Comparative proteome bioinformatics of VAMP subfamilies

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Complete sequencing of model genomes has allowed to infer whole proteome sequences, hence to perform comparative analyses of regulatory systems among different kingdoms, phyla or species. Regulation of protein trafficking is a central theme in eukaryote cell biology and it is well-known that coiled-coil SNARE domains play a crucial role in mediating membrane fusion. Coiled-coil SNARE domains seem to have a common ancestor as they show a conserved hydrophobic heptad register and a specific polar residue, distinguishing Q- and R-SNAREs. However, slight differences in the local distribution of hydrophobic and polar residues, as well as differences in the steric hindrance i.e. the presence of a small or bulky residue - even when belonging to the same class - at a certain position, may regulate interaction specificity. In addition to coiled-coil domains, the SNARE proteins show extra domains which are likely to regulate the formation and/or disassembly of the fusion complex. In fact, syntaxins show a three-helical N-terminal HAHBHC domain which is able to regulate their capacity to contibute to the formation of a fusion complex, inhibiting intermolecular interactions by intramolecular binding to the coiled-coil Q-SNARE domain.
We have recently identified in VAMPs a novel SNARE domain which is possibly crucial to the regulation of membrane fusion. VAMPs sharing such domain represent a new VAMP subfamily more conserved among eukaryotes than classic VAMPs. Analysis in silico of both the coiled-coil and novel SNARE domains in VAMPs from different eukaryotes shows that the variation in sequences and in the representativeness of each subfamily might depend on special mechanisms and roles in the regulation of cell trafficking. In particular, animals (including humans) and plants show a really different representativeness of VAMPs with or without the novel domain, whose variation is ensured in the two kingdoms by different strategies.