Poster

Investigation of the molecular architecture of *Candida auris* ribosome

A. Atamas[1], D. Incarnato[1], A. Stetsenko[1], S. Billerbeck[1], A. Guskov[1]

[1]Groningen Biomolecular Sciences and Biotechnology Institute (GBB), University of Groningen, Groningen, 9747 AG, the Netherlands

a.atamas@rug.nl

Candida auris has emerged as a significant pathogen due to its increased resistance to antimicrobial agents, warranting heightened attention in the medical community [1]. Developing effective strategies to combat this pathogen necessitates a profound understanding of its molecular biology, including the intricacies of its genetic machinery. The exceptional drug resistance observed in *C. auris* might be partially attributed to distinctive characteristics inherent in its ribosomal configuration. Presently, investigations are scrutinizing the translational responses of *C. auris* to antifungal agents [2], yet studies specifically dedicated to ribosomal structure in this context are insufficient.

The study of ribosomes holds great promise in many regards. Ribosomes serve as a major target for numerous antibiotics and antifungal drugs. Moreover, delving into ribosome studies may provide insights into the evolutionary trajectory and genetic adaptations of this pathogen, which is crucial for a comprehensive understanding of its prevalence and adaptability in different environments.

Ribosomal RNA (rRNA) plays a pivotal role in protein synthesis, constituting an integral component of the ribosome. The difference in rRNA from one organism to another is the appearance of additional sites, such as extension segments. It is assumed that such features emerged to perform specialized functions [3]. In addition, the study of ribosome proteins is of great importance in understanding various aspects of protein synthesis and cellular function. For example, the study of the features of the ribosome of *C. albicans* showed some changes in the ribosomal protein eL42 that lead to resistance of this pathogen to cycloheximide [4]. In our previous work, we investigated the *C. albicans* ribosome and the specifics of its interaction with the emetine analog cephaeline [5].

In this study, we have investigated the structure of the *C. auris* ribosome using rRNA sequence sequencing data as well as bioinformatic and structural analyses. The structure of the ribosome was elucidated using single particle cryo-electron microscopy (cryo-EM), providing high-resolution insight into its architecture and potential functional features. Our study will help to reveal new aspects of molecular adaptation of *C. auris* and may serve as a basis for the development of new therapeutic and preventive measures against infections caused by this pathogen.

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