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RELATIONSHIP BETWEEN TFBS ABUNDANCE AND GENE EXPRESSION IN CARBOHYDRATE METABOLISM-RELATED GENES DURING FLOWERING IN RICE

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Abstract: The abundance of transcription factor binding sites (TFBSs) on promoter sequences differs from gene to gene. Understanding how this difference affects gene expression would enable us to develop superior lines through allele mining based genomic selection or genome editing. To understand the relationship between the TFBSs abundance and transcription in carbohydrate metabolism-related genes that are central to growth and grain yield in rice. For this, we first analysed the expression pattern of four carbohydrate metabolism-related enzymes - Sucrose Phosphate Synthase (SPS), PME (Pectin Methyl Esterase), Galacturonosyl transferase (GalAT) and Phosphoglucomutase (PGM). Then, we obtained a reliable set of TFBSs on the core and distal promoters of these genes following Support Vector Machine (SVM) method and stringent cut off of 90% TFBS motif similarity. Fold change in gene expression during phenology change from vegetative to flowering showed a linear relationship with the TFBS abundance in the case of an SBP family transcription factor, SPL12. Further, identification of CpG islands in the promoters explained the deviations in this linear relationship between gene expression and TFBS abundance. Using two DNA parameters - the TFBS abundance and the CpG islands - we provide predictive insights to the gene expression of carbohydrate metabolism-related genes in rice.

Keywords: Transcription factor binding sites, Gene expression, Carbohydrate metabolism, Phosphoglucomutase, Rice

GENETIC DIVERGENCE STUDIES FOR YIELD AND YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.)

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Abstract: Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, forty rice genotypes were raised at Regional Agricultural Research Station, Karjat during *Kharif*, 2020 to identify diverse genotypes. They were evaluated for fifteen yield and yield attributing characters using D^2 analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 6 clusters. Maximum number of genotypes i.e. 33 and 11 were grouped under cluster I and II, respectively and while clusters III, IV, V, VI were solitary. Maximum inter cluster D^2 value was observed between cluster IV and VI ($D= 22.174$) followed by cluster V and VI ($D = 22.138$), cluster II and V ($D= 22.066$), cluster II and III ($D=21.455$), cluster III and VI ($D=19.528$), cluster II and VI ($D =17.256$) and cluster I and VI ($D = 17.217$). The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. The intra cluster distance was maximum in cluster II ($D=9.890$) followed by cluster I ($D=8.839$). The cluster III, IV, V and VI recorded no intra cluster distance being solitary.

Keywords: Cluster, Genetic divergence, Genotypes, Rice

CHARACTERIZATION OF THE BIOACTIVE CONSTITUENTS PRESENT IN THE HEXANE EXTRACT OF *TERMINALIA CHEBULA* FRUITS

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Abstract: A study was conducted to assess the biochemical constituents present in the fruits of *Terminalia chebula*. The hexane extract of *Terminalia chebula* fruits was prepared by using soxhlet apparatus and the extract was subjected to GC-MS and FTIR analysis. The hexane extract of *T. chebula* fruits showed the presence of large number of phytoconstituents that possess antioxidant, antibacterial and antifungal activities. FTIR analysis revealed the presence of functional groups such as OH, CH, C=O, NH, C=C, CF, =CH that represents the presence of polyphenols, tannins, terpenoids, flavonoids, carbohydrate and protein compounds in *T. chebula*.

Keywords: *Terminalia chebula*, phytoconstituents, GCMS, FTIR

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GENETIC VARIABILITY STUDIES FOR YIELD COMPONENTS IN RICE (*ORYZA SATIVA* L.)

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Abstract: Forty eight genotypes were assessed for variability at RARS Karjat Dist. Raigad during *Kharif* 2020. The analysis of variance revealed highly significant differences due to treatments for all the fifteen characters under study. The estimates of PCV were slightly higher than their corresponding GCV for all the traits studied but the difference is very less indicating the presence of environmental influence to some degree in the phenotypic expression of the traits. All the characters except no of tillers per plant showed high broad sense heritability. High heritability estimates coupled with high genetic advance as per cent of mean were observed for number of filled spikelets per panicle, total number of spikelets per panicle, straw yield per plant, number of unfilled spikelets per panicle, plant height, test weight, grain yield per plant and harvest index indicating the preponderance of additive type of gene action for the expression of these characters and selection may be effective for improving these characters. Thus, these characters may serve as an effective selection parameter during breeding programme.

Keywords: Rice, Variability, Heritability, Genetic advance, Yield components

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SOIL PROPERTIES AND NUTRIENT AVAILABILITY UNDER TEAK BASED AGROFORESTRY SYSTEM

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Abstract: Since the last century, unwise utilization of soil resource has caused dramatic reduction in soil organic carbon pool, a foundation of soil life. Considering this fact, the present research experiment was carried out to assess the role of teak based agroforestry systems in improving the soil organic carbon status of soil and its influence on soil fertility. The results revealed that alkalinity and salinity of soil were significantly decreased under teak based agroforestry systems as compared to nearby agricultural land. Moreover, soil organic carbon (SOC) was increased by 59.61 per cent in soil of teak based agroforestry over the agricultural soil. Like SOC, the availability of primary nutrients (N, P₂O₅ and K₂O) and DTPA-extractable Fe and Zn were also significantly improved in soil of teak based agroforestry systems grown under South Gujarat agroclimatic condition.

Keywords: Soil organic carbon, Agroforestry system, Available primary nutrients, DTPA- extractable Fe, Zinc

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COMPARATIVE EFFICACY AND ECONOMICS OF DIFFERENT INSECTICIDES AND BIOPESTICIDES AGAINST TOMATO FRUIT BORER [*HELICOVERPA ARMIGERA* (HUBNER)] ON TOMATO (*SOLANUM LYCOPERSICUM* L.)

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Abstract: The field trial was conducted at SHUATS, Prayagraj, during *Rabi*-2022-23. Experiment was laid out in RBD (Randomized Block Design) with eight treatments replicated three evaluated against *Helicoverpa armigera* i.e., T₁ Novaluran 10% EC, T₂ Emamectin benzoate 5% SG, T₃ Chlorantraniliprole 18.5% SC, T₄ *Beauveria bassiana* 1x10⁸CFU, T₅ Neem oil 4%, T₆ Spinosad 45% SC, T₇ Nisco Sixer Plus and T₈ untreated Control. Were tested to compare the efficacy against *Helicoverpa armigera* and their influences on yield of Tomato. The best and most economical treatment is Chlorantraniliprole 18.5% SC (260q/ha) followed by Spinosad 45% SC (245q/ha), Emamectin benzoate 5% SG (225q/ha), Nisco Sixer Plus (200q/ha) Novaluran 10% EC (185q/ha), Neem oil 4% (163q/ha) *Beauveria basiana* 1x10⁸ CFU (149q/ha) and as compared to control T₈ (80q/ha). After calculating the benefit cost ratio of different treatments highest B:C ratio of different treatments was observed Chlorantraniliprole 18.5% SC (1:6.02) followed by Spinosad 45% SC (1:5.65), Emamectin benzoate 5%SG (1:5.30), Nisco Sixer Plus (1:4.72), Novaluran 10% EC (1:4.32), Neem oil 4% (1:3.83), *Beauveria basiana* 1x10⁸CFU (1:3.53), as compared to untreated control T₈ (1:1.96) having the lowest B:C ratio.

Keywords: Biopesticides, Insecticides, *Helicoverpa armigera*, Chlorantraniliprole, Tomato, Yield