antisera, and Miss M. Tyzzer for technical assistance. The work was supported by the Medical Research Council.

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Received October 4, 1972.

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Chromosome Location of Genes Conditioning Stem Rust Resistance Transferred from Diploid to Hexaploid Wheat

A survey of a large number of accessions of diploid wheat (Triticum monococcum L. and T. boeoticum Boiss.) revealed two potentially useful genes conditioning resistance to stem rust (Puccinia graminis Pers. f. sp. tritici Eriks. and E. Henn). The practical utilization of diploid resistance at higher levels of ploidy in breeding presents no technical prob-Vardy and Zohary1 proposed the use of an interspecific triploid hybrid bridge to transfer rust resistance from diploid to tetraploid wheat. A resistant derivative from the cross T. durum cv. Spelmar² × T. boeoticum G21 was isolated, and its behaviour to stem rust studied by Gerechter-Amitai et al.². In my study this tetraploid was backcrossed once to the hexapoid wheat cultivar Steinwedel, and two resistant lines were isolated and accessioned as W3588 and W3589 respectively. (W numbers refer to the Sydney University Wheat Accession Register).

A resistant hexaploid derivative W3591 was isolated from the cross (T. aestivum W1569 \times T. boeoticum C68-123) \times Chinese Spring, an interspecific triploid hybrid bridge was not necessary for this particular transference. Two additional resistant hexaploid lines were studied: W3534, Marquis⁵ × (Stewart³ × T. monococcum RL5244) F₄ (obtained from Drs. P. L. Dyck and E. R. Kerber, Canada), and W3586 (T. durum W304×T. monococcum ev. Einkorn)× unknown T. aestivum F_5 (obtained from Dr. R. A. McIntosh,

On the basis of stem rust reactions these five lines were divided into two groups. The first group which included W3586, W3588, and W3591 was resistant to all Australian components of standard races 21, 34, and 126 of P. graminis, but susceptible to all components of standard races 15 and 17. The remaining lines, W3534 and W3589, which constituted the second group were resistant to all Australian strains.

Genetic and pathological tests showed that each of the five

lines possessed a single dominant gene derived from its diploid parent, and that the lines within each group possessed the same gene. Results of monosomic analyses confirmed this, and indicated that chromosome 2A was implicated in the three lines in the first group. Nullisomic F₂ segregants for choromosome 2A were susceptible, and at meiosis showed reduced chromosome pairing typical of nulli-2A plants3. The main differentiation provided by Einkorn in the standard stem rust differential set seems to be attributable to this gene. If so all components of standard races which are avirulent on Einkorn should be avirulent on these lines. This is supported by the observation that a single dominant gene controls avirulence in crosses between P. graminis cultures^{4,5}. No previously identified gene conditioning stem rust reaction has been located on chromosome 2A; and so I propose that this gene be designated Sr21.

The gene present in the second group was located on chromosome 7A. F₂ telocentric mapping utilizing W3534 and telocentric chromosome 7AL of Chinese Spring showed that it is located on the long arm, and linkage of 0.27 ± 0.042 with the centromere was estimated. I propose this gene be designated Sr22. It is highly improbable that Sr22 is allelic with Sr15, because Sr15 is closely linked with Pml6, and Pml is independent of the 7A centromere7.

Results from further investigations to test other linkages will be published in detail at a later date.

Financial assistance was provided by the Rural Credits Development Fund, Reserve Bank of Australia.

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Received October 23, 1972.

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Erratum

In the article "Induced Transmitter Release from Schwann Cells and its Suppression by Actinomycin D" (Nature New Biology, 241, 85; 1973) the authors' names should appear in alphabetical order: S. Bevan, W. Grampp and R. Miledi.

Editorial, Advertising and Publishing Offices of NATURE MACMILLAN JOURNALS LIMITED 4 LITTLE ESSEX STREET, LONDON WC2R 3LF Telephone Number: 01-836 6633. Telegrams: Phusis London WC2R 3LF Telex 262024

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