CEREAL RUSTS BULLETIN

VOLUME 14 PART 2 1986

EDITED BY N.H. CHAMBERLAIN AND R. JOHNSON

PUBLISHED BY

THE EUROPEAN AND MEDITERRANEAN CEREAL RUSTS FOUNDATION

Cereal Rusts Bulletin Vol 14, Part 2, 1986

CONTENTS

Cereal Rusts Bulletin Vol 14, Part 2, 1986

GENETICS OF STEM- AND LEAF RUST RESISTANCE OF THE WHEAT CULTIVAR MEPHISTO

BY

P. BARTOS, J. KOSNER, E. STUCHLIKOVA, R. HANUSOVA

Research Institute for Crop Production,
Praha - Ruzyne, Czechoslovakia

SUMMARY

The results of our trials with stem rust including monosomic analysis suggest that the cv. Mephisto carries the gene Sr5 and at least one other gene for stem rust resistance. The gene Sr5 governs IT 0;, the other gene IT 2,2-3. This gene was effective to some isolates that were virulent to Sr5. At the adult stage in the cv. Mephisto a few pustules of IT 3-4 appeared at waxy ripeness even when inoculated with race 21 (isolate G 69) avirulent to Sr5. The same was observed in F_2 generation of the crosses. Obviously the resistance is expressed by the reduced number of pustules at the adult stage.

We presume that resistance at the adult stage is governed by the same genes as at the seedling stage; however, presence of gene(s) only for adult plant resistance cannot be excluded.

Our analysis of leaf rust resistance showed that one dominant gene for leaf rust resistance is possessed by the cv. Mephisto. This gene is different from the genes of the standard differential varieties. The supposition based on preliminary results that this gene might be an allele of Lr1 was not confirmed. Monosomic analysis failed because of technical error. All lines segregated in the ratio 3R:11S.

INTRODUCTION

The spring wheat cultivar Mephisto originates from the Federal Republic of Germany and was derived from the cross Weihenstephaner Stamm x Opal (Saatzucht von Rümker). It was also grown in Czechoslovakia (licenced in 1975 and restricted in 1982).

The cultivar Mephisto shows resistance to some races of stem- and leaf rust. We studied resistance of this cultivar in several experiments. Results of our studies are summarized in this paper.

MATERIALS AND METHODS

Seed of the cultivars Mephisto and Jara (susceptible Czechoslovak spring wheat) was identical with the seed in National Yield Trials. Seeds of other cultivars were obtained from the Department of Genetic Resources of the Research Institute for Crop Production, Praha-Ruzyne. Common rust races from the Czechoslovak rust survey were used in the experiments.

In the greenhouse, inoculation was carried out by rubbing the wetted first leaf with urediospores diluted with talc. The inoculated

plants were sprayed with tap water and kept for 48 hours under covered glass cylinders. Infection types were classified after Stakman et al. (1962). The greenhouse temperature varied between 18-22°C.

In the field, spreader rows (cv. Michigan Amber) were inoculated by hypodermic needle with water suspension of urediospores of stem rust race 21 (isolate G 69). Degree of infection was evaluated in F_1, F_2 and F_3 generations of the cross Mephisto x Jara. In the greenouse reactions of cv. Mephisto were tested with 19 stem- and 15 leaf rust isolates from the rust surveys 1980-1982.

Monosomic analysis using Chinese Spring monosomic series was also carried out in the greenhouse to locate genes for resistance.

RESULTS AND DISCUSSION

Stem rust

Cv. Mephisto was tested with 19 isolates of stem rust. It was resistant to four stem rust isolates avirulent on the standard differential variety Reliance. It was susceptible to all except three of the isolates virulent on Reliance. To these cv. Mephisto displayed infection type 2 or 2-3. No relation between this reaction and reactions of standard differentials was established.

Monosomic analysis of stem rust resistance of the cultivar Mephisto was carried out with race 21 (isolates G 69). Observed ratios (Table 1) were checked for fit to a 13:3 ratio that was found for the disomic line indicating one dominant and one recessive gene. The critical line for the dominant gene is evidently 6D.

The monosomic analysis was not successful in locating the other gene for stem rust resistance indicated by the 13:3 ratio. Lines 5A and 7D had a significantly higher number of resistant plants than expected, whereas the line 2A had a lower number of resistant plants.

Three genes for stem rust resistant have been described on chromosome 6D, namely Sr5, Sr29 and Sr27. The observed resistant reaction of Mephisto to races avirulent on Reliance indicates that Mephisto probably possesses the gene Sr5. This presumption is supported by the results obtained with the cross Sonora 64 x Mephisto. Sonora possesses Sr5 and Sr11 (Luig, 1983). No segregation was observed in the stem rust reaction in F_2 population of this cross when inoculated with stem rust race 21 (isolate G 69). However, the population consisted of only 127 plants and was therefore too small to prove the identity of one gene in both parents if three or more resistance genes were present.

In the field inoculated with race 21 (isolate G 69), the degree of infection in the cross Mephisto with the susceptible cultivar Jara was determined in F_1, F_2 and F_3 generations. It was possible to carry out the analysis on the basis of infection types because at the time of evaluation (waxy ripeness) IT was 3-4 in all plants.

Plants of F_1 generation had an average infection degree of 10%. The F_2 generation segregated. Degree of infection varied from 5 to 60% (Table 2). Distribution of plants with various degrees of infection indicates that 35% of infection can be considered as maximal for the category of resistant plants. Plants with 40% of infection and more were classed as susceptible when F_2 and F_3 generations were classified.

On the basis of this classification the results in the F_2 fit a 13R:3S ratio (Table 2) indicating the action of two genes for stem rust resistance, one dominant and one recessive. In F_3 generation 48 lines were tested in the field for their reaction and segregation. The results (Table 3) confirm the conclusion that two genes are involved in the stem rust reaction of the cultivar Mephisto to race 21 (isolate G 69). We presume that these genes are the same as the genes we found at the seedling stage. It is known that Sr5 governs resistance at the seedling as well as adult stage.

Earlier we have found in the cultivar Bezostaya 1, which possesses Sr5 (Bartos et al., 1970) that during ripening some pustules of susceptible type appear on plants. Resistance in the crosses with susceptible varieties was expressed then by reduced number of pustules of IT 3-4. Parallel field- and greenhouse tests of F_3 lines indicated that low IT in the greenhouse corresponded with a low degree of infection in the field. We presume a similar situation in the cultivar Mephisto.

The gene Sr5 is not effective against race 11 of stem rust. The cv. Mephisto showed IT 2-3 or 3 when inoculated with this race 11 (isolate G 425) in the greenhouse and was moderately resistant in the field inoculated with the same isolate. We presume that the undetermined gene in our trials with race 21 governs the intermediate reaction to race 11. However, the results obtained with the segregating F_2 generation of the crosses Mephisto x Jara and Jara x Mephisto were not conclusive because the infection level was low in this trial and the number of plants limited. Lines of the F_3 generation were not studied.

Leaf rust

The cultivar Mephisto was resistant to 8 out of 15 leaf rust isolates used in the trial. All cultures that were avirulent on Mephisto were also avirulent on Lr1 and Lr2a. However, some cultures avirulent on Lr1 and Lr2a were virulent on Mephisto. The most common race in 1981, namely UN 3-61 comprised avirulent as well as virulent isolates on Mephisto. Obviously none of the resistance genes possessed by standard differentials governs leaf rust resistance of the cv. Mephisto.

When we started to analyze the leaf rust resistance of Mephisto we thought that an allele of Lr1 might be involved in its leaf rust resistance. Therefore we crossed Mephisto with cultivars possessing Lr1: Th^6-Centenario and Sonora 64. Sonora 64 was also crossed with Th^6-Centenario. The segregation in F_2 generation of the cross Mephisto x Th^6-Centenario and Sonora 64 x Mephisto inoculated with an isolate of race UN 3-61 avirulent on both parents showed that gene for leaf rust resistance in Mephisto is not allelic with Lr1 (Table 4). The results obtained with the cross Sonora 64 x Th^6-Centenario confirm that both cultivars have at least one gene in common (Lr1).

The monosomic analysis carried out with race UN 3-61 (isolate 436) failed probably because of technical error in the preparation of lines. However, it proved that one dominant gene was involved in the leaf rust resistance of the cv. Mephisto. All monosomic lines CS x Mephisto segregated in the ratio 3R:1S. Out of 1,862 plants of all monosomic lines and one disomic check, 465 plants were susceptible (P for 3:1 = 0,99-0,95).

REFERENCES

BARTOS, P., GREEN, G.J. and DYCK, P.L. (1970). Reactions to stem rust and genetics of stem rust resistance in European wheat varieties. Can. J. Bot. 48: 1439-1443.

LUIG, N.H. (1980). A survey of virulence genes in wheat stem rust Puccinia graminis f.sp. tritici. Paul Parey, Berlin - Hamberg.

STAKMAN, E.C., STEWART, D.M.. and LOEGERING, W.Q. (1962). Identification of physiologic races of Puccinia graminis var. tritici. Minn. Agr. Exp. Sci. J. Ser. Paper 4691.

Table 1 - Monosomic analysis of stem rust resistance of the cv. Mephisto to race 21 (isolate G 69).

Monosomic line	Number and % of plants				χ^2
	resistant		susceptible		
	IT 0; 1 1-2, 2	%	IT 3, 3-4	%	13 : 3
1A	148	82.22	32	17.78	0.112
1B	162	80.20	40	19.80	0.147
1D	173	79.72	44	20.28	0.332
2A	34	66.67	17	33.33	7.120xx
2B	180	86.12	29	13.88	3.260
2D	165	78.57	45	21.43	0.989
3A	124	85.52	21	14.48	1.733
3B	165	85.49	28	14.51	2.280
3D	179	84.43	33	15.57	1.411
4A	164	83.25	33	16.75	0.517
4B	168	83.58	33	16.42	0.718
4D	177	84.29	33	15.71	1.270
5A	212	89.08	26	10.92	9.567xx
5B	123	86.01	20	13.99	2.130
5D	138	79.77	35	20.23	0.249
6A	163	80.69	39	19.31	0.041
6B	161	76.67	49	23.33	2.896
6D	176	93.62	12	6.38	18.874xxx
7A	138	78.41	38	21.59	0.932
7B	108	83.72	21	16,28	0.517
7D	180	86.96	27	13.04	4.425x
Disom.	156	82.98	32	17.02	0.369
Σ	3394	83.17	687	16.83	9.833xx
Σ - 6D	3218	82.66	675	17.34	5.089

Table 2 - Segregation of F_2 population of the cross Mephisto x Jara in the field trial inoculated with race 21 (isolate G 69)

	Number of plants with percentage of rust infection								
	5-10	15	20	25	30	35	40	50	60
Found	28	17	14	8	12	2	12	5	4
	Σ 81						Σ 21		
Expected for 13R : 3S	83						19		
P = 0.8 - 0.5									

Table 3 - Segregation of F_3 lines of the cross Mephisto x Jara in the field trial inoculated with race 21 (isolate G 69)

	Number of lines	
	Found	Expected for 13R : 3S
Resistant non segregating	22	21
Susceptible non segregating	2	3
Segregating (3S : 1R)	6	6
Segregating (3R : 1S)	7	6
Segregating (13R : 3S)	11	12
P = 0.99 - 0.95		

Table 4 - Segregation of F_2 populations of the crosses involving Mephisto and cultivars possessing Lrl. Greenhouse tests with race 61 isolate 628.

Cross	Number of plants		
	R	S	total
Mephisto x Th^6-Centenario	125	4	129
Sonora 64 x Mephisto	113	14	127
Mephisto x Sonora 64	125	6	131
Sonora 64 x Th^6-Centenario	139	0	139

Cereal Rusts Bulletin Vol 14, Part 2, 1986

IDENTIFICATION OF GENES FOR REACTION TO STEM RUST IN WHEAT LINES AND CULTIVARS WITH SINGLE GENES FOR REACTION TO LEAF RUST

BY

R.N. SAWHNEY, L.B. GOEL

Division of Genetics, Indian Agricultural Research Institute, New Delhi-110012 (India)

SUMMARY

Near isogenic lines and cultivars of wheat with single leaf rust resistance genes Lr2a, Lr19, Lr21, Lr22, Lr23, Lr24 ('Agent'), Lr25 ('Transec'), Lr26 ('Benno'), Lr27 ('Gatcher') and LrKT ('Klein Titan') were resistant to Indian stem rust cultures also. The stem rust resistance of single gene lines/cultivars carrying Lr19, Lr21, Lr24, Lr26 was suggested to be due to known genes Sr25, Sr21, Sr24, Sr31, respectively. Similarly, resistance to stem rust in the lines with Lr2a and Lr23 could be attributed to Sr30 and Sr11, respectively, which are known to be present in the progenitors of these Lr gene lines. Resistance in the line and cultivar with Lr22 and Lr25 is due to unknown associated or additional genes effective to Indian stem rust cultures. Cultivar 'Klein Titan' may have a stem rust resistance gene common to that in 'Barleta Benvenuto' (BB). The stem rust resistance of cv. 'Gatcher', however, is due either to interaction between a number of known Sr genes or additional unknown gene(s) effective to Indian cultures of P. graminis.

