Short communications

Taxonomy of tenuiviruses and the relationship between tenuiviruses and negative-strand viruses. BC Ramírez, M Nguyen, AL Haenni (*Institut Jacques-Monod, 2, place Jussieu, tour 43, F-75251 Paris cedex 05, France*)

Five viruses belong to the recently recognized tenuivirus group: rice stripe virus (RSV), maize stripe virus (MStV), rice hoja blanca virus (RHBV), European wheat striate mosaic virus, and rice grassy stunt virus (RGSV). These viruses infect plants of the Graminae family. They are persistently transmitted by planthoppers in which they are transovarially passed. The 'viral particles' isolated from tenuivirus-infected plants have a flexuous, circular thread-like morphology. The genome of tenuiviruses is composed of 4 (RSV, RHBV, RGSV) or 5 (MStV) single-stranded RNA. Unequal amounts of RHBV RNA4 of the 2 polarities, viral (v) and viral complementary (vc), as well as a subgenomic RNA4, are encapsidated. RHBV RNA4 directs the synthesis *in vitro* of a non-structural 21 kDa protein designated NS4. NS4 corresponds to the non-structural protein that accumulates in RHBV-infected rice plants but is not detected in RHBV-infected planthoppers. RNA 3 directs the synthesis *in vitro* of a non-structural 23 kDa protein designated NS3. None of the RHBV RNA species directs the *in vitro* synthesis of the nucleocapsid (NC) protein. The sequences of the RHBV RNA4 and RNA3 confirm the use of the ambisense strategy for the expression of these 2 RNA. vRNA4 contains the open reading frame (ORF) of NS4, and vcRNA4, an ORF corresponding to a 32.5 kDa protein. vRNA3 contains the ORF of NS3, and vcRNA3 the ORF of NC. The ambisense strategy is also used by the *Arenaviridae* and some members of the *Bunyaviridae*. The tenuiviruses mRNA are synthesized *via* a cap-snatching mechanism similar to the one described for the synthesis of the mRNA of influenza virus, and some members of the *Arenaviridae* and *Bunyaviridae* families. It has been proposed to create a new family for the tenuiviruses, the *Tenuiviridae*, that together with the *Ortomyxoviridae*, *Bunyaviridae* and

Arenaviridae, would compose the order of the Multinegavirales.

Captures au piège AGRAPHID de cicadelles vectrices de virus nuisibles aux poacées. JP Moreau (*INRA, unité de zoologie, F-78026 Versailles, France*)

À la suite des pullulations de pucerons des céréales (*Sitobion avenae* F) de 1973 à 1975 en Europe de l'Ouest, il a été décidé l'installation en France, à l'instar du réseau britannique, d'un réseau de pièges à succion (AGRAPHD). Les données recueillies ont été exploitées pour l'établissement des prévisions de risques vis-à-vis de nombreuses espèces de pucerons et en particulier les vecteurs des virus de la jaunisse nanisante de l'orge. Parmi les homoptères capturés figurent aussi les auchénorrhynques vecteurs des autres virus des céréales. En effet, comme les formes ailées des pucerons, les cicadelles adultes font partie du plancton aérien. Dans les pièges de l'INRA-Versailles, on a enregistré les captures de certaines espèces majeures dont le delphacidé *Javesella pellucida* Fall et le cicadellidé *Psammotettix alienus* Fall. Cette dernière espèce, vectrice du virus du nanisme du blé, a causé récemment d'importants dégâts en France. L'importance des populations de ces cicadelles dans les prises du réseau pourrait constituer un élément complémentaire permettant une meilleure appréciation des risques viraux dans les semis des céréales d'automne.

Replication of BYDV in Poaceae and ultra-structural alterations. MA Favali ¹, R Musetti ¹, R Pedrazzini ² (¹ *Dipartimento di Biologia Applicata alla Difesa delle Piante, Università di Udine, Udine*; ² *Dipartimento di Biologia Evolutiva e Orto Botanico, Università di Parma, Parma, Italy*)

Barley yellow dwarf is one of the most widespread and economically important virus disease of Poaceae, infecting barley, wheat, oat, sorghum, rye, triticale, maize, rice and many wild

grasses. It is caused by members of the luteovirus group, some of which are closely related serologically and share common aphid vectors. BYDV particles occur in very low concentration in phloem tissue and are similar to ribosomes.

