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Erratum

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A region of heterogeneity adjacent to the 5*s* ribosomal RNA gene of cereal rusts

W. K. Kim [1], T. Zerucha [2], and G. R. Klassen [2]

[1] Agriculture Canada, Research Station, 195 Dafoe Road, Winnipeg, Manitoba R3T 2M9, Canada
[2] Department of Microbiology, University of Manitoba, Winnipeg, Manitoba R3T 2N2, Canada

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On page 102 of the paper starting on page 101 of volume 22 there were unfortunately one error. The paragraph concerned is now printed correctly below.

Materials and methods

Polymerase chain reaction. Total DNA from each organism (100 μg/ml) was diluted 10-fold in TE buffer (10 mM Tris-HCl, pH 7.6, 1 mM EDTA) and PCR was done in a 100 μl reaction volume which included 10 μl of 10 × Perkin Elmer Cetus PCR buffer (100 mM Tris-HCl, pH 8.3; 500 mM KCl; 15 mM Mg Cl_2, 0.1% gelatin), 8 μl of dNTP mix contributing 200 μM of each nucleotide to the final concentration of the reaction mixture, 1.5 μl (10 pmole) of each primer [primer Q (dACGCCTCTAAGTCAGAAT) was based on an yeast sequence (Gutell and Fox 1988) while primer Y (dTCGCAGAGCGAACGGGAT) was based on published 5*s* sequences (Wolters and Erdman 1988)], 1.0 μl (10 ng) of template DNA solution; 0.5 μl (2.5 units) of *Taq* polymerase, and 77.5 μl of ultrapure, sterilized water. The DNA was heated for 5 min at 94 °C just before addition to the reaction solution. Fifty μl of mineral oil were placed over the reaction solution and then the reaction tube was subjected to a heating and cooling protocol in a DNA thermal cycler (Perkin Elmer Cetus Instruments) using the step cycle program (Myers et al. 1989). The amplification was started with the denaturation step at 94 °C for 1 min, followed by annealing at 55 °C for 1 min and polymerization at 72 °C for 1 min. The sequence was repeated for 27 cycles and at the end of the cycle, the polymerization step at 72 °C was extended for 5 min. The amplification products were electrophoresed directly on 1.3% agarose gels or first precipitated in ethanol and then resuspended to TE buffer before electrophoresis (Kim et al. 1988). The PCR product yield was sufficient for staining of bands in gels with ethidium bromide and for restriction digestion.