

Application of genetically modified microorganisms for potential human amyloids search

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Amyloids are fibrous protein structures often found in patients with severe diseases, such as Alzheimer's, Parkinson's diseases etc. A number of studies have shown that the production of heterologous amyloidogenic proteins in *Saccharomyces cerevisiae* strains results in formation of amyloid aggregates with properties similar to those found in mammals.

Amyloid aggregates formed in yeasts usually do not have their own phenotypic manifestation. To assess amyloidogenic potential of individual proteins a yeast test-system was developed under supervision of Prof. Y.O. Chernoff. The system is based on usage of genetically modified *S. cerevisiae* cells auxotrophic for certain growth factors, allowing effective phenotypic selection to search for amyloidogenic proteins within proteomes of various organisms [1]. Using this test-system, our laboratory evaluated amyloid potential of a spectrum of human proteins, the amyloidogenicity of which was previously predicted by bioinformatics algorithms. The proteins that have shown amyloidogenic potential in yeast-based model are being currently tested *in vitro* and *in vivo*. Some mutant *Escherichia coli* strains can be applied for studying propensity of heterologous proteins to form amyloids *in vitro*. Thus, application of genetically modified microorganisms makes it possible to identify new human amyloidogenic proteins and to improve predictive ability of bioinformatics algorithms.

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REFERENCE

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