P4
«Evolutionary relationships of Microbial Transglutaminases»

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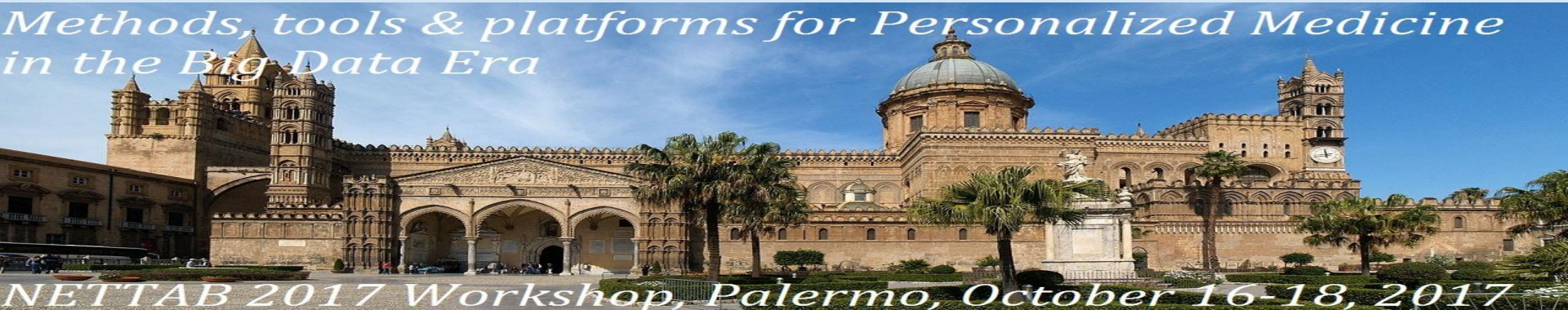
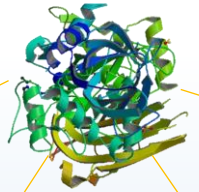
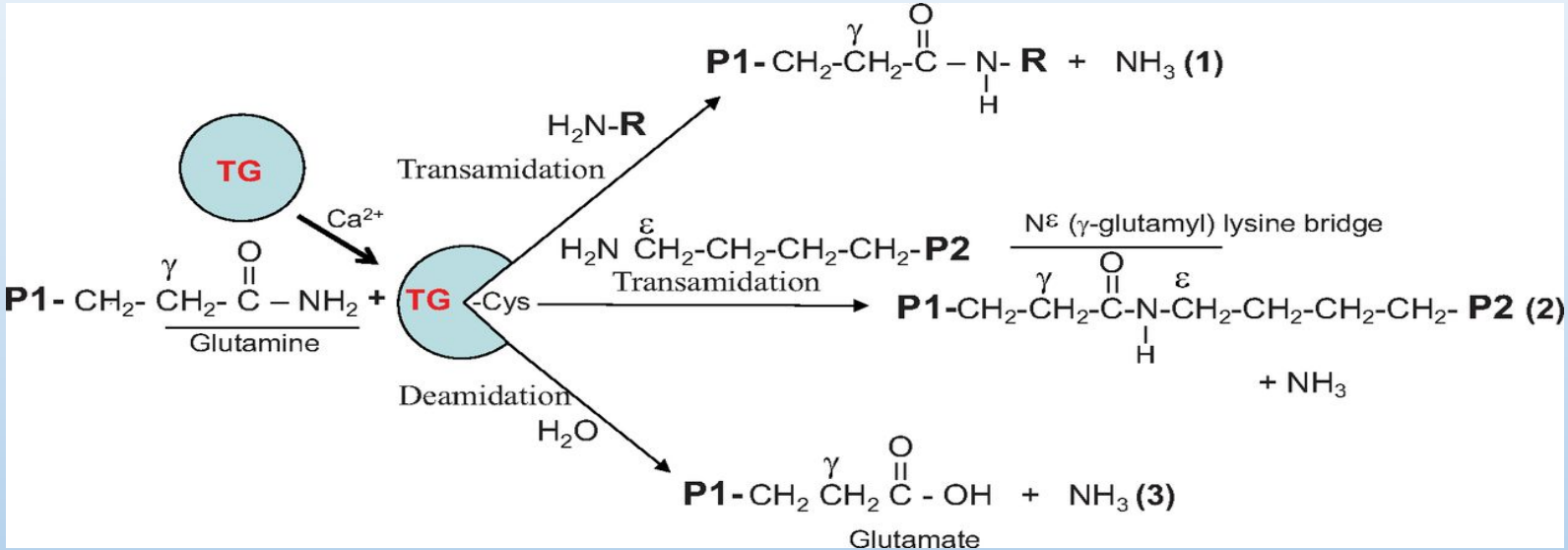


