

Evidence of *olive mild mosaic virus* transmission by *Olpidium brassicae*

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Abstract Transmission of three strains of OMMV by an *Olpidium* sp. was evaluated and compared. The three strains were 1) an OMMV wild type (WT) recovered from olive trees, 2) an OMMV variant (L11) obtained after 15 serial passages of single local lesions induced in *Chenopodium murale* plants, and 3) a construct OMMV/OMMV L11 in which the coat protein (CP) gene replaced that of the wild type. A single-sporangial culture derived from Chinese cabbage (*Brassica pekinensis*) used as a bait plant grown in soil of an olive orchard, was identified as *Olpidium brassicae* based on the size and sequence of the generated amplicon in PCR specific tests. Each of the three virus strains was soil transmitted to cabbage roots in the absence of the fungus at similar rates of 30 to 40%. Separate plant inoculation by *O. brassicae* zoospores incubated with each viral strain resulted in enhanced transmission of OMMV, reaching 86% of infection whereas that of the other two strains remained practically unaffected at ca. 34%. Binding assays showed that the amount of virus bound to

zoospores, estimated spectrophotometrically, was 7% in the case of OMMV, and practically nil in the case of the other two viral strains. Substitution of the coat protein (CP) gene of OMMV by that of the OMMV L11 strain, drastically reduced viral transmissibility in the presence of zoospores to the level of that observed in their absence. Our data shows that OMMV soil transmission is greatly enhanced by *O. brassicae* zoospores and that the viral CP plays a significant role in this process, most likely by facilitating virus binding and later entrance into the host plant roots.

Keywords Coat protein · Fungal transmission · OMMV mutants

Introduction

Olive mild mosaic virus (OMMV) is a recent member of genus *Necrovirus*, family *Tombusviridae* originally isolated from olive trees in Portugal (Cardoso et al. 2005). New sequence data submitted to Genbank (accession numbers EF 201608, EF 201607, EF 201606 and EF 201605) reveals that it also infects tulips, and is the causal agent of Augusta disease (Pham et al. unpublished), which was previously ascribed to Tobacco necrosis virus (TNV) (Kassanis 1949). The virus has a diameter of ca. 28 nm and a single stranded positive-sense RNA genome, 3683 nts long, containing 5 open reading frames (ORF).

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