Resistance of Wild Wheat to Stripe Rust: Predictive Method by Ecology and Allozyme Genotypes

By
Eviatar Nevo, Zeev Gerechter-Amitai, Avigdor Beiles, and Edward M. Golenberg

(Received June 5, 1985)

Key Words: Angiosperms, Poaceae, Triticum dicoccoides; Uredinales, Puccinia striiformis. — Wild emmer, pathogene resistances, ecology, allozyme genotypes, statistic analyses. — Flora of Israel.

Abstract: From 114 accessions of wild emmer wheat from 11 sites in Israel, known for their allozymic variation (Nevo & al. 1982), individual genotypes were tested for resistance to one isolate of stripe rust both in the seedling stage in a growth chamber and in the adult plant stage in the field. The results indicate that resistance to stripe rust in seedlings and adults are significantly correlated ($r_s = 0.40, p < 0.001$). Genetic polymorphisms of resistance to stripe rust vary geographically and are predictable by climatic, as well as allozymic markers. Three variable combinations of rainfall, evaporation, and temperature explain significantly $0.40-0.53$ of the spatial variance in disease resistance to stripe rust, suggesting the operation of natural selection. Several allozyme genotypes are significantly associated with disease resistance. We conclude that natural populations of wild emmer wheat in Israel contain large amounts of disease resistance genes. These populations could be effectively screened and then utilized by the phytopathologist for identifying resistant genotypes and producing new resistant cultivars.

The best hope for future genetic improvements of the increasingly depauperating cultivated crops lies in exploiting the rich gene pool of the plants’ wild progenitors (Harlan 1976). Modern plant breeding practices have also drastically reduced the genetic variability of cultivated wheat (Frankel & Bennett 1970, Feldman 1979, Feldman & Sears 1981) which is the prime food crop of man. Consequently, cultivated wheats became vulnerable to diverse diseases which cause drastic cuts in yields. A major way to increase wheat production is by introducing disease resistance genes from the wild to the cultivated gene pool.

1 Patterns of Resistance of Wild Wheat to Pathogens in Israel II.
Tetraploid wild wheat, *Triticum dicoccoides* KOERN., contains large amounts of genetic variation, displaying local and regional adaptive differentiations to different climates, soils and pathogens (Nevo & al. 1982, 1985). Thus, it is suitable for breeding programmes to introduce into cultivated wheats resistance to a broad range of diseases, pests, and for tolerance to poor soils and climatic extremes. Such procedures could stabilize and extend agriculture into marginal environments. Furthermore, gains are likely to be longer lasting if more than one gene for resistance or tolerance could be transferred successfully to a cultivar (Plucknett & al. 1983) by sampling across the range of distribution of this species.

Pioneering work has already been completed to exploit *T. dicoccoides* for breeding programmes. These include, among others, resistance to stripe rust (Gerechter-Amotai & Stubbs 1970, Gerechter-Amotai & Grama 1974, Grama & Gerechter-Amotai 1974, Grama & al. 1983, 1984).

In our preliminary study of this series, we have indicated that patterns of resistance of wild wheat to powdery mildew and leaf rust are predictable by ecology and allozyme genotypes (Nevo & al. 1985). We demonstrate here that these predictive methods are also applicable to stripe rust. Thus, both ecology and allozyme markers could be effectively used for primary screening in the utilization of wild wheat for producing resistant wheat varieties.

**Materials and Methods**

The present study involves the analysis of a *T. dicoccoides* KOERN., collection, consisting of 114 accessions, for resistance to one isolate of stripe rust, *Puccinia striiformis* West. All populations were described in detail geographically, ecologically, and allozymically in Nevo & al. (1982). The populations tested are illustrated in Fig. 1 and summarized in Table 1. Seeds are deposited in the Institute of Evolution, University of Haifa.

In our studies of resistance in the seedling stage, we used culture Gyr-22 of *P. striiformis*, belonging to race 2EO (Johnson & al. 1972). Which had been isolated from *T. dicoccoides* growing in its natural habitat at Almagor, Israel. The test were performed in a controlled environment growth chamber. Methods of inoculation and growth conditions were described elsewhere (Gerechter-Amotai & al. 1984).

The infection type (IT) produced by the reactions were read on a 1–9 scale from very resistant to very susceptible: 1 = very resistant; 2 = resistant; 3 = moderately resistant; 4 = low intermediate; 5 = intermediate; 6 = high intermediate; 7 = moderately susceptible; 8 = susceptible; 9 = very susceptible. The reactions to infection were summarized by combining the IT into three groups with resistant (R) = 1–3; intermediate (I) = 4–6; and, susceptible (S) = 7–9.

At the Bet Dagan Experimental Farm, the 114 entries were evaluated in the adult plant stage, under conditions of an artificially induced epidemic with a composite of stripe rust races, including race 2EO (isolate GYR-22).

We report here on the geographical distribution of resistance to one isolate of stripe rust in a survey of 11 populations of *T. dicoccoides* in Israel and determine