

P11**Epidemiology of *Alfalfa mosaic virus* (AMV) in Spain: its incidence and effects in lucerne and genetic diversity of populations from different hosts**

María Bergua, María Elena Vargas-Mainar, Marisol Luis-Arteaga, Fernando Muñoz, Fernando Escriu

Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), 50080 Zaragoza, Spain

Alfalfa mosaic virus (AMV, *Alfamovirus*, *Bromoviridae*) is widespread all over the world on its main natural host, lucerne. It may be transmitted through lucerne seeds and by at least 15 aphid species in a non-persistent manner to more than 150 natural hosts, including some vegetable crops of economic importance, like tomato or pepper. In spite of its high potential of spreading there is little information on the epidemiology of this virus, particularly in Spain, which holds the third position in the ranking of lucerne production of the European Community, with an important fodder-dehydration industry. Local lucerne-ecotypes are cultivated in Spain, for which the incidence and the impact of AMV infection are not known. We report on three aspects of the epidemiology of AMV in Spain: the incidence of AMV in lucerne crops, the effects of AMV infection on the yield and quality of fodder, and the variability and genetic structure of AMV populations from different hosts.

AMV incidence were studied in two different ecological areas of lucerne cultivation and varied between 10 to 87%, in average, increasing with the age of fields at different rates for each ecological area. Analysis of data suggested that differences in incidence within each area were mainly determined by initial rates of seed infection. Effects of AMV infection on the yield and quality components of fodder were assayed in four Spanish lucerne-ecotypes. A variable reduction of fodder yield was observed after three years of cultivation in three of them. Analysis of sequences of 60 AMV Spanish-isolates from different hosts, including lucerne, tomato, pepper, broad bean, borrago and weeds, determined in four genomic regions (P1, P2, MP, and CP) covering about 25% of the genome, indicated low genetic diversity and different degree of selective constraints acting on each region. Neighbour-joining phylogenies showed two clusters (I and II) of sequences in P1, MP and CP regions, with further subdivision of cluster II in MP and CP regions, one of the new subclusters being only comprised by Spanish isolates. Genetic structure of the analyzed AMV-populations revealed the existence of geographic subdivision, which was also observed among isolates from different world areas, suggesting that seed transmission of AMV in lucerne and the agronomic properties of this crop are important factors on the epidemiology of AMV. In addition to the economic importance of AMV-induced disease in lucerne, these results are relevant in order to provide information on the epidemiological role of lucerne as an AMV-reservoir for vegetable crops, which frequently coexist with lucerne.