



International Conference

FROM SEED TO PASTA III

A SUSTAINABLE DURUM WHEAT CHAIN
FOR FOOD SECURITY AND HEALTHY LIVES



Bologna - Italy, 19-21 September 2018

DECIPHERING THE GENETIC BASIS AND MOLECULAR DEFENSE MECHANISMS OF SPOT BLOTCH DISEASE RESISTANCE OF DURUM WHEAT: AN EMERGING TREAT TO WHEAT PRODUCTION IN SOUTH-EAST ASIA.

¹Chethana C.K., ^{1*}RudraNaik,V., ¹Suma S Biradar., ²Desai S.A., ³Narendra Kadoo,
⁴I. K. Kalappanavar, ⁴Avinalappa Hotti

*Corresponding author: rvnaikgpb@gmail.com

¹Wheat Improvement Project, University of Agricultural Sciences (UAS), Dharwad-580005, Karnataka, INDIA

²Registrar, Protection of PPV& FRA, Ministry of Agriculture & Farmers Welfare, GOI, New Delhi, INDIA

³Principal Scientist (AcSIR), CSIR-NCL, Pune 411008, India. ⁴Professor of Plant pathology, U AS, Dharwad

Spot blotch (SB) is an emerging disease caused by *Bipolaris sorokiniana* affecting the wheat production in warm and humid regions of India and in other South Asian countries. The tetraploid (durum) wheats are endowed with natural resistance to brown and black stem rusts diseases but are highly susceptible to spot blotch posing severe yield losses. The study was conducted to elucidate the genetics and molecular mechanisms of SB resistance in durum wheat. The highly resistant (NIDW-295) and susceptible (Bijaga Yellow) durum genotypes in field and in glasshouse conditions were selected for further studies. The six generation (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) mean analysis was used to study the gene action indicated that duplicate gene interaction and additive \times dominance genetic effects were governing the SB resistance. The detailed infection pattern of *Bipolaris sorokiniana* at different time points after inoculations was studied and observed that successful infection of fungus by 24 hpi and disease symptoms were appeared on 4 dpi. The studies revealed that six host resistant components *viz.*, number of trichomes on leaves, number of spore per lesion, spore germination, lesion size and lesion frequency were differed significantly in resistant and susceptible genotypes. The expression stability of five housekeeping genes (*TaCDC48*, β -*tubulin*, *TaSAND*, *HveIF4E* and *EF-1 α*) were analyzed by Best keeper, gNORM, Norm Finder and comprehensive ranking methods suggested that *CDC 48* was found most stable and selected as housekeeping gene for quantitative RT-PCR. The relative expression profiling of defense related genes during SB infection were analyzed at different time points after infection and showed significant up regulation of *PR* genes [*PR 1.1*, *PR3 (Chitinase)* and *PR2 (β -1,3-glucanase)*], salicylic acid pathway genes (*NPR1-3*, *ICS1* and *PAL*), jasmonic acid biosynthesis and transduction pathway genes (*LOX2*, *AOS2*, *AOC*, *MYC2* and *PDF 1.2*) at early hours of infection in resistant genotype NIDW-295 compared to susceptible genotype Bijaga Yellow implying their role in the elucidating the defense response against SB infection in durum wheat.

ABSTRACT