INTRODUCTION

Interaction between lines carrying specific genes for resistance and pathogen isoates provides a means of postulating genes in a host. The information on all the known loci for leaf rust resistance to Indian cultures of Puccinia recondita Rob. ex. Desm. has been reported (Sawhney et al., 1977; Sawhney and Goel, 1983). For the identification of identical or associated genes for resistance to Puccinia graminis f. sp. tritici, seedlings of a series of near-isogenic lines and cultivars carrying known specific genes for resistance to leaf rust (Lr genes) were studied against the Indian stem rust races. The present study has revealed that some of the lines and cultivars with known genes for resistance to leaf rust also carry associated or additional genes imparting resistance against Indian races of stem rust. Additional genes identified for resistance to stem rust would be useful for providing a broadened genetic base in resistance breeding programmes.

MATERIALS AND METHODS

Near-isogenic lines in Thatcher background and other cultivars each with a known leaf rust resistance gene, including Lr13 backcrossed into 'Prelude' were separately inoculated at seedling stage with the prevailing Indian races (14, 21, 34, 40, 40A, 42, 42B, 117A-1 and 122) of stem rust. The spores of rust cultures were procured initially from the Indian Agricultural Research Institute (IARI), Regional Research Station, Shimla and were derived from single spores. Standard procedures for inoculation of seedlings and recordings of the reactions were followed (Stakman et al., 1962). The tests were conducted in a glasshouse at the IARI, New Delhi at a temperature not exceeding 22°C. The results were confirmed in the temperature controlled laboratory at the Division of Genetics, IARI, New Delhi, at temperatures ranging from 12°-22°C where adequate fluorescent light was provided for the proper development of rust infection.

RESULTS

A comparison of infection types on single gene lines for resistance to the leaf rust and a carrier line 'Thatcher' against stem rust cultures 40 and 122, the pathotypes that were virulent on 'Thatcher', is given in Table 1. Since 'Thatcher' is resistant to a number of stem rust pathotypes (21, 24, 34, 40A, 42B, 117, 117A-1), it was not possible with these cultures to establish whether the complete spectrum for resistance to stem rust in single gene lines for resistance to leaf rust was due to associated/additional stem rust resistance genes or to stem rust resistance in the carrier line, 'Thatcher'. The line carrying Lr13 that was available in 'Prelude' background was, however, observed to be susceptible to all the pathotypes tested.

The stem rust resistance of Tc+Lr2a to pathotype 122; of Tc+Lr19 or cv. 'Agatha' (Table 2) to all the pathotypes tested; of Tc+Lr21 and Tc+Lr23 to the pathotype 40; of Tc+Lr22 to both the pathotypes 40 and 122 needs special comments. Among the cultivars studied, 'Agatha' (Lr19), 'Agent' (Lr24), 'Benno' (Lr26) and 'Gatcher' (Lr27) were observed resistant to all the stem rust pathotypes whereas 'Transec' (Lr25) and 'Klein Titan' (LrKT) were effective to the Indian cultures of race 42 (Table 2).

DISCUSSION

The resistance to stem rust pathotype 122 in Tc+Lr2a is possibly due to Sr30, a stem rust resistance gene known to be present in 'Webster', the donor of Lr2a. Sr30 was reported to be effective to pathotype 122 (Sawhney and Goel, 1981).

A leaf rust resistance gene, Lr19 both in Tc+Lr19 and cv. 'Agatha' is known to be either identical or closely linked with stem rust resistance gene Sr25 and was derived from Agropyron elongatum. Sr25 gives resistance to all the Indian stem rust pathotypes (Sawhney and Goel, 1981). The stem rust resistance in Tc+Lr21 is reported to be identical with Sr21 from the diploid 'Einkorn' (McIntosh, 1981). This is supported by our seedling data where 'Einkorn' (Sr21) was found resistant to pathotype 40 and susceptible to pathotype 122

(Sawhney and Goel, 1981), a behaviour identical to that of Tc+Lr21 for reactions to these pathotypes. Lr21 was initially derived from Aegilops squarrosa var. meveri (Syn. Triticum tauschii). The resistance in Tc+Lr22 to stem rust pathotypes 40 and 122 could be due to an additional gene obviously derived from Aegilops squarrosa var. strangulata the source of Lr22. Lr23 in Tc+Lr23 was derived from 'Lee' which is reported to carry Sr9g, Sr11 and Sr16 (Luig, 1983). Resistance common to the pathotype 40 identified in Tc+Lr23 in this study and that in a line carrying Sr11 reported earlier (Sawhney and Goel, 1981) indicates that the stem rust resistance in Tc+Lr23 is possibly due to Sr11.

The resistance to stem rust in cv. 'Agent' (Lr24) and in cv. 'Benno' (Lr26), may be due to the well known identical or associated genes Sr24 and Sr31, respectively. Both these genes are completely effective to all Indian cultures of stem rust races tested (Sawhney et al., 1983).

Cultivar 'Gatcher' has been reported to possess Sr2, Sr5, Sr6, Sr8, Sr9g and Sr12 (Luig, 1983) in addition to two complementary dominant genes (Lr27 + an undescribed gene) for leaf rust resistance (Singh and McIntosh, 1984). The complete effectiveness for stem rust in 'Gatcher' could be due either to interaction between a number of known Sr genes or additional unknown ones, because the rust reaction on the cultivar is synergistic as compared with reaction produced by the six known stem rust resistance genes (Sawhney and Goel, 1981).

Cultivars 'Transec' (Lr25 and 'Klein Titan' (LrKT) produced incompatible reactions to the Indian culture of stem rust race 42. The stem rust resistance of 'Transec' to pathotype 42 is possibly due to an undescribed gene as 'Transec' does not carry any known stem rust resistance gene. Along with 'Klein Titan', cultivar 'Barleta Benvenuto' was also tested against pathotype 42. Both these cultivars were found to be resistant to this stem rust pathotype. This supports pathologically, the suggestion that these two cultivars share a common gene for resistance to stem rust (R.A. McIntosh, personal communication).

The stem rust resistance genes identified in the single gene lines/cultivars for leaf rust resistance in the present study should be of added advantage to breeders for incorporating simultaneously resistance to both the rusts.

ACKNOWLEDGEMENTS

We wish to express our sincere gratitude to Dr. R.A. McIntosh for helpful comments and to Dr. Roy Johnson for reading the manuscript. We also thank Dr. S. Nagarajan and his colleagues at IARI Regional Station, Shimla for supplying the initial spore inoculum of stem rust cultures.

REFERENCES

LUIG, N.H. (1983). A survey of virulence genes in wheat stem rust, Puccinia graminis f.sp. tritici. Advances in Plant Breeding, Vol. 11, pp.198, Paul Parey, Berlin.

McINTOSH, R.A. (1981). A gene for stem rust resistance in non-homoeologous chromosomes of hexaploid wheat progenitors. Proceedings XIII International Botanical Congress, Sydney, 274.

SAWHNEY, R.N., NAYAR, S.K., SINGH, S.D. & CHOPRA, V.L. (1977). Effectiveness of Lr genes for resistance against Indian races of leaf rust (Puccinia recondita Rob. ex. Desm.). Sabrao Journal 9: 13-20.

SAWHNEY, R.N. and GOEL, L.B. (1983). Effectiveness of newly described leaf rust resistance genes against Indian cultures of standard races and biotypes of leaf rust in wheat. Wheat Information Service 56: 34-36.

SAWHNEY, R.N. and GOEL, L.B. (1981). Race specific interactions between wheat genotypes and Indian cultures of stem rust. Theoretical and Applied Genetics 60: 161-166.

SAWHNEY, R.N., GOEL, L.B. and MATHUR, H.C. (1983). Genes for resistance to wheat stem rust. Indian Phytopathology 36: 730-732.

SINGH, R.P. and McINTOSH, R.A. (1984). Complementary genes for reaction to Puccinia recondita tritici in Triticum aestivum 11. Cytogenetic studies. Can. J. Genet. Cytol. 26 (6): 736-742.

STAKMAN, E.C., STEWART, D.M. and LOEGERING, W.Q. (1962). Identification of physiologic races of Puccinia graminis var. tritici. United States Department of Agriculture, Agriculture Research Service No. E617, 53.

TABLE 1 - Infection types on near isogenic lines for leaf rust resistance genes against Indian cultures of stem rust races virulent on 'Thatcher' (Tc), a carrier line.

Near isogenic lines	Infection types with pathotypes	
	40	122
Tc+Lr1	3	3
Tc+Lr2a	3	0;-2
Tc+Lr2b	3	3
Tc+Lr2c	3-4	3
Tc+Lr2d	4	3
Tc+Lr3 (Democrat)	4	3
Tc+Lr3 (Aniversario)	4	3
Tc+Lr3 (Bage)	3-4	3
Tc+Lr9	3	3
Tc+Lr10	4	3
Tc+Lr11	4	3-4
Tc+Lr12	3	4
Tc+Lr14a	3-4	3-4
Tc+Lr14b	4	3
Tc+Lr14ab	4	3
Tc+Lr15	3	4
Tc+Lr16	3	3
Tc+Lr17	3	4
Tc+Lr18	3	4
Tc+Lr19	0;-2	0;-1
Tc+Lr21	0;	3
Tc+Lr22	0;	0;-2
Tc+Lr23	0;-2	4
Thatcher (Tc) (Carrier line)	4	3-4

IT 0;, 0;-1, 0;-2 = resistant; IT 3, 4 = susceptible

TABLE 2 - Infection types on cultivars with known genes for leaf rust resistance when tested with prevalent and virulent Indian cultures of stem rust races.

Cultivar	Infection types with pathotypes									
	21	24	34	40	40A	42	42B	117	117A-1	122
'Agatha' (Lr19)	0;	0;	0;	0;	0;	0;-2	0;-1	0;	0;	;
'Thew' (Lr20)	4	2-3*	4	4	4	3	4	3-4	3	4
'Agent' (Lr24)	0;-2	0;	0;	0;	0;	0;	0;-1	0;-1	0;-2	0;-2
'Transec' (Lr25)	4	3	3-4	3	3-4	0;	3-4	3-4	3-4	3
'Benno' (Lr26)	0;	0;-1	0;	0;-1	0;	0;	0;-1	0;	0;	0;-2
'Gatcher' (Lr27)	0;	0;	0;	0;-1	0;-1	0;	0;-2	0;	0;	0;-2+
'Klein Titan' (LrKT)	3	4	3	3-4	3	0;	4	3	4	3-4

IT 0;, 0;-1, 0;-2, 0;-2+ = resistance; IT 3, 3-4, 4 = susceptible; * IT 2-3 = low infection.

Cereal Rusts Bulletin Vol 14, Part 2, 1986

DIVERSITY FOR RESISTANCE TO LEAF RUST IN TRITICUM DURUM (DESF.)

BY

D.L. Sharma* R.G. Saini, A.K. Gupta and Sangeeta Gupta
Department of Genetics
Punjab Agricultural University
Ludhiana-141 004, India

* Present Address : Regional Research Station, H.P. Agricultural University (HPKVV), Bajaura-175 125 (Kullu), India.

SUMMARY

Reactions of thirty-six wheats (Triticum durum) to eight Puccinia recondita cultures developed from Indian races were studied to establish diversity for leaf rust resistance genes. Based on the infection types these wheats were classified as nine diverse groups. All the wheats were susceptible to culture IL004 which is avirulent on all the known Lr genes from Triticum aestivum except Lr20. Nine wheats did not show resistance to any of the rust cultures but the remaining 27 were resistant to one or more of these rust cultures. Although these 27 wheats were susceptible to culture IL004, the weakest ever known leaf rust culture reported from India, these wheats were resistant to culture IL001 from the most virulent and predominant leaf rust race 77 indicating that the 27 durums are useful sources of resistance to this race and may possess new and as yet undescribed leaf rust resistance genes.

INTRODUCTION

Resistance to leaf rust caused by Puccinia recondita has been identified from many durum wheats and its inheritance in some of these wheats has also been reported (Statler, 1973; Rashid et al., 1976). However, not much is yet known about the diversity of resistance genes from durum wheats. Leaf rust culture IL004 (race 1) from India is avirulent on all the known Lr genes except Lr20 from T. aestivum and alien genes Lr26 and Lr28. All wheats showing susceptibility to culture IL004 and resistance to other highly virulent cultures should have Lr20 or new and yet undescribed leaf rust resistance genes. The present paper reports diversity for leaf rust resistance from thirty-six durum wheats showing susceptibility to culture IL004 and differential resistance to seven additional cultures of Puccinia recondita from India.

