POSTER ABSTRACTS

AGRICULTURAL SCIENCES

1. COMBINATORIAL EFFECT OF RICE BLAST RESISTANCE GENES TAGGED USING RESTRICTION FRAGMENT LENGTH POLYMORPHISM

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Restriction fragment length polymorphism (RFLP) mapping using greenhouse phenotypic data of recombinant inbred lines (RILs) identified four major genes for blast resistance against five races of rice blast pathogen in Southern USA. Using the markers bracketing the gene or closely linked to the resistance gene as tag for each gene, lines with different gene and their combinations were evaluated at the blast nursery. Analyses of the performance of the lines using three parameters: area under disease progress curve (AUDPC), percent disease leaf area (%DLA), and IRRI standard Evaluation System for blast (SES rating) indicated the presence of direct gene effect and gene x gene interaction. In particular, Pi-q6 significantly interacted with other tagged genes while Pi-q1, Pi-b2 did not. Regression model revealed that the best fitting combinations were Pi-q5, and Pi-q6 for %DLA and AUDPC and Pi-q5, Pi-q6, and Pi-b2 for SES rating. Results further revealed that the genes and their interaction can explain only 20-25% of the variation observed at the blast nursery and the remaining differences may be attributed to the minor genes or unidentified major genes in the RIL population.

Keywords: rice blast, RFLP, gene expression, major gene, gene interaction, gene mapping, disease resistance, *Oryza sativa*

2. GENETIC MAPPING WITH AMPLIFIED FRAGMENT LENGTH POLYMORPHISM (AFLP) IN RICE

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Genetic map construction and tagging of genes for qualitative and quantitative traits in rice have been conducted mainly through the use of restrictive fragment length polymorphism (RFLP) and random amplified DNA (RAPD) markers. These markers, however, are limited in the number of loci they can assay per reaction and amplified fragment length polymorphism (AFLP) has been proposed as a valuable tool for gene mapping in many plant species. To test the usefulness of AFLP's for genetic mapping in rice, 54 AFLP bands using seven *Eco*R1 +3: Mse1 +3 primer combination on an F_2 population derived from an indica/japonica cross were assayed. Only 4 of the 54 bands scored deviated from the expected 3:1 Mendelian ratio for dominant markers ($P<0.05$). Using the program Mapmaker and a framework map of RFLPs and RAPDs, 50 AFLPs were mapped to rice chromosome except chromosome 12. The AFLPS located on each chromosome varied from 1 to 8 and appeared to be randomly distributed. Using the resulting genetic map, quantitative trait loci (QTLs) for seed and reproductive traits were identified with 7 QTLs bordered by AFLP markers. These results indicate that AFLP technology could be a tool for genetic studies in rice.

Keywords: AFLP, QTL, mapping, rice, PFLP, RAPD, genetic

3. RESTRICTION FRAGMENT LENGTH POLYMORPHISM ANALYSIS OF GENETIC VARIATION IN STRAINS OF *Pseudomonas* (RALSTONIA) *solanacearum* INFECTING *Musa and Heliconia* FAMILIES

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The Philippine population of banana-infecting strains of *Pseudomonas solanacearum* was analyzed in relation to foreign strains infecting Musa and Heliconia families through restriction fragment length polymorphism (RFLP). Probes which harbor the genes for extracellular polysaccharides (E36, 07 050), endoglucanase (pHE3), trytophan biosynthesis (p T161), a random clone from Z04 library (p Z1217) and the repititive element (pM114) were used for the purpose, RFLP patterns were affected by the kind of probes used. Different RFLP types were noted among strains using different probes. Composite RFLP analysis, however, resolved 16 haplotypes grouped into five clusters at 65% similarity level.

4. FACTORS INFLUENCING GENE EXPRESSION AND T-DNA TRANSFER IN *A. tumefaciens*-MEDIATED TRANSFORMATION OF RICE

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Rice has been routinely transformed using the directs DNA uptake methods. Recent developments in rice genetic transformation using *A. tumefaciens* as a natural vector necessitate the investigation of factors that will promote optimum gene expression and T-DNA transfer in the recalcitrant indica rice varieties. Activities of three different promoters were investigated transiently using *gus*A after particle bombardment of suspension cells. Actin and ubiquitin promoters were found to induce higher GUS activity. A binary vector pCGN1558 was modified to contain these promoters in front of the *gus* A-intron. *A. tumefaciens* strain EHA 101 and A136 were transformed with the derivatives of the binary vector and transformed colonies were tested for infectivity to coleoptile bases of IR54 and IR72 seedlings. GUS activity of the infected coleoptile bases showed that the *A. tumefaciens* colonies were comparable but not better than the positive control At656. Possible reasons for the results were discussed with emphasis on the importance of the compatibility of the *A. tumefaciens* strains with the binary vector, the border sequences, and the Ti-plasmid present.

