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 co-expression 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 15961 (high root) were phenotyped for yield, spikelet associated traits, Th9c and root traits under aerobic condition. The population was genotyped with 115 polymorphic and root traits under aerobic condition. The population was genotyped with 115 polymorphic

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 temperature fluctuations, soil moisture stress) and biotic stresses in Maharashtra under recent years 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, Pedagao were evaluated and for trait associated with drought stress tolerance at ICAR-NIASM. Thirty-six genotypes including three local checks were evaluated based on two levels of irrigation i.e. irrigation (irrigation at 50% depletion of available soil moisture) and irrigation (irrigation at 75% depletion of available soil moisture at 15 days interval, respectively). The images and spectral signatures were captured at 30 and 15 days interval, respectively. As stress indicators using thermal imaging camera and spectroradiometer, respectively, as stress indicators using thermal imaging camera and spectroradiometer, respectively, images and spectral signatures were captured at 30 and 15 days interval, respectively.

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); Rice-wheat-mungbean (R-W-T-M; zero tillage) with 100% residue retention/Incorporation (S2); Rice-wheat-mungbean (R-W-T-M; zero tillage) with 100% residue retention (S3); Malhe-wheat-mungbean (R-W-T-M; zero tillage) with 50% maize and 100% of wheat-mungbean residue retention (S4). 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) in next generation sequencing. Results clearly showed that all four scenarios were dominated by Basidimycota and Glomeromycota based on the fungal taxonomic diversity. Ascomycota ranges from 55 to 74%, in an order of increase in ScC 5% ScC5% ScC4, however, Basidimycota and Glomeromycota did not follow any trend both of these were found to be 5%. Amongst 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 were varied among scenarios. Presence of different species was studied in all scenarios which showed 49, 91, 85 and 95 types of species were found respective scenario of 1, 3, 5 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 is increasing to meet the culinary market. Its production is markedly different from growing conditions. The production is markedly different from what is harvested earlier than the conventional cultivation results for yield reduction. A holistic approach to minimise yield reduction is essential as one factor operates independently. Four cultivars (K. Kityati, K. Kimsana, K. Pukhral and K. Pushkar) were evaluated in AICRP (Potato) under contrasting growing environments to assess the effects of location, cultivars and harvesting time together, as well as interaction effects of Location, Cultivars and Harvesting time. The existence of varied results among growing environments and cultivars. The interaction effects of Location x Cultivars x Harvesting time exhibited highly significant results. The yield of small (10.0-25.0g), medium (25.0-50.0g) and large (>50.0g), total yield and tuber yield and (1.0g) across cultivars and harvesting time. Although, K. Kimsana recorded the highest yield with the greatest per cent of small and medium size tubers suitable for baby potatoes, whereas, K. Kityati and K. Pukhral are recommended for baby potato production under tropical conditions.

REARING TEMPERATURE EFFECTS ON GROWTH, MUSCLE MORPHOLOGY AND GENE EXPRESSION OF TILAPIA, OREOCROMIS 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 gene 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 weight (g) and muscle fiber frequency and qRT-PCR of myoD and myostatin gene. The reared at 30°C grew significantly higher than the 25 and 34°C, the frequency distribution of white muscle fibres in the <5 μm diameter class was similar at 25 and 30°C, and significantly higher for fishes reared at 34°C. The frequency distribution of 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. The myostatin gene expression was similar at all the three rearing temperatures. The investigation suggests that rearing temperature affect fish growth, cellularity and gene expression in juvenile tilapia.

CHARACTERIZATION AND IDENTIFICATION OF MUTATION IN TMBIM6 GENE IN RESPONSE TO HEAT STRESS IN GOATS OF SEMI ARID REGION

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BAX inhibitor-(Bcl-1) gene, known as TMBIM6, is evolutionarily conserved and regulates cell survival in response to various stress in animals and plants. The present study were undertaken to characterize the TMBIM6 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 heat 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 TMBIM6 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 Jakhana goat. The mutation at base position 55 was found to be causing change in the amino acid sequence at base position 8. Similarly the mutation at base position 56 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.

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 2010, 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 growing 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 area 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 W397 and Arka Pimplar and red accessions Acc. 1565 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 allelic traits and the mechanism inducing drought tolerance in these lines.
EFFICACY OF CASTOR CULTIVARS ON CONSUMPTION AND UTILIZATION INDICES IN THE ERI SILKWORM, SAMIA CYTHIA 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 (64.66 g/larva), mean growth rate with GAUCH-1 (0.35 g/larva) and mean efficiency of conversion of ingested food in the cultivar DCH-177 (18.59 %). 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 (4.35 g/larva, 5.17 g/larva, 0.35 g/larva 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.

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 cytherea ricini Balsdual. 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 (86.76 %), crude protein (33.95 %) and total protein (39.45 mg/g) contents. Chlorophyll 'a' and 'b' and total chlorophyll contents were high with GCH-4 cultivar (1.909, 0.335 and 2.165 mg/g) and total sugar content was found with fresh weight of the cultivar DCH-177 (2.783 mg/g). However, the lower volumes of leaf moisture content was found in DCH-519 (71.99 %), crude protein content in Bengaluru local (20.71 %), 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, phosphorous, potassium, calcium, magnesium and sulphur contents were higher with the cultivar GAUCH-1 (5.423 %, 0.272 %, 3.761 %, 4.185 %, 2.215 % and 0.933 %, respectively). Whereas least elemental composition of nitrogen content was found in Bengaluru local (3.316 %), phosphorous and nitrogen contents in GCH-4 (0.200 % and 1.918 %, respectively), phosphorous and potassium contents in 48-1 (3.218 %, 3.328 %) and 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.

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 disease. The present study aims to analyze heat stress mediated changes in expression patterns of immune response genes involved in innate immune mechanisms against invading microbes. Blood samples were collected from the indigenous cross-bred (Sahial) and cross-bred (Friesial) 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 37°C for one hour followed by incubation at 37°C for recovery time. The kinetics of gene expression patterns for heat shock protein 70 (Hspt70) and genes of immune system (TLR2, TRC, IL4 and IFN gamma) were analyzed at different recovery intervals of 0, 2, 4, 6 and 8 h. The higher level of expression of Hspt70 mRNA was detected at 2 h after heat stress treatment followed by gradual decline to the normal level. Samples from Sahial cow exhibited higher expression of Hspt70 mRNA compared to the Friesial cattle. Acute inflammatory cytokines, IL2 and IFN gamma increased in both indigenous and cross bred cattle. However the expression was more pronounced Sahial cow compared to the Friesial. The innate immunity protein TLR2 did no 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.

EXPRESSION OF TRANSCRIPTION FACTOR ATSHINE1 TO IMPROVE ABIOCIC 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 leaf quality is influenced by growth condition and various abiotic stresses such as drought and salinity are known to reduce stress tolerant mulberry plants. The expression of ATSHINE1 gene was found in at the young leaf of mulberry. The expression was induced by constitutively over-expressing Arabidopsis SHINE1 (ATSHINE1), a transcription factor. The gene is known to improve leaf surface wax synthesis and Impacts stress tolerance under laboratory conditions. Better cell membrane stability, chlorophyll content and cell viability in transgenic plants than wild type under drought and salinity stress. The overall data from abiotic stress experiments suggested that over-expression of ATSHINE1 in mulberry can improve cellular tolerance traits. Since ATSHINE1 is an upstream regulatory protein, the stress tolerant phenotype observed could be due to the activation of multiple downstream genes.