THE PROPOSED BROWN RUST OF WHEAT (*PUCCINIA RECONDITA* F. SP. *TRITICI*) VIRULENCE MONITORING SYSTEM.

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ABSTRACT

A new system of virulence identification of brown rust of wheat (*Puccinia recondita* f. sp. *tritici*) consisting of three sets of differentials (Set 0, A and B) is proposed. The zero set has no role in identifying virulences, but consists of universal susceptible, a resistant line and currently popular cultivars. Set A has a maximum loading capacity of nine entries and at present consists of eight *Lr* lines or lines with known genes. Reactions on these are grouped either as R or S. Using binary notation and decanary value, a number to denote the reaction on set A is arrived. Set B, that has the same nine lines capacity, has at present five entries from the international set. Reaction on this set is also assigned a number following the same procedure.

WHEN Biffin in 1905 demonstrated that disease resistance is inherited in a simple Mendelian way, there was a sense of optimism. Disease-resistant varieties that were bred and made popular, soon became susceptible to the vary same pathogen. This led to the theory of race and a system of race identification 'stem rust' was proposed. To separate minor differences in reaction of race to bio-types, additional differentials were recommended. When the gene-for-gene theory was widely accepted, it was clear that the race nomenclature is not on a sound principle. The *Phytophthora infestans* and potato system was the first to change. Following these, numerous procedures were suggested[1,2].

Stakman and Christensen opined that conclusions regarding race were limited by the varieties available at a given time. Based on their experience with stem rust race 15 and 15B they felt it necessary to periodically revise the classification of races. Recent studies[3] have generated some basic information and we now propose a system of virulence identification that will be followed in India.

CONSTITUTION OF THE PROPOSED SETS

The routine seedling house procedures were followed in standardising the proposed sets (table 1). The zero set consists of universal susceptible, an Indian line resistant to all races which would serve as a watchdog, currently cultivated or useful five bread wheats and two maccroni wheats. Reaction on this set is not considered in the nomenclature. Instead, it shows the behaviour of the currently cultivated varieties, meeting requirements of extension workers. The universal susceptible on infection shows that the test is uniform and the watchdog, when susceptible would identify any new race that may creep-in.

Set A, can have a maximum of nine entries, but at present has eight lines with known *Lr* genes. By repeated tests, the strength of these genes was evaluated and has been accordingly arranged in ascending order. Hence, *Lr* 14a which gives resistant reaction for only 4 races was the first line in set A. The *Lr* 19 gene resistant to all the races was the eighth and others were midway between except *Lr* 24. The pedigree of the lines constituting set A, has been shown in table 2.

Set B has the same capacity of nine lines but has at present four lines from the international set with known resistant genes and Thew an additional differential has been arranged in the following way as per their strength: Loros (*Lr* 2c), Webster (*Lr* 2a), Democrat (*Lr* 3), Thew (*Lr* 20) and Malakoff (*Lr* 1). This set is able to identify most of the races, and establish a link with the earlier system of race identification. Two weeks after inoculation[3] disease reactions are to be

TABLE 1

The proposed brown rust (Puccinia recondita tritici) virulence identification set.

Set 0	Set A	Set B
Agra local	*Lr* 14a	Loros (*Lr* 2c)
Karchia mutant (*Lr* 9+?)	*Lr* 24	Webster (*Lr* 2a)
WL 711	*Lr* 31	Democrat (*Lr* 3)
Sonalika (*T. aestivum*)	*Lr* 13	Thew (*Lr* 20)
Kalyansona (*T. aestivum*)	*Lr* 17	Malakoff (*Lr* 1)
IWP 94 (*T. aestivum*)	*Lr* 15	
NI 5439 (*T. aestivum*)	*Lr* 10	
Jayaraj (*T. durum*)	*Lr* 19	
HD 4502 (*T. durum*)		

TABLE 2

Pedigree of the Lr lines in Set-A

Lr line	Pedigree
14a	Selkirk × Thatcher[6]
24	Prelude[6] × Agent
31	Timvera (W 1308)
13	Egret
17	Thatcher[6] × K. lucero
15	Kenya × W 1483
10	Thatcher[6] × Lee
19	Agatha (T 4 lines)

TABLE 3

The binary coding system

Pustule type	Reaction	Binary number
0 0 1 2	R	0
3 4	S	1

recorded into any of the seven category (table 3). These reactions can be grouped either as resistant or as susceptible. After repeated tests a master table on the reaction of the test lines was prepared and is given in table 4. Races were found to interact differentially with *Lr* genes, and that reaction of no two races was identical. Each virulence was found to infect varying number of genes.