Keywords: gene expression, I-DNA transfer, *A. tumefaciens*, rice

5. IDENTIFICATION OF RAPD MARKERS LINKED TO A MAJOR BRUCHID RESISTANCE GENE IN MUNGBEAN (*Vigna radiata L.*)

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Random amplified polymorphic DNA (RAPD) was used to identify markers linked to major bruchid resistance gene in mungbean. Four pairs of pear-isogenic lines------------*(V. radiata var. sublobata)*, a wild relative of mungbean and the source of resistance to bruchid *(genus Callosobruchus)* of the resistant NILs, were used. RAPD reactions were based on the protocol by Williams et al. (1991), with modifications. Eighty-four Operon primers were screened, of which 66 were succesful in amplifying loci from the NILs DNAs. Twenty markers were found polymorphic in at least 2 pairs of NILs. Two markers, $S01_{946}$ and $Q14_{695}$, were found polymorphic in all pairs of NILs. Segregation analysis and subsequent mapping of the putative markers were done using a set of recombinant inbred lines from the cross Pagasa 7 XTC1996.

Keywords: RAPD, mungbean, *V. radiata*, insect resistance, *Callosobruchus maculatus*, near isogenic lines, recombinant inbred lines.

6. RANDOM AMPLIFIED POLYMORPHIC DNA ANALYSIS OF PAPAYA RINGSPOT VIRUS-RESISTANT INTERSPECIFIC HYBRIDS

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Papaya production worldwide has been markedly reduced by papaya ringspot virus type-P(PRSV-P). Interspecific hybrid of papaya (*Carica papaya* L.) and a wild relative, *Carica cauliflora* Jacq. were produced to develop resistance to PRSV-P. An improved embryo rescue technique was used for the production of interspecific hybrid plants. Resultant hybrid embryos were of (two) types (single and multiple) and were variable in size, colour, and developmental stages. Regeneration via embryogenesis variable F_1, phenotypes. Random amplified polymorphic DNA (RAPD) markers were used to identify hybrids. Genomic DNA of parents and a hybrid was screened using 72 decamer primers of which 57 showed polymorphism between the two parents. On the hybrid, 17 primers revealed polymorphic banding patterns (1-2 bands) of both parents. Five (OPA-07, OPA-9, OPA-19, OPB-12, OPC-06) out of the 17 primers which consistently resolved polymorphis of the parents were used to assess hybridity of 120 interspecific hybrid. All plants analysed contained at least 1 band from *C. cauliflora* as shown by any of the 5 primers, indicating that they are hybrids. In addition, all plants produced had some intermediate morphological traits of papaya and *C. cauliflora.* Pollen fertility of the hybrid is low (0.6-130%), in contrast to the high (93-100) fertility of the parents.

Keywords: *Carica papaya* L., *Carica cauliflora* Jacq., embryo rescue, interspecific hybrids, papaya ringspot virus type-P, primers, random amplified polymorphic DNA, resistant

7. STRUCTURE AND EXPRESSION OF A β-GLUCANASE MULTIGENE CLUSTER IN RICE

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Plants produce high levels of β-glucanases in roots during seed germination and flower formation and response to invasion by pathogenic microbes. To understand the role of these enzymes in the defense response and various developmental stages, 3 β-glucanase genes in rice were cloned and characterized in structure and expression, *Gns2*, *Gns3*, and *Gns4* were tandemly arranged within a 9 kb region in the same orientation of transcription. These genes encoded a mature peptide of 3.2-3.3 kD in size. Both *Gns2* and *Gns3* specified an acidic mature peptide, in contrast to *Gns4* which encoded a basic mature peptide. The *Gns2*, *Gns3*, and *Gns4* isozymes likely had a $\beta_{1,3}$-glucanase activity, and may be extracellular because the genes specify a signal peptide but not a C-terminal wextension. *Gns2* was expressed at low levels in germinated seed and mature leaf. Neither *Gns2* nor *Gns3* was induced by exogenous and stress treatments. *Gns4* was found to be the most active gene. It may have exogenous hormones important growth and defense-related functions. It was expressed substantially in germinated seed, and in response to exogenous GA, auxin, ABA, and the defense signal salicylic acid.

