

Nilgiri Wheat News

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Race surveillance and preemptive breeding against black and brown rusts of wheat in Nilgiri hills

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Race 77-5 of brown rust was found to be the most predominating followed by 77-7 and 77-8 in Nilgiri hills. For stem rust, only two races viz. 40A and 40-1 occurred with equal frequencies. It is alarming to note that majority of the released varieties are susceptible to one or other races of leaf rust surviving in Nilgiris. Matching virulent races against *Lr* genes viz. *Lr*10, *Lr*13, *Lr*23, *Lr*26 commonly used in released varieties are available in Nilgiri hills. *Lr*24 effective against all prevailing races, hold promise against brown rust, however, deployment of single gene with major effect over large area is prone to breakdown due to evolution of matching virulence. Pyramiding of *Lr*24 with other major or minor genes may pre-empt such threat. Linkage of *Lr*24 with *Sr*24 and availability of matching virulence against *Sr*24 in black rust race 40-1 existing in Nilgiris calls for pyramiding of additional *Sr* genes in such cultivars, if envisaged for cultivation in central and peninsular parts of India. Presence of race 77-7 and its increasing trend in the recent years, renders other highly effective gene *Lr*9 useless, if used alone in central and peninsular India.

The ability of two races 40A and 40-1 of black rust prevailing in Nilgiris to infect varieties of central and peninsular India having genes *Sr*7b, *Sr*9b, *Sr*9e, *Sr*11, *Sr*24 etc. renders deployment of these genes

alone or in combination useless. However, use of *Sr*2 in combination of two or more of these genes is able to provide complete protection from both the races. IARI, Regional station, Wellington has undertaken backcross breeding programme, to pyramid the highly effective rust resistant genes into already tested and improved agronomic background and developed a large number of genetic stocks. Most of these stocks exhibited adult plant resistance continuously for five years to black and brown rusts under natural epiphytotics at Wellington. Wheat breeders from national wheat improvement programmes are invited to make use of these stocks available in the crossing block of the station during both summer and winter seasons.

Stem and Leaf Rust Resistance in Wild Relatives of Wheat With D Genome

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Resistance to stem rust and leaf rust in five D genome species of wheat viz., 267 accessions of *Aegilops tauschii* Coss., 39 of *Ae. cylindrica* Host, 17 of *Ae. ventricosa* Tausch, 4 of *Ae. crassa* Boiss. and 8 of *Ae. juvenalis* (Thell.) Eig were evaluated in adult plant stage. Two hundred and thirty nine (90%) accessions of *Ae. tauschii* Coss., 30 (77%) of *Ae. cylindrica* Host, 16 (94%) of *Ae. ventricosa* Tausch, three (75%) of *Ae. crassa* Boiss. and five (62.5%) of *Ae. juvenalis* (Thell.) Eig were resistant to stem rust pathotypes prevalent in South India at Wellington (hot spot for leaf and stem rusts) under field condition. Invariably, all the accessions of the five species were resistant to leaf rust pathotypes. Quantitative measurement of disease using area under disease progress curve (AUDPC) also revealed the slow progress of disease in the resistant accessions compared to susceptible check (Agra Local). Since the D genome is common in all the

five species, it could be concluded that the genes present in D genome might play a vital role in leaf rust resistance, but in case of stem rust resistance wide range of differential response is noticed among the accessions. Among the species evaluated, *Aegilops tauschii* Coss., is exploited to a larger extent, followed by *Ae. ventricosa* Tausch and *Ae. cylindrica* Host for leaf and stem rust resistance because of the homology of D genome with hexaploid bread wheat. *Ae. crassa* Boiss. and *Ae. juvenalis* (Thell.) Eig could not be utilized so far, possibly due to partial homology which makes the transfer of traits difficult. So, these species have considerable potential as a source of rust resistance and may enhance the existing gene pool of resistance to stem and leaf rusts.

