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Whey and whey by-products as drivers of yeast microbial diversity

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INTRODUCTION

Whey is largely discarded during cheese manufacture. However, at moderate extent, whey may be concentrated to whey powder products (WC, WPC, WPI) or transformed into fresh ricotta which, in turn, may be salted or fermented (*ricotta forte*)[1-2]. The deproteinized whey (namely *scotta*) derived from ricotta production together with the unprocessed whey are used to fuel biogas reactors, feed cattle or are disposed as waste. During whey transformation a number of physico-chemical and microbiological changes occur. Whey-borne yeasts are poorly studied, but the knowledge of their phenotypic traits could be exploitable for whey byproducts fermentation as well as for different biotechnological uses.

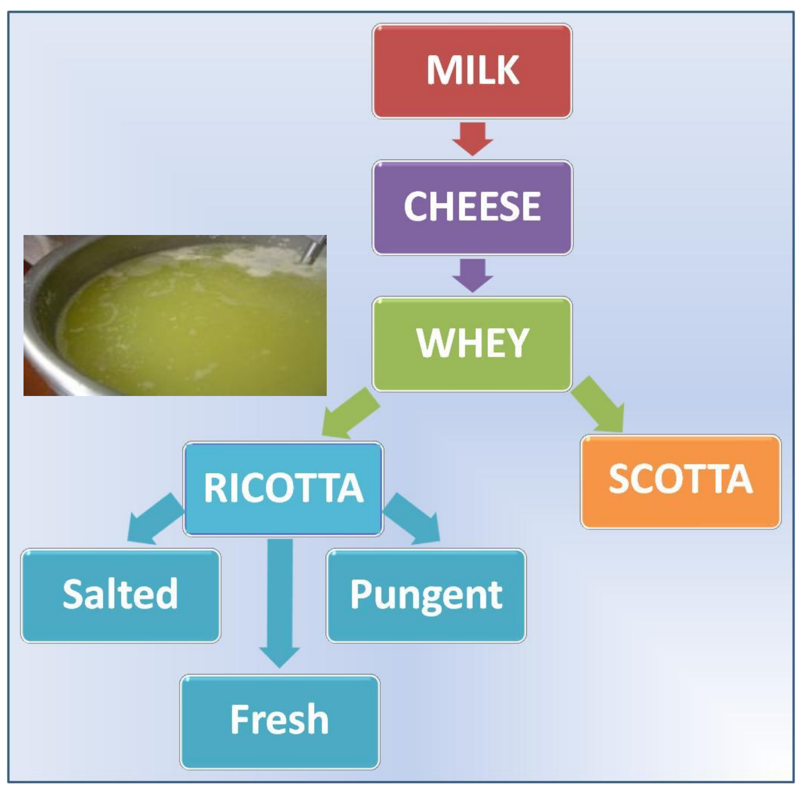
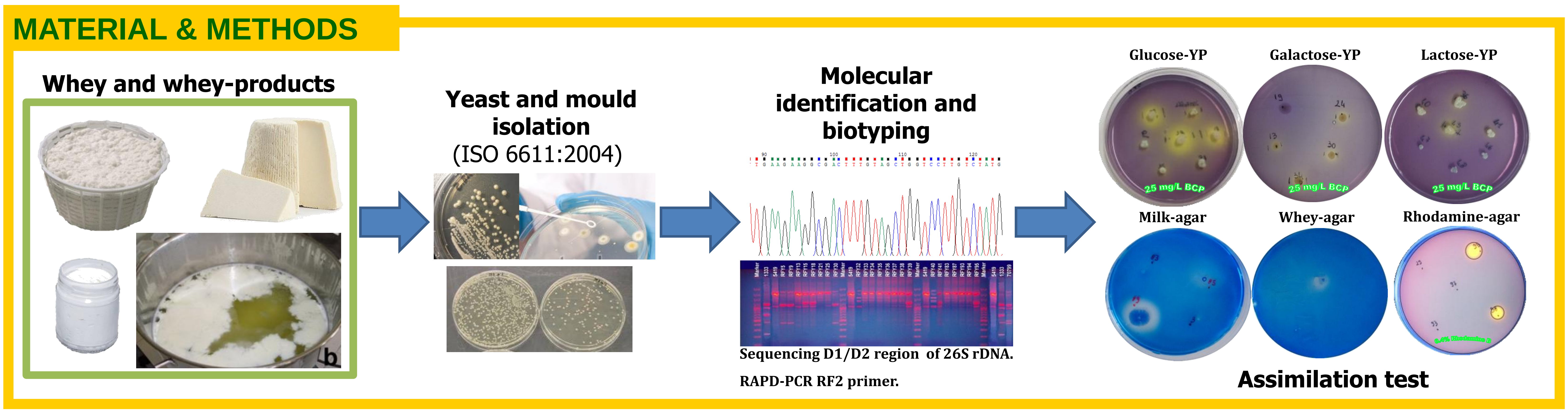