HOW VIRULENCE IS TO BE NAMED?

The nomenclature of physiological races, has a function of providing a concise name suitable for both spoken and written word. Though various systems have been proposed, all of them have some weakness or the other The binary notation system[4] and the yellow rust identification procedure developed thereafter[1] have the merits of precise nomenclature while the American and Australian system emphasise lines with known genes[2,5,6]. The proposed system of Flowerdale cares for the reaction of present day cultivars but it is not considered in virulence identification. This helps to keep a constant watch over the performance of released varieties to field isolates of the pathogen.

In identifying and naming of the races, the binary notation system would be followed. In both set A and B lines have been arranged, serially as per their strength. If the set has more than nine entires, then the value ascribed to a race may exceed 1000. Three-digit nomenclature is easy to remember and communicate and hence, each set has a maximum of nine entries. Table 5 shows the procedure followed in the race nomenclature. The decanary procedure follows raising a number of the base, 2, and no. total of two number will be identical. Hence, a set which has nine entires would have a value of 2^8, the total if all the entries susceptible (2^0 to 2^8) will be 511.

TABLE 5

Procedure for coding reaction. Example race 77 Set A

Details *Lr*	14a	24	31	13	17	15	10	19
Decanary value decoded	2^0	2^1	2^2	2^3	2^4	2^5	2^6	2^7
Decanary value	1	2	4	8	16	32	64	128
Reaction of race 77	1	2	4	8	16	32	64	
Binary value	S	R	S	S	R	S	R	R
Decanary value for the race in set A	1	0	4	8	0	32	0	0
Summary of decanary value multiplied by binary value 1 4 8 32 = 45								

When an isolate of the pathogen is tested on the *Lr* lines, following the binary coding resistants are denoted as 0 and susceptible as 1. If we arrange the reactions of race 77 on set A it would be, 10110100, which means *Lr* 14a, *Lr* 31, *Lr* 13 and *Lr* 15 are susceptible while *Lr* 17, *Lr* 10 and *Lr* 19 are resistant (table 5). This sequential value is multiplied by the decanary value, and is totalled. The total value is the number to denote the reaction in set A. Reaction of race 77 on set A gets a value of 45 and the corresponding reaction on set B is 31. So race can be renamed 45R31. The alphabet capital 'R' that separates the values of set A from B, denotes that the virulence is that of brown rust (*P. recondita tritici*).

This nomenclature system when followed shows that:

Race 77 = 45 R 31
Race 12A = 5 R 13
Race 63 = 0 R 8

Gene *Lr* 17 gave susceptible reaction at higher light and temperature conditions. Reaction of *Lr* 13 and *Lr*

TABLE 4

Master table showing the reaction of races against Lr lines of Set A and B.

Lr	10	11	12	12A	12B	17	20	63	77	77A	77A–1	104	104A	104B	106	107	108	162	162A
14a	–	R	–		–	–	–	R	–	–	–	–	–	–	R	–	–	–	–
24	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
31	–	R	–	–	R⁺	–	–	R	–	–	–	R	–	–	R⁺	–	–	–	–
13	–	R	R⁺	R⁺	R⁺	–	R	R	–	–	–	R	R	–	R	–	–	–	
17	R⁺	R	R⁺	R⁺	R⁺	–	R	R	R⁺	R⁺	R⁺	*	*	*	R	R	R	*	*
												–	–	–				–	–
15	R	R	R	R	R	—	R	R	–	–	–	R	R	R	R	–	R	R	R
10	R	R	R	R⁺	R⁺	R	R	R	0	0	R	R	R	R	R	R	R	0	0
									–	–								–	–
19	R	R	R	R	R	R	R	R	R	–	R	R	R	R	R	R	R	R	R
2c	–	R⁺	–	–	–	R	–	R	–	–	–	–	–	–	*	–	–	–	–
															–				
2a	–	R	R	R	R	–	–	R	–	–	–	0	0	0	R	–	–	–	–
												–	–	–					
3	R	R	–	–	–	R	R	R	–	–	–	–	–	–	R	R	R	–	–
20	R	–	R	–	R	–	–	–	–	–	R	R	–	R	–	R	–	R	–
1	–	R	R	R	R	–	–	R	–	–	–	–	–	–	R	R	–	R	R