A high yielding and multiple rust resistant bread wheat variety HW 5216 (Pusa-Navagiri) released for cultivation in Southern Hill Zone, India

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A high yielding wheat variety conferring multiple rust resistance was released for cultivation in Southern Hill Zone of India and notified. The Southern hills in India are known as the main foci for leaf and stem rust and acts as source for fresh epidemics of rusts to the plains of India when wheat crop raised in winter. Although area wise southern hill zone is a small zone but strategically very important zone for India, particularly to control the rusts. Therefore the continuous efforts in diversifying the genetic basis of rust resistance, release of such varieties and there by containing the rust inoculum is of national importance in order to arrest the dissemination of uredospores to the plains of the country to avoid any rust epidemics. The variety HW 5216 yielded significantly superior over checks viz., HW 2044 and CoW(w)1 (*aestivum*) over four of testing periods and recorded highest zonal mean grain yield of 45.6q/ha. It recorded overall yield advantage of +11.82% over best check CoW(W)1 occurred 10/11 times in first non-significant group as compared to best check var. CoW(W)1 indicating wider adaptability and stability in performance across zones. Significant yield advantage for HW 5216 ranged from 2.7% to

51.0% over the checks indicating its yielding ability in the proposed zone and has the highest yield potential of 62.4q/ha. When tested for varied irrigation levels it recorded no significant yield loss. HW 5216 exhibited high degree of seedling resistance to most stem, leaf and yellow rust pathotypes under artificial epiphytotic conditions. It produces good appearing grains with higher test weight (81.47kg/hc) and better grain quality (>12% protein and 44.75 sedimentation value)

Hybrid Necrosis in Wheat: evolutionary significance or potential barrier for gene flow?

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One hundred and four released varieties of bread wheat (*Triticum aestivum* L ssp. *aestivum*) in India were crossed to two *T.aestivum* testers, namely, C306 (*Ne₁Ne₁ ne₂ne₂*) and HD2329 (*ne₁ne₁ Ne₂Ne₂*) to determine the frequency and distribution of genes for hybrid necrosis present in them. Sixty seven varieties (65.4%) showed the presence of *Ne₂* gene and only eight varieties (7.7%) had *Ne₁* gene in their background. Twenty nine varieties (27.9%) were non carrier (*ne₁ne₁ ne₂ne₂*) for both the genes. Most of the *Ne₁*-carriers are of Indian origin and their pedigree revealed the involvement of landraces and old varieties as parents. Predominance of *Ne₂* gene in Indian varieties happened after the introduction of semi-dwarf Mexican wheat varieties, which are mostly *Ne₂* carriers and also due the extensive and continuous use of germplasm from Mexican and European origin in the hybridization programme. Moreover varieties with *Ne₂* gene is selected for their linked beneficial traits mainly rust resistance genes. The phenomenon of hybrid necrosis is one among the post zygotic barrier speciation process which acts as a barrier for either intra or inter specific gene flow. The genetic architecture of hybrid necrosis in wheat is simple following the minimal predictions of the Bateson – Dobzhansky-Muller (BDM) model . Widespread occurrence of dominant genes for hybrid necrosis in Indian varieties is of great concern to wheat breeders as it often interferes in the choice of elite parents and imposes restrictions on the productivity of crosses.

Protein marker as an easy tool to detect secale cereale-derived linked genes *Sr31*, *Lr26*, *Yr9* and *Pm8* genes in wheat

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The high yielding potential associated with IRS.IBL translocation involving the short arm of rye chromosome 1R and the long arm of wheat chromosome 1B were well exploited world over for developing disease resistant and high yielding wheat varieties. This was due to the translocation of the effective disease resistance linked genes *Sr31* for resistance to stem rust (*P.graminis f.sp.tritici*), *Lr26* for resistance to leaf rust (caused by *Puccinia triticinia*), *Yr9* for resistance to stripe rust (*P.striiformis f.sp.tritici*), *Pm8* for resistance against powdery mildew (caused by *Erisiphe graminis f.sp. tritici*) along with useful agronomic traits. However now virulent pathotypes have been reported which has overcome these rust resistance genes. The *Sr31* gene complex have close linkage with the genes controlling secalins (*Sec-1*). Thus *Sec-1* acts as a marker for the identification of *Sr31*, *Lr26*, *Yr9* and *Pm8* genes. SDS-PAGE was used to examine the presence of 1BL.1RS translocation in six Indian wheat genotypes viz. HP 1205, HD 2329, HD 2285, WH 147, Lok-1 and J 24 introgressed with *Sr31*+ gene complex with the aim to eliminate the lines carrying these genes, since it is tightly linked to poor baking quality. The SDS-PAGE results showed that all the lines carry *Sec-1* band and are therefore likely to carry the IBL.IRS translocation and the linked genes *Sr31*, *Lr26*, *Yr9* and *Pm8*. This technique could be well exploited to detect the presence of linked genes *Sr31*, *Lr26*, *Yr9* and *Pm8* in wheat cultivars as it is an easy, efficient, faster and economical tool to eliminate the lines with 1BL.1RS translocation and developing wheat varieties for better end use quality and reducing the risk to Ug99 stem rust race threat.

