

CONSERVATIVE AMYLOIDOGENIC REGIONS IN NUCLEOPORINS WITH FG REPEATS

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Amyloids are a group of protein aggregates possessing a set of unusual features. Many functional amyloids required for different biological processes have been discovered. In these cases, protein aggregation seems to be beneficial for an organism. Therefore, this property might be conservative for orthologous proteins. At least one known example supports this hypothesis. The amyloid aggregates of the CPEB protein were suggested to play an important role in the long-term memory formation in *Aplysia californica*, *Drosophila melanogaster*, and *Mus musculus*. We suppose that the list of functional amyloid candidates can be extended with orthologous proteins which possess conservative regions with amyloid properties. A perspective example is nucleoporins with FG-repeats. For several of them from different species were demonstrated amyloid properties. We speculate that this feature may be common for the whole protein family. Nup49, Nup57, Nup100, Nup145, and Nsp1 are the most abundant proteins with FG-repeats in the yeast nuclear pore complex. For each of these nucleoporins, we retrieved at least 170 orthologous sequences of different Opisthokonta species from the EggNOG database. Further, we analyzed them with the ArchCandy program in combination with the IUPred tool to find unstructured aggregate-prone regions. According to the results, almost all orthologs of investigated nucleoporins can potentially form amyloids. We aligned protein sequences of the nucleoporin orthologs and assigned amyloidogenic scores to the alignment positions to find conservative aggregation-prone regions. Such fragments were found in Nup49, Nup57, and Nup145 proteins, and their orthologs, but not in Nup100 and Nsp1. Thus, we suggest that only three nucleoporins with FG-repeats possess conservative amyloid regions, which might reflect the potential functional role of their aggregation. The research was supported by the RFBR grant 20-34-70073.