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# plant disease

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[Home](#) > [Plant Disease](#) > [Table of Contents](#) > [Full Text HTML](#)  
[Previous Article](#) | [Next Article](#)

February 2018, Volume 102, Number 2  
Page 448  
<https://doi.org/10.1094/PDIS-08-17-1161-PDN>

## DISEASE NOTES

### Detection of *Puccinia graminis* f. sp. *tritici* Race RRTTF in Ecuador in 2016

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Wheat stem rust is a devastating disease that has incited severe epidemics, resulting in extreme yield losses over the past century. Stem rust infection in plots of wheat line UC11075, known to carry the *Sr38* resistance gene, was unusual and severe in February 2016 in a nursery at the Instituto Nacional de Investigaciones Agropecuarias Austro station near Cuenca, Ecuador. Stems with heavy infection by *Puccinia graminis* f. sp. *tritici* (*Pgt*) were sent for genotyping in labs at Ottawa, ON, and St. Paul, MN, and for phenotyping at Morden, MB. None of the samples received directly from the field had viable spores, but genotyping was done in Ottawa and St. Paul using DNA extracted from spores or infected plant materials killed in ethanol. DNA was extracted using the OmniPrep kit (G-Biosciences, St. Louis, MO). Results from the Ottawa genotyping lab using 11 of 20 simple sequence repeat markers (Stoxen 2012) indicated that all February 2016 samples from the Austro station were genotypically identical, and 9 of 11 markers matched to *Pgt* isolate 10-Eth-1-2 from Ethiopia (collected in 2010), which previously was pathotyped to race TRTTF. Results from the St. Paul genotyping lab using 17 selected single nucleotide polymorphism markers also found that all samples were genotypically identical and grouped into *Pgt* clade III (Olivera et al. 2015) along with isolates 14ETH136-2 from Ethiopia (2014), 86PAK1030a from Pakistan (1986), and 06YEM34-1 from Yemen (2006), which previously was pathotyped to race RRTTF or TRTTF. Original samples collected in February were increased in August 2016 in Ecuador. These, along with other samples collected in December 2016, were sent to Morden for phenotyping in February 2017. Five of 18 samples that were sent were viable. Each sample was first increased on susceptible McNair in isolation and then inoculated on 20 single-gene differential lines. Infected seedlings were rated for infection type at 14 days postinoculation, and the letter-code nomenclature (Jin et al. 2008) was used to identify the race. Four isolates had mixed infection, but isolate 16-ECU-22 was clearly pathotyped to race RRTTF and matched to results from both genotyping labs. Isolate 16-ECU-22 is a urediniospore increase from the original field collection at the Austro station in February 2016 that was sent for genotyping and was

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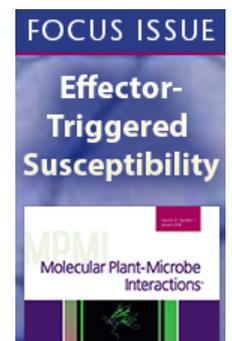
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increased in a greenhouse in Ecuador in August. Race RRTTF is distinctive by its combined virulence to genes *Sr38* and *Sr13* and poses a significant threat to wheat production in North and South America. Previous seedling assessment found that 55% of Canadian hard red spring wheat varieties were susceptible to *Pgt* race RRTTF from Pakistan (Fetch et al. 2012). The origin of *Pgt* race RRTTF in Ecuador is unknown, but it was clearly similar to isolates of RRTTF from Asia, eastern Africa, and the Middle East. It is unknown whether race RRTTF is a recent long-distance exotic introduction into Ecuador or a de novo variant of an existing South America lineage that was introduced earlier. Further study is needed to determine how widespread this race is in Ecuador and its potential to migrate to large-scale wheat production areas in South and North America.

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Section:

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