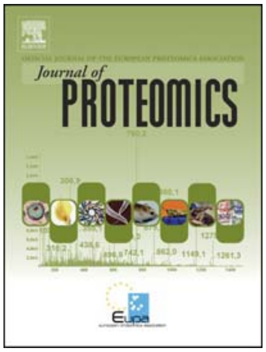

Proteomic analysis of the adaptative response of *Mucor* spp. to cheese environment

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Significance

The *Mucor* genus consists of a multitude of poorly known species. In the food context, few species are known for their positive role in the production of various food products, including cheese, while others are spoiling agents. The present study focused on the analysis of morphological and proteome differences of various *Mucor* spp. representative strains known as either positively (hereafter referred as "technological") or negatively (hereafter referred as "contaminant") associated with cheese or non-related to cheese (endophyte) on two different media, a synthetic medium and a cheese-mimicking medium. The main goal was to assess if adaptative traits of «technological» strains to the cheese environment could be identified. This work was based on observations we did in a recently published physiological study (Morin-Sardin *et al.*, 2016). One of the important innovative aspect lies in the use for the first time of an extensive 2-DE approach to compare proteome variations for 4 strains on two different media. Results obtained offered an insight in the metabolic mechanisms associated with growth on a given medium and showed that adaptation to cheese environment is probably supported by species specific proteins. The obtained data represent an essential step point for more targeted studies at the genomic and transcriptomic levels.

Highlights

- Proteome of 4 *Mucor* strains were compared in synthetic and cheese-mimicking media

- 289 proteins differentially accumulated were identified according to the medium

- Cheese related strains showed a higher diversity of biological processes in cheese environment

- The low number of common accumulated proteins among strains is in line with specific adaptive responses