MATERIALS AND METHODS

The thirty-six wheats were grown in aluminium trays in a growth chamber maintained at a temperature of 20°C ± 1°C and relative humidity between 80-90 per cent. The first leaf of seven days old seedlings of each cultivar was inoculated using a uredospore-talc mixture. Five plants of each of these wheats were also grown in 0.5 metre long rows placed 30 cm apart in a polythene house with

temperature ranging between 18°C to 24°C. Three flag leaves from each of the two randomly selected adult plants of all these wheats were inoculated with a uredospore-talc mixture of culture IL011. Standard conditions for disease development were maintained and disease reaction as infection types (IT) on seedlings as well as the adult plants were scored 14 days after inoculation using a modification of the scale given by Stakman et al. (1962). The seedlings as well as the adult plants with infection types 0;, 1, 1^+, 2, 2^+, 3^C and 3^N were given an overall resistant rating while those with infection types 3, 3^+ and 4 were classified as susceptible.

The codes of the cultures used, their source race and avirulence/virulence formulae as determined on a single gene leaf rust resistant lines in Thatcher background (T. aestivum) are given in Table 1.

RESULTS AND DISCUSSION

Depending upon similarity of the overall reaction to eight leaf rust cultures the 36 wheats have been classified into nine diverse groups which are given in Table 2.

Cultivars Jaya, NP52, Moha, Malwi Local, AW3673, ND64-76, N59, D19329-28-11Y and T77 were susceptible to all the rust cultures at both adult plant and seedling stages. The four cultivars of group II were susceptible to all the cultures at the seedling stage while the adult plants were resistant to culture IL011 (race 77A). In addition to adult plant resistance, cultivars Wells, ND62-21, ND64-207, ND64-217 and MACS-9 in group III also showed some, but not complete, seedling resistance to culture IL011. All the stocks in group IV and V have complete seedling and adult plant resistance to culture IL011. Cultivars in group IV have a gene for resistance to culture IL016. Cultivar ND63-36 in group V has a gene for resistance to culture IL015. The cultivars in group VI have resistance to cultures IL011, IL015 and IL016 which may or may not be due to the same resistance factor(s). Cultivars in group VII have resistance to cultures IL011, IL016, IL015 and IL013, Group VIII cultivars, NP404 and MACS 825 show resistance to cultures IL005, IL009, IL013, IL015, IL016 and IL011. Maximum resistance appears to be present in ED3009 and NP400 belonging to group IX which showed resistance to seven out of the eight cultures used for the present work, being susceptible only to culture IL004.

All the cultivars tested are susceptible to culture IL004 which is avirulent on all the known Lr genes from T. aestivum except Lr20. Resistance of ED3009 and NP400 to cultures IL005, IL009 and IL016 and susceptibility to IL004 may indicate the presence of Lr20 or a new and yet undescribed gene or genes effective against these three cultures. If Lr20 is present it must be combined with additional gene(s) that give resistance to cultivars IL007, IL011, IL013 and IL015 all of which are virulent for Lr20. Similarly, cultivars NP404 and MACS 825 are resistant to the three cultures that are avirulent for Lr20 and susceptible to IL004. Again, this could indicate the presence of Lr20 but only in association with other genes giving resistance to cultures IL011, IL013 and IL016. A further problem in the suggestion that Lr20 may be present is that the role of ploidy level on expression of leaf rust resistance genes in wheat is not yet known. Lr20 was originally identified from a hexaploid wheat cultivar, Thew (Browder, 1972). This adds to the difficulty of

assessing the possible presence of Lr20 in the cultivars using the present data.

All the wheats tested here except for those in group I are resistant to the most virulent and predominant Indian leaf rust race 77 (biotype A) from which culture IL011 has been derived. Susceptiblity of all the durum wheats to culture IL004 which is the weakest ever known culture of leaf rust from India and their resistance to a highly virulent race like 77 suggests that the presently studied durums may have genes which are different than the genes identified from Triticum aestivum. Pandey and Rao (1984) have also indicated differences between the Lr genes identified from Triticum durum and those from Triticum aestivum.

Resistance against race 77 and its biotypes is not common in Triticum aestivum. Although the alien genes Lr9, Lr18, Lr19, Lr21, Lr24, Lr25 and Lr28 confer resistance against race 77 both at seedling and adult plant stage (Saini et al., 1986), their use in wheat has not been successfully demonstrated because of their association with many undesirable traits. The durum wheats are known as good donors of many quality characteristics. The present report indicates that durums may also be good donors of diverse resistance genes against some highly virulent races of leaf rust.

REFERENCES

BROWDER, L.E. (1972). Designation of two genes for resistance to Puccinia recondita in Triticum aestivum. Crop Sci., 12 : 705-706.

PANDE, H.N. and M.V. RAO (1984). Differential behaviour of aestivum and durum wheats to races 77 and 106 of leaf rust (Puccinia recondita Rob. ex. Desm.). Wheat Inform. Serv. 58 : 34-35.

RASHID, G., J.S. QUICK and G.D. STATLER (1976). Inheritance of leaf rust resistance in three durum wheats. Crop Sci., 16 : 294-296.

SAINI, R.G., A.K. GUPTA and D. ANAND (1986). Expression of some leaf rust resistance genes at different grown stages in wheat against race 77-A Curr. Sci., 55 : 802-804.

STAKMAN, E.C., D.M. STEWART and W.Q. LOEGERING (1962). Identification of physiological races of Puccinia recondita tritici. Minn. Agric. Exp. Sta. Sci. J. Series Paper 4691.

STATLER, G.D. (1973). Inheritance of resistance to leaf rust in Waldron wheat. Phytopathology, 63 : 346-348.

Table 1 - Leaf rust cultures, their source race and avirulence/virulence formulae.

Culture Code	Source race	Avirulence/virulence formulae
IL004		PLr1,2,3,10,11,12,13,14,15,16,17,18,21,22,23,27,30/pLr20
IL005, IL009*	162A	PLr1,11,15,20/pLr2,3,10,12,13,14,16,17,18,21,22,23,27,30
IL007	108	PLr3,15,27/pLr1,2,10,11,12,13,14,16,17,18,20,21,22,23,30
IL011	77A	PLr18,21,27/pLr1,2,3,10,11,12,13,14,15,16,17,20,30
IL013	106	PLr11,23/pLr1,2,3,10,12,13,14,15,16,17,18,20,21,22,27,30
IL015	106	PLr13,15,18/pLr1,2,3,10,11,12,14,16,17,20,21,22,23,27,30
IL016	107	PLr1,15,20,21/pLr2,3,10,11,12,13,14,16,17,18,22,23,27,30

*IL005 and IL009 give a 0; and 3^N reaction on Lr11, respectively.

Table 2 - Reactions of some durum wheats to 8 Indian leaf rust cultures

Group	Cultivars/Genetic stock	Source*	Leaf rust culture and reaction								
			IL004	IL005	IL009	IL007	IL013	IL015	IL016	IL011	
										Seedlings	Adult plants
I	Jaya,NP52, Moha, Malwi Local	AICWIP	4	3	3	3^{+}-4	3	3	3	3	3
	AW3673,ND64-76,N59, D19329-28-IIY	ISWN	3-4	3	3	3	3	3	3	3	3
	T-77	RAMC	4	3	3	3-3^{+}	3	3	3	3	4
II	ND64-32,ND64-33,DT-182,DT-184	ISWN	3	3	3	3	3	3	3	3	0;
III	Wells,ND62-21	ISWN	3	3	3	3	3	3	3	0;-2^{+}	0;
	ND64-207, ND64-217	ISWN	3	3	3	3	3	3	3	0;	0;
	MACS 9	AICWIP	3	3	3	3	3	3	3	2^{+}	2
IV	ND62-53, ND62-73	ISWN	3	3	3	3	3	3	2	0;-1	0;
V	ND63-36	ISWN	3	3	3	3	3	2^{+}	3	0;	0;
VI	D60-114,ND64-202, ND64-210	ISWN	3	3	3	3	3	2-2^{+}	2-2^{+}	0;	0;
	RL3686, Roussia,DT-183,Leeds	ISWN	3	3	3	3	3	2-2^{+}	2-2^{+}	2^{+}	0;
	Herculese,ND59-12,ND 63-60	ISWN	3	3	3	3	3	2-2^{+}	1^{+}	0;	0;
VII	18888-1M-3Y-5M-2Y,D14497-B-5M-9Y	ISWN	3	3	3	3	0;-2	2-2	0;-1	0;-1	0;
	NP401	AICWIP	3	3	3	3	1-2	-	-	0;-1	1
VIII	NP404	AICWIP	3	1	0;	3	0;-1	1	1	0;-2^{+}	0;
	MACS825	AICWIP	3	0;	3^{N}	3^{+}	0;	0;-1	0;	0;	0;
IX	NP400	AICWIP	3	1-2	0;-1	1	1-2	3^{N}	2	0;-1	0;
	ED3009	ISWN	3	2	0;-1	2	0;	1	1	0;-1	0;

* AICWIP = All India Coordinated Wheat Improvement Programme.
ISWN = International Spring Wheat Nursery
RAMC = University of Sydney, Australia

Cereal Rusts Bulletin Vol 14, Part 2, 1986

THE FUNCTION OF MYCOVIRUSES IN CEREAL RUSTS

BY

A.C. NEWTON

Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA, UK

Isolates of several species of cereal rusts contain double-stranded RNA (dsRNA) or virus-like particles (VLPs) (Newton et al., 1984; Lecoq et al., 1974; Mussel et al., 1973; Rawlinson & MacLean, 1973; McDonald & Heath, 1979) and VLPs have been noted in other rust fungi (Littlefield & Heath, 1974). Although it is difficult to quantify the proportion of isolates which contain dsRNA or mycoviruses, some reports indicate that they are found in most, if not all isolates (Newton et al., 1985) while others indicate a frequency of ca. 20% (Bozarth, 1972). However, in a few cases where the presence of dsRNA has been associated with a phenotypic expression, its occurrence was almost ubiquitous (Tavantzis & Smith, 1979; Ushiyama, 1979; Rawlinson et al., 1973; Zanzinger et al., 1984). It is reasonable, therefore, to speculate if the apparently ubiquitous occurrence of dsRNA in the cereal rusts is indicative of an important role in their life cycle, or whether it is due merely to an efficient transmission mechanism.

Molecular genetical investigations may elucidate the mechanisms of transmission of dsRNA, for example, whether integration into the nuclear genome occurs. However, the evidence from dsRNA banding patterns (Newton et al., 1985) and from hybridisation experiments described below may indicate a role for dsRNA which in some cases ensures its selection for efficient transmission.

Newton et al., (1985) reported that all isolates of Puccinia striiformis f. sp. tritici tested showed an identical dsRNA banding pattern and all isolates of f. sp. hordei showed identical dsRNA banding patterns in all but two groups of bands (group B & C) where bands were often vague. However, the two formae speciales had different banding patterns which clearly differentiated them. All other isolates of different rust species examined had unique banding patterns. P. striiformis differs from the other cereal rusts examined in that it has no known sexual cycle. However, it has been demonstrated that isolates of P. striiformis f. sp. tritici readily exchange nuclei between dikaryotic hyphae resulting in progeny of either parental genotype or two non-parental genotypes (Goddard, 1976; Little & Manners, 1969; Taylor, 1976; Wright & Lennard, 1980) up to c 10% being of the latter type (Little & Manners, 1969). Although such events have been reported in other rust fungi (e.g. Garret, 1960; Bridgmon & Wilcoxson, 1959), they do not rely solely upon this mechanism of nuclear reassociation. It is not yet known whether this somatic nuclear exchange occurs in P. striiformis f. sp. hordei as well as in f. sp. tritici although work on this question is in progress.

From the above facts we may speculate whether there is any direct causal correlation between dsRNA pattern uniformity and ability to readily exchange nuclei. In Ustilago maydis (Day & Dodds, 1979) and in Saccharomyces cerevisiae (Bevan & Mitchell, 1979) dsRNA encoded toxins ensure inter-isolate killing which is an extreme form of incompatibility. In cereal rusts, differences in dsRNA may also be expressed as differences in toxin production causing vegetative incompatibility. An individual isolate must be protected from the effects of its own toxin and thus compatibility would occur in interactions between isolates producing identical toxins. Therefore, if identical dsRNA banding patterns, as in P. striiformis f. sp. tritici, is indicative of identical toxin production, compatibility is ensured. It follows that any isolates of P. striiformis with differing dsRNA patterns would be incompatible if they affected the toxin encoding bands. Experimental evidence has demonstrated that incompatibility may occur between isolates of P. striiformis f. sp. tritici and f. sp. hordei (Newton et al., 1986). Thus toxin encoding bands may be amongst the 'D' group bands which clearly differentiate these two formae speciales (Newton et al., 1985). Furthermore, it is possible that a change in the dsRNA banding patterns gave rise to the two separate formae speciales of this species. However, further speculation as to whether toxin encoding bands are involved and where they are located depends upon further investigation and ultimately upon molecular genetical characterisation of these and other bands. Such characterisation may also provide evidence on the evolutionary relationships of the different formae speciales of P. striiformis. The evolutionary significance of mycoviruses in the cereal rusts may be considerable.

