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Biodiversity of chloroquine resistance transporter

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Abstract. The bioinformatic analysis of chloroquine resistance transporter (PFCRT) was provided. The protozoan are concerned to be such organisms the influence of chlorine on which is potentially inefficient.

Key words: Chloroquine Resistance Transporter (PfCRT), biodiversity, alighment, malaria parasites.

The spread and emergence of chloroquine-resistant *Plasmodium falciparum* malaria parasites has become a disaster for world health level. Resistance is conferred by mutations in the Chloroquine Resistance Transporter (PfCRT), a membrane protein of the protozoan internal digestive vacuole. These mutations cause the accumulation of chloroquine (CQ) by the protozoa. The mechanism by which this occurs is unknown. In [1] there has been detected resistant forms and wild-type of PfCRT at the surface of *Xenopus laevis* oocytes. It was shown that the resistant form of PfCRT transported CQ, whereas the wild-type protein did not. CQ transport via the mutant PfCRT was inhibited by the resistance-reverser verapamil. Thus, CQ resistance is suspected to direct transport of the chemical substances via mutant form of PfCRT.

Antimalarial drugs (e.g. chloroquine and its analogues) were developed primarily to treat malaria disease; however, they are beneficial for many infectious diseases, for which they are used mostly in modern medicine [2]. Chloroquine and hydroxychloroquine, two of the most fascinating drugs, are increasingly recognized

for their effectiveness in non-malarial diseases. In [2], chloroquine and hydroxychloroquine have been shown to have immunomodulatory and immunosuppressive effects, and currently have established roles in the management of rheumatic diseases [2]. Recently, chloroquine analogues have also been found to have antithrombotic, cardiovascular, antineoplastic and metabolic effects.

The aim of this study was to detect the organisms which contain Chloroquine Resistance Transporter and thus the effect of antimalarial drugs including chlorine on which can be potentially inefficient.

Materials and methods. Alignment was performed using protein sequences of the Chloroquine Resistance Transporter (PfCRT) of *Plasmodium* obtained from National centre of Biothechnology Information via program ―BLASTP 2.2.32+‖ [3] The dendrogram tree was produced using BLASTp progfame. BLASTp computes a pairwise alignment between a query and the database amino acid sequences searched. It does not explicitly compute an alignment between the different database sequences. For purposes of this sequence tree presentation an implicit alignment between the database sequences is constructed, based upon the alignment of those (database) sequences to the query. It may often occur that two database sequences align to different parts of the query, so that they barely overlap each other or do not overlap at all. In that case it is not possible to calculate a distance between these two sequences and only the higher scoring sequence is included in the tree [4].

Results. Results of research are presented in Fig. 1.

Conclusions. According to bioinformatic analysis of chloroquine resistance transporter (PFCRT) the organisms *Plasmodium falciparum*, *Plasmodium fragile*, *Plasmodium reichenowi*, *Plasmodium vivax*, *Plasmodium cynomolgi*, *Plasmodium yoelii*, *Plasmodium berghei*, *Plasmodium vinckei*, *Toxoplasma gondii* are concerned as such the influence of chlorine on which is potentially inefficient.

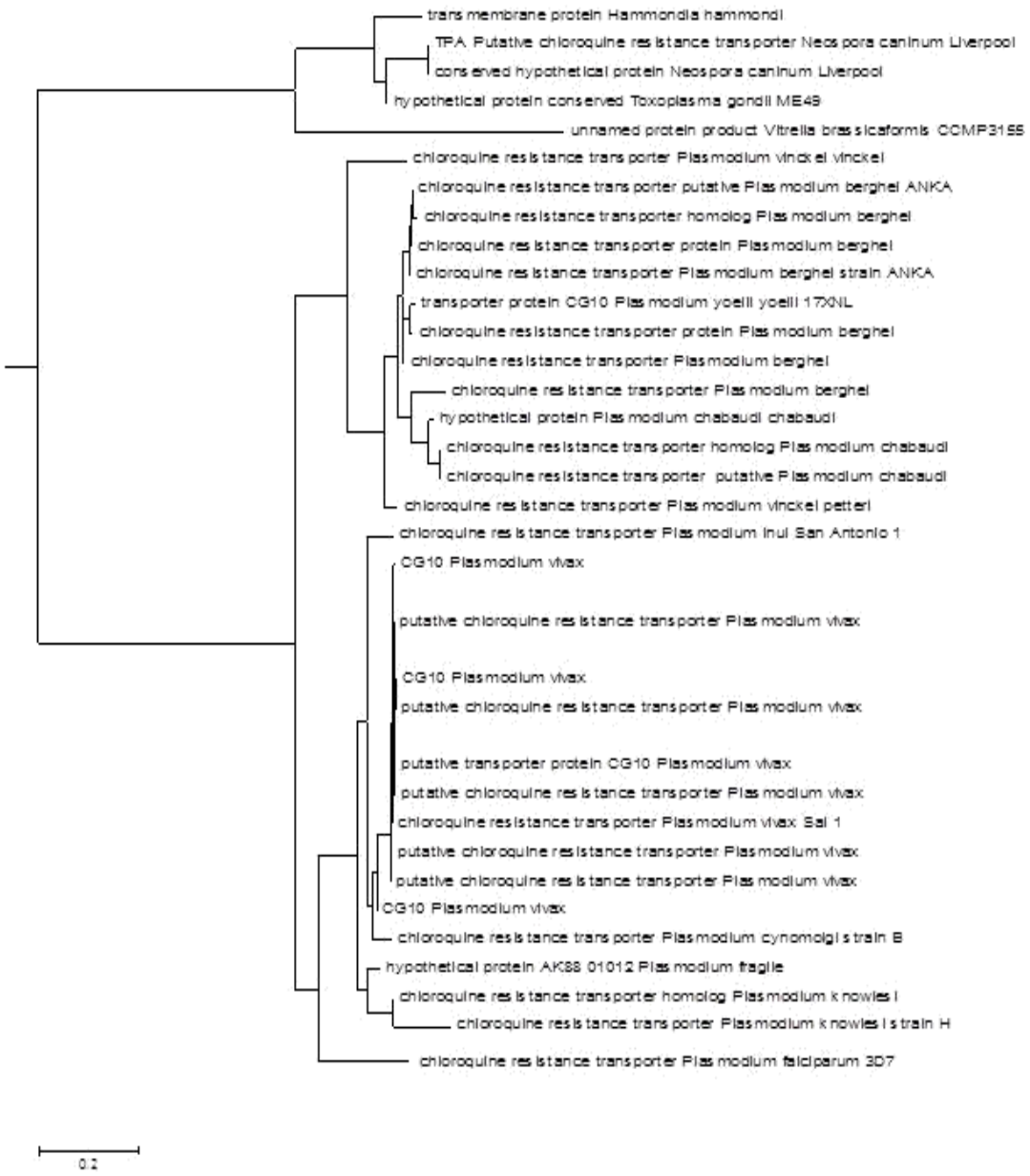

Fig. 1. Clustering dendrogram constructed on the basis of alignment of Chloroquine Resistance Transporter (PfCRT)

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