM1 HEATMAP



- The SD81 microbiome catabolized 43% and 88.5% of the tested carbon and nitrogen source, showing a high phenotypic diversity compared to SD84 and SD82. In comparison, SD84 and SD82 microbiomes were only able to catabolise 33.4% and 29% of nitrogen sources and 38% and 8% of carbon sources, respectively. Overall, the microbiomes of SD81 and SD84 showed greater phenotypic diversity compared to that of SD82.

- pH and total titratable acidity (TTA) values agree with what is found in the literature [4]. All sourdoughs showed comparable $C0_2$ production, with a higher T'1 value for SD84 (h 7:40 VS 5:30)

NGS-16S analysis shows fewer bacterial species compared to culture-dependent methods, likely due to the high similarity in the V3-V4 region of 16S rRNA in the *Lactobacillaceae* family [3]. In contrast, NGS-ITS analysis detects more yeast species than culture-dependent methods.

REFERENCES

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[4] Arora, K., Ameur, H., Polo, A., Di Cagno, R., Rizzello, C. G., & Gobbetti, M. (2021). Thirty years of knowledge on sourdough fermentation: A systematic review. Trends in Food Science & Technology, 108, 71-83.

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