REFERENCES

BEVAN, E.A., & MITCHELL, D.J., 1979. The killer system in yeast. In: Viruses and Plasmids in Fungi. Series in Mycology. Volume 1. Ed. by P.A. Lemke, pp 162-201. Marcel-Dekker, New York.

BOZARTH, R.F., 1972. Mycoviruses: a new dimension in microbiology. Environmental Health Perspective 2: 23-29.

BRIDGMON, G.H., & WILCOXSON, R.D., 1959. New races from mixtures of varieties of Puccinia graminis. Phytopathology 44: 428-429.

DAY, P.R., & DODDS, J.A., 1979. Viruses of pathogenic fungi. In: Viruses and Plasmids in Fungi. Series in Mycology. Volume 1. Ed. by P.A. Lemke, pp 201-239. Marcel-Dekker, New York.

GARRET, W.N. 1960. Production of new races of Puccinia graminis var tritici by tissue transplants. Phytopathology 50 : 636.

GODDARD, M.V. 1976. Production of a new race 105 E 137, of Puccinia striiformis in glasshouse experiments. Transactions of the British Mycological Society 67, 395-398.

LÉCOQ, H., SPIRE, D., RAPILLY, F., & BERTRANDY, J., 1974. Mise en evidence de particules de type viral chez les Puccinia. Comptes Rendus de l'Academie de Sciences (Paris) Serie D 279: 1599-1602.

LITTLE, R., & MANNERS, J.G., 1969. Somatic recombination in yellow rust of wheat (Puccinia striiformis). I. The production and possible origin of two new physiologic races. Transactions of the British Mycological Society 53, 251-258.

LITTLEFIELD, L.J., & HEATH, M.C., 1979. Parasites of Rust Fungi. In: Ultrastructure of the Rust Fungi. Chapter 9, pp 242-249. Academic

Press, New York.
McDONALD, J.G., & HEATH, M.C., 1979. Unpublished reports cited in Littlefield, L.J. & Heath, M.C. 1979. Ultrastructure of the Rust Fungi. pp 242-245. Academic Press, New York.
MUSSEL, H.W., WOOD, M.A., ADLER, J.P., & BOZARTH, R.F., 1973. 2nd International Congress of Plant Pathology, Minneapolis, USA. Abstract No. 0908.
NEWTON, A.C., CATEN, C.E., & JOHNSON, R., 1985. Variation for isozymes and double-stranded RNA among isolates of Puccinia striiformis and two other cereal rusts. Plant Pathology 34: 235-247.
NEWTON, A.C., JOHNSON, R., & CATEN, C.E., 1986. Attempted somatic hybridization of Puccinia striiformis f. sp. tritici and P. striiformis f. sp. hordei. Plant Pathology 35: 108-113.
RAWLINSON, C.J., HORNBY, D., PEARSON, V., & CARPENTER, J.M., 1973. Virus-like particles in the take-all fungus, Gaeumannomyces graminis. Annals of Applied Biology, 74: 197-209.
RAWLINSON, C.J., & MACLEAN, D.J., 1973. Virus-like particles in axenic cultures of Puccinia graminis tritici. Transactions of the British Mycological Society 61: 590-593.
TAVANTZIS, S.M., & SMITH, S.H., 1979. Virus-like particles transmitted by and detected in spawn of the cultivated mushroom Agaricus bisporus. Phytopathhology 69: 104-107.
TAYLOR, E.C., 1976. The production and behaviour of somatic recombinants in Puccinia striiformis. Proceedings of the fourth European and Mediterranean Cereal Rust Conference, Interlaken. pp. 36-38.
USHIYAMA, R., 1979. Fungal viruses in edible fungi. In: Fungal viruses, pp. 29-33. Ed. by H.P. Molitoris, M. Hollings & H.A. Wood. Wien & New York: Springer Verlag.
WRIGHT, R.G. & LENNARD, J.H., 1980. Origin of a new race of Puccinia striiformis. Transactions of the British Mycological Society 74, 283-287.
ZANZINGER, D.H., BANDY, B.P., & TAVANTZIS, S.M., 1984. High frequency of finding double-stranded RNA in naturally occurring isolates of Rhizoctonia solani. Journal of Cereal Virology 65: 1601-1605.

Cereal Rusts Bulletin Vol 14 Part 2, 1986

POSTULATION OF GENES FOR STEM RUST RESISTANCE IN 24 CHINESE WHEAT CULTIVARS

BY

CHANG-CHENG HU & A.P. ROELFS

Cereal Rust Laboratory, USDA, ARS, Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108 USA
Senior Author address now, Institute of Plant Protection, Agric. Acad. of China Ma-Lin-Wa, Beijing, Peoples Republic of China

ABSTRACT

The presence of genes for resistance to stem rust (Puccinia graminis Pers. f. sp. tritici) was studied in 24 Chinese wheat cultivars by determining their reactions to 23 stem rust isolates. These were the most widely grown cultivars in the 1960 and 1970's. Only 7 genes for stem resistance: Sr5, 6, 8a, 11, 17 and Tmp of the 25 Sr genes evaluated were postulated as being present in any cultivars. Yang-Mai possessed genes for resistance other than those studied. No Sr genes for resistance were detected in Beijing 6, Beijing 8, Beijing 15, Shi-Jia-Zhung 34, Feng-Chen 3 and Ai-Feng 4. Sr5 was postulated in Dong-Fang-Hong 2, Dong-Fang-Hong 6, Ke-Feng 1, Beijing 10, An-Hewi II, Jing-Hong 1, Jing-Hong 2 and Qing-Chung 5. SrTmp was postulated in Nung-Ta 311, Nung-Ta 139, Beijing 9, Beijing 11, Bai-Yu-Bao, Yen-An 15, Xuzhow 14 and Beijing 10. Sr8 was postulated in E-Gan-Zao and An-Hewi II. Sr17 was postulated in E-Gan-Zao, Jing-Hong 1 and Jing-Hong 2 while Sr6 and Sr11 probably occur in Qing-Chung 5.

INTRODUCTION

Many genes for stem rust resistance have been used in the development of commercial wheat cultivars. When the plant pathologist and plant breeder know which gene(s) for resistance to stem rust are present or lacking in a wheat cultivar, a better choice of parents can be made. Additionally the risk of stem rust developing when these cultivars are used in commercial production can be better determined if the virulence of the pathogen population is monitored.

Based upon the gene-for-gene concept, the presence of the specific resistance gene(s) in the host can be postulated with suitable combinations of genes for avirulence and virulence in the pathogen (3,4). Therefore, 24 Chinese wheat cultivars were tested for the presence of stem rust resistance genes Sr5, 6, 7a, 7b, 8a, 9a, 9b, 9d, 9e, 10, 11, 12, 13, 14, 15, 16, 17, 23, 24, 25, 26, 29, 31, 36, and Tmp.

MATERIALS AND METHODS

Seed of 24 Chinese wheat cultivars were from seed storage at Cereal Rust Laboratory, St. Paul. These cultivars were all important commercial cultivars in China during the period of 1960 to 1970. Bima 1 and McNair 701 were added as checks. Bima 1 was a major commercial

cultivar in China in early 1950's. McNair 701 has been used by the Cereal Rust Laboratory as a standard check for susceptibility among winter wheats. The seeds of Bima 1 wwere furnished by Professor H.R. Wang and Mr K.N. Wang of China. The origin and year of release of each of the Chinese cultivars are given in Table 1. The 23 cultures of stem rust used are given in Table 2. The evaluation of the 24 Chinese wheat cultivars to stem rust were made at the Cereal Rust Laboratory, St. Paul. The infection type produced by the selected isolates on the designated monogenic lines are presented in Table 3.

Plants were grown in 7 cm^2 plastic pots of vermiculite. Each set of 6 pots was placed in a plastic tray (16 cm x 24 cm) with 4 lines per pot. Five days after planting the plants were fertilized with a water-soluble fertilizer (23-19-17, N-P-K) at a rate of 2.5 g per tray. The 7-day-old plants were inoculated with a spore suspension in a light weight mineral oil carrier, then placed in a dew chamber at 18°C overnight. The next morning the chamber was illuminated (10,000 lux) and the temperature gradually was raised to 30°C over a 4-hour period so the dew evaporated slowly. Then the plants were placed in a greenhouse at 18°C supplemented with 11,000 lux of fluorescent light. The infection types were scored 14 days after inoculation (7).

The presence of genes for resistance to stem rust was postulated by the comparison of the infection type of the tested cultivars with 25 selected monogenic lines which have been described elsewhere (1,2,6,8).

RESULTS

The low infection type (I.T.) produced on 24 Chinese wheat cultivars by isolates of stem rust and their postulated genotypes for stem rust resistance are summarised in Table 4.

The cultivars Beijing 6, Beijing 8, Beijing 15, Shi-Jia-Zhung 34, Feng-Chen 3, Ai-Feng 3, Bima 1 and McNair 701 were susceptible to all cultures. Ten cultivars had only one gene tested for, five cultivars have 2 genes and 2 cultivars have 3 genes. Yang-Mai 1, has unknown gene(s) as shown by I.T. 23CN with races QSH, QFB, RHR, RSH and GCC.

Dong-Fang-Hong 2, Dong-Fang-Hong 6 and Ke-Feng 1 have Sr5 as shown by I.T. 0; with races BBC, BCC, HJC, KBC, DKC, GDC, GCC and GCC. However, Dong-Fang-Hong 2 and Dong-Fang-Hong 6 may have other resistance gene(s) as shown by I.T. 0; with races RKH, RTH, RKQ. Ke-Feng 1 also has a gene(s) for resistance to races TTR, MBC, QSH, QFB, QCM and RKH.

Nine cultivars, Nung-Ta 311, Nung-Ta 139, Beijing 9, Beijing 10, Beijing 11, Bai-Yu-Bao, Ai-Feng 4, Xuzhou 14 and Yeng-An 15 have SrTmp. Beijing 10 may have Sr5 in addition as shown by I.T. 0; with races BBC, BCC, HJC, KBC, DKC, GDC, GCC and GCC.

Jing-Hong 1 and Jing-Hong 2 have Sr5 and Sr17, in addition they have another resistance shown by I.T.; with races TNM virulent on Sr17 (column 1) and MBC. If it was Sr6 then QFB, QCM should have resulted in a 0; IT. E-Gan-Zao has Sr8, 17 and an additional gene (low I.T. with races RHR, RSH, RLQ and HJC). Qing-Chun 5 has Sr5, 6, and 11, as well as resistance to races RSH, RTH and RTQ.

DISCUSSION

The distribution of the Sr genes for resistance to P. graminis for which we tested was limited in these Chinese cultivars. Only six of the known genes were detected. However, some of them such as Sr5, 6, 8, 11, and 17 are important genes world-wide, and virulence for them individually is common. Eight of the cultivars have SrTmp. The low I.T. of SrTmp of 2- occurred in wheats with the Triumph-type background (5). The isolates virulent on SrTmp in this test are of races 15 and 56 which are important races in North America. Seven of the important commercial wheat cultivars had none of the genes for stem rust resistance detected by the isolates used in this test. Special attention must be given to find out what virulences exist in the pathogen population in China and to select resistance genes effective against them.

REFERENCES

LUIG, N.H., 1983. A survey of virulence genes in wheat stem rust, Puccinia graminis f. sp. tritici. Verlag Paul Parey. Berlin and Hamburg.

MCINTOSH, R.A., 1983. A catalogue of gene symbols for wheat (1983 Edition). Proc. 6th International Wheat Genetics Symposium, Kyoto, Japan pp. 1197-1254.

MCVEY, D.V. 1986. Postulation of genes for stem and leaf rust resistance in the International Wheat Performance Nursery XII and XVII. Proc. 4th International Wheat Conf. May 2-5, 1986; Rabat, Kingdom of Morocco. (In press).

MCVEY, D.V., & ROELFS, A.P., 1975. Postulation of genes for stem rust resistance in the entries of the Fourth International Winter Wheat Performance Nursery. Crop Science. 15:335-337.