A combined ultrastructural and autoradiographic study on leaves of maize, barley and oat, healthy and infected with BYDV, has been carried out in order to detect the possible sites of virus synthesis and to compare the alterations caused by the BYDV in the different hosts. Therefore susceptible varieties of barley (*Hordeum vulgare* var Pirate), maize (*Zea mays* L) and oat (*Avena byzantina* L) were grown in the greenhouse and inoculated with PAV strain of BYDV by the aphid vector *Rhopalosiphum padi* (L). One month after inoculation, small samples of leaf tissues were floated for 20 min and 3 h at 27°C on sterilized water containing 500 µCi/ml [³H]-uridine, and then prepared for EM autoradiography. The ultrathin sections were examined on a Philips CM 10 electron microscope, operated at 80 kV. The EM observations demonstrated that nuclei were the organelles the most sensitive to the BYDV infection. Moreover EM autoradiography showed that [³H]-uridine was incorporated almost exclusively into the phloem nuclei, which show typical alterations, and after only 3 h of uptake they are also found in the cytoplasm where virus particles were observed. From these experiments it seems that the host cell nuclei are involved in BYDV RNA synthesis.

Geminiviruses: genome organization and protein functions. B Gronenborn¹, M Bendahmane¹, C David¹, C Desbiez¹, F Heyraud², I Jupin¹, A Kheyr-Pour¹, J Laufs¹, S Schumacher¹, L Wartig¹ (¹ CNRS, Institut des sciences végétales, F-91198 Gif-sur-Yvette, France; ² Max-Planck-Institut für Züchtungsforschung, D-50829 Cologne, Germany)

Geminiviruses are small plant pathogens with a circular single-stranded DNA genome encapsidated within a particle of an architecture unique among all known viruses. The virion consists of 2 incomplete icosahedrons attached to each other forming a 'twin' or 'geminat' particle. The viral genome consists of either 1 (monopartite) or 2 (bipartite) circular molecules of about 2.6 to 3.0 kb.

Geminiviruses are classified into 3 subgroups. Subgroup I comprises monopartite geminiviruses, eg maize streak virus (MSV), *Digitaria* streak

virus (DSV) or wheat dwarf virus (WDV), all pathogens of Poaceae including important cereal crops as maize, wheat and barley. With the single exception of tobacco yellow dwarf virus (TYDV) the subgroup I geminiviruses infect monocotyledonous plants, and the diseases caused by them occur in both temperate and tropical climates. They are transmitted by cicadellid leafhoppers, for instance, by *Psammotettix alienus* in the case of wheat dwarf virus, the only geminivirus of Poaceae in Europe.

The main member of subgroup II is beet curly top virus (BCTV), a geminivirus that represents an intermediate (recombinant) between leafhopper-transmitted subgroup I and the whitefly-transmitted subgroup III geminiviruses.

The geminiviruses of subgroup III are transmitted by the whitefly *Bemisia tabaci* and occur worldwide in subtropical and tropical habitats. In general, the whitefly-transmitted geminiviruses have bipartite genomes consisting of an A- and a B-DNA component. Exceptions to this rule include the Mediterranean and Near East/African tomato yellow leaf curl viruses (TYLCVs) and tomato leaf curl virus (ToLCV) from Australia, all being monopartite geminiviruses.

Upon infection, the single-strand encapsidated within the twinned virion is converted by host enzymes into a double-stranded, replicative DNA (minichromosome). To initiate the synthesis of the complementary strand, subgroup I geminiviruses encapsidate a small (80 nt) DNA primer molecule. The double-stranded DNA serves as template for divergent transcription of both plus- and minus-strands, originating at promoters within a large intergenic region or in an about 250 bp 'common region' in the case of geminiviruses with a bipartite genome. Central to the large intergenic as well as the common regions is a conserved palindromic sequence able to form a hairpin-loop structure. The loop of this hairpin contains a 9-base sequence motif identical within all known geminiviruses.

This nonanucleotide TAATATT↓¹AC is part of the replication origin with the penultimate A being the first base of virus-strand DNA synthesis.

Contrary to most plant viruses, geminiviruses do not code for a replicase. Rather, they rely on host polymerases for their genome replication. They do encode, however, a multifunctional protein of *M_r* 41 kDa essential for their DNA replication, the Rep protein. The Rep protein of the whitefly-transmitted geminiviruses is a single contiguous polypeptide chain (*M_r* 41 kDa),