Fig. 1. Fate of whey and whey by-products.

AIM

Samples of whey and whey by-products were analyzed for the biodiversity of yeast microbiota. Isolates were molecularly identified and characterized for their milk sugar assimilation and lipid and protein hydrolysis.

MATERIAL & METHODS



Whey and whey-products

Yeast and mould isolation
(ISO 6611:2004)

Molecular identification and biotyping

Sequencing D1/D2 region of 26S rDNA.

RAPD-PCR RF2 primer.

Glucose-YP **Galactose-YP** **Lactose-YP**

Milk-agar **Whey-agar** **Rhodamine-agar**

Assimilation test

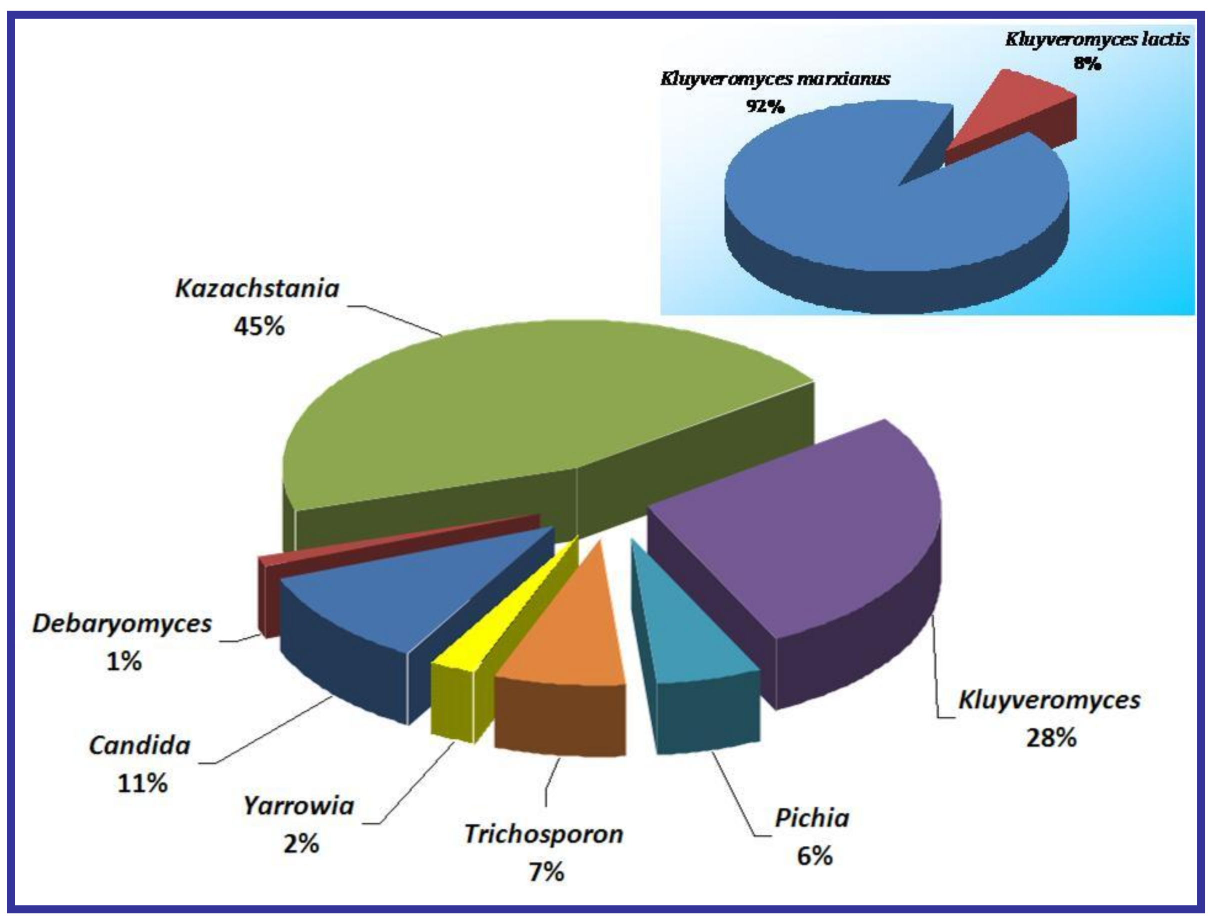


Fig. 2. Yeasts in whey and whey by-products.

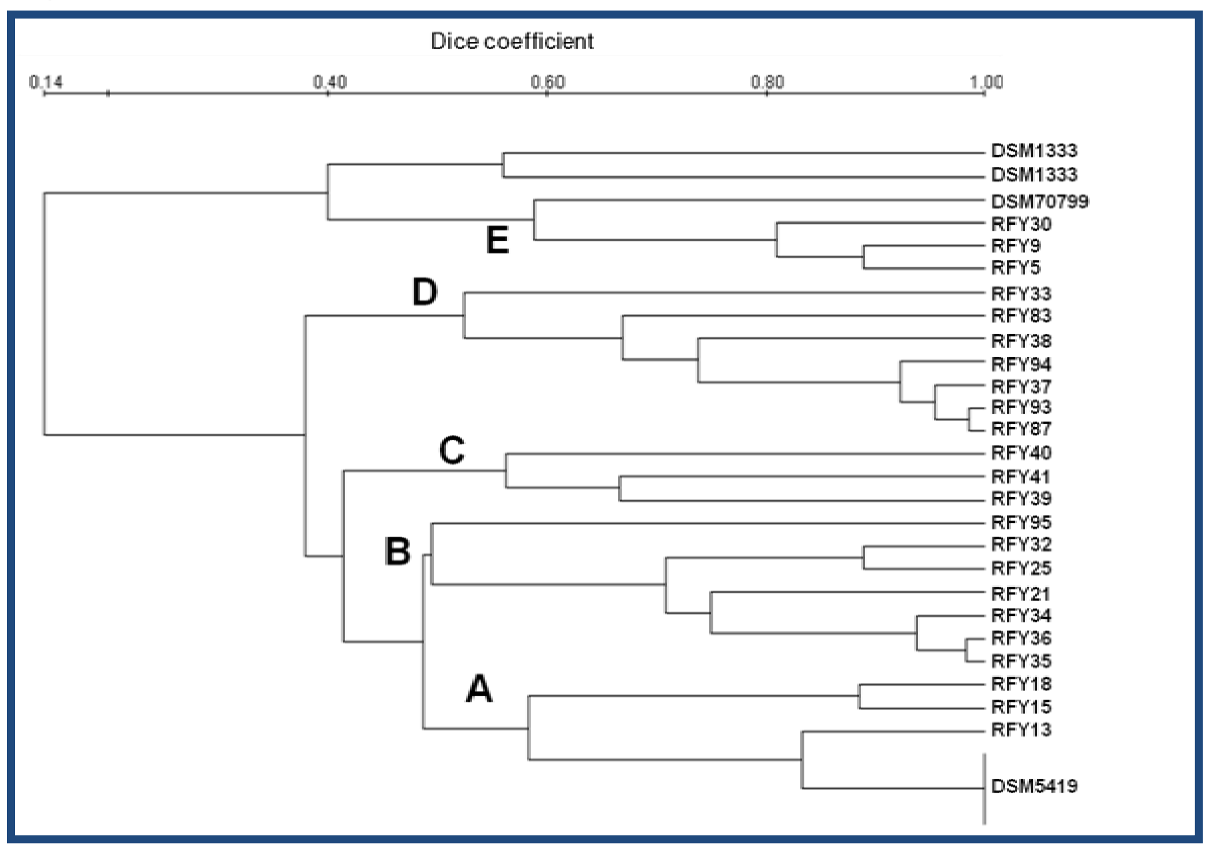


Fig. 3. Cluster analysis of *Kluyveromyces* spp. isolates from whey and whey by-product samples. Silimarities were calculated with UPGMA.

