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Abstracts



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VALIDATION OF ASSOCIATED SSR MARKERS IN RECOMBINANT INBRED LINES IN RICE (*ORYZA SATIVA L.*) FOR DROUGHT ADAPTIVE TRAITS

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Several diverse traits need to be pyramided into a single genetic background to achieve a comprehensive improvement in drought adaptive traits. Most of these traits are quantitatively inherited polygenic traits and their introgression can be effectively achieved only through a focused molecular breeding approach. Therefore, the challenge is to discover/identify heritably stable major QTLs that function irrespective of genetic background. In this direction mapping population comprising of 230 recombinant inbred lines developed by crossing Thanu (high WUE) and IET 15963 (high root) were phenotyped for yield, spikelet associated traits, ¹³C and root traits under aerobic condition. The population was genotyped with 115 polymorphic SSR markers reported to be linked with yield under drought, spikelet associated traits, ¹³C and root traits. QTLs for important traits like yield under drought, ¹³C, roots and traits associated with spikelet fertility were discovered. QTLs governing ¹³C flanked by RM125-RM180 and RM180-RM246 on chromosome 7 was characterized by the presence of RM180 (¹³C) marker identified by association mapping at our centre. QTL identified for root length by linkage mapping is on the chromosome 4 at the marker RM307, which is again validating the marker/QTL from the association study. QTL detected at the same marker intervals in two different approaches indicate that QTLs are stable as well as heritable.

Abstract ID: B110

IDENTIFYING SUGARCANE GENOTYPES FOR INTERMITTENT DROUGHT TOLERANCE THROUGH THERMAL IMAGING AND SPECTRAL SIGNATURE

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Sugarcane (*Saccharum officinarum L.*) is one of the most important commercial crops widely grown in tropics and subtropics of the world. The cane yield is markedly influenced by many extrinsic and intrinsic factors. Thus, any fluctuation in the sugarcane production on account of abiotic (such as maximum-minimum temperature fluctuations, soil moisture stress) and biotic stresses in Maharashtra in recent times would have considerable socio-economic implications. Drought is one of the main constraints for sugarcane production in Maharashtra, which causes considerable decline in cane yield and even no harvest in extremely severe cases. In order to provide modern and non-destructive tools for investigating the drought tolerance in sugarcane, thirty-six genotypes collected from SBI, Coimbatore; VSI, Pune; MPKV Central Sugarcane Research Station, Padegaon were maintained and evaluated for traits associated with drought tolerance at ICAR-NIASM. Thirty-six genotypes including three local checks were evaluated with two levels of irrigation i.e. 11- Full irrigation (Irrigation at 50% depletion of available soil moisture) and 12-Limited irrigation (Irrigation at 75% depletion of available soil moisture at formative and grand growth period), replicated thrice in a split plot design. Data were generated based on genetic variability in physiological as well as yield traits under moisture stress and irrigated conditions. Canopy temperature and spectral signature based indices were developed as stress indicators using thermal imaging camera and spectro-radiometer, respectively. IR images and spectral signatures were captured at 30 and 15 days interval, respectively to optimize the use of these non-destructive tools for identifying drought tolerant genotypes. It was found that distinct genotypes viz., Co-99004, Co 86032, Co-0115, CoC-671, Co-2010-01, Pad 9046, Co-2000-12, CoM 265, CoVSI-03102 and CoM-09057 kept their canopy cooler even under moisture stress conditions. These genotypes having cooler canopy also showed higher transpiration rate under water stress condition. However, perusal of yield data indicates CoM-99022, Co-0115, Co-11001, Co-3102, CoM-265, Co-11025, Co-671, Co-99004, Co-11025 and CoM-09057 are having more yield potential under moisture stress condition.



