https://doi.org/10.17816/ecogen568129

Identifying novel amyloid candidates using bioinformatics algorithms and a yeast model approach

Andrew A. Zelinsky, Aleksandr A. Rubel, Marina V. Ryabinina

Saint Petersburg State University, Saint Petersburg, Russia

Amyloids are protein aggregates characterized by their insolubility in detergents and ability to form fibrils. They are often associated with various diseases, including neurodegenerative disorders, type 2 diabetes and certain forms of cancer. Amyloids also play important roles in bacteria and different physiological processes in both lower and higher eukaryotes.

Together with the laboratory of Prof. Y.O. Chernoff we have developed a comprehensive approach for screening new potentially amyloidogenic proteins. This involves using bioinformatics algorithms to predict protein amyloidogenicity and further verifying using a yeast model. We have created a yeast test system specifically designed to study changes in phenotype in genetically modified *Saccharomyces cerevisiae* strains [1]. This system involves the production of recombinant amyloidogenic proteins fused with reporter proteins Sup35N or YFP. Using yeast assay, we have investigated 22 human proteins that were predicted to be amyloidogenic by ArchCandy algorithm [2]. Currently, additional *in vitro* biochemical tests are underway with proteins that have shown the potential to form amyloids in yeast models. There are also plans to evaluate the amyloid-forming ability of specific human proteins in mammalian cell cultures. These various approaches appear to be enhancing our comprehension of the impact of amyloid formation in health and disease.

This research was funded by Russian Science Foundation (grant 20-14-00148-П).

Keywords: amyloids; bioinformatics; yeasts.

REFERENCES

1. Chandramowlishwaran P, Sun M, Casey KL, et al. Mammalian amyloidogenic proteins promote prion nucleation in yeast. *J Biol Chem*. 2018;293(9):3436–3450. DOI: 10.1074/jbc.m117.809004

2. Ahmed AB, Znassi N, Château M-T, Kajava AV., et al. A structure-based approach to predict predisposition to amyloidosis. *Alzheimer's & Dementia*. 2014;11(6):681–690. DOI: 10.1016/j.jalz.2014.06.007

AUTHORS' INFO

Andrew A. Zelinsky, M. Sci. (Biol.), Researcher, Laboratory of Amyloid Biology; Saint Petersburg State University, Saint Petersburg, Russia; ORCID: 0000-0003-2068-3024; eLibrary SPIN: 5832-1192; e-mail: andrew_zelinsky@mail.ru

Aleksandr A. Rubel, Dr. Sci. (Biol.), Head, Laboratory of Amyloid Biology; Saint Petersburg State University, Saint Petersburg, Russia; ORCID: 0000-0001-6203-2006; eLibrary SPIN: 3961-4690; e-mail: arubel@mail.ru

Marina V. Ryabinina, B. Sci. (Biol.), Laboratory Assistant, Laboratory of Amyloid Biology; Saint Petersburg State University, Saint Petersburg, Russia; ORCID: 0000-0002-5504-7362; eLibrary SPIN: 7113-6941; e-mail: marina.v1205@gmail.com