Marker assisted selection in introgression of rust resistance genes (*Yr10* and *Sr26*) in some select Indian Wheat cultivars (*Triticum aestivum*) by PCR Based Markers

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Yellow rust resistance locus *Yr10* located on short arm of chromosome 1B in Moro and originated from the Turkish line PI178383 was investigated in terms of polymorphism in 12 segregating lines of two different cultivars WH147x *Yr10* in BC₁ generation, LOK-1 x *Yr10* in BC₃ generation to confirm the transfer of *Yr10* resistance gene through molecular marker (SSR – *XPSP 3000*). The microsatellite marker *Xpsp3000* is inherited in a co dominant manner and linked with the yellow rust resistant gene *Yr10*, with a distance of 1.2cm. It could be used in Marker Assisted selection. *Agropyron elongatum*-derived *Sr26* gene is located on the long arm of chromosome 6A.It is confirmed at the molecular level by using AFLP marker *Sr26#43* in the segregating lines from 4 varieties along with their five different sources were screened. The plant materials used for molecular confirmation of rust resistance gene *Sr26* included BC₁ BC₂ and F₂ plants from various cross combinations. Usefulness of molecular markers for the detection of rust resistance genes in different genotypes is discussed. Out of fifty lines of different cross combination, screened for the presence of stem rust resistance gene *Sr26*, Forty six lines of genotypes revealed the presence through PCR analysis with the primers specific to *Sr26* gene at 200bp and 207bp.The dominant gene *Yr10* showed polymorphism for the Microsatellite locus *Xpsp3000* with the 260bp respectively in 12 segregating lines of WH147x*Yr10* (BC1) and LOK-1 x *Yr10* (BC3). Since *Yr10* was located on the short arm of chromosome 1B, only nine SSR markers distributed on the short arm of chromosome 1B were chosen for screening for polymorphism between the resistant and susceptible varieties. The unique genetic associations of *Yr10* specific alleles of *Xpsp3000* will be useful in Marker- Assisted selection and gene pyramiding. *Yr10* showed close genetic association with alternate alleles at the *Xpsp3000* and or Gli-B1

could be used in marker assisted selection for pyramiding *Yr10* with other stripe rust resistance genes.

Underlying mechanisms of disease resistance in wheat against *Puccinia triticina*, the incitant of brown rust

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Two wheat cultivars including a leaf rust susceptible PBW226 (PBW226-*Lr24*) and its resistant near isogenic line HW2016 (PBW226+*Lr24*) carrying the dominant seedling leaf rust resistance gene *Lr24* were used for comparative transcriptome studies. Seedlings of the two NILs (HW 2016+*Lr 24*) and (PBW226-*Lr 24*) showed no difference on the leaf surface at 0 and 48 hr after leaf rust inoculation. However, the seedlings of the susceptible genetic stock (PBW226-*Lr 24*) exhibited halo spots at spore germinating sites; these pale-halo spots transformed into brown coloured chlorotic spots and were associated with the emergence of pustules in the centre of the chlorotic spots, causing breakage of the epidermal cells along the surface of the infected leaf. Chlorotic spots and pustules were not appeared in resistant wheat stock HW 2016 + *Lr24*. Comparison of amplification pattern between infected resistant and susceptible mRNA sample using the RAPD primers indicated that around 88 bands were differentially expressed and some of the bands appeared to exhibit a common to both the samples. A total of 88 TDF's were identified and out of which 12 TDF's that were amplified with primers. Out of 23 TDFs sequenced 12 (52%) were expressed in resistant NIL HW 2016 and 11 (48%) TDFs were expressed in susceptible genetic stock (PBW226-*Lr 24*). TDFs expressed in resistant line (HW 2016+ *Lr 24*) were similar to MYB3R transcription factor, resistance protein LR10, CBF4-like protein, fasciclin-like protein FLA29, heat shock protein HSP26, Pm3b-like disease resistance protein 15Q1, WRKY transcription factor, Na⁺/H⁺ antiporter of *Triticum aestivum*. TDFs expressed in susceptible line PBW 226 showed similarity with ent-kaurene oxidase, salt tolerant-related protein, wali2 protein, wheatwin6-b defence protein, ubiquitin-protein ligase and fimbrin/plastin-like protein of *Triticum aestivum*. One TDF had similarity with Ubiquitin ligase , Ubiquitin

