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Carbon Based Classification of Aquaporin Proteins: A New Proposal

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Abstract : Major Intrinsic proteins (MIPs), actively involved in the passive transport of small polar molecules across the membranes of almost all living organisms. MIPs that specifically transport water molecules are named aquaporins (AQPs). The permeability of membranes is actively controlled by the regulation of the amount of different MIPs present but also in some cases by phosphorylation and dephosphorylation of the channel. Based on sequence similarity, MIPs have been classified into many categories. All of the proteins are made up of the 20 amino acids, the only difference is there in their orientations. Again all the 20 amino acids are made up of the basic five elements namely: carbon, hydrogen, oxygen, sulphur and nitrogen. These elements are responsible for giving the amino acids the properties of hydrophilicity/hydrophobicity which play an important role in protein interactions. The hydrophobic amino acids characteristically have greater number of carbon atoms as carbon is the main element which contributes to hydrophobic interactions in proteins. It is observed that the carbon level of proteins in different species is different. In the present work, we have taken a sample set of 150 aquaporins proteins from Uniprot database and a dynamic programming code was written to calculate the carbon percentage for each sequence. This carbon percentage was further used to barcode the aqauporins of animals and plants. The protein taken from Oryza sativa, Zea mays and Arabidopsis thaliana preferred to have carbon percentage of 31.8 to 35, whereas on the other hand sequences taken from Mus musculus, Saccharomyces cerevisiae, Homo sapiens, Bos Taurus, and Rattus norvegicus preferred to have carbon percentage of 31 to 33.7. This clearly demarks the carbon range in the aquaporin proteins from plant and animal origin. Hence the atom level analysis of protein sequences can provide us with better results as compared to the residue level comparison.

Keywords : aquaporins, carbon, dynamic prgramming, MIPs
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