Keywords: ABA, auxin, β-glucanase, calli, coleoptide, ethylen, GA, protein, seed germination

8. STRUCTURE AND EXPRESSION OF A NOVEI DEFENSE-RELATED GENE IN *Oryza sativa Linn*

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Knowledge about molecular mechanisms underlying the plant defense response is still fragmentary. To help better understand this process, the genes encoding the β-glucanases in rice, which are among the pathogenesis-related proteins produced by plants in response to pathogen invasion were A β-glucanase gene, *Gns9*, that has structural and expression properties was cloned. The *Gns9* mature protein products was unusually long, consisting of 322 amino acids (34.5 kDa), about 15 residues longer than the typical higher plant β-glucanase. Its preprotein also contained an N-terminal signal peptide and a C-terminal extension, presumably for vacuolar transport. *Gns9* consisted of two exons and usually short intron (99bp). Analysis of transcript (message) levels showed that unlike many plant β-glucanase genes, *Gns9* was only weakly induced by a fungal elicitor and wounding, and was not stimulated by salicylic acid. However, it was strongly activated by the stress hormone ethylene, and thus may function in an ethylene-dependent defense response. *Gns9* was highly espressed in calli, immature seed, root, and coleoptile, and was strongly responsive to exogenous GA, auxin and ABA, indicating a possible role also in growth and development.

Keywords: ABA, auxin, β-glucanase, calli, coleoptile ethylene GA, protein, root, seed

9. TRANSIENT ACTIVITY OF THE CAMV35S PROMOTER LACKING THE METHYLATION TARGETS IN RICE AND EFFICIENT SELECTION OF TRANSFORMED RICE CELLS USING THE BAR GENE

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Gene silencing is usually caused by promoter or gene methylation. The activity of a cauliflower mosaic virus (CaMV)35S promoter with lesser number of methylatable cytosine on gene expression was studied. A plasmid (pSan9) with the CaMV35s promoter mutated at the TGACG motifs (methylation target free (MTF 35S) and CaM35S plasmid (pSan2) driving the *gus*A gene was used. The activity of the MTF 35S and CaMV35S promotes to drive the expression of *gus*A reporter gene was determined transiently in rice variety Radon using the polyethylene glycolmediated transformation. Transient GUS activity of two-day DNA-treated protoplast showed an expected lower activity in the protoplast treated with pSan9. Radon protoplasts were co-transformed with the selectable marker *bar* gene and with either pSan2 or pSan9. Plants were regenerated from the DNA-treated protoplast at a high selection and co-transformation efficiencies. Two transgenic plants produce with minimum integration events shown in the southern blot analysis exhibited high GUS activity using a fluorimetric assay. However, most of the plants regenerated contained high multiple integration events resulting to each inability to determine the activity of the MTF35S promoter in stable conditions.

Keywords: cauliflower mosaic virus, methylation, promoter, GUS activity, B-glucu ronidase, polythylene glycol, protopists, transformation, *Oryza sativa*, transgenic, *bar* gene

10. MOLECULAR MAPPING OF RESISTANCE TO *Thrips palmei* IN POTATO: I. POLYMORPHISM SURVEY AND INHERITANCE STUDY OF RAPD MARKERS

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Random Amplified Polymorphic DNA (RAPD) marker technique was employed to find additional polymorphic DNA markers between *S. tuberosum* and *S. berthaultii* parents of the two mapping populations (BCT and BCB) used in this study. Atotal of 115 short, random oligonucleotide primers from Operon Technologies were surveyed for differences between the parental genotypes used. Eighty (80) RAPD bands were found polymorphic between the parents. Segregation analyses of all polymorphic RAPD bands identified wereconducted in the two backcross populations. Chi-square test suggest that only 14% of the segregating RAPD bands observed followed the expected Mendelian ratio. The mapped portion of the RAPD markers identified in this study is currently being located into the existing RFLP map of potato. Ultimately, the combined RFLP/RAPD map will used to map the position of the genes for resistance to *Thrips palmei*.