MCVEY, D.V., & HAMILTON, K., 1985. Stem rust resistance gene from Triumph 64 identified in four other winter wheats. Plant Disease 69: 217-218.

ROELFS, A.P., & MCVEY, D.V. 1979. Low infection types produced by Puccinia graminis f. sp. tritici and wheat lines with designated genes for resistance. Phytopathology 69: 722-730.

ROELFS, A.P., 1984. Race specificity and methods of study, pp. 131-164. In The Cereal Rusts Vol I. Origins, Specificity, Structure, and Physiology, W.R. Bushnell and A.P. Roelfs, eds. Academic Press, Orlando.

ROELFS, A.P., 1985. Wheat and rye stem rust, pp. 3-37. In The Cereal Rusts Vol. II. Diseases, Distribution, Epidemiology and Control, A.P. Roelfs and W.R. Bushnell, eds. Academic Press, Orlando.

TABLE 1. The source of 24 Chinese wheat cultivars that were widely grown in the 1960's and 1970's.

Cultivar	Origin	Year released	Pedigree
Nung-ta 311	Beijing Agric Univ	1963	Triumph/Ya-ta 1817
Nung-ta 139	Beijing Agric Univ	1968	Nung-ta 183/Virgillo// Yan-ta 1817/30983
Dong-Fang-Hong 2	Beijing Agric Univ	1968?	Nung-ta 45, Selection
Dong-Fang-Hong 6	Beijing Agric Univ	1968?	Nung-ta 45, Reselection
Beijing 6	Chinese Acad Agric Sci	1961	North China 187, Selection
Beijing 8	Chinese Acad Agric Sci	1963	Bima 4/Early Premium
Beijing 9	Chinese Acad Agric Sci	1964	Shi-te 14/Skorospelka L-1//Shan-Xi 54//Early Premium/3/ Nung-ta 183
Beijing 10	Chinese Acad Agric Sci	1965	North China 672/Xin-Shi-Mai//Skorospelka L-1/North China 672
Beijing 11	Chinese Acad Agric Sci	1968	5711 66/Beijing 8
Beijing 15	Chinese Acad Agric Sci	1970	North China 187/Shi-te 14// Skorospelka L-1/3/Early Premium/Bima 4//Skorospelka L-1
Jing-Hong 1	Chinese Acad Agric Sci	1967	Orofen/N. P. 798
Jing-Hong 2	Chinese Acad Agric Sci	1967	Orofen/N. P. 798
Shi-Jia-Zhung 34	Agric Acad Hebei Prov	1963	Shi-Jia-Zhung 407/Mentana
Bia-Yu-Bao	Yan tai Agric Instit Shandong Prov	1970	You-Zi-Mai/Bao-ta-San-Bai-Pao
Xuzhou 14	Xuzhou Agric Instit Jiangsu Prov	1962	Early Premium/Mentana
Yang Mai 1	Yangzhou Agric Instit Jiangsu Prov	1972	Funo, Selection
E-Gan-Zao	Agric Acad Jiangsu Prov	1964	Tevere/East China 6
An-Hwei 11	Agric Acad Anhwei Prov	1966	Forlani/Early Premium
Feng-Chen 3	Northwest Agric College	1966	Heine Hvede/Xi-Nung 6028
Ai-Feng 3	Northwest Agric College	1971	Xian-Nung 39/58(18)2// Feng-Chen 3
Ai-Feng 4	Northwest Agric College	1971	Xian-Nung 39/58(18)2// Feng-Chen 3
Bima 1	Northwest Agric College	1947	Ma-Zha-Mai/Quality
Qing-Chun 5	Agric Acad Qing Hai Prov	1969	Abbondanza/Orofen
Ke-Feng 1	KeShen Agric Instit He-Long-Jiang	1968	Merit/CI 12268/4/Ke-53-652/ Yican 304/3/CI 12356/5/Funo/ 6/Yuan 142//CI 12268/3/Funo

TABLE 2. Test cultures of *Puccinia graminis* f. sp. *tritici* used to postulate the *Sr* genes for resistance in 24 Chinese wheat cultivars.

Race[1] CRL	Culture no.	Virulence formula[2]
TNM	74-21-1409-A	5,7a,7b,8a,9d,9e,10,11,12,14,16,17,23,36,Tmp
TNM	74-04-01-A	5,7a,7b,8a,9d,9e,10,11,12,14,16,23,36,Tmp
TTR	81-SA-BZ-05-A	5,6,7a,7b,8a,9a,9b,9d,9e,10,11,12,14,15,16,17,23,36,Tmp
MBC	59-14-19	5,7a,7b,10,15,16,17,Tmp
QSH	69-21-399	5,6,7a,8a,9b,9d,10,11,12,14,15,16,17
QFB	80-21-599-3	5,8a,9a,9d,12,14,15,16,17
QCM	84-CA-89-C	5,7a,9a,9d,10,12,14,15,16,17,36
RHR	71-21-584-B	5.6.7a,7b,9a,9b,9d,10,12,14,15,16,17,23,36
RKH	72-ETH-5-2	5,6,7a,7b,8a,9a,9b,10,12,15,16,23
RSH	72-18-0630-B	5,6,7a,7b,8a,9b,9d,10,11,12,14,15,16,17
RKQ	70-11-0098-B	5,6,7b,8a,9a,9b,9d,12,14,15,16,36
RTH	84-MOR-445-A	5,6,7a,7b,8a,9a,9d,9d,10,11,12,14,15,16,17
RKQ	72-25-0639-C	5,6,7b,8a,9a,9b,9d,12,14,15,16,17,36
RTQ	72-00-0053-C	5,6,7b,8a,9a,9b,9d,11,12,14,15,16,36
BBC	75-45-1385-A	10,14,15,16,17,23
BCC	72-22-1160-2	7a,9a,10,12,14,15,16,17
HJC	70-44-64-A	6,7a,7b,8a,9d,10,12,14,15,16,17
LBB	111-S2	5,15
KBC	25-0-JBR-A	7b,9d,9e,10,12,14,15,16,17
DKC	75-45-1622-A	6,7a,8a,9a,9e,10,14,15,16,17
GDC	75-45-1550-C	7a,8a,9d,10,14,15,17,23
GCC	74-45-1328-B	7a,9a,9d,10,14,15,16,17
GCC		7a,9a,9d,10,12,14,16,23

1 = See Roelfs (8).
2 = *Sr5*, *6*, *7a*, *7b*, *8a*, *9a*, *9b*, *9d*, *9e*, *10*, *11*, *12*, *13*, *14*, *15*, *16*, *17*, *23*, *24*, *25*, *26*, *27*, *29*, *31*, *36* and *Tmp* evaluated.

TABLE 3. Low infection types produced by interaction of 23 cultures of Puccinia graminis f. sp. tritici and 25 wheat lines with a single known gene for resistance.

SR	Pathogen cultures (Table 2)																				
gene	TNM	TNM	TTR	MBC	QSH	QFB	QCM	RHR	RKH	RSH	RKQ	RTH	RKQ	RTQ	BBC	BCC	HJC	LBB	KBC	DKC	GDC	GCC	GCC
5															;	;	;		;	;	;	;	;
6	;	;		;		;	;								;	;		;	;		;	;	;
7a						23C					23C		23C	XCN	23C			;1C	2C				
7b					2-	2	2								2	2		2-		2-	2-	2	2
8a				2-			2	2							2	2-		2=	2=			2	2
9a	2-	2-		2-	2					2					2		2	23	2=		2=		
9b	2	2		2		2	2								2	2	2	2-	21	2	2-	2+	2
9d				1											1	1-		1		1-			
9e				;1	;1	;1=	;1	;1-	;1	;1=	;1	;1	;1	;1	;	;	;1	;1=			;1-	;	;1
10						1N					1N		1N	1N				1CN					
11				;		;	;2-	1	;2-		21		2		2=	;	;	1=C	;1-	;	;	;	;2-
12				X=											23C			X=		X=	X-	X=	
13	2	2	2	2	2	2	2	2	2	2	2+	2	2	2-	2	2	2	2=	2	2	2-	2	2
14				21CN														;				2	
15	XCN	XCN																					:1+N
16																2		2=			2=		
17		;							;		;	;		;		;		;					;1N
23				23C	23C					23CN						23CN	23CN	;		23CN		;1-	
24	2	2	2	2-	2=	2=	2=	2	2	2-	2	2	2	2	2	2=	2-	2=	2=	2	2=	2=	2=
25	2	2-	2-	2-	2	2=	2=	2	2	2	2-	2-	2	2	2	2	2=	2=	2=	2=	2-	2=	2=
26	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=
29	2	2=	2=	2-	2=	2-	2-	2-	2-	2-	2-	2-	2	2-	2	2-CN	2=	2=	2=	2=	2-	2=	2=
31	2-	2=	2=	2=	2=	2=	2=	2=	2=	1	2=	2=	2=	2=	1	;1C	;1-	1	;1	;1-	2=	;	;
36				0;	0	X-			0;	0		0;			0	0	0	0	0	0	0	0	0;
Tmp					2=	2=	2-	2	2=		2=	2-	2-	2=	2=	2=	2=	;	2=	2=	2=	2=	2-

1. Infection types after Roelfs (7)

TABLE 4. Postulated genotype and low infection types produced by interaction of 23 cultures of Puccinia graminis f. sp. tritici and 24 commercially important wheat cultivars grown in China between the 1960 and 1970.

	Pathogen cultures (from Table 2)																						SR
Cultivar	TNM	TNM	TTR	MBC	QSH	QFB	QCM	RHR	RKH	RSH	RKQ	RTH	RKQ	RTQ	BBC	BCC	HJC	LBB	KBC	DKC	GDC	GCC	GCC	[1]gene(s)
Bima 1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	Check
McNair 701	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	Check
Beijing 6																								None
Beijing 8																								None
Beijing 15																								None
Shi-Jia-Zhung 34																								None
Feng-Chan 3																								None
Ai-Fang 3																								None
Dong-Fang-Hong 2									0;		23C	0	0		2-	0	0	0	0	0	0	0	0	Sr5+
Dong-Fang-Hong 6									0		23C	0	0		0	0	0	0	0	0	0	0	0	Sr5+
Ke-Feng 1			1+	12	23C	3C	X-		0			0;1	0		0	0	0	0	0	0	0;1	0	0;	5+
Nung-ta 311					2	2	2	2	2	2	2	2	2-	2	2-	2	2-	2	2	2	2	2	22+	Tmp
Nung-ta 139					2	2	2	2	2	2	2	2	2	2	2	12	2	2	2	2	2	2	2	Tmp
Beijing 9					2	2	23	2	2-2	32	22+	2	2	2	0	2-	2	2	2	2+	2	2	2	Tmp
Beijing 11						2	2	2+	2	22+	2	2	2	2	2	2+	2	2	2	2	2	2	2	Tmp
Bai-Yu-Bao					23	2	2	2	0;2	0	2	2	2	2	2	2-	2	2	2-	2	2	2+	2	Tmp
XuZhou					2+	23	23	2	2+	22+	22+	2	23	2	2	2+	2	23	23	2	23	2	23	Tmp
Ai-Fang 4					23	23	23	1+2	2	2+3	12C	2+	23	2	2	2	2	2H	2	2+	23	2	23	Tmp
Yen-An 15						23	22+	;1N	2	2	;1CN	2+	2		2	2	;2-	2H	2H	2+	23	2	2+	Tmp
Beijing 10					2	2	23	23	23	2	2	0;	0	2	0;	;	0	0	0;	0;	0	0	0	Tmp,5
An-Hwei 11				2	2	2	2	0;1	0;-	0	;1-	0;	02		2	0;		0	0	0	2-	0	0	5,8a
E-Gan-Zao		0;		2			2	;1N	2	2	2	;1	12-	X	12N	02	X	2	2+		;2	2	:12	8a,17,+
Jing-Hong 1	0;	0;			X-		23	;2	01-		2-2	;	0?	0;	0;	0;	0;	0;	0;	0;	0;	0;	0;1	5,17,+
Jing-Hong 2	;	0;			0;-	2	23	0;	0;		2-	;	2	0;	0;	0;	0;	0;	0;	0;	0;	0;	0;	5,17,+
Qing-Chun 5		0;	0;	0;		02-	X-	0;?	0?		2+	0	0?	0;	0	0	0	0	0;	0	0;	0	0	5,6,11
Yang-Mai 1				12-	23C	23C	2	23C	12	23C		2	02-		2	12N		2	2	3+C		2	23	?

