

Journal of Biological Research

Bollettino della Società Italiana di Biologia Sperimentale



**91st SIBS Congress on the role of the
Italian Society for Experimental Biology
in the Italian research**

Ancona, Italy, 9-10 November 2018

ABSTRACT BOOK

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its activation by oxidant stress involves the band 3 (AE1) membrane protein. Tyr phosphorylation (AE1) occurs during *P. falciparum* growth leading to the release of microparticles containing hemichromes and RBCs structural weakening. Syk inhibitors block these events interacting with protein catalytic site. We have performed *in vitro* and *in silico* studies and compared the obtained results. *In vitro* we treated parasitized erythrocytes with different concentrations of Syk inhibitors and we evaluate the Tyr phosphorylation levels in Band 3 residues by proteomic analysis. In presence of Syk inhibitors we observed a marked decrease of band 3 phosphorylation according to drug concentration increase. The proteomic data trend relating to the inhibition values IC_{50} correspond to the computational studies. *In silico* studies were based on different approaches of molecular modeling aimed to deepen the knowledge about the ligand-protein interaction in order to obtain the highest efficacy *in vitro*. This study allow to optimize the structure of these compounds and to design and discover new promising antimalarial drugs.

PRELIMINARY DATA ON THE MODULATORY EFFECTS OF DIFFERENT PLANT EXTRACTS ON JELLYFISH VENOM

Gian Luigi Mariottini^{1*}, Laura Cornara^{1,2}, Paolo Giordani³, Antonella Smeriglio⁴, Domenico Trombetta⁴, Lucrezia Guida⁵, Silvia Lavorano⁶, Bruno Burlando^{2,3}

¹Department of Earth, Environment and Life Sciences (DISTAV), University of Genova, Genova, Italy; ²Biophysics Institute, National Research Council (CNR), Genova, Italy; ³Department of Pharmacy (DIFAR), University of Genova, Genova, Italy; ⁴Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Messina, Italy; ⁵Department of Experimental Medicine (DIMES), Section of Biochemistry, University of Genova, Genova, Italy; ⁶Acquario di Genova, Area Porto Antico, Ponte Spinola, Genova, Italy

*E-mail: Gian.Luigi.Mariottini@unige.it

Jellyfish are toxic sea organisms representing a health issue for both recreational and occupational activities. Given that herbal products are attracting increasing interest, we examined plant extracts from *Carica papaya* L., *Ananas comosus* (L.) Merr., and *Bouvardia ternifolia* (Cav.) Schltdl., known for protective properties against different animal venoms. The interference of these extracts with the toxicity of tissue homogenates from the jellyfish *Pelagia noctiluca*, *Phyllorhiza punctata*, and *Cassiopea andromeda*, were evaluated on L929 mouse fibroblasts, used as an *in vitro* skin cell model. The quantification of jellyfish cytotoxicity was achieved by MTT cell viability assays, deriving dose response curves and IC_{50} values. Each of the extracts of *C. papaya* and *A. comosus* significantly lowered the cytotoxicity of *P. noctiluca* and *P. punctata*, but enhanced the toxic effect of *C. andromeda*. The extract of *B. ternifolia* reduced *P. punctata* cytotoxicity, showed no effect against *P. noctiluca*, and increased *C. andromeda* cytotoxicity. In summary, the modulatory effects of plant extracts on jellyfish homogenates cytotoxicity resulted to be species-specific, showing either protective or worsening effects. More specifically, extracts with protease activities, like *A. comosus* and *C. papaya*, seem to protect from jellyfish with toxic peptides like phospholipase A.

EXTREMOPHILES ORGANISMS AS VALUABLE SOURCE OF RADICAL SCAVENGERS: APPLICATIONS IN THE BLUE-BIOTECHNOLOGIES

Concetta M. Messina^{1*}, Massimo Cocchi², Andrea Santulli^{1,3}

¹University of Palermo, Department of Earth and Sea Science,

Laboratory of Marine Biochemistry and Ecotoxicology, Trapani, Italy; ²University of Bologna, Department of Veterinary Sciences, Bologna, Italy; ³Consorzio Universitario della Provincia di Trapani, Marine Biology Institute, Trapani, Italy

*E-mail: concetta.messina@unipa.it

A significant contribution to the discovery of new bioactive molecules was given by the study of species that have adapted to live in extreme environments, such as acidophilous organisms, halophilic, cryophilic and thermophilic. These are microorganisms that have developed unique physiological characteristics, which allow them to survive extreme physical and chemical conditions, such as high temperatures, high salt concentrations or extreme pH levels and therefore, can adapt itself and can proliferate in environments recognized as inhospitable to life. This is possible, because they are specialized to produce, in a modulated way, molecules that allow them to adapt to changes in the chemical-physical conditions of the environment. A large part of these microorganisms belongs to the domain of the Archea, ancestral bacteria that represent a considerable fraction of the prokaryotic world in terrestrial and marine ecosystems; their unusual properties make them a potentially valuable resource in the development of new biotechnological processes and industrial applications such as new pharmaceuticals, cosmetics, food supplements, molecular probes and enzymes.

HYPERGLYCEMIA AFFECTS ANION EXCHANGE THROUGH BAND 3 PROTEIN: AN IN VITRO AND IN VIVO STUDY ON HUMAN ERYTHROCYTES

Rossana Morabito^{1*}, Alessia Remigante^{1,2}, Saverio Loddo³, Vincenzo Trichilo³, Silvia Dossena², Angela Marino¹

¹Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Messina, Italy; ²Institute of Pharmacology and Toxicology, Paracelsus Medical University, Salzburg, Austria; ³Department of Clinical and Experimental Medicine, AOU Policlinico Universitario G. Martino, Messina, Italy

*E-mail: rmorabito@unime.it

Band 3 protein (B3p) accounts for erythrocytes homeostasis, namely ion balance, gas exchange and membrane deformability. In the present investigation, the effect of hyperglycemia, related to metabolic dysfunctions, has been evaluated on erythrocytes *in vitro* exposed to increasing concentrations of glucose (5-15-35-50 mM) for different time intervals (3-24 h) as well as on erythrocytes from patients with high glycated hemoglobin (HbA1c) levels. The rate constant for SO_4^{2-} uptake, accounting for the efficiency of anion exchange through B3p, along with levels of MDA, GSH, -membrane -SH groups and osmotic fragility have been measured. The incubation with high glucose concentrations (15-35 mM) for 24 h exacerbated osmotic fragility, compromising the measurement of anion exchange through B3p. When erythrocytes were exposed to high glucose for 3 h, being MDA, GSH and membrane -SH levels unchanged, SO_4^{2-} trapped by the cells was significantly reduced with respect to control (5 mM). Under high HbA1c levels, the rate constant was higher than control and SO_4^{2-} content higher than both control and high glucose-treated erythrocytes. The present findings show that: i) measurement of the rate constant for SO_4^{2-} uptake is a suitable tool to monitor the effect of hyperglycemia on erythrocytes; ii) hyperglycemia due to high glucose applied for 3 h affects anion exchange capability without producing lipid peroxidation; iii) high HbA1c levels seem to accelerate anion exchange capability through B3p. Future studies will evaluate whether this acceleration depends on an altered Bp3 conformation, affecting crosslink with Hb, or on altered phosphorylative signaling underlying B3p function.