Keywords: potato, *S. tubersum*, *S. berthaultii*, RAPD, DNA markers

11. MOLECULAR MAPPING OF RESISTANCE TO *Thrips palmei* IN POTATO: II. EVALUATION OF GLANDULAR TRICHOME TRAITS AND THRIPS RESISTANCE REACTION IN TWO BACKCROSS POPULATIONS

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Parent and progenies of two backcross population, BCT and BCB, derived from a cross between a diploid *Solanum tubersum* and a wild diploid species, *S. berthaultii*, were evaluated for glandular trichome traits and resistance to *Thrips palmei* under Philippine conditions. Both parental genotypes exhibited the expected variation for glandular trichome traits and contrasting resistance reaction to thrips infestation. *S. berthaultii* expressed both trichome types, A and B, and highly resistant reaction to thrips infestation. Evaluation of the BCT population indicated that the progenies showed a wide range of variation in trichome density and MEBA scores. However, only type *A trichomes* were found in all the 147 BCT progenies tested. Results of the thrips resistance evaluation showed that all BCT progenies succumbed to thrips damage before the final damage rating could be conducted. On the other hand, the BCB population showed a wide range of variation in resistance reaction to thrips infestation. Trichome traits analyses of the BCB are currently underway. Ultimately, result of this study will be used in mapping the location of thrips resistance gene(s) in potato.

Keywords: potato, glandular trichomes, MEBA, *Thrips palmei*, insect resistance, mapping

12. DEVELOPMENT OF RINGSPOT VIRUS RESISTANT PAPAYA

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Papaya ringspot virus (PRSV) is a serious problem in papaya production worldwide. It is likely that the planting of resistant papaya cultivars will overcome this

problem. Interspecific hybridization between papaya (*Carica papaya* L.) and the resistant wild species, *Carica cauliflora* Jacq., has been done with the aid of embryo rescue to produce interspecific hybrids. An improved embryo rescue protocol was adapted and subsequently utilized for efficient production of interspecific hybrid between papaya and PRSV-resistant *C. cauliflora* from 90- and 120-day-old embryos. Pre-incubation of hybrid embryos for 5 days on either liquid or solid germination medium full-strength De Fossard nutrients plus 10 uM BAP 3 0.25 μM NAA, and 58 μM sucroser induces germination of hybrid embryos. Subsequent transfer of germinated embryos tp a hormone-free nutrient medium allowed good growth pf hybrid seedlings in-vitro. Hybrid seedling are now flowering in the glasshouse and are currently being backcrossed with papaya. This wide hybridization work is an attempt to transfer PRSV resistance from the wild to cultivated species.

Keywords: *Carica papaya, C. cauliflower*, embryo rescue, inter-specific hybridization, papaya ringspot virus

13. TEMPORAL EXPRESSION OF QUANTITATIVE TRAIT LOCI FOR BLAST RESISTANCE IN RICE

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Thirteen quantitative trait loci (QTLs) in 9 chromosome were identified for blast resistance using phenotypic data the blast nursery. Eight of these loci were located using IRRI's Standard Evaluation System for blast (SES rating) at 41 days after seeding (DAS) while 6 loci were found for percent diseased lead area (%DLA) at 40 DAS. The markers closely linked to each QTL were analyzed using being data gathered at 19, 26, 33 and 47 DAS to determine if the same QTLs were being expressed at different ages after seeding. Analyses showed that all marker x phenotype associations except for I were not significant at 19 DAS for % DLA but not for SES rating. Most associations were found significant at 26 DAS. Putative QTLs near the major gene (s) were consistently identified at 26 and 33 DAS but not at 19 and 47 DAS for both %DLA and SES rating.

Keywords: rice blast, RFLP, gene expression, quantitative traits locus (QTL), minor gene, gene mapping, disease resistance, *Oryza sativa*

14. TRANSFER OF TUNGRO VIRUS RESISTANCE FROM THE WILD RICE *Oryza rufipogon* GRIFF. TO THE CULTIVATED RICE *O. Sativa L.*

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Rice tungro disease is the most severe and widespread viral disease of rice bringing about substantial losses in many rice-growing areas especially in South and Southeast Asia. Strategies and current status of work on the development of tungro-resistant varieties by transferring resistance genes from the wild relatives of rice to the cultivated rice through wide hybridization was presented. Accession 105908, 105909 and 105910 of *Oryza rufipogon* were subjected to enzyme-linked immunosorbent assay (ELISA) and found to be resistant to the rice tungro spherical virus (RTSV) and rice tungro bacilliform virus (RTBV). Those were crossed to IR64, a susceptible commercial variety. The F1 hybrid *O. rufipogon* (100909) x IR64 was backcrossed to IR64 producing 279 BC1F1 plants. Selected BCl Fl plants were further backcrossed to the recurrent parent producing 1650 BC2F1 plants which constituted the mapping population. Backcrossed plants were selected based on morphological similarity to IR 64 and resistance to the two viruses. Genetic similarity to IR64 based on RFLP and RAPDS parental served as basis for further backcrossing to reconstitute the genetic background of IR64. RFLP and RAPDS parental survey revealed high level of polymorphism between *O. rufipogon* and IR64.