Transglutaminase (TGase) availability and its function

Keratinocyte
TGase
Tissue TGase
Epidermal TGase
Prostate TGase
Plasmatic TGase
TGase 5/6/7



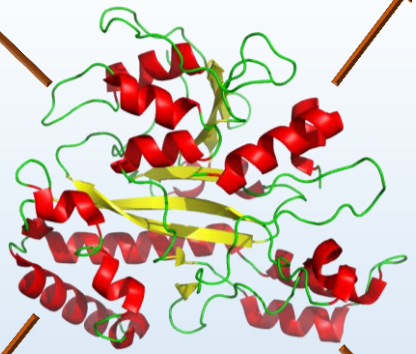


MTGase industrial applications

Research and biotechnology

In order to create:

- Protein-DNA conjugates
- Protein-Polimer conjugates
- Protein-Protein conjugates



Textile industry

Acting on wool fibers by:

- Cross-linking
- Grafting

Pharmacological field

In order to create substances which can be used:

- For mineral supplements for children and adults
- For reducing the allergenicityof certain proteins

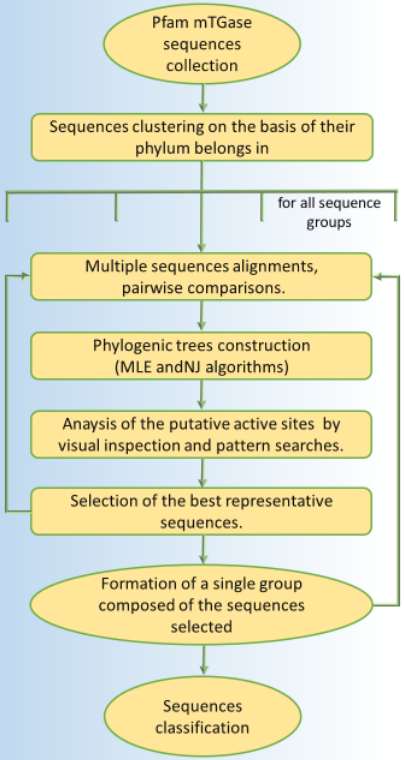
Food industry

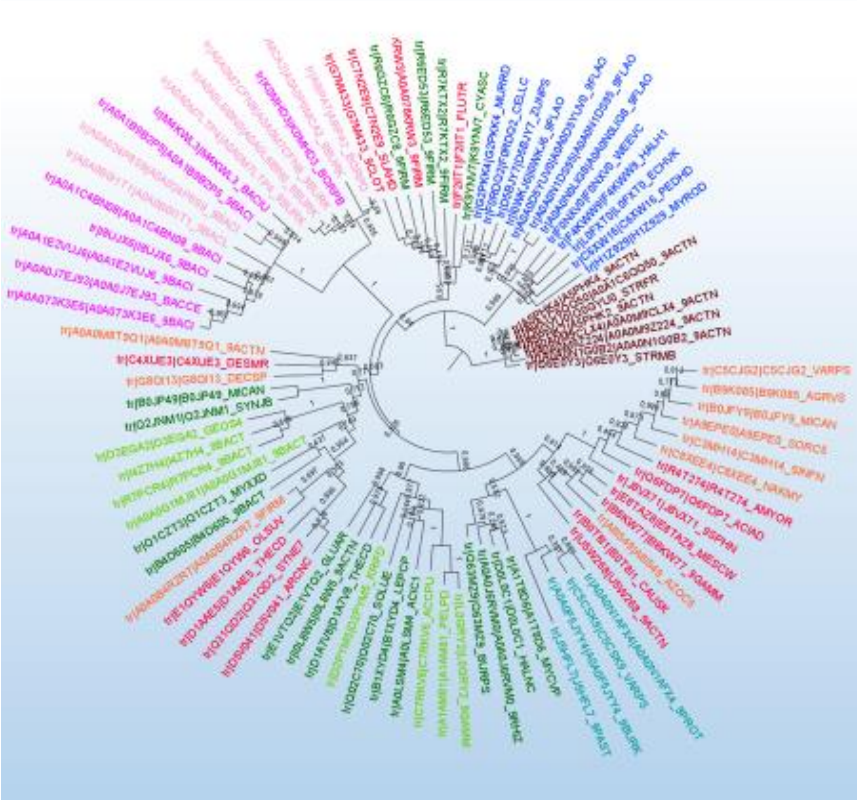
Influences the following protein properties:

- Gelatinization capacity
- Viscosity
- Thermal stability
- Capacity of water retention
- Nutritional value

Workflow and Results: a preliminary classification of novel forms of microbial TGase

Workflow





Group I : MTGases similar to the MTGase of *Chryseobacterium sp.*, a novel form of MTGase, which is very different from all the other MTGases known.