proteosome system influences many process such as the cell cycle, signal transduction, transcription, and stress reponses including defence. E3 Ubiquitin ligases mediating plant defence signalling. One of the TDF from a susceptible line was up-regulated, similar to wheatwin6-b defence protein from *Triticum aestivum*, which belongs to the pathogenesis-related PR 4 family.

Occurrence of Aecial Stage of Stem and Leaf

Rusts on Barberry species in Nilgiris hills

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Role of alternate host particularly species of Barberry accustomed to Nilgiri hills particularly at higher elevation were investigated in detail. Systematic surveys at fortnight intervals were carried out throughout the year (April 2012 to March 2013) . During the critical observations in interior regions of Nilgiri forests, it was observed that several species of Barberry were infected with plenty of aecial cups of different sizes and shapes. Pycnial stages were also noticed in some of the samples. A total of about 100 samples of leaves with such aecial cups were collected by following random sampling method from the forests in Nilgiris. Generally, aecia cup formation was abundant during the months of *Rabi* as compared to few cups formed in summers. Aeciospores were gently collected by using sterile scalpel and dispensed a drop of sterile water amended with teepol as an adjuvant. These suspensions of aeciospores were inoculated on one week old seedlings of different species of *Triticum* including *Triticum monococcum*, *Triticum dicoccum*, *Triticum aestivum* and rye (*Secale cereale*). The pathogenesis studies under glass house conditions indicated the infective nature of few isolates on *Triticum dicoccum* and *Triticum aestivum*. Repeatedly, inoculated seedlings expressed both brown and black rust symptoms. Further purification and taxonomic analysis studies are in progress.

Summer Nursery Notice

Off- season sowing for crops such as Wheat, barley, mustard, sunflower, lentil, Bengal gram, pea, safflower etc. will commence in the month of May, 2013. Following points are hereby brought to the kind notice of all concerned:

1. Seed materials of wheat, barley and triticales (main emphasis) and other crops of your centre must reach Regional Station, IARI, Wellington latest by 20th May, 2013.
2. A proper sowing plan as well as pedigree details should accompany your material.
3. Summer nursery facility is mainly extended to breeding materials for generation advance, corrective crossing, multiplication of seeds to a limited scale and disease scoring under natural hot spot environment.
4. The purpose of planting should be duly indicated along with your choice for material to be harvested or not. Also mention if disease (rusts, powdery mildew etc.) are required to be recorded.
5. Summer nursery facility to organizations other than ICAR institutes, SAUs and any other Govt. sponsored institutes will be on payment basis and the details will be supplied on demand. Private agencies have to sign MoU for consultancy project with IARI before availing the summer nursery facility.
6. It will be appreciated if user or representative are present physically at the time of sowing.
7. Important contacts:
 - Dr. M. Sivasamy, Sr. Scientist – Farm Incharge (09442350239), Dr P. Jayaprakash, Sr. Scientist – Summer Nursery Incharge (09842506455), Dr. V.K. Vikas, Incharge guest house (09442921061)

News

New joining and Transfers

- Mr. Rajesh Kumar Meena, T-1 joined station in January, 2013.
- Sh. Mohan Lal Meena, T-6 joined station in February, 2013.
- Dr. (Mrs.) Shilpi Aggarwal, T-3 transferred to IARI, New Delhi.

Retirement:

- Mr. H. Krishnan, SSS superannuated on 31st March, 2013 after putting his 34 years of dedicated services at the station. Staff , IARI,

Regional Station, Wellington wishes him a happy retired life.

Award

- Congratulations to Dr. C. Umamaheshwari for having won the woman scientist award conferred by Indian Society of Mycology and Plant Pathology, RCA, Udaipur