

**Microbial Transglutaminases investigations for selecting putative forms of industrial interest**

Deborah Giordano (1,2), Angelo Facchiano (1)

- (1) Istituto di Scienze dell'Alimentazione, CNR, via Roma 64, Avellino, Italy
- (2) Dottorato di Ricerca in "Innovazione e management di alimenti ad elevata valenza salutistica",  
Università di Foggia, Italy

**Motivation**

Microbial Transglutaminase (MTGase) is an enzyme belonging to the class of transferases. Enzymes of this family (E.C. 2.3.2.13) catalyze post-translational modification in many proteins by acyl transfer reactions, deamidation and crosslinking (polymerisation) between protein intra- or inter-chain glutamine (acyl donor) and lysine (acyl acceptor) peptide residues (1). Even if the functions of transglutaminases in bacteria are unknown, now they are become an important tool for industry, but also for research and biotechnology fields. The interest in these enzymes is also focused on various biological processes and clinical applications (2-4) as well as on their important role in the prevention of allergy and food intolerance, including celiac disease (5-6).

Since the early 1990s, many MTGase-producing strains have been found, and production processes have been optimized. Nowadays the MTGase produced by *Streptomyces mobaraensis* is commercially available and widely used in biopolymers industry, in cosmetics, in clinical applications, in wool textiles, and in the food processing industry. We are interested to explore the existence of different MTGases that may maintain or improve the functional features of the mTGase currently in use.

**Methods**

Databases searches have been performed in order to identify amino acid sequences of potential transglutaminases in microorganisms. NCBI databases, UniProt and specific microbial genome databases have been searched by querying the sequence from *Streptomyces mobaraensis* sequence and human tissue TGase, as reference to human form, by BLAST tools.

**Results**

Microbial sequences annotated as "hypothetical transglutaminases" are largely present in databases. Searches based on the selected query sequences evidence a even more high number of MTGases. Among them, we find different characteristics in terms of length, presence of domains, position of amino acids with expectable functional roles. The results suggest a variety of forms within the microbial universe, and this encourage us for the search of novel proteins to be investigated for in vitro activity.

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