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Peptidomics characterization of allergenic and non allergenic tropomyosin orthologs.

Dr. Cristian Piras[1], Dr. Alessio Soggiu[1], Prof. Luigi Bonizzi[1], Dr Krisztina Takács[2], Dr Andras Nagy[2], Dr Éva Gelencsér[2], Dr Thomas Holzhauser[3], Dr Joana Costa[4], Dr Annette Kuehn[5], Prof Karin Hoffmann[6], Prof Andrea Urbani[7,8], Dr Viviana Greco[8], Prof Francesco Ria[9], Dr Chiara Autilio[10], Dr Paola Roncada[11]

[1]University of Milan, Department of Veterinary Medicine DIMEVET, Milano, Italy, [2]NARIC Food Science Research Institute, Department of Biology, Budapest, Hungary, [3]Recombinant Allergen Therapeutics, Division of Allergology, Paul-Ehrlich-Institut, Federal Institute for Vaccines and Biomedicines, Langen, Germany, [4]REQUIMTE-LAQV/Faculty of Pharmacy, University of Porto, Porto, Portugal, [5]Allergology - Immunology - Inflammation Research Unit, Department of Infection and Immunity, Luxembourg Institute of Health, , Luxembourg, [6]Dept. of Pathophysiology and Allergy Research, Medical University of Vienna, Vienna, Austria, [7]Santa Lucia Foundation, Rome, Italy, [8]Istituto di Biochimica e Biochimica Clinica, Università Cattolica del Sacro Cuore, Rome, Italy, [9]Institute of General Pathology, Università Cattolica del S. Cuore, , Italy, [10]Dipartimento di Diagnostica e Medicina di Laboratorio, Laboratorio di Biologia Molecolare Clinica, Policlinico "A.Gemelli", Università Cattolica Del Sacro Cuore, Rome, Italy, [11]Istituto Sperimentale Italiano "Lazzaro Spallanzani", Milano, Italy

Background
The cleavage and the digestion patterns of allergenic proteins play a key role in allergenicity. The transformation of food proteins starts with their denaturation by the acidic environment of the stomach. However, protein denaturation is not enough to completely remove allergenic properties of a protein, but it is necessary a complete enzymatic digestion. Whether the enzymatic digestion is not efficient, the persistence of bigger peptides can occur and put the basis for the development of the sensitization process.The hypothesis of the current work takes into consideration the probability that shrimp tropomyosin (TM) is not fully digested or presents a digestion pattern that generates some peptides that can be immunogenic.Therefore, the work plan designed, aims to study the cleavage pattern of: purified chicken TM, recombinant chicken TM, purified TM of Penaeus monodon (Pen m 1), recombinant TM of Penaeus monodon (rPen m 1) and recombinant TM of Crangon crangon (rCrac c 1).
Methods
One mg of each ortholog has been processed through simulated mouth, gastric and intestinal digestion. The sample was frozen to block the digestion and, after this step, concentrated and cleaned through protein precipitation. The protein pellet was processed for peptidomic analysis through 1D Tricine gel electrophoresis, 2D Tricine gel electrophoresis and mass spectrometry.
Results
Simulated gastric digestion pattern of shrimp TM highlighted the presence of a resistant band at an average MW of 25 kDa that could be involved in the immunogenic process.
Conclusions
This innovative approach (peptidomics study through 1D-2D Tricine/MS) could represent a milestone for the study of digestion patterns of allergenic proteins or for the study of allergenic potential of novel foods.

Keywords
Tropomyosin, digestomics, peptidomics, allergenic peptides

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