1 = after Roelfs, (8)

Cereal Rusts Bulletin Vol 14, Part 2, 1986

POSTULATION OF GENES FOR STEM RUST RESISTANCE IN 13 CHINESE WHEAT CULTIVARS

BY

CHANG-CHENG HU & A.P. ROELFS

Cereal Rust Laboratory, USDA, ARS, Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108 USA
Senior Author address now Institute of Plant Protection, Agric. Acad. of China Ma-Lin-Wa, Beijing, Peoples Republic of China

ABSTRACT

Thirteen current commercial cultivars of Chinese wheat were tested for the presence of gene(s) for resistance to stem rust (*Puccinia graminis* f. sp. *tritici*) by use of 23 stem rust isolates. Dong-Xie 3 and Dong-Xie 4 possess *Sr5* and *31*. Feng-Kang 2, Feng-Kang 8, Jing-Dan 106, Yi 78-4078, Lu-Mai 1 and Yan 7770-4 probably have *Sr31*. Feng-Kang 13 has *Sr5* plus another unidentified gene. Fu 63, Jing-Mai 11, Yan-An 15, and Bei-Nong 3217 probably have an undesignated resistance gene(s) effective against only a few cultures.

INTRODUCTION

Six genes (*Sr5*, *6*, *8a*, *11*, *17*, and *Tmp*) for wheat stem rust resistance were postulated in a set of 24 commercial Chinese wheat cultivars grown during the period 1960 to 1970 (2). This study evaluates 13 commercial cultivars from the 1970-1980 period. The information concerning the gene or genes for resistance to stem rust enables a better choice of parents for crosses and for determining whether these cultivars can be used as a base of resistance on which to build in future years.

Based upon the gene-for-gene concept of Flor, the presence of specific resistance gene(s) in the host can be demonstrated with suitable combinations of genes for avirulence and virulence in the pathogen (4,5). The 13 current commercial Chinese wheat cultivars were tested for the presence of stem rust resistance genes *Sr5*, *6*, *7a*, *7b*, *8a*, *9a*, *9b*, *9d*, *9e*, *10*, *11*, *12*, *13*, *14*, *15*, *16*, *17*, *23*, *24*, *25*, *26*, *29*, *31*, *36*, and *Tmp* (3,6,8).

MATERIALS AND METHODS

The Chinese wheat cultivars were from the Institute of Crop Breeding and Cultivation, Chinese Academy of Agricultural Science, Beijing. The origin of these cultivars is shown in Table 1. Cultures of *Puccinia graminis* Pers. f. sp. *tritici* of stem rust are given in Table 2. Plants were grown in vermiculite in a plastic tray (16 cm x 24 cm) holding 6 plastic pots (7 cm x 7 cm) with four lines per pot. Five days after planting the plants were fertilized with a water-soluble fertilizer (23-19-17, N-P-K) at a rate of 2.5 g per tray. The 7-day-old plants were inoculated with a spore suspension in a light weight mineral oil carrier, then placed in a dew chamber at

18°C overnight. The next morning the chamber was illuminated (10,000 lux) and the temperature was gradually raised to 30°C over a 4-hour period so the dew evaporated slowly. Then the plants were placed in a greenhouse at 18°C supplemented with 11,000 lux of fluorescent light. The infection types were recorded 14 days after inoculation (7).

RESULTS

The reaction and the genotypes postulated of 13 Chinese wheat cultivars to 23 isolates of stem rust resistance are presented in Table 4. Four cultivars (Jing-Mai 11, Yan-An 15, Bei-Nong 3217 and Fu 63) have none of the designated genes for stem rust resistance detected by the isolates used in this test. This resistance was generally inadequate against many of the cultures evaluated and was effective only against cultures selected for their avirulence.

Eight cultivars probably have Sr31: Dong-Xie 3, Dong-Xie 4, Feng-Kang 2, Feng-Kang 8, Yi 78-4078, Yan 7770-4, Jing-Dan 106 and Lu Mai 1. This resistance has been effective worldwide to date. The low infection type was similar to that for Sr31 (Table 3 & 4).

Dong-Xie 3 and Dong-Xie 4 also have Sr5 as shown by the low infection type (0-0;) with races BBC, HJC, KBC, DKC, GDC, GCC and GCC. Feng-Kang 13 also has Sr5 in combination with an undesignated resistance gene. Resistance of Fu 63 was shown by low infection type with races QCM, RKQ, KBCS, DKCS, GDC, GCC and GCC. Jing-Mai 11 was resistant to races MBC, QCM, RKQ, BBC, BBC and LBB. Yan-An 15 was resistant to QCM, RHR, RKH, RKQ and KBC. Bei-Nong 321 was susceptible to all races except KBC.

DISCUSSION

The distribution of the Sr genes for resistance to P. graminis for which we tested was very limited in this set of Chinese cultivars of current importance. Eight cultivars have Sr31 probably due to the wide use of 'Lovrin 10' and 'Lovrin 13' (1) as parental material. Sr31 is linked to Lr26 and Yr9 and they are located on the chromosome 1R/1B which was transferred from rye. This translocation has been introduced into many wheats worldwide from the Russian cultivars, 'Aurora' and 'Kavkaz'. Four cultivars (Fu63, Jing-Mai 11, Yan-An 15, and Bei-Nong 321) have none of the designated genes for stem rust resistance detected by the isolates used in this test. These cultivars probably have an inadequate base of resistance for use in commercial production in areas where stem rust occurs. It is now necessary to determine the virulence genes of the pathogen population in China as well as to select resistance genes to use in China.

REFERENCES

BARTOS, P., 1984. Genes for stem rust resistance in European wheats. Proc. Eur. Mediterr. Cereal Rusts Conf. VI., Grignon, France, pp. 29-32.

HU, C.C., & ROELFS, A.P., 1986. Postulation of genes for stem rust resistance in 24 Chinese wheat cultivars. Cereal Rusts Bulletin 14: 61-67.

LUIG, N.H., 1983. A survey of virulence genes in wheat stem rust, Puccinia graminis f. sp. tritici. Verlag Paul Parey. Berlin and

Hamburg.
MCVEY, D.V., 1986. Postulation of genes for stem and leaf rust resistance in the International Winter Wheat Performance Nursery XII and XVII. Proc. 4th International Wheat Conf. May 2-5, 1986; Rabat, Kingdom of Morocco. (In Press).
MCVEY, D.V., & ROELFS, A.P., 1975. Postulation of genes for stem rust resistance in the entries of the Fourth International Winter Wheat Performance Nursery. Crop Science. 15:335-337.
ROELFS, A.P., & MCVEY, D.V., 1979. Low infection types produced by Puccinia graminis f. sp. tritici and wheat lines with designated genes for resistance. Phytopathology 69: 722-730.
ROELFS, A.P., 1984. Race specificity and methods of study, pp. 131-164. In The Cereal Rusts Vol I. Origins, Specificity, Structure, and Physiology, W.R. Bushnell and A.P. Roelfs, eds. Academic Press, Orlando.
ROELFS, A.P., 1985. Wheat and rye stem rust, pp. 3-37. In The Cereal Rusts Vol. II. Diseases, Distribution, Epidemiology and Control, A.P. Roelfs and W.R. Bushnell, eds. Academic Press, Orlando.

TABLE 1. The source of 13 Chinese wheat cultivars that were important commercially in the 1970 and 1980's.

Cultivar	Origin	Pedigree
Dong-Xie 3	Beijing	Double 6/Predgorinaya 2//Double 3
Dong-Xie 4	Beijing	You-Bao 36/Lovrin 13
Feng-Kang 2	Beijing	Awn-white 4/Lovrin 10
Feng-Kang 8	Beijing	Awn-red 7/Lovrin 10
Feng-Kang 13	Beijing	Kang-Bai 14/Kang-Yin 655
Jing-Dan 106	Beijing	You-Bao/Awn-red 7//Double 6/Predgorinaya 213/Awn-red 7/Lovrin 10
Yi 78-4078	Hebei	E-Gan-Zao/Lovrin 10
Lu-Mai 1	Shan-Dong	Feng-Chen 3//Meng-Xian 205/Neuzucht
Fu 63	Shan-Dong	You-Bao/Orofen (irradiated)
Yan 7770-4	Shan-Dong	Yan-Nung 685/Ai Bian 1
Jing-Mai 11	Shaan-Xi	Wei-Dong 7/Wei-Dong 8
Yan-An 15	Shaan-Xi	Bulgarian 10/Tai-Gu 49//Beijing 5
Bei-Nong 3217	Zheng-Zhou	Funo/Nei-Xiang 5//Xian-Nong 39/3/Xi-Nong 64L4743/Yan-Ta 24

TABLE 2. Test cultures of *Puccinia graminis* f. sp. *tritici* used to postulate the *Sr* genes for resistance in 24 Chinese wheat cultivars.

Race[1] CRL	Culture no.	Virulence formula[2]
TNM	74-21-1409-A	5,7a,7b,8a,9d,9e,10,11,12,14,16,17,23,36,Tmp
TNM	74-04-01-A	5,7a,7b,8a,9d,9e,10,11,12,14,16,23,36,Tmp
TTR	81-SA-BZ-05-A	5,6,7a,7b,8a,9a,9b,9d,9e,10,11,12,14,15,16,17,23,36,Tmp
MBC	59-14-19	5,7a,7b,10,15,16,17,Tmp
QSH	69-21-399	5,6,7a,8a,9b,9d,10,11,12,14,15,16,17
QFB	80-21-599-3	5,8a,9a,9d,12,14,15,16,17
QCM	84-CA-89-C	5,7a,9a,9d,10,12,14,15,16,17,36
RHR	71-21-584-B	5.6.7a,7b,9a,9b,9d,10,12,14,15,16,17,23,36
RKH	72-ETH-5-2	5,6,7a,7b,8a,9a,9b,10,12,15,16,23
RSH	72-18-0630-B	5,6,7a,7b,8a,9b,9d,10,11,12,14,15,16,17
RKQ	70-11-0098-B	5,6,7b,8a,9a,9b,9d,12,14,15,16,36
RTH	84-MOR-445-A	5,6,7a,7b,8a,9a,9d,9d,10,11,12,14,15,16,17
RKQ	72-25-0639-C	5,6,7b,8a,9a,9b,9d,12,14,15,16,17,36
RTQ	72-00-0053-C	5,6,7b,8a,9a,9b,9d,11,12,14,15,16,36
BBC	75-45-1385-A	10,14,15,16,17,23
BCC	72-22-1160-2	7a,9a,10,12,14,15,16,17
HJC	70-44-64-A	6,7a,7b,8a,9d,10,12,14,15,16,17
LBB	111-S2	5,15
KBC	25-0-JBR-A	7b,9d,9e,10,12,14,15,16,17
DKC	75-45-1622-A	6,7a,8a,9a,9e,10,14,15,16,17
GDC	75-45-1550-C	7a,8a,9d,10,14,15,17,23
GCC	74-45-1328-B	7a,9a,9d,10,14,15,16,17
GCC		7a,9a,9d,10,12,14,16,23

1 = See Roelfs (8).
2 = *Sr5*, *6*, *7a*, *7b*, *8a*, *9a*, *9b*, *9d*, *9e*, *10*, *11*, *12*, *13*, *14*, *15*, *16*, *17*, *23*, *24*, *25*, *26*, *27*, *29*, *31*, *36* and *Tmp* evaluated.

TABLE 3. Low infection types produced by interaction of 23 cultures of Puccinia graminis f. sp. tritici and 25 wheat lines with a single known gene for resistance.

SR	Pathogen cultures (Table 2)																				
gene	TNM	TNM	TTR	MBC	QSH	QFB	QCM	RHR	RKH	RSH	RKQ	RTH	RKQ	RTQ	BBC	BCC	HJC	LBB	KBC	DKC	GDC	GCC	GCC
5															;	;	;		;	;	;	;	;
6	;	;		;		;	;								;	;		;	;		;	;	;
7a						23C					23C		23C	XCN	23C			;1C	2C				
7b					2-	2	2								2	2		2-		2-	2-	2	2
8a				2-			2	2							2	2-		2=	2=			2	2
9a	2-	2-		2-	2					2					2		2	23	2=		2=		
9b	2	2		2		2	2								2	2	2	2-	21	2	2-	2+	2
9d				1											1	1-		1		1-			
9e				;1	;1	;1=	;1	;1-	;1	;1=	;1	;1	;1	;1	;	;	;1	;1=			;1-	;	;1
10						1N					1N		1N	1N				1CN					
11				;		;	;2-	1	;2-		21		2		2=	;	;	1=C	;1-	;	;	;	;2-
12				X=											23C			X=		X=	X-	X=	
13	2	2	2	2	2	2	2	2	2	2	2+	2	2	2-	2	2	2	2=	2	2	2-	2	2
14				21CN														;				2	
15	XCN	XCN																					:1+N
16																2		2=			2=		
17		;							;		;	;		;		;		;					;1N
23				23C	23C					23CN						23CN	23CN	;		23CN		;1-	
24	2	2	2	2-	2=	2=	2=	2	2	2-	2	2	2	2	2	2=	2-	2=	2=	2	2=	2=	2=
25	2	2-	2-	2-	2	2=	2=	2	2	2	2-	2-	2	2	2	2	2=	2=	2=	2=	2-	2=	2=
26	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=	2=
29	2	2=	2=	2-	2=	2-	2-	2-	2-	2-	2-	2-	2	2-	2	2-CN	2=	2=	2=	2=	2-	2=	2=
31	2-	2=	2=	2=	2=	2=	2=	2=	2=	1	2=	2=	2=	2=	1	;1C	;1-	1	;1	;1-	2=	;	;
36				0;	0	X-			0;	0		0;			0	0	0	0	0	0	0	0	0;
Tmp					2=	2=	2-	2	2=		2=	2-	2-	2=	2=	2=	2=	;	2=	2=	2=	2=	2-

Low infection type as described by Roelfs (8)

TABLE 4. Low infections produced by interaction of 23 cultures of Puccinia graminis f. sp. tritici and 13 wheat cultivars which were important commercially during the 1970 and 1980's in China.