FUNGAL METAGENOME STUDY OF SOILS UNDER CONSERVATION AGRICULTURE BASED MANAGEMENT SCENARIOS

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The diversity and abundance of soil fungi was studied in different conservation agriculture (CA) based management scenarios in reclaimed sodic soils. These scenarios were based on wide range of indicators (crop rotation, tillage, crop establishment, residue management etc). The four scenarios viz., Rice {conventional tillage (CT)/transplanted rice (TPR)}-wheat rotation (Farmers practice; Sc1); Rice-wheat-mungbean {CT/TPR-ZT (zero-tillage)-ZT} with 100% residue retention/incorporation (Sc2); Rice-wheat-mungbean (ZT-ZT-ZT) with 100% residue retention (Sc3), Maize-wheat-mungbean (ZT-ZT-ZT) with 65% of maize and 100% of wheat-mungbean residue retention (Sc4). As most of the biochemical decomposition of organic plant biomass is carried out by heterotrophic microorganisms, among which fungi plays an important role. Soil microbial abundance study was carried out using molecular tool of high throughput sequencing technology (pyrosequencing/ next gen sequencing). Results clearly showed that all four scenarios were dominated by Ascomycota followed by Basidiomycota and Glomeromycota based on the fungal taxonomic diversity. Ascomycota ranges from 55 to 74%, in an order of increase in Sc1 < Sc2 < Sc3 < Sc4, however, Basidiomycota and Glomeromycota did not follow any trend both of these were found 0 to 3%. Amongst 11 observed classes, Sordariomycetes was found in all scenarios with highest abundance followed by Dothideomycetes and Eurotiomycetes. Dominating orders in all four scenarios were Sordariales, Hypocreales and Pleosporales belongs to Ascomycota phylum. Pattern of abundance of these three was similar in all four scenarios Sordariales > Hypocreales > Pleosporales. The Ascomycota and Basidiomycota phyla are dominating fungi in soils and mainly belong to the saprotrophic soil fungi and are responsible for decomposition of organic residues. Diversified cropping systems (maize-wheat-mungbean) in north-west with CA based best management practices showed the positive effect on residue decomposing fungal community. We also found that the composition of soil fungal communities at the phylum, class, and order levels was almost similar in all four scenarios but their abundance was varied among scenarios. Presence of different species was studied in all scenarios which showed 54, 91, 85 and 95 types of species were found respective scenario of 1, 2, 3 and 4. Diversity indices such as species richness, evenness (E) and Shannon-Wiener diversity index (H) were also recorded.



MULTIVARIATE INTERACTION ANALYSIS FOR ENHANCED BABY POTATO PRODUCTION UNDER TROPICAL CONDITIONS

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Potatoes are consumed in different forms from cooked to fry across the world. In recent times, the demand for small potatoes with target sizes of 20-40mm in diameter is increasing to meet the culinary market. Its production is markedly different from ware potato, as harvested earlier than the conventional results greater yield reduction. A holistic approach to minimise yield reduction is essential as not one factor operates independently. Four cultivars (K. Khyati, K. Himsona, K. Pukhraj and K. Pushkar) evaluated in AICRP (Potato) under contrasting growing environments to assess the main as well as interaction effects of Location, Cultivars and Harvesting time together, revealed a highly significant difference for all the three main effects indicating the existence of variation among growing environments and cultivars. The interaction effect of Location x Cultivars, Cultivars x Harvesting time exhibited highly significance for small (10.0-25.0g), medium (25.0-50.0g) and large (>50.0g), total yield and tuber dry matter content indicating these traits strongly influenced by them. The location Chinndwara was found to produce greater per cent of small and medium sized tubers, having greater efficiency in producing small (2.45), medium (2.1), large (1.6) and total tuber yield (1.9) across cultivars and harvesting time. Although, K. Himsona recorded with the greatest per cent of small and medium size tubers suitable for baby potatoes, the yield of this category was found greatest in K. Khyati and at par with K. Pukhraj across locations and harvesting time, hence can be recommended for baby potato production under tropical conditions.

Abstract ID: B005

REARING TEMPERATURE EFFECTS ON GROWTH, MUSCLE MORPHOLOGY AND GENE EXPRESSION OF TILAPIA, OREOCHROMIS MOSSAMBICUS

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Oreochromis mossambicus, tilapia is a fast growing fish able to adapt to a range of environmental conditions. The study was conducted with the aim to understand the effect of rearing temperatures on juvenile tilapia growth, muscle cellularity and expression of myoD and myostatin genes. Tilapia larvae were reared at 25, 30 and 34°C for 60 days. Fish growth was measured in terms of body weight, white muscle fiber frequency and qRT-PCR of myoD and myostatin gene. At 60 day, tilapia juveniles reared at 30°C grew significantly higher than the 25 and 34°C, the frequency distribution of white muscle fibres in the <25 µm diameter class was similar at 25 and 30°C but was significantly higher for fishes reared at 34°C. The frequency distribution of white muscle fiber of diameter 25-50 µm was significantly higher at 30°C in comparison to 25 and 34°C. MyoD mRNA level was significantly higher in 34°C than 25 and 30°C. Myostatin gene expression was similar at all the three rearing temperatures. The present investigation suggests that rearing temperature affect fish growth, muscle cellularity and gene expression in juvenile tilapia.