New Name	13R19	0R8	5R5	5R13	1R5	61R26	5R27	0R8	45R31	109 R 31	109R 23	17R23	21R31	29R23	0R9	45R3	13R27	93R7	93R15

*gives X reaction but variable.
gives -X (more resistant pustules) once in a way.
0sensitive to light and temperature.

Note: *Lr* 17 with race 77 group gives R reaction under proper light and temperature only.

31 were also dependant on temperature. During 1981, race 77 dominated the flora and is at present the most virulent race able to attack 9 genes out of 13, in our set and gives variable reaction on *Lr* 17. Race 12A that occurs in ver low frequency has virulence for 4 genes, while race 63 not traced for the last many years has virulence for just 1 gene. This is clearly reflected by the values assigned in the new nomenclature system. The more virulent (able to infect greater number of resistant genes) gets a higher number. In other words, higher the number, complex is the race and hence, the nomenclature itself quantifies the reaction potentials.

The procedure to decode and arrive at the susceptible genes is easy and involves simple arithmetic. Supposing we have 132 R 7 virulence. Refer table 5 and follow the following steps.

A. Which is the nearest smaller decanary value?
B. Detect that value from the value of the virulence.
   Example: Nearest to 132 is 12B (Line 8 – *Lr* 19)
   132 – 12B = 4.
C. Check the nearest value to the balance number.
D. Minus that from total.
E. Keep going till the end.
   Example: The balance is 4 which fits with line 3 (*Lr* 31).

In set B, value 7 means that line 3 which has a value of 4 is susceptible (7–4 = 3), line 2 is also susceptible which has a value 1 is left, it is clear line 1 is also susceptible ($2^0 = 1$). The virulence analysis shows that 132 R 7 is virulent against *Lr* 19, *Lr* 13, *Lr* 2c, *Lr* 2a and *Lr* 3.

Identification of genes in the host by matching technique would be initiated once pure cultures are established. This system would be implemented from the 1981 crop year onwards, at Flowerdale, Simla, India which has the national mandate for monitoring and analysis of the cereal rust pathogen.

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METHYL PARATHION IMPACT ON THE REGULATION OF PHOSPHORYLASE ACTIVITY IN SELECTED TISSUES OF THE SNAIL, *PILA GLOBOSA* (SWAINSON)

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ABSTRACT

Sublethal studies of methyl parathion showed depletion of total carbohydrates and glycogen contents in the selected tissues of the snail, *Pila globosa*. The activity levels of phosphorylase 'a' showed a significant decrease while phosphorylase 'b' showed a variable trend. The results are discussed in relation to the regulation of glycogen breakdown.

INRTODUCTION

OF the several factors that contribute to the disturbance and imbalance of an ecosystem, the pesticides are noteworthy[1], since they form potential toxins used to eradicate pests and insects[2]. The imbalance of an ecosystem has profound influence on several non-target species[3]. Recent reports indicate that many of these pesticides cause cytogenic, mutagenic[4] and pathological changes[2]. This paper presents a study on the sublethal effects of methyl parathion (0–0 dimethyl 0–4 nitrophenyl phosphorothioate, a widely used organophosphate pesticide) on the glycolytic pathway, taking the key enzyme phosphorylase in the selected tissues of the fresh water snail, *Pila globosa*. This species was selected because it forms an integral part of the fresh water and rice field ecosystems.