	Pathogen cultures (from Table 2)																						SR
Cultivar	TNM	TNM	TTR	MBC	QSH	QFB	QCM	RHR	RKH	RSH	RKQ	RTH	RKQ	RTQ	BBC	BCC	HJC	LBB	KBC	DKC	GDC	GCC	GCC	[1]gene(s)
Feng-Kang 13				2			22+		1		2+	;1	2+	2	0	0	0;		0;	0;	0;	0;	0;	5,+
Dong-Xie 3	2	2	12-	;	2	2	2	2	;1	2	;1	;1	1	;1	0;	01-	0;	2	0;1	0;	0;1	0;	0	5,31
Dong-Xie 4	2	2	2	;	2	2	;1	2	;1	2+	2	;	;1	2	12	01-	0	2	0;	0;	0;	0;	0;	5,31
Yi 78-4078	2	2	2-	0;	2	2-	-	2	2-	2	X-	2=	2	2	2	0	2-	2	0	12	;1	;1	2-	31
Yan 7770-4	2	2	2-	2	2	2	2	2	2	2	2	2-	;1-	2	12C	2	2	12-	;	2	2	2-	;	31
Feng-Kang 2	2	2	2	;1	2	2	0;	2	;1	2	;1	;	;1	2	12C	2	2	12	2	2	2	;1	;	31
Feng-Kang 8	2	2	2	2	2	2	2	2	;1	2	2-	;1	2	2	12C	2-C	2	2-	2	2	2	2	2	31?
Lu-Mai 1	2	2	2-	;1-	2	2	2	2	2-	0	2-	2	2-2	2	2	0	2-	0?	2	2	2	2	2	31?
Jing-Dan 106	2	2	2	;1-	2	2	;1	2	;1	2	;1	;1	2	2	;1-	2	2	2-	2	2	2	;1	2	31?
Fu 63							2						;2						2	0;	2	2	0;	?
Jing-Mai 11				2			;1						2		X-	2			2					+
Yan-An 15							2	;1N	2		23N								2					+
Bei-Nong 321																			2					+
Bima 1	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	Check
McNair 701	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	H	Check

1. Low infection types described by Roelfs, (8); + indicates an additional gene(s) for resistance

Cereal Rusts Bulletin Vol 14, Part 2, 1986

Resistance sources in barley to Puccinia hordei

BY

Mareike Reinhold and E.L. Sharp
Department of Plant Pathology
Montana State University
Bozeman, MT 59717
USA

SUMMARY

Numerous resistance sources were discovered when 146 cultivars were subjected to infection with Puccinia hordei. The 11 virulence types originated from different areas of the world and represented a broad range of virulence patterns. Cultivars with the genes Pa3 and Pa7, respectively were resistant to all isolates. Several varieties of unknown origin exhibited similar reaction patterns.

INTRODUCTION

Leaf rust (Puccinia hordei Otth.) of barley (Hordeum vulgare L.) is considered a serious threat to barley production in many areas (Levine and Cherwick 1952, Moseman and Greeley 1965, King and Polly 1976, Saari and Prescott 1977, Celoni 1979). A steady increase of infection with leaf rust has been reported from Western Europe. Rintelen (1975) considered leaf rust of barley the most common cereal rust in West Germany. The release of new barley cultivars with resistance to powdery mildew (Erysiphe graminis f. sp. hordei) and stripe rust (Puccinia striiformis West.) gives the later appearing leaf rust a chance for unrestricted development (Rintelen 1975, Walter and Lehman 1980). Previous evaluations of resistance sources in different countries resulted in the description of the nine resistance genes PA through PA9 (Roane and Starling 1967, Clifford 1974, Nover and Lehman 1974, Tan 1977a, 1977b).

Only few commercially grown barley cultivars in Europe however possess specific resistance to leaf rust (Rintelen 1979, Walter and Lehmann 1980). The same was observed for cultivars grown in the United States (Reinhold and Sharp 1982). Parlevliet et al. (1980) however found a considerable amount of partial resistance in a number of western European cultivars.

The appearance of new virulent strains of leaf rust which were able to overcome existing resistance genes (Walter and Lehmann 1980) and the rarity of currently known resistance genes makes it necessary search for new and different sources of resistance in order to provide the plant breeder with potentially useful material. The following study describes the evaluation of 146 barley cultivars/lines to 11 isolates of the pathogen representing a wide spectrum of virulence.

MATERIALS AND METHODS

Samples of barley cultivars/lines were obtained from Drs J.R. Smith, Jr., Beltsville, MD USA, B.C. Clifford, Aberystwyth, Wales, and J.E. Parlevliet, Wageningen, The Netherlands, as well as from the barley collection maintained at Montana State University (MSU). The pathogen was collected from local cultivars in the Mediterranean area and the United States by MSU-researchers. One isolate (Tel Aviv) originated from the alternate host, the common star of Bethlehem (Ornithogalum umbellulatum spp.). Cultures from the United States were obtained from widely separated locations in Montana, Minnesota and Texas. Single pustule cultures of all isolates were maintained on the cultivar Moore CI 7251. The virulence types of the isolates were determined by the reaction of 13 barley cultivars representing the resistance genes PA through PA9 (Table 1).

Eight to ten seedlings per cultivar were sown in 10 cm pots in sterilized Bozeman silt loam. The pots were placed in a growth chamber with a 12-hr daily photoperiod (2.2 - 3.3 x 10 ergs/cm/sec) at 15/24 + 1C (dark/light). Seedlings were inoculated with uredospores suspended in distilled water when 9-10 days old. For most cultivars 1-2 replications were carried out, especially when unstable reactions were observed. After inoculation plants were placed into a darkened dew chamber at 20C for 20-24 hours to allow spore germination and infection. Plants were then returned to the growth chamber. Plants were evaluated for disease reaction 12 days after inoculation using the following infection type scale.

0 no visible pustules (resistant)
1 small pustules, infrequently with chlorosis and necrosis (resistant)
2 definite chlorosis surrounding moderate size pustules (intermediate)
3 large pustules, occasionally slight chlorosis (susceptible).

RESULTS AND DISCUSSION

Eight cultivars listed at the top of Table 2 were resistant to all isolates used. The resistance genes Pa3 (Aim and Estate) and Pa7 (Cebada Capa, Forrajera Klein/Rika 7 and La Estanzuela) were thus effective against all 11 virulence types. Three lines (Giza 117/Baktim/Giza 118, Giza 119/Tannekasse 105 and 386-16-2) all selected at Sakha, Egypt showed a similar reaction pattern. A crossing analysis is under way to determine the genetic background of the resistance reaction. Cultivars reportedly carrying the Pa2 gene (Ariana, Juliaca and Peruvian) or its complex (Batna, Reka, Ricardo, Bolivia and Quinn) gave different reactions indicating the involvement of more than one gene. Inconsistent reactions have earlier been reported for Pa2 (Reinhold and Sharp 1983). Sudan, Oderbrucker and Speciale are assumed to carry the Pa gene (Roane 1962). Oderbrucker and Speciale reacted similar to 10 isolates but gave a different reaction when inoculated with the Sakha isolate. Sudan, on the other hand displayed a considerably higher resistance reaction to the 11 virulence types than either Oderbrucker or Speciale. It is assumed that Sudan either carries additional genes for resistance, or that the gene in Sudan is different from the one described for the other two

cultivars. Multiple alleles in the Pa locus similar to the Ml-a locus for mildew resistance in barley may also be present in these three cultivars.

Pa4 in Lechtaler and Gold was ineffective against the virulence types used in this study. Twelve cultivars/lines listed at the bottom of Table 2 did not express any resistant reaction to Puccinia hordei.

It becomes evident that by using 'exotic' virulence types of the pathogen new genes for resistance can be detected and more information about already known genes can be gained. This study indicates that specific as well as unspecific resistance to barley leaf rust is abundant and readily detectable. Resistance to every virulence type used in the investigation was found. The combination of two or three of the described genes should result in good protection of a cultivar against Puccinia hordei.

REFERENCES

CELONI, C. (1979). Puccinia hordei in Italy. A preliminary survey on the virulence characteristics of fungus in our country. Cereal Rusts Bull. 6:11-16.

CLIFFORD, B.C. (1974). The choice of barley genotypes to differentiate races of Puccinia hordei Otth. Cereal Rusts Bull. 2:5-6.

KING, J.E. and R.W. POLLEY (1976). Observations on the epidemiology and effects on grain yield of brown rust in spring barley. Pl. Path. 25:63-73.

LEVINE, M.N. and W.F. CHEREWICK (1952). Studies on dwarf leaf rust of barley. USDA - Tech. Bull. No. 1056, 17pp.

MOSEMAN, J.G. and W. GREELEY (1965). New pathogenic strains of Puccinia hordei among physiologic races identified in the United States from 1959 through 1964. Plant Dis. Rep. 49:575-578.

NOVER, I. and C.O. LEHMANN (1974). Resistenzeigenschaften im Gersten - und Weizensortiment Gatersleben 18. Prufung von Sommergersten auf ihr Verhalten gegen Zwergrost (Puccinia hordei Otth.). Kulturpflanze 22:25-43.

PARLEVLIET, J.E., LINDHOUT, W.H., Van OMMEREN, A., and H.J. KUIPER. (1980). Level of partial resistance to leaf rust Puccinia hordei in West European barley and how to select for it. Euphytica 29:1-8.

REINHOLD, M. and E.L. SHARP (1982). Resistance to leaf rust of barley in Southern Texas. Cereal Rusts Bull. 10:4-10.

RINTELEN, J. (1975). Physiologic specialization of Puccinia hordei Otth. and reaction of barley varieties and cultivars to physiological races. Proc. 3rd Inter. Barley Genet. Symp., Ganshsing, Federal Republic of Germany 7-12 July. 464-467.

ROANE, C.W. (1962). Inheritance of reaction to Puccinia hordei I. Genes for resistance among North American race differentiating varieties. Phytopathology 52:1288-1295.

ROANE, C.W. and T.M. STARLING (1967). Inheritance of reaction to Puccinia hordei in barley. II. Gene symbols for loci in differential cultivars. Phytopathology 57:66-68.

SAARI, E.E. and J.M. PRESCOTT (1977). Barley diseases and their surveillance in the region. 4th Regional Winter Cereal Workshop - Barley. Amman, Jordan. April 24-28. 2:320:330.

TAN, B.H. (1977a). A new gene for resistance to Puccinia hordei in certain Ethiopian barleys. Cereal Rusts Bull. 5:39-43.

TAN, B.H. (1977b). Evaluating host differentials of Puccinia hordei. Cereal Rusts Bull. 5:17-26.

WALTER, U., and C.O. LEHMANN (1980). Resistenzeigenschaften im Gersten - und Weizensortiment Gatersleben. 24. Prufung von Sommergersten auf ihr Verhalten gegen Zwergrost (Puccinia hordei Otth.). Kulturpflanze 28:277-238.

Table 1 - Reaction of differential cultivars to eleven isolates of *Puccinia hordei*

CI Number	Cultivar	Isolates*										
		I1	I2	I3	I4	I5	I6	I7	I8	I9	I10	I11
3410	ESTATE	R	R	R	R	R	R	R	R	R	R	R
6193	CEBADA CAPA	R	R	R	R	R	R	R	R	R	R	R
6489	SUDAN	R	R	I	R	R	S	S	I	I	S	S
3391	BATNA	R	I	R	S	S	I	I	I	S	R	S
1243	HOR. 2596	I	I	I	S	R	R	I	I	I	R	I
1257	BOLIVIA	S	I	R	I	I	S	S	I	I	I	I
653	PERUVIAN	R	R	I	I	I	I	I	S	S	S	S
6306	RICARDO	R	I	R	I	I	I	I	S	S	S	S
1024	QUINN	I	R	I	R	I	I	S	S	S	S	S
13807	MAGNIF 104	I	I	I	R	S	S	S	S	S	S	S
5051	REKA 1	S	S	S	S	S	S	S	S	S	S	R
1145	GOLD	S	S	S	S	S	S	S	S	S	S	S
6481	EGYPT	I	S	S	S	S	S	S	S	S	S	S

* I1 = Merchouch, Morocco, I2 = San Antonia, TX, USA, I3 = Marrakech, Morocco, I4 = Tel Aviv, Israel, I5 = Fretissa, Tunisia, I6 = Ismir, Turkey, I7 = Tel Hadia, Syria, I8 = Rabat, Morocco, I9 = Homs, Syria, I10 = Creston, MT, USA, I11 = Sakha, Egypt.

Table 2 - Reaction of 146 barley cultivars/lines to eleven isolates of Puccinia hordei.

CI/PI Number	Cultivar/line	Isolates* I1	I2	I3	I4	I5	I6	I7	I8	I9	I10	I11
0	386-16-2	R	R	R	R	R	R	R	R	R	R	R
3737	AIM	R	R	R	R	R	R	R	R	R	R	R
6193	CEBADA CAPA	R	R	R	R	R	R	R	R	R	R	R
0	G119/TANNEK.105	R	R	R	R	R	R	R	R	R	R	R
328102	LA ESTANZUELA	R	R	R	R	R	R	R	R	R	R	R
11801	F.KLEIN/RIKA 7	R	R	R	R	R	R	R	R	R	R	R
0	08438/SAHRAM-2	R	R	R	R	R	R	R	R	R	R	R
3410	ESTATE	R	R	R	R	R	R	R	R	R	R	R
0	G117/BAKT./G118	R	R	R	R	R	R	R	R	R	R	R
0	FORD 1203	I	R	R	R	R	I	I	I	R	I	S
0	CCIM-13	I	R	I	R	R	I	S	I	I	R	I
1243	HOR.2596	I	I	I	S	R	R	I	I	I	R	I
4974	4974	R	R	I	R	I	I	R	I	S	I	R
0	GIZEH 134	R	R	R	R	R	R	R	I	S	I	S
0	MARI/ATHENAIS	R	R	R	R	R	R	R	I	S	I	S
0	ASSE/NACTA	R	R	R	R	R	R	R	S	S	R	I
0	ATHENAIS/NOPAL	R	R	I	R	I	S	R	R	S	R	R
4798	4978	R	R	R	R	S	R	S	I	I	R	I
8612	8612	I	R	S	R	R	R	S	I	S	R	I
10501	ATHENIAS	R	R	R	R	R	S	I	I	S	S	R
1021	WEIDER	I	I	I	I	I	S	I	S	I	R	S
2524	ARIANA	I	I	R	I	S	I	I	I	S	I	S
3634	3634	R	S	I	R	R	I	I	R	R	S	S
1257	BOLIVIA	S	I	R	I	I	S	S	I	I	I	I
6306	RICARDO	R	I	R	I	I	I	I	S	S	S	S
653	PERUVIAN	R	R	I	I	I	I	I	S	S	S	S
399487	BREVIA	R	I	R	R	I	S	S	R	S	R	S
371630	ASSE	R	I	R	R	I	S	S	R	S	I	S
0	BIGO 3	I	S	I	R	R	I	I	S	S	I	S
11577	HOR 728	I	S	R	R	R	I	I	S	S	R	S
6489	SUDAN	R	R	I	R	R	S	S	I	I	S	S
4979	RABAT	I	I	I	I	R	I	S	S	S	I	S
8158	FORRAJERA	R	R	R	S	R	S	S	R	I	I	S
3391	BATNA	R	I	R	S	S	I	I	I	S	R	S
3212	MODJO	I	S	I	I	S	I	S	I	I	I	S
13119	AMBER	I	S	I	I	S	S	I	I	I	S	I
1024	QUINN	I	R	I	R	I	I	S	S	S	S	S
4975	4975	R	R	R	R	R	S	S	S	S	R	S
2674	GORDON	R	R	R	R	I	S	S	I	S	S	S
4976	4976	R	I	I	R	S	S	S	I	S	R	S
7629	ANOIDIUM/RABAT	R	I	I	S	S	S	S	I	S	I	I

0	LOFA ABED	I	I	I	S	S	I	S	S	I	I	S
4251	DELTA	I	S	I	I	S	I	S	I	S	S	R
7480	BADAJOY	R	S	R	S	I	I	S	R	S	I	S
11533	SAN CARLOS	R	S	S	S	S	R	S	R	I	I	I
410862	SUNDANCE	I	S	I	R	R	I	I	S	S	S	S
6200	6200	S	I	I	S	I	S	S	I	I	R	S
0	11069/GIZA117-1	I	I	S	I	R	S	S	S	S	S	I
0	11068/GIZA117-2	R	I	S	I	I	S	S	S	S	S	I
1114	JULIACA	R	R	R	I	S	S	S	S	S	I	S
11331	UNION	R	I	I	I	S	S	S	I	S	S	S
0	MU4335/CI12010	I	R	I	S	S	S	R	S	S	S	I
1017	MONTE CHRISTO	I	I	S	I	S	S	I	S	I	S	S
3403	LYALLPUR	I	S	I	I	S	S	I	S	I	S	S
13611	BIGO 1	I	S	I	S	I	I	I	S	S	S	S
0	MALA ABED	I	S	I	S	S	I	S	I	I	S	S
4219	4219	I	S	I	S	S	S	R	I	S	I	S
657	CHILE BREWING	I	S	I	S	S	S	S	I	S	I	I
1227	BENTON	I	S	S	I	I	S	I	I	S	S	S
1700	MAROCCO	R	S	S	S	S	I	S	S	R	I	I
13807	MAGNIF 104	I	I	I	R	S	S	S	S	S	S	S
6483	AUSTRAL	R	R	S	R	R	S	S	S	S	S	S
0	MAGNUM	R	S	R	R	S	S	S	S	S	I	S
5862	MENELIK	R	S	I	S	S	S	I	S	I	S	S
0	BIGO 2	I	S	I	S	S	I	I	S	S	S	S
7089	HAMILTON	I	S	S	I	S	S	S	S	I	I	S
13667	ZEPHYR	I	S	S	I	S	S	I	S	I	S	S
5595	5595	S	S	I	S	R	S	S	I	R	S	S
6482	CRUZAT	S	S	I	S	R	S	S	S	I	S	I
6488	LECHTALER	I	S	S	S	S	S	I	S	I	I	S
5559	5559	I	S	S	S	S	S	S	S	R	I	I
3245	3245	S	S	I	S	S	S	S	I	S	I	R
13575	PEROGA	R	S	I	S	S	S	S	R	S	S	S
7890	7890	R	S	I	S	S	S	S	I	S	S	S
1701	MAROCCO	R	S	I	S	S	S	S	S	S	S	I
8025	8025	R	S	R	S	S	S	S	S	S	S	I
1433	CHILEAN D	S	S	I	S	S	S	S	S	I	S	I
6305	PSAKNON	S	S	I	S	S	S	S	S	I	S	R
0	3309-AT-XV2240	I	I	S	S	S	I	S	S	S	S	S
0	08438/SAHRAINCE	S	S	R	S	I	S	S	S	S	R	S
1703	MAROCCO	S	S	I	S	S	I	S	I	S	S	S
0	FORD 1200	S	S	I	S	S	S	I	S	S	S	I
6486	FRIEDRICH.BERG	S	S	S	S	S	I	I	S	I	S	S
15368	SAFRA	I	S	S	S	S	S	I	S	I	S	S
3623	3623	I	S	S	S	S	S	S	I	S	I	S
653	PERU	S	S	I	S	S	S	S	I	I	S	S
2330	MANCHURIAN	I	S	S	S	S	S	S	S	R	S	R
0	FORD 1190	S	S	S	S	S	S	I	S	I	S	I
1088	ABACUS	S	S	S	S	I	S	S	S	I	S	R
410858	MARIS OTTER	I	S	I	S	S	S	S	S	S	S	S
13150	DELISA	I	S	I	S	S	S	S	S	S	S	S

9174	ROGERS	I	S	S	S	S	S	S	S	I	S	S
5267	PEATLAND	I	S	S	S	S	S	S	S	I	S	S
5109	BURBANK HULLESS	S	S	I	S	S	S	S	S	S	S	I
15225	M.C. 20	S	S	I	S	S	S	S	S	S	S	I
9537	HUSKY	S	S	S	S	S	S	S	S	I	S	R
12443	INGRID	S	S	S	S	S	S	S	S	I	S	I
6518	PALLIDIUM 043	S	S	S	S	S	S	S	S	I	S	R
12467	ESPERANCE	S	S	I	S	S	S	S	S	S	I	S
1179	ALGERIAN	I	S	S	S	I	S	S	S	S	S	S
1702	MAROCCO	I	S	S	S	S	S	S	S	S	S	I
12254	FLORIDA 102	S	S	S	S	S	S	I	S	I	S	S
11790	EMIR	S	S	R	S	S	S	I	S	S	S	S
2221	2221	S	S	S	S	S	S	S	S	S	I	I
8097	HERTA	I	S	S	S	S	S	S	S	S	S	S
13834	JULIA	I	S	S	S	S	S	S	S	S	S	S
7510	LICHT	I	S	S	S	S	S	S	S	S	S	S
0	ATHOS	I	S	S	S	S	S	S	S	S	S	S
3906	3906	I	S	S	S	S	S	S	S	S	S	S
6481	EGYPT	I	S	S	S	S	S	S	S	S	S	S
10667	HARRISON	I	S	S	S	S	S	S	S	S	S	S
10648	LARKER	I	S	S	S	S	S	S	S	S	S	S
428006	RATNA	S	S	I	S	S	S	S	S	S	S	S
11189	BONUS	S	S	R	S	S	S	S	S	S	S	S
1237	ABYSSINIAN	S	S	S	I	S	S	S	S	S	S	S
15556	MARIS MINK	S	S	S	S	S	S	S	S	S	S	S
261	CLUB MARRIOT	S	S	S	S	I	S	S	S	S	S	S
447012	GEORGIE	S	S	S	S	I	S	S	S	S	S	S
2444	NIGRATE	S	S	S	S	S	I	S	S	S	S	S
0	CORACLE	S	S	S	S	S	S	S	R	S	S	S
7250	PLAINS	S	S	S	S	S	S	S	S	R	S	S
466726	MONA	S	S	S	S	S	S	S	S	I	S	S
0	ATLAS	S	S	S	S	S	S	S	S	S	S	I
5051	REKA 1	S	S	S	S	S	S	S	S	S	S	R
940	ODERBRUCKER	S	S	S	S	S	S	S	S	S	S	R
3208	3208	S	S	S	S	S	S	S	S	S	S	I
9538	TRAIL	S	S	S	S	S	S	S	S	S	S	S
13541	EMIR	S	S	S	S	S	S	S	S	S	S	S
8093	BONUS	S	S	S	S	S	S	S	S	S	S	S
531	HANNCHEN	S	S	S	S	S	S	S	S	S	S	S
182	ODESSA	S	S	S	S	S	S	S	S	S	S	S
7131	BALDER	S	S	S	S	S	S	S	S	S	S	S
7021	QUEENS	S	S	S	S	S	S	S	S	S	S	S
7251	MOORE	S	S	S	S	S	S	S	S	S	S	S
9561	PROCTOR	S	S	S	S	S	S	S	S	S	S	S
11808	VADA	S	S	S	S	S	S	S	S	S	S	S
2962	SOUTH RUSSIAN	S	S	S	S	S	S	S	S	S	S	S
13837	SULTAN	S	S	S	S	S	S	S	S	S	S	S
392	MOLDAVIA	S	S	S	S	S	S	S	S	S	S	S
7536	SPECIALE	S	S	S	S	S	S	S	S	S	S	S
5438	COMPANA	S	S	S	S	S	S	S	S	S	S	S

7022	NASSAU	S	S	S	S	S	S	S	S	S	S	S
9558	PIROLINE	S	S	S	S	S	S	S	S	S	S	S
6250	ATSEL	S	S	S	S	S	S	S	S	S	S	S
1145	GOLD	S	S	S	S	S	S	S	S	S	S	S
14119	ABATE	S	S	S	S	S	S	S	S	S	S	S

* I1 = Merchouch, Morocco, I2 = San Antonio. TX, USA, 13 = Marrakech, Morocco, I4 = Tel Aviv, Israel, I5 = Fretissa, Tunisia, I6 = Ismir, Turkey, I7 = Tel Hadia. Syria, I8 = Rabat, Morocco, I9 = Homs, Syria, I10 = Creston, MT, USA, I11 = Sakha, Egypt.