

minimum disease severity (40.91 and 36.3 %) resulting in maximum grain yield (74.27 and 77.89 q/ha) during spring 2018 and 2019 respectively. The plant height and cob height was found maximum on this date. As sowing date was delayed, severity of charcoal rot increased, thus decreasing grain yield, plant height and cob height. Among meteorological factors, disease severity was found positively correlated with mean temperature and negatively correlated with mean relative humidity and total rainfall. Multiple regression equation depicting all the dependent variables revealed that when there was increase in one unit of mean temperature the percent disease severity increased by 6.08 percent. However, increase in one unit of rainfall will lead to 0.42 percent decrease in disease severity. The effect of three irrigation schedules (additional irrigation at tasseling and silking stage, local practice and stress at tasseling and silking stage) on the development of charcoal rot showed that application of an additional irrigation at tasseling and silking stage had least mean disease severity (36.28%) compared to other irrigation schedules and resulted in highest mean grain yield (72.61 q/ha). Water stress at tasseling and silking stage of the crop aggravated the disease development. Thus it can be concluded that inoculating the plant at most susceptible stage, delayed sowing and water stress at flowering and tasseling stage predisposes the plant to charcoal rot during spring season in Punjab.

II-48. PROFILING OF LOW-NITROGEN STRESS RESPONSIVE MIRNAS IN MAIZE USING HIGH-THROUGHPUT SEQUENCING

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The post green revolution agriculture is based on generous application of nitrogen (N)-based fertilizers and high-yielding genotypes. Generally, plants cannot utilize more than 40% of the applied nitrogenous fertilizer; hence more than half of the applied fertilizer is lost to the environment and results in environmental pollution via acidification, eutrophication, and depletion of ozone layer by emission of greenhouse gas. Therefore, genetic improvement in nitrogen use efficiency (NUE) in crops is desirable for a sustainable and profitable agriculture. There is a need to identify key regulatory factors playing pivotal role in acquisition, transportation and utilization of N in plants. Among other factors, microRNA (miRNA) mediated gene regulation plays a crucial role in controlling low N stress adaptation and tolerance in plants. In this endeavor, the present study was undertaken to identify N stress responsive miRNAs in maize in tropical maize using high-throughput sequencing. The HKI-163 maize inbred line was grown hydroponically with sufficient nitrogen (2mM) and without nitrogen for 21 days. Observations were recorded on all important shoot and root physiological parameters. The root and shoot samples were deep sequenced for miRNA study. The expression analysis revealed 23 known miRNAs (11 up & 12 down-regulated) in leaf and 3 known miRNAs (1 up & 2 down-regulated) in root, which expressed differentially under N stress. We also identified 53 (20 up & 33 down-regulated) and 26 (9 up & 17 down-regulated) novel miRNAs in leaf and roots respectively. The knowledge gained will help understand the important roles that miRNAs play in maize, while responding to a nitrogen limiting environment.