CHARACTERIZATION AND IDENTIFICATION OF MUTATION IN TMB1M6 GENE IN RESPONSE TO HEAT STRESS IN GOATS OF SEMI ARID REGION

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BAX inhibitor-1 (BI-1) gene, known as TMB1M6, is evolutionary conserved and regulates cell survival in response to various stress in animals and plants. The present study was undertaken to characterize the TMB1M6 gene in relation to stress susceptible and tolerant phenotypes in different goat breeds by high resolution melting (HRM) analysis. Phenotyping of individuals were carried out basing on heart rate (HR) and respiration rate (RR) during peak heat stress period and recognized as heat stress-tolerant (HST) and heat stress-susceptible (HSS). Genotyping of TMB1M6 gene was carried out in 40 animals during peak heat stress period by HRM. HRM analysis indicated four different groups in the analysed samples. HRM analysis indicated that the phenotyping based on physiological response was concordant with 80% of the population. Two novel mutations were observed in heat stress-tolerant and stress-susceptible individuals in analysed samples. The nucleotide polymorphisms were identified at base position 55 in heat stress-tolerant (HST) individual in Barbari goat. Similarly the mutation at base position 96 was observed in heat stress-susceptible (HSS) individual in Jakhrana goat. The mutation at 55 base position was from T to C causing change in the amino acid sequence at base position 18. Similarly the mutation at base position 96 changes in amino acid position at 31. The nucleotide sequence analysis showed 98 percent similarity between goat breeds and 84% similarity was observed in cattle, human and mouse. SNP in heat stress susceptible and heat stress tolerant phenotype were identified.

Abstract ID: B008

SCREENING ONION GENOTYPES FOR WATER DEFICIT STRESS TOLERANCE

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Water deficit stress is one of the major constraints limiting onion productivity worldwide. Identifying and implementing the novel genetic resources in the breeding program for the development of drought tolerant varieties is one of the important alleviating strategies. The field experiment was carried out to identify the level of water deficit stress tolerance in onion genotypes. During Rabi 2015, 58 onion genotypes (19 red onion genotypes and 39 White onion genotypes) were screened for water deficit stress on the basis of their leaf senescence rate and bulb yield. Water deficit stress was imposed on 45 days old onion seedling by withholding irrigation for continuous 50 days, whereas in control, normal irrigation schedule was practiced throughout the growth period. Relative water content (RWC) which directly reflects the plant water status was measured from both controlled and stressed plants. Stressed plants showed 65-70% RWC as compared to 75-85% RWC in controlled plants. In plants, the major indicator of drought susceptibility is the reduction in leaf greenness and yield. We categorized onion genotypes as tolerant, intermediate and susceptible lines based on leaf senescence rate and percentage change in bulb yield. The white onion accessions, W 397 and Arka Pitamber and red accessions Acc. 1656 were identified as water deficit stress tolerant lines as they showed less leaf senescence rate and minimum reduction in bulb weight/yield (< 30%) under stressed condition. Further, the study is needed to get insight knowledge on the favourable adaptive traits and the mechanism inducing drought tolerance in these lines.

Abstract ID: B316

EFFICACY OF CASTOR CULTIVARS ON CONSUMPTION AND UTILIZATION INDICES IN THE ERI SILKWORM, SAMIA CYNTHIA RICINI BOISDUVAL

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An investigation was undertaken to know to screen some of the selected castor (*Ricinus communis* L.) cultivars (DCH-519, 48-1, DCS-9, GCH-4, DCH-177, GAUCH-1, JC-12 and Bengaluru local) through consumption and utilization indices of eri silkworm on both fresh and dry weight basis. The results emanated from the study revealed that total food consumption, total food digestion and mean approximate digestibility on fresh weight basis were higher with the cultivar JC-12 (31.35 g/larva, 22.65 g/larva and 84.99 %, respectively), mean consumption index with GAUCH-1 (6.06), mean growth rate with GAUCH-1 (0.35) and mean efficiency of conversion of ingested food in the cultivar DCH-177 (18.69 %). On dry weight basis, GCH-4 cultivar registered higher total food consumption of 13.97 g/larva, GAUCH-1 resulted in highest total food digestion, mean consumption index, growth rate and efficiency of conversion of digested food (4.55 g/larva, 5.17, 0.35 and 20.72 %, respectively). However, mean approximate digestibility was highest in the cultivar JC-12 (84.99 %) and lowest in DCH-177 (80.17 %). The results of the study inferred that consumption and utilization indices in eri silkworm were found better with cultivar GAUCH-1 over other cultivars and can be conveniently exploited for rearing of eri silkworm for production of eri cocoons.