CONCLUSIONS

Unlike the most represented *K. servazzii*, *K. marxianus* strains was well adapted to whey environment because of their phenotypic features. On the other hand, the dominance of *K. servazzii* suggested possible synergistic interactions with lactose-fermenting species like *K. marxianus* or lactic acid bacteria.

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RESULTS

Most of 83 yeast isolates belonged to *Kazachstania servazzii* and *Kluyveromyces* spp. (Fig. 2). Interestingly, *K. servazzii* predominated in fermented ricotta cheese and scotta. By contrast *Kluyveromyces marxianus* and *K. lactis* also were found together with other species in whey. These results were consistent with those found in natural whey starter [3]. In addition, *K. servazzii* was also associated with *K. marxianus* and lactic acid bacteria in *koumiss* [4], whereas *K. marxianus* was occurred in ripened Pecorino di Farindola cheese [5]. RAPD-PCR and cluster analysis revealed a large heterogeneity among *Kluyveromyces* isolates (Fig. 3). Overall, 20 biotypes was identified. Furthermore, glucose and galactose were highly metabolized by almost all tested yeasts, whereas lactose was only assimilated by *K. marxianus* and *K. lactis* strains. RFY9, RFY30 and RFY34 were lactose negative. Interestingly, the strain RFY95 showed lipolytic activity like *Candida* spp. *Yarrowia lipolytica* and *Trichosporon* spp. isolates. In addition, 15 isolates of *K. marxianus* and *K. servazzii,* showed proteolytic activity towards milk total proteins and *K. marxianus* RF15 was able to hydrolyze only whey proteins (Fig 4).

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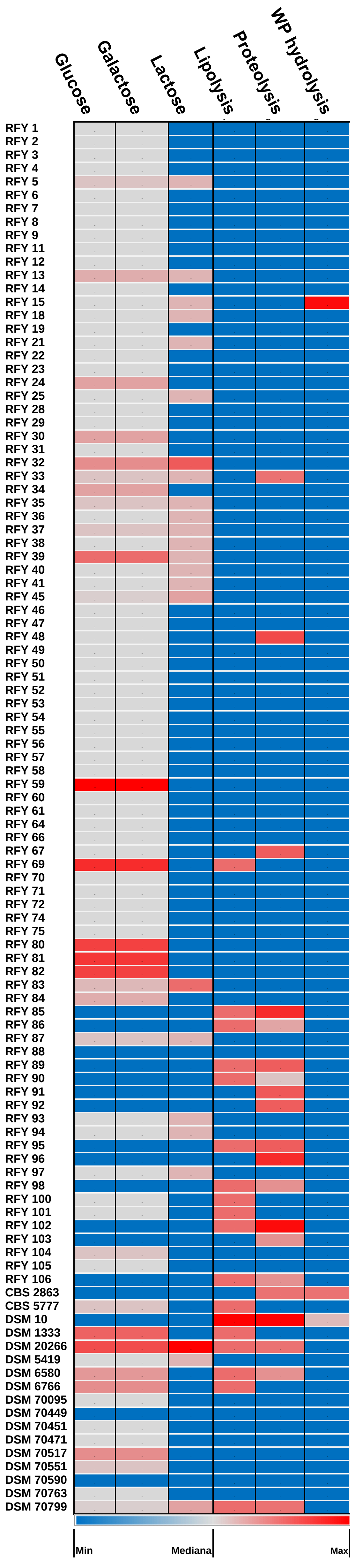

Fig. 4. Phenotypic patterns of yeast isolates from whey and whey by-products.

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