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DISEASE NOTES



# First Report of *Groundnut ringspot orthotospovirus* Infecting Field Pea (*Pisum sativum* L.) Crop in Brazil



## Authors and Affiliations

M. G. Fontes, Dept. Fitopatologia, UnB, Brasília-DF, Brazil

M. F. Lima

M. E. N. Fonseca

L. S. Boiteux<sup>†</sup>, Embrapa Vegetable Crops (CNPV), Brasília-DF, Brazil.

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Field pea (*Pisum sativum* L.) cultivar Axé with symptoms of orthotospovirus infection ( $\approx$  5% incidence) were collected under open field conditions in Brasília-DF, Central Brazil. Ten leaf samples displaying apical chlorosis, necrosis, and deformation were evaluated via serology (ELISA) using antisera (produced at Embrapa Vegetable Crops) specific to the nucleocapsid (N) protein of three *Orthotospovirus* species: *Tomato chlorotic spot orthotospovirus* (TCSV), *Tomato spotted wilt orthotospovirus* (TSWV), and *Groundnut ringspot orthotospovirus* (GRSV). ELISA tests indicated that all symptomatic pea plants were positive for GRSV with some cross reaction with TCSV. Reverse-transcription (RT) PCR assays were conducted to confirm the virus species infecting field pea. Total RNA from one infected pea sample (ER1 isolate) was extracted using TRIzol reagent (Invitrogen, Carlsbad, CA), and the purified nucleic acid preparation was used for RT-PCR assays. For cDNA synthesis, the enzyme M-MLV (Promega) was used with the J13 primer (5'-CCC-GGA-TCC-AGA-GCA-AT-3'), which has eight conserved nucleotides that are present at the 3' termini of the small (S), medium (M), and large (L) genomic RNAs of orthotospoviruses. To determine consistently the viral species associated with the disease symptoms, the cDNA was used as a template in PCR assays with a GRSV-specific primer pair (5'-AGA-GCT-TCC-TTA-GTG-TTG-TAC-TT-AG-3' and 5'-GAA-AGG-TCT-AGA-TCT-AAA-CTG-CCA-C-3'), a TCSV-specific primer pair (5'-CTC-GGT-TTT-CTG-CTT-TTC-3 and 5'-

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TAT-AGC-3' and 5'-CAC-AAG-GCA-AAG-ACC-TTG-AG-3'), targeting regions of the N protein-coding gene (Webster et al. 2011). PCR assays showed N gene-derived amplicons (≈600 bp) only when using primers specific for GRSV. A consensus sequence (gb\KY778230) was obtained by direct sequencing of the PCR amplicons from the sample ER1. The sequence alignment displayed nucleotide identity above 94% with a wide range of GRSV isolates available at GenBank. *Fabaceae* members have been reported as natural TSWV hosts in Brazil, including chickpea (Boiteux et al. 1995), lentil (Fonseca et al. 1995), and field pea. So far, only peanut has been reported as a *Fabaceae* host of GRSV in the country (Camelo-García et al. 2014). In fact, to our knowledge, this is the first worldwide report of pea-infecting GRSV isolates. GRSV infection may result in negative yield impact in peas, especially in early-infected plants. In addition, the identification of field pea as a new GRSV host might have epidemiological consequences in Central Brazil because this crop is usually cultivated either in rotation or side-by-side with processing tomatoes, for which most of the leading hybrids are highly susceptible to GRSV (Giordano et al. 2010). In this scenario, novel management strategies should be implemented, including chemical control of viruliferous thrips in these susceptible crops, adoption of proper crop rotation systems, and deployment of GRSV-resistant cultivars.

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## The American Phytopathological Society

(APS)

📍 3285 Northwood Circle, Suite 100, St. Paul,

MN 55121 USA

☎ +1.651.454.7250

**FAX** +1.651.454.0766

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