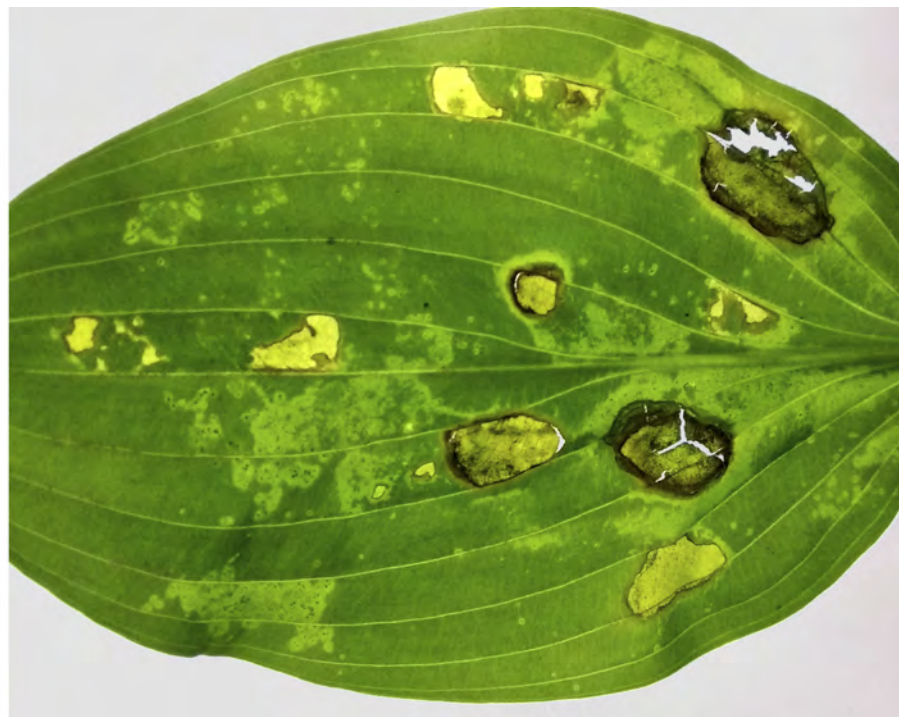


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DISEASE NOTES



First Report of *Alternaria alternata* Causing Leaf Spot on *Rumex crispus* in Uruguay

T. E. Kaspary, M. A. García, S. Stewart, G. Casaroto, R. F. Ramos, and C. Bellé

Affiliations ✓

Authors and Affiliations

T. E. Kaspary^{1 †}

M. A. García¹

S. Stewart¹

G. Casaroto²

R. F. Ramos³

C. Bellé³

¹Instituto Nacional de Investigación Agropecuaria–INIA, La Estanzuela, Colonia, Uruguay

²Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil

³Universidade Federal de Santa Maria, Santa Maria, Rio Grande do Sul, Brazil

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Rumex crispus L. (curled dock), a member of the family Polygonaceae, is considered an important weed in grasslands and crops (Hejcmán et al. 2012). Curled dock decreases yield and nutritive value of different species by competition for space, water, and nutrients (Zaller 2004). In addition, it may be an alternative host of pests and diseases of crops (Abbasi et al. 2018). In October 2018, *R. crispus* plants

with severe spotting on their leaves were observed in a field at La Estanzuela, in Colonia, a department in southwestern Uruguay. Symptoms were small, circular, light brown spots that eventually turned into irregular, dark brown lesions, although a few remained circular with concentric rings. Leaf lesion samples were surface sterilized (70% ethanol for 30 s, 1% NaClO for 2 min, rinsed three times in sterile water, dried on sterilized filter paper) and placed on potato dextrose agar (PDA). To identify the causal fungus, morphological analysis was conducted, followed by molecular characterization through the amplification and sequencing of the internal transcribed spacer (ITS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), the second largest subunit of RNA polymerase II (RPB2), and the translation elongation factor (TEF-1 α) gene regions, using the method described by [Woudenberg et al. \(2013\)](#). Colonies were round, composed of cottony mycelium of dark olivaceous hyphae. Conidiophores were septate, light-to-olive golden brown, with a conidial scar where conidia were produced in long chains. Conidia ($n = 50$) were obclavate to obpyriform, golden brown, with a cylindrical or coniform beak at the tip, and measured 25.9 to 61.5 μm long \times 12.5 to 16.5 μm wide with two to six transverse and one to three longitudinal septa. Sequences of the studied DNA regions were submitted to GenBank, and accession numbers were received (ITS, MK635345; GAPDH, MK639185; RPB2, MK645322; TEF-1 α , MK639186). BLAST searches showed 99 to 100% identity with the existing sequences (including ex-type CBS 916.96) of *Alternaria alternata* (Fr.) Keissl. (1912) (ITS, AF347031; GAPDH, AY278808; RPB2, KC584375; TEF-1 α , KC584634). To confirm Koch's postulates, six plants of *R. crispus* were inoculated with a suspension of 10^6 conidia/ml, whereas six plants to which distilled water was applied were considered as controls. All plants were enclosed in plastic bags and incubated in a growth chamber at $25 \pm 2^\circ\text{C}$ for 24 h with a 12-h photoperiod. At the end of the 24-h period, plastic bags were removed. Ten days after inoculation, leaves displayed symptoms similar to those observed in the field, whereas controls remained symptomless. The fungus reisolated from inoculated leaves had the same morphological and molecular traits as the initial isolate. Pathogenicity tests were carried out two times. Our findings highlight the relevance of *R. crispus* as a reservoir for an important crop pathogen as well as a major crop competitor. To our knowledge, this is the first report on *A. alternata* affecting *R. crispus* plants in Uruguay.

The author(s) declare no conflict of interest.



The American Phytopathological Society (APS)

📍 3340 Pilot Knob Road, St. Paul, MN 55121 USA

☎ +1.651.454.7250

FAX +1.651.454.0766



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