

P004 Characterization of the N-terminal segment used by the barley yellow dwarf virus movement protein

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The N-terminal sequence of the Barley Yellow Dwarf virus movement protein (BYDV-MP) is known to promote the transport of viral RNA into the nuclear compartment of host plant cells. Here, graphical analysis predicts that this sequence would form a membrane interactive amphiphilic α -helix. Confirming this prediction, NT1, a peptide homologue of the BYDV-MP N-terminal sequence, was found to be α -helical in the presence of vesicles mimics of the nuclear membrane (65%). The peptide increased the fluidity of these nuclear membrane mimics (rise in wavenumber of *circa* $0.5 \text{ cm}^{-1} - 1.0 \text{ cm}^{-1}$) and induced surface pressure changes of 2 mN m^{-1} in lipid monolayers with corresponding compositions. Thermodynamic analysis showed that the peptide stabilized the lipid organization of the monolayers, changing their Gibbs free energy (ΔG_{Mix}), interaction parameter (α) and enthalpy of mixing (ΔH) from positive to negative. In combination, these data strongly suggest that BYDV-MP forms an N-terminal amphiphilic α -helix, which partitions into the nuclear membrane primarily through thermodynamically stable associations with the membrane lipid headgroup region. It is suggested that the N-terminal sequence of BYDM-MP may play a role in targeting its parent protein to the nuclear membrane.