15. ASSESSMENT OF GENETIC DIVERSITY IN THE PHILIPPINE ABACA *Musa textilis Nee.* GERMPLASM COLLECTION USING DNA MARKERS

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The technique of Random Amplified Polymorphic DNA (RAPD) analysis was employed to assess the extent of genetic diversity among abaca accessories collected and maintained in existing germplasm banks. A total of 104 random, short oligonucleotide primers from Operon technologies were tested to reveal DNA polymorphisms among selected abaca accessions. Fifty-six out of 104 primers screened showed intense and well resolved amplification products. RAPD analysis was subsequently conducted on DNA samples of 106 abaca accessions obtained from existing gene bank collections. Cluster analysis and principal component analysis (PCA) of the RAPD data were analysed using NTSYS-pc computer software. Correlation between RAPD markers and morphological traits were likewise analysed.

Keywords: abaca, *Musa textilis*, DNA markers, RAPD, genetic diversity, germplasm collection

16. APPLICATION OF DNA FINGERPRINTING IN RESOLVING THE IDENTITY OF A POPULAR FARMERS' VARIETY

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The study aimed to illustrate the usefullness of simple PCR-based markers in establishing the identity of rice varieties with uncertain origin. The study used Banay-banay 7-Toner, a high quality rice variety in Mindanao, which has an uncertain origin. Compared to IR64, both are agro-morphologically very similar. Results of the study showed no significant difference between Banay-banay and IR64 in 18 quantitative and 8 qualitative agro-morphological traits observed. Amylose contents of the two varieties were also found to be comparable and both contain intermediate amylose (21-22%). In the absence of Banay-banay pedigree information randomly amplified polymorphic DNA and simple sequence length polymorphisms (SSR) to fingerprint Banay-banay 7-tonner and IR64 were used. From a total of 360 loci generated by RAPD analysis the 2 samples were different in 8 bands only (2.27) or a similarity of 97.87. SSR analysis also indicated that both varieties had almost the same set of alleles in most of the 24 loci assayed. Compared with other high quality varieties like PSB Rc14, BPI-76 and C4-63G. Banay-banay clustered with IR64. Thus, DNA fingerprinting results strongly supported the earlier observation that Banay-banay 7-Tonner is very similar if not the same as IR64.

Keywords: DNA fingerprinting, rise, Banay-banay, IR64

17. INFLUENCE OF HOST SELECTION ON THE POPULATION STRUCTURE OF *Xanthomonas oryzae PV. oryzae*

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The influence of host genotypes on the genetic structure of the populations of *X. oryzae pv. oryzae* was evaluated in plots established in the Philippines over a two year period. Bacterial populations were from three near-isogenic rice cultivars containing the *Xa4*, *Xa7* or *Xa10* genes for resistance to *X. o. pv. oryzae* and the susceptible parent IR 24. The genetic structure of the pathogen population was monitored by using two polymerase chain reaction-based assays. Two genetic lineages (B and C) of *X. o. pv. oryzae* were detected. Lineage C, composed of races, 3 (virulent to *Xa4* and *Xa10*) and 9 (virulent to *Xa4* and *Xa10* and moderately virulent to *Xa7*) dominated the population at both sites. In all cultivars, there was a reduction in the population diversity over the two years. After 2 years selection, populations on the cultivar with *Xa 10* consisted of lineage C haplotypes (C-01 and C-05) that were races 3 and 9. Populations on the cultivar with the *Xa7* gene were race 9 and were mostly of srains from the common lineage C, haplotype C-01 and a rare population from C-05. Molecular changes in strains from *Xa7* that were adapted on *Xa7* were compared. Four distinct groups with increased virulence were defined, indicating that virulence to *Xa7* occurred through 4 different evolutionary pathways.

Keywords: host selection, xanthomonas oryzae, rice genetic structure

18. ESTERASE ISOZYME ANALYSIS OF ASIAN CORN BORER (*Ostrinia furnacalis GUENEE*) POPULATIONS FROM THE PHILIPPINES AND JAPAN

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Thirteen genotypes of esterase-1 were observed in three populations of Asiatic corn borer, 11 from the Laguna population with 5 allele (t, u, v, w, x) 7 from Leyte with 6 alleles (t, u, v, w, x,y) 7 from Cotabato with 5 alleles (t, u, v, w, x). Only the Leyte population had allele. The Asiatic cornborer populations from Laguna and South Cotabato had heterozygosity values of 0.202 and 0.200 higher than that of Leyte with 0.162. The Laguna population was significantly different from that of Leyte and South Cotabato although the latter two were not significantly differentfrom each other. The Japanese population of corn borers from one site had six genotypes of esterase-1 with 4 alleles (t, u, v, w) and heterozygosity value of 0.286 and which were different from the genotypes of the Philippines populations.

