Identification and classification of potyviruses on the basis of coat protein sequence data and serology

Brief Review

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Summary. The identification and classification of potyviruses has been in a very unsatisfactory state due to the large size of the group, the apparent vast variation among the members and the lack of satisfactory taxonomic parameters that will distinguish distinct viruses from strains. In the past, use of classical methods, such as host range and symptomatology, cross-protection, morphology of cytoplasmic inclusions and conventional serology, revealed a "continuum" implying that the "species" and "strain" concepts cannot be applied to potyviruses. In contrast, nucleic acid and amino acid sequence data of coat proteins has clearly demonstrated that potyviruses can be divided into distinct members and strains. This sequence data in combination with information of the structure of the potyvirus particle has been used to develop simple techniques such as HPLC peptide profiling, serology (using polyclonal antibody probes obtained by cross-adsorption with core protein from trypsin treated particles) and cDNA hybridization. These findings, along with immunochemical analyses of overlapping synthetic peptides have established the molecular basis for potyvirus serology; explained many of the problems associated with the application of conventional serology; and provided a sound basis for the identification and classification of potyviruses. As a result, the virus/strain status of some potyviruses has been redefined, requiring a change in the potyvirus nomenclature. These new developments necessitate a re-evaluation of the earlier literature on symptomatology, cross-protection, cytoplasmic inclusion body morphology and serology.

Introduction

The potyvirus group is the largest and economically most important of the 28 plant virus groups and families currently recognized [67]. The potyvirus group was established in 1959 as one of the plant virus groups with elongated particles...
At that time the number of viruses recognized in the group was only 14. Since then a large number of new members have been discovered and added to the list of potyviruses to make it the most rapidly growing of all the plant virus groups [30]. By 1971 the number of potyviruses had increased to 25 [106], by 1976 to 45 [28], by 1979 to 73 [65], by 1982 to 115 [67], by 1985 to 152 [30], and by 1988 to 175 [49, 54, 59, 60, 70, 82, 92, 96, 99].

Although it has been suggested that many viruses included in the group may be synonymous [29], recent molecular analysis reveals that the number of distinct viruses being recognized is increasing much faster than the number of recognized synonyms. Thus, while pepper mottle virus (PeMV) appears to be a strain of potato virus Y (PVY) [86] and the N strain of soybean mosaic virus (SMV-N) a strain of watermelon mosaic virus 2 (WMV 2) [31, 109], sugarcane mosaic virus (SCMV) and SMV have each been shown to consist of four distinct potyviruses [82, 92, unpubl. results] and bean yellow mosaic virus (BYMV) strains to consist of more than one distinct virus [41, 96]. Thus, it appears that the number of distinct potyviruses recognized is going to increase dramatically. While the present 175 definitive and possible members account for about 30% of all known plant viruses, we believe that this figure may increase to 50% once the strains of many of the potyviruses are properly characterized, particularly those infecting legumes [7, 10, 16, 51, 58, 98].

Most potyviruses have narrow, often extremely restricted host ranges. They flourish in a wide range of crops and environmental conditions [46, 47]. In 1974 they were reported to infect 1,112 species of 369 genera in 53 plant families [23]. Since then many more species, genera and families would have been added as hosts of potyviruses. Their economic importance is highlighted by the fact that, in a recent survey of the ten most important filamentous viruses from each of the ten major world regions, 73% were potyviruses [70].

Definitive potyviruses are transmitted in the non-persistent manner by many aphid species while some possible members have fungus, mite or whitefly vectors. Definitive and possible members of the group investigated so far have all been found to induce characteristic “pinwheel” cytoplasmic inclusion bodies in infected plant cells [46, 47].

Potyvirus particles are flexuous rods, 680–900 nm long and 11 nm wide, consisting of a single protein species of $M_r$ ranging from 30,000 to 37,000 and a single molecular of ssRNA of $M_r$ 3.0 × $10^6$ to 3.5 × $10^6$ [46]. For a detailed description of the structure of potyvirus particles and their coat proteins, see Shukla and Ward [83] and for genome organization and function, see Dougherty and Carrington [19].

It has been repeatedly pointed out by taxonomists and reviewers that the taxonomy of the potyvirus group is in a very unsatisfactory state and that successful resolution of potyvirus taxonomy presents a major challenge for plant virologists [30, 42, 46, 47] that would have tested Linnaeus [70]. The current unsatisfactory state of potyvirus taxonomy has been due to the large size of the group, the apparent vast variation among the members and the lack