

Errata

The author line for the article that appeared on page 778 of Volume 82 was incorrect. Consequently, the article should have read as follows:

Molecular Plant Pathology

Genetic Diversity of *Rhizoctonia solani* Anastomosis Group 2

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ABSTRACT

Liu, Z. L., Sinclair, J. B., and Chen, W. 1992. Genetic diversity of *Rhizoctonia solani* anastomosis group 2. *Phytopathology* 82:778-787.

Genetic diversity among 70 isolates of *Rhizoctonia solani* anastomosis group (AG) 2 was studied by isozyme polymorphism and DNA restriction analyses. Five genetically distinct intraspecific groups (ISGs) (ISG 2A [9 isolates], 2B [13 isolates], 2C [22 isolates], 2D [14 isolates], and 2E [12 isolates]) were distinguished within AG 2 based on binary characters of isozyme alleles and restriction sites by using numerical cladistic analysis with isolate ISG 1C19 (AG 1-IC type) as an outgroup. Isozyme phenotypes were developed for these groups. Some isozyme alleles and loci were identified as useful molecular markers for population studies. DNA restriction mapping showed that these groups shared the same gene of mitochondrial small subunit rDNA and a high level of similarity in nuclear rDNA for internal transcribed spacers (ITS), including the 5.8S ribosomal

RNA gene. The polymerase chain reaction (PCR) amplified DNA fragments varied for the five groups. In the ITS region, groups 2A and 2E had the same lengths (0.69 kb) but differed at one *EcoRI* site; groups 2B, 2C, and 2D had the same lengths (0.74 kb) but differed from one another by at least one restriction site, *MspI* or *TaqI*. ISG 2A corresponded to AG 2-1; 2B to AG 2-2 IIIB; 2C to AG 2-2 IV; 2D to a newly defined group related to AG 2-2; and 2E to a newly defined group, previously identified as AG 2-2, related to AG 2-1. When evaluated from a single source and developed at different levels, ISGs 2A and 2E were closely related, and ISGs 2B-D were closely related. The merits of using isozyme and DNA analyses for the study of *R. solani* populations or ISGs are discussed.

Additional keywords: molecular differentiation, phylogeny, *Thanatephorus cucumeris*.
