

Human and Mosquito Lysozymes in Malaria: Old Molecules for New Approaches towards Diagnosis, Therapy and Vector Control

Mauro Prato^{1,2*}

¹Dipartimento di Genetica, Biologia e Biochimica, Università di Torino, Torino, Italy

²Dipartimento di Neuroscienze, Università di Torino, Torino, Italy

As a consequence of the global eradication program recently launched by charity foundations [1], World Health Organization (WHO) officially registered in 2010 a decline in estimated malaria cases and deaths, with 655,000 deaths counted among more than 200 million clinical cases worldwide, of which 91% due to *Plasmodium falciparum* [2]. Nevertheless, malaria remains so far an alarming emergency in developing countries, as the vast majority of cases occur in Africa (81%) and South-East Asia (13%) [2]. Thus, it appears still urgent to identify any parasite or host molecules which might serve as new affordable markers for early diagnosis of malaria complications [3], or as new targets for primary and adjuvant therapy [4] along with vector control [5].

In this context, lysozymes could be good candidate molecules. These enzymes are antibacterial proteins defined by their ability to hydrolyze β -1,4-glycosidic linkage between N-acetylmuramic acid and N-acetylglucosamine of peptidoglycan in the cell wall of bacteria (muramidase activity) [6]. Three major distinct lysozyme types showing high level of homology have been identified in the animal kingdom: c-type (chicken-type), present in several members of the Chordata, including humans, and different classes of the Arthropoda, including mosquitoes; g-type (goose-type), in few members of the Chordata and in some bivalve mollusks; and i-type (invertebrate-type), in the invertebrates [6]. Human lysozyme was the first mammalian lysozyme to be sequenced and served as a model protein for a wide variety of studies [7]. Interestingly, in the recent years the involvement of both human and mosquito lysozymes in malaria has been observed independently by several research groups.

Natural haemozoin (nHZ, malarial pigment), a lipid-bound ferriprotoporphyrin IX crystal produced by *Plasmodium* parasites after haemoglobin catabolism, was shown to promote *in vitro* the early release of human lysozyme from adherent monocytes [8]. Such an effect was mediated by the increased production of three pro-inflammatory molecules (TNF α , IL-1 β and MIP-1 α /CCL3), and was dependent on activation of p38 mitogen-associated protein kinase (MAPK) and NF- κ B pathways [9]. Moreover, 15-hydroxyeicosatetraenoic acid (15-HETE), a major component of the lipid moiety of nHZ, was identified very recently as the molecule responsible for the most part of these effects [10].

Consistently, the plasma levels of lysozyme [11] and the number of nHZ-containing leukocytes in the peripheral blood of *P. falciparum*-infected patients [12-14] correlated well with parasitaemia degree or disease severity. On the other hand, the mosquito homologue of human lysozyme was shown to bind to oocysts of *Plasmodium berghei* and *falciparum* in *Anopheles gambiae*, *stephensi*, and *dirus*, and therefore facilitate their development within the vector [15,16].

These findings suggest that human lysozyme may represent a likely marker for early diagnosis of complicated malaria as well as a putative target for adjuvant therapy, whereas mosquito lysozyme could be addressed as a new target for insecticides to be used in vector control. Although further investigation is certainly required, it is intriguingly to

speculate that old well-known enzymes such as lysozymes might reveal themselves as very relevant molecules to be targeted by innovative and cost-effective tools to fight malaria.

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***Corresponding author:** Mauro Prato, Dipartimento di Neuroscienze, Università di Torino, Corso Raffaello 30, 10125, Torino, Italy, Tel: +39-011-6708198; Fax: +39-011-6708174; E-mail: mauro.prato@unito.it

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