Abstract ID: B317

SCREENING OF CASTOR (*RICINUS COMMUNIS* L.) CULTIVARS THROUGH BIO-CHEMICAL ASSAY FOR CHAWKI REARING OF ERI SILKWORM

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In the current study, eight castor (*Ricinus communis* L.) cultivars (DCH-519, 48-1, DCS-9, GCH-4, DCH-177, GAUCH-1, JC-12 and Bengaluru local) were subjected to assess their suitability through bio-chemical assay for rearing of eri silkworm, *Samia cynthia ricini* Boisduval. The results of the current investigation revealed that, castor cultivars raised under rainfed condition differed significantly with respect to biochemical and mineral constituents. Cultivar GAUCH-1 registered higher leaf moisture content (80.76 %), crude protein (33.95 %) and total protein (39.45 mg/g) contents. Chlorophyll 'a' 'b' and total chlorophyll contents were high with GCH-4 cultivar (1.903, 0.350 and 2.165 mg/g) and total sugar content was found with cultivar DCH-177 (7.783 mg/g). However, the lower volumes of leaf moisture content was found in DCH-519 (71.99 %), crude protein content in Bengaluru local (20.72 %), total protein content in DCS-9 (21.33 mg/g), chlorophyll 'a', 'b' and total chlorophyll contents in Bengaluru local (1.483, 0.143 and 1.732 mg/g) and total sugar content in 48-1 (2.670 mg/g), respectively. Elemental composition of castor cultivars viz., nitrogen, phosphorus, potassium, calcium, magnesium and sulphur contents were higher with the cultivar GAUCH-1 (5.432 %, 0.272 %, 3.761 %, 4.185 %, 2.215 % and 0.935 %, respectively). Whereas least elemental composition of nitrogen content was found in Bengaluru local (3.316 %), phosphorus and potassium contents in GCH-4 (0.200 % and 1.918 %, respectively), calcium in 48-1 (3.218 %), magnesium in DCS-9 (1.695 %) and sulphur in DCH-519 (0.453 %). The results of the study inferred that, bio-chemical and mineral constituents of leaves were significantly superior in GAUCH-1 cultivar and can be exploited for rearing of the eri silkworm to maximize eri cocoon production.

Abstract ID: B318

EFFECT OF HEAT STRESS ON EXPRESSION PATTERN OF IMMUNE SYSTEM GENES IN INDIGENOUS AND CROSS BRED DAIRY CATTLE

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Higher temperatures of summer months and impending climate change scenario have increased the risk of heat stress in dairy cattle. Heat stress severely impacts productive performance and immune potential of animals making them more susceptible to diseases. The present study aims to analyze heat stress mediated changes genes expression patterns involved in innate immune mechanisms against invading microbes. Blood samples were collected from the indigenous breed (Sahiwal) and cross-bred (Frieswal) dairy cattle. The Peripheral blood mononuclear cells (PBMC) isolated and were subjected to in vitro thermal stress. The heat stress was given to the PBMC sample groups at 42°C for one hour followed by incubation at 37°C for recovery time. The kinetics of gene expression patterns for heat shock protein 70 (Hsp70) and genes of immune system (TLR2, TLR4, IL4 and IFN gamma) were analyzed at different recovery intervals of 0, 2, 4, 6 and 8 h. The higher level of expression of Hsp70 mRNA was detected at 2 h after heat stress treatment followed by gradual decline to the normal level. Samples from Sahiwal cattle showed higher expression of Hsp70 mRNA compared to the Frieswal cattle. Acute inflammatory cytokines, IL2 and IFN gamma increased in both indigenous and cross bred cattle. However the expression was more pronounced Sahiwal cattle compared to the Frieswal. The innate immunity protein TLR2 did not show much variation where as TLR4 was induced by heat stress. These preliminary studies indicated that the immune-related genes differentially expressed during thermal stress among native and crossbred cattle. Enhanced expression of immune genes may provide evidence for the adaptability status of indigenous cattle breeds in higher temperatures of tropical climate.

Abstract ID: B319

EXPRESSION OF TRANSCRIPTION FACTOR ATSHINE1 TO IMPROVE ABIOTIC STRESS TOLERANCE IN MULBERRY (*MORUS ALBA* L.)

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Leaf quality in mulberry (*Morus* sp.) is one of the major factors contributing for silkworm (*Bombyx mori* L.) growth and development. The silkworm growth and cocoon yield is largely influenced by the freshness and nutritional quality of the mulberry leaves. Mulberry foliage yield and leaf quality is influenced by growth condition and various abiotic stresses such as drought and salinity are known to reduce leaf quality and yield. In this regard, an attempt has been made to develop stress tolerant mulberry plants through transgenic approach by constitutively over-expressing Arabidopsis SHINE1 (AtSHN1), an AP2-domain containing transcription factor. The gene is known to improve leaf surface wax synthesis and impart stress tolerance. The selected transgenic mulberry plants showed PEG-induced desiccation stress tolerance under laboratory conditions. Better cell membrane stability, chlorophyll content and cell viability in transgenic plants than wild type under drought stress condition indicated the relevance of AtSHN1 in stress acclimation. In summary the overall data from abiotic stress experiments suggested that over-expression of AtSHN1 in mulberry can improve cellular tolerance traits. Since AtSHN1 is an upstream regulatory protein, the stress tolerant phenotype observed could be due to the activation of multiple downstream genes.