Group II: MTGases similar to the MTGase of *Bacillus Subtilis* (Tgl-like), some of them do not preserve all the catalytic residues.

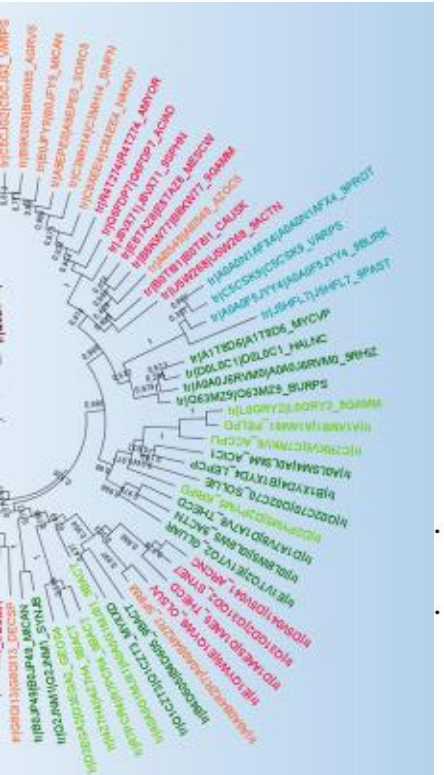
Group III: MTGases that preserve the main catalytic triad of *Streptomyces mobaraensis* MTGase, in the order Cys Asp His.

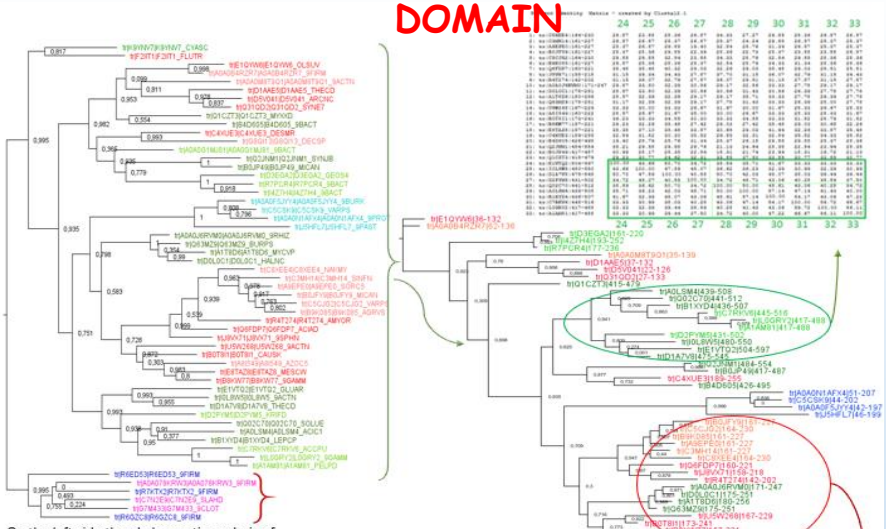
Group IV: a little group of proteins from Proteobacteria.

Group V: MTGases, similar to the eukaryotic TGases and preserving their typical catalytic triad order, i.e. Cys, His, Asp. This last group need further deep analysis in order to evaluate the possibility to obtain a more detailed classification.

Preliminary classification of microbial TGase belonging to group V

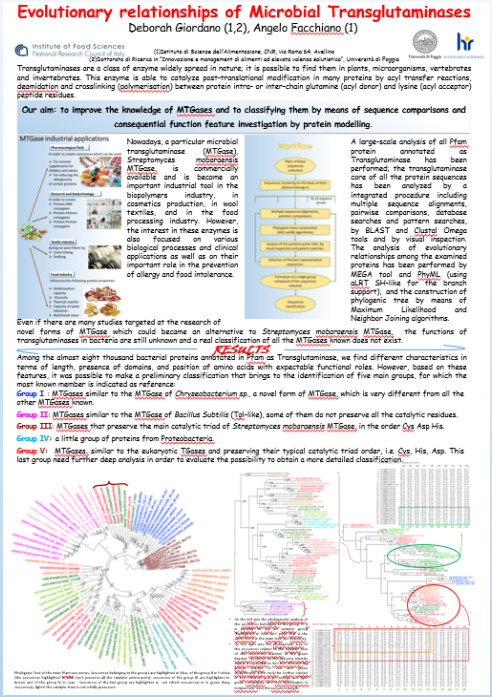
GROUP V → **ANALYSIS ON THE CATALYTIC DOMAIN**





