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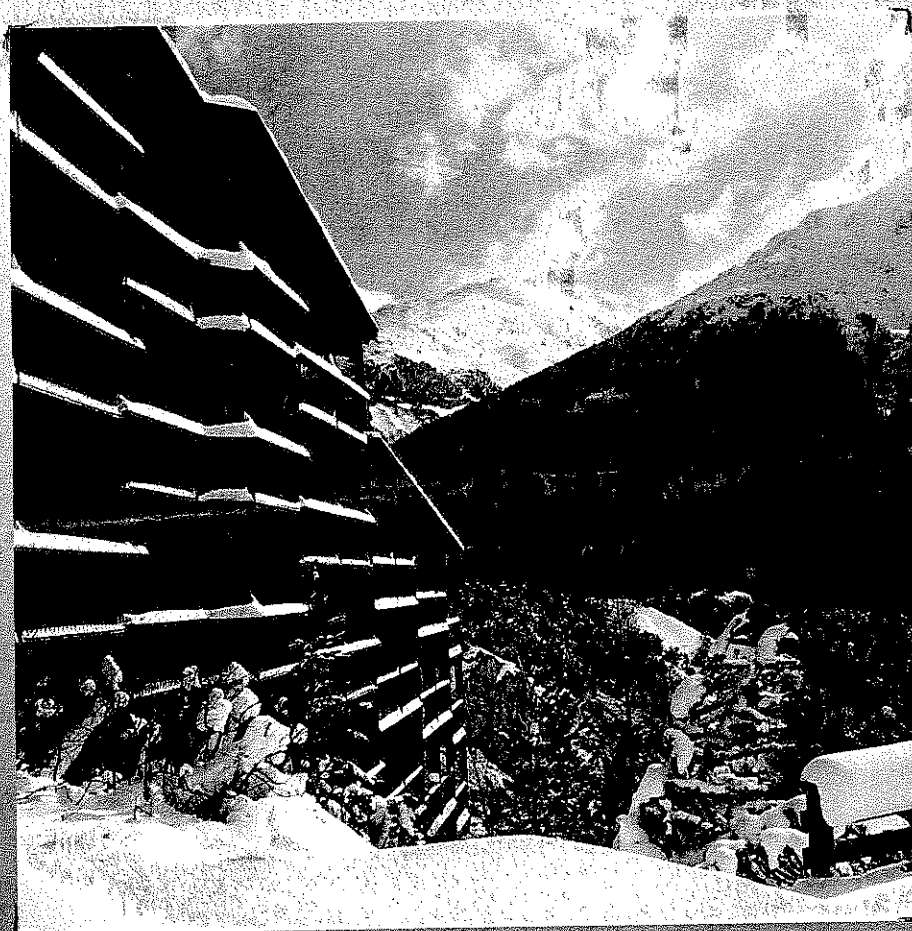
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13^{èmes} rencontres de virologie végétale



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53- Structural disorder in plant virus proteins

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The structure-to-function paradigm has changed with the discovery of intrinsically (or natively) disordered domains in proteins. By contrast to the vast majority of globular proteins, intrinsically disordered proteins (IDP) do not fold as a unique 3D structure. Under physiological conditions, IDPs exist as a dynamic ensemble of conformations containing no or only few secondary structure elements (helices and sheets). About 50% of the proteins coded by higher eukaryotes genomes are predicted to contain disordered domains ((Dunker et al. 2008).). Many of them are involved in cellular regulation processes requiring their interaction with several different partners. Structural disorder is likely to allow the surface plasticity necessary to this multi-partnership. Interestingly many proteins encoded by animal RNA viruses are also predicted to be rich in disordered domains. For instance, there are strong experimental evidences that the measles virus N-tail intrinsic disorder is associated with multipartners interactions, (Bourhis et al. 2004). Up to now, intrinsic disorder has been poorly investigated in plant viruses. VPgs are the only exception to date. VPgs are proteins linked to the 5' end of the genome of many plant and animal RNA viruses. Although sharing this common feature, VPgs are highly diverse in size, sequence and function. They are involved in key steps of the viral cycle such as genome replication, protein translation and viral movement in plant hosts (Sadowy et al. 2001). Using several disorder predictors, we showed that *Lettuce mosaic virus* (LMV) and *Rice yellow mottle virus* (RYMV) VPgs are predicted to possess disordered regions. We next extended these results to 14 VPgs representative of the viral diversity. Disordered regions were predicted in all VPg sequences whatever the genus and the family suggesting that intrinsic disorder is a common feature of VPgs (Hébrard et al, 2009). We will show that intrinsic disorder is also predicted in other major proteins of several phytoviral species.

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