DETERMINANTS OF INTRACELLULAR LOCALISATION OF NATIVE SACCHAROMYCES CEREVISIAE VIRUSES

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Saccharomyces cerevisiae yeast are widely used in many industrial and scientific fields. Many natural and laboratory yeast strains contain native viruses which belong to *Totiviridae* family [1], including the satellite virus M and helper viruses ScV-LA (L-A) and ScV-LBC (L-BC). Totiviruses replicate inside of host cell and are only transmitted during reproduction and sporogenesis, therefore no extracellular state is detected [2]. Co-existence of M and L-A viruses determines the biocidal activity of yeast. However, it is often implied, that L-A (or L-BC) on its own has no significant impact on host cells [3]. Yet more detailed studies on native yeast viruses are relevant in order to assess their impact on yeast more accurately.

The aim of this research is to study localisation patterns and establish localisation determinants of native *S. cerevisiae* viruses. For this purpose, fluorescent proteins were used to mark endoplasmic reticulum of *S. cerevisiae* and Gag proteins of Totivirus capsid. Fluorescence microscopy demonstrated different localisation of L-A and L-BC viruses: L-A is found in nucleus, while L-BC is spread throughout cytosol. Although the structures of these viruses are very similar, some previous research suggest that the C terminal domain of L-A virus protein might determine the translocation to nucleus of host cell [4]. In addition, plasmids were constructed differing by -1 ribosomal frameshift, which is necessary for fused Gag-Pol viral protein synthesis. Different interactions with native viruses were observed: when proteins are translated without ribosomal frameshift, native L-A viruses are eliminated. Meanwhile, synthesis of full-length protein does not interfere with the replication of native L-A virus. Further research will be continued regarding the topic of localisation of native viruses in different strains of *S. cerevisiae* yeast, as well as determinants of localisation of these viruses.

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