- On the left side the phylogenetic analysis of the sequences belonging to the group V: it is possible to see an isolated group (highlighted in blue and pink) that is the same found in the main tree (red brackets).
- On the right side the phylogenetic tree of the sequences related to the catalytic core of the sequences selected in the green bracket : as shown by the percents identity matrix it is possible to find two different big groups (circled in red and green respectively), wich could be further divided in two different groups (orange and light green rectangles), and this classification is indipendent from the sequence length.

For all the information please visit poster n°4



Evolutionary relationships of Microbial Transglutaminases

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(2)Università di Ricerca in "Innovazione e management di alimenti ad elevato valore salutistico", Università di Foggia

Transglutaminases are a class of enzyme widely spread in nature; it is possible to find them in plants, microorganisms, vertebrates and invertebrates. This enzyme is able to catalyze post-translational modification in many proteins by acyl transfer reactions, deamidation and crosslinking (polymerization) between protein intra- or inter-chain glutamine (acyl donor) and lysine (acyl acceptor) peptide residues.

Our aim: to improve the knowledge of MTGases and to classifying them by means of sequence comparisons and consequential function feature investigation by protein modelling.

MTGase industrial applications

Nowadays, a particular microbial transglutaminase (MTGase), *Streptomyces mobaraensis* MTGase, is commercially available and is become an important industrial tool in the biopolymers industry, in cosmetics production, in wool textiles, and in the food processing industry. However, the interest in these enzymes is also focused on various biological processes and clinical applications as well as on their important role in the prevention of allergy and food intolerance.

Workflow

A large-scale analysis of all Pfam protein annotated as Transglutaminase has been performed; the transglutaminase core of all the protein sequences has been analyzed by a integrated procedure including multiple sequence alignments, pairwise comparisons, database searches and pattern searches, by BLAST and Clustal Omega tools and by visual inspection. The analysis of evolutionary relationships among the examined proteins has been performed by MEGA tool and PhyML (using aLRT SH-like for the branch support), and the construction of phylogenic tree by means of Maximum Likelihood and Neighbor Joining algorithms.

Even if there are many studies targeted at the research of novel forms of MTGase which could become an alternative to *Streptomyces mobaraensis* MTGase, the functions of transglutaminases in bacteria are still unknown and a real classification of all the MTGases known does not exist.

RESULTS

Among the almost eight thousand bacterial proteins annotated in Pfam as Transglutaminase, we find different characteristics in terms of length, presence of domains, and position of amino acids with expectable functional roles. However, based on these features, it was possible to make a preliminary classification that brings to the identification of five main groups, for which the most known member is indicated as reference:

Group I : MTGases similar to the MTGase of *Chryseobacterium sp.*, a novel form of MTGase, which is very different from all the other MTGases known.

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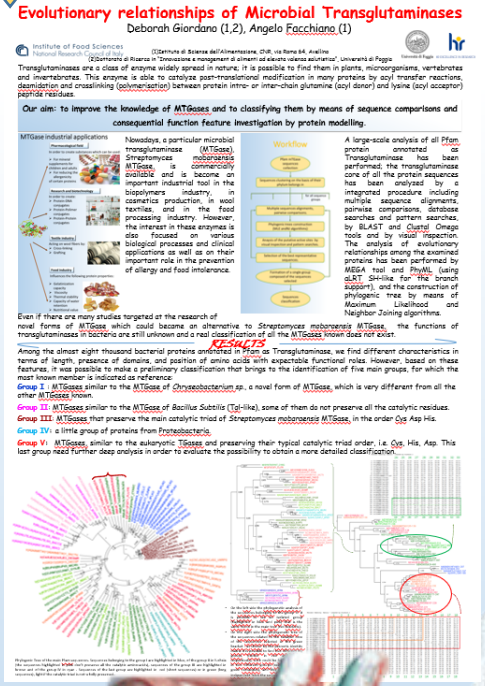

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Thanks for your attention!!!