Characterisation of putative potassium channel proteins from *Chlorella* Viruses

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Viruses can be considered as an interesting source of proteins with robust function and minimal size. Examples of such a minimal design are ion channels, which are now found in an increasing number of viruses including the influenza viruses A, B and C, HIV and many others.

Bioinformatic analysis of the three *Chlorella* Viruses PBCV-1, ATCV-1, MT325 and NY-2A proteome (Fitzgerald et al. 2007a-c) identified three open reading frames (ORFs) A201L, A621L and A624L, which encode for putative transmembrane proteins with some hallmarks of K\(^+\) channels. I tested possible K\(^+\) channel function of the A201L homologs and the A621L homolog z688R of the ATCV-1 Virus in yeast growth assays. These assay systems showed negative results. Therfore the heterologous expression of the proteins did not rescue growth of yeast mutants with defect K\(^+\) uptake systems. Furthermore an expression of the protein in HEK293 cells also revealed no clear-cut evidence for a conductance of the viral proteins in patch clamp studies.

An interesting side aspect of this work was related to the observation that z688R of the ATCV-1 Virus, which shows high similarity of the Kcv like protein from virus NY-2B, exhibited peculiar sorting in HEK293 cells. This protein was found to accumulate in donut like structures. They seem to be endoplasmic reticulum (ER) generated protein depots, which lead in combination with autophagosome formation to ER-associated protein degradation (Korkhov, 2009). Colocalisation studies with the autophagosome markerprotein microtubule-associated protein1 light chain 3 beta (LC3) suggests that the protein structure of z688R may contain information for the sorting of membrane proteins into autophagosomes.