Keywords: Asiatic corn borer, *Ostrinia furnacalis* Guenee, isozymes, esterase, insect biotypes

19. KINETIC PROPERTIES AND ACTIVITIES OF CORN LEAF NITRATE REDUCTASE AND ROOT PHOSPHOENOLPYRUVATE CARBOXYLASE AT DIFFERENT LEVELS OF SALINITY

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With the increasing demand for food, utilization of marginal lands like the saline areas become important. Breeding for salt tolerant varieties of otherwise salt sensitive crops is one of the strategies undertaken in crop improvement. The biochemical mechanism of salt tolerance in corn using enzyme markers was, therefore, investigated. The kinetic studies revealed that leaf NR was stable at O-6°C and showed maximum activity at 29°C. Both ph optimum and ph stability were observed at 7.8 Root PEPC was stable at 30-50°C and showed maximum activity at 30°C. Its ph optimum was 8 and stable at kph 6-8 its Km for PEP was 16 um. Salt level of 25 mM significantly decreased leaf NR and root PEPC activities of both the salt-sensitive (P1 1) and salt-tolerant (P31) corn inbreds. Leaf NR and root PEPC of P31 showed higher activities than that of P1 1. The activity of root NR of P31 showed sensitivity to high salt levels, while P1 1 root NR activity significantly increased at salt levels>75 mM. Leaf PEPC of P31 showed greater tolerance to high salt concentrations than P1 1 leaf PEPC. Results suggest that NR and PEPC might play significant roles in salt tolerance in corn.

Keywords: kinetic properties, nitrate reductase, phosphoenolpyuvate carboxylase, salt tolerance, corn

20. PHENYLACETIC ACID-ENHANCED ANTHER CULTURE RESPONSE IN INDICA RICE (*Oryza sativa L.*)

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Anther culture is employed to complement conventional rice breeding approach for development of breeding lines tolerant to abiotic stress (cold and saline). The standard protocol utilizes 2,4-D at 2 mg/L level, as the main plant growth regulator for callus induction and formation. Efficiency of this protocol with *indica* rice is far below the targeted 3% green plant regeneration based on number of anthers plated. Hence the effect of phenylacetic acid (RAA) at 10 mg/L in combination with 4 mg/L NAA and 0.5 mg/L of either kinetin or 6-benzylminopurine, in improving anther culture response of *indica* rice was investigated. Nine out of 17 parental genotypes formed more calli in PAA-enriched callus induction medium compared to 2,4 D-enriched medium. Likewise, with 4F$_1$ crosses, an increase of 2 times callus formation was obtained in PAA-enriched medium. No significant enhancement in green plant regeneration, however, was observed with the treatments employed. In some genotypes, especially those which usually form calli but never differentiate and regenerate green plants, such as Arkansas and C22, PAA treatment induced green callus differentiation and green plant regeneration. Direct plant regeneration from callus, that is, without transferring from callus induction into regeneration medium, was also obtained. Further investigation on optimizing the culture condition for enhancement regeneration of PAA-treated calli will be conducted.

Keywords: anther culture, phenylacetic acid, 2,4-D, NAA, kinetin, 6-benzylaminopurine, callus induction, callus formation, plant regeneration, abiotic stress

21. BIOLOGICAL CONTROL OF GINGER RHIZOME ROT USING TRICHODERMA SP.

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A study to evaluate the efficacy of *Trichoderma sp.* at different time of application against *Sclerotium rolfsii* and *Fusarium sp.* causing rhizome rot ginger was conducted in Kidapawan, Cotabato from July 1992 to 1994. Laboratory tests revealed that the introduction of *Trichoderma sp* simultaneously and one week ahead of the pathogen significantly inhibited the growth of *Sclerotium rolfsii* and *Fusarium sp* at a spore density of 29,000/10ml of distilled water. In a greenhouse experiment, the introduction of *Trichoderma sp* one week ahead of the pathogen (*S. rolfsii* and *Fusarium sp*), introduced simultaneously, and pathogen introduced one week ahead of the *Trichoderma sp* gave a percentage infection of 58.33%; 39.58%; 66.67% and severity of 59.5%; 71.66% and 66.67%, respectively. Verification in farmers field was conducted using *Trichoderma sp* in CFA form at 50 gms/hill as basal and 50gms two months after planting as experimental practice and no *Trichoderma* application for farmers practice. Results showed a percentage infection of 8.5% with 12.0% severity while farmers practice with 12.5% and 18.5% infection and disease severity, respectively. *Trichoderma sp*, applied in spore suspension and CFA form is, therefore, a potential biocontrol agent (BCA) against *S. rolfsii* and *Fusarium sp* causing rhizome rot in ginger.

Keywords: biological control, ginger rhizome rot, *Trichoderma*, *Sclerotium rolfsii*, *Fusarium*

22. VARIETAL DIFFERENCES IN THE CELLULOSE, LIGNIN AND SILICA CONTENTS OF THE DIFFERENT PLANT PARTS OF RICE (*Oryza sativa L.*)

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The amount of variation and of cell-wall constituents i.e., cellulose, lignin, and silica in the different parts of the rice plants were investigated. A total of 53 varieties (47 indica and 6 japonica) was used. There were highly significant varietal differences in the cell-wall constituents of the different rice varieties. Cellulose was the most abundant component of the cell wall followed by lignin and then silica. Downward from leaves to the roots, lignin and cellulose contents increased but the silica content decreased. There was insignificant amount of silica in the roots and the absorbed silica was mainly accumulated in the shoots particularly in the leaf blade. Several patterns of distribution of cellulose, lignin and silica contents within the different plant parts were observed. Majority of the varieties have low amounts of cellulose, lignin and silica. In the varietal classification, Pokkali, slat tolerant, contains high amount of cellulose in the roots but low cellulose and lignin in the shoot. Salt tolerant IR 4595-41-13, had low cellulose and silica in all parts but with high lignin in the leaf blade and root, and high cellulose content with low silica in the leaf sheath and stem.

Keywords: acid-detergent fiber, cell-wall constituents, rice, salt tolerant, varietal differences

23. INSECTICIDAL ACTION OF PLANT VOLATILE OILS ON SEVERAL INSECT PESTS

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Volatile oils derived from four plant species, namely *Blumea balsamifera*, *Vitex negundo*, *Ageratum conyzoides* and *Chrysanthemum indica*, were evaluated for toxicity against insect pests of different orders. Generally, all the volatile oils were highly toxic to *Spodoptera exempta* and *Nilaparvata lugens*, moderately toxic to *Plutella xylostella*, *Dysdercus cingulatus* and *Musca domestica*, and slightly toxic to *Spodoptera litura* and stored grain insects such as *Callosubruchus chinensis*, *Rhizopertha dominica*, *Sitophilus zeamays* and *Tribolium castaneum*. No toxicity was noted for *C. indica* to *T. castaneum*. Based on the mean LD_{50} values from all test insects, the order of decreasing toxicity of the volatile oils was as follows: *V. negundo* >*B. balsamifera* > *A. conyzoidex* > *C. indica*. The insecticidal potential of these plant species therefore warrant further investigative study toward a practical agricultural application.

Keywords: plant volatile oils, insect pests, biopesticides

24. *Chalcomyza ipomoeaphaga* MARTINEZ: A NEW LEAFMINER PEST OF SWEET POTATO (*Ipomoea batata* LAMARK)

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Dipterous leafminers in sweet potato create conspicuous tunnels in the leaves that can hamper photosynthesis during serious infestation. Sweet potato leaf miner collections from Pinaod, San Ildefonso, Bulacan yielded a new insect pest which has never been recorded in the Philippines. Diagnostic works showed *Chalcomyza ipomoeaphaga* Martines from Guadaloupe to be present. This pest in known to attack sweet potato in Americas. The bioecology of this pest should be studied closely since it poses a potential threat to the production of sweet potatoes in the Philippines.

Keywords: leaf miner, pest, Diptera, sweet potato *Chalcomyza ipomoeaphaga*

25. FIELD PERFORMANCE OF THERMALLY SELECTED POPULATIONS OF *Diadegma semiclausum*, A LARVAL PARASITOID OF DIAMONDBACK MOTH

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Diadegma semiclausum is suited to cold areas at temperature lower than 24°C. In view of the desire to release this parasitoid in the lowland because of its higher rate of parasitism (90%) than *Cotesia plutellae* on diamondback moth, *Plutella xylostella*, *Diadegma* was selected for resistance to high temperature.

The *Diadegma* population collected from Benguet was reared for three generations in a screenhouse at 29 to 34°C prior to selection and sensitivity of the F_4 adult *Diadegma* to different temperatures was determined by exposure in thermo-regulated incubator (TRI). The adult LT_{50} (Lethal Temperature) was exposed for 6 hrs. at 35°C. The selection was made by rearing the parasitized DBM at 35°C inside the TRI at intervals of three generations between selection pressure. Percent developed *Diadegma* cocoons gradually increased from 17 to 55% (F_{38}) while the percent adult emergence was relatively stable from F_5 to F_{38} ranging from 85 to 95%. The sex ratio was not affected. Fifty-pairs of the heat-resistant *Diadegma* (HRD) and original heat-susceptible *Diadegma* (OSD) were released once in the field on separate plot of cabbage infested with DBM and enclosed within a mosquito net (two trails). The number of cocoons and the rate of parasitism of HRD was higher than OSD. HRD parasitism was comparable to *C. plutellae* (CP). The additive parasitism of HRD + CP was higher than HRD or CP only. The OSD cocoons were much lower than HRD or CP only. Six weeks after harvest of the experimental cabbage, the *Diadegma* parasitism on nearby crucifer fields was 33%. The results showed the possibility of releasing HRD in the lowland.

Keywords: *Diadegma semiclausum*, parasitoid, diamondback moth, moth

26. LABORATORY SELECTION OF *Diadegma semiclausum*, A LARVAL PARASITOID OF DIAMONDBACK MOTH, FOR RESISTANCE TO HIGH TEMPERATURE

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Diadegma semiclausum is suited for the management of diamondback moth (*Plutella xylostella*), the most destructive pest of crucifers, in higher elevation with temperature below 25°C. In view of the desire to release this parasitoid in the lowland because of its higher rate of parasitism (90%) than *Cotesia plutellae*, *Diadegma* was selected for resistance to high temperature. The *Diadegma* populations were collected from Benguet and reared for three generations in a screenhouse at 29 to 34°C prior to selection. The sensitivity of the F_4 adult *Diadegma* to different temperatures was determined by exposure in thermoregulated incubator (TRI). The adult LT_{50} (Lethal Temperature) was exposed to 6 hrs. at 35°C. The selection was made by rearing the parasitized DBM at 35°C inside the TRI at intervals of 3 generations between selection pressure. The developed *Diadegma* cocoons gradually increased from 17 to 55% (F_{38}) while the adult emergence was relatively stable from F_5 to F_{38}, ranging from 85 to 95%. The sex ratio was not affected. A 48% survival of the laboratory-selected heat resistant *Diadegma* was observed when initially exposed in the field at 35°C and RH of 66%. This

indicates that a heat-resistant *Diadegma* can be mass-reared and released in crucifer-growing areas in lowland elevation to supplement *C. plutellae*.

Keywords: *Diadegma semiclausum*, larva parasitoid, laboratory-selected, high temperature resistance, diamondback moth, crucifers

27. OCCURRENCE, MORTALITY FACTORS AND WITHIN-PLANT DISTRIBUTION OF BOLLWORM, *Helicoverpa armigera* (Hubn) ON COTTON

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The seasonal occurence of cotton bollworm (*Helicoverpa armigera*), mortality factors, and egg and larval distribution on cotton were determined.

The peak of occurence of the pest was recorded at 57, 78 and 106 days after emergence (DAE) on cotton planted within the season, in Guimba, Nueva Ecija; Pozorrubio, Pangasinan; and Polomolok, South Cotabato, Philippines, respectively. The pest occurred earlier in late-planted cotton than in the early-planted ones, with peaks of occurrence at 54 and 75 DAE, respectively. Rainfall, relative humidity, air temperature, and sunshine duration did not significantly influence the population trend of the pest.

The mortality factors on the various insect stages were: physiological defects, diseases, natural enemies, and dispersion.

The eggs were predominantly laid on the top young leaves and growing terminals of the upper third portion of the cotton plant. The larvae were confined on the upper third-portion from 43 to 64 days after emergence (DAE), at the middle third-portion from 78 to 85 DAE and the upper third from 92 to 106 DAE. The availability and type of fruiting forms were the primary cues for the pattern in the egg and larval distribution within the cotton plant.

Keywords: occurence, mortality factors, eggs and larval distribution, bollworm, population trend

28. THE NATURAL ENEMIES OF PADDY CLIMBING WORM, *Pseudaletia separata* (WALKER) (LEPIDOPTERA: NOCTUIDAE)

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The paddy climbing worm or rice eating caterpillar can decimate large tracks of harvestable rice overnight. Nevertheless, the present of natural enemies effectively check this pest. One species of predator, 11 species of parasitoids and 1 entomopathogenic fungus were collected and identified. The predator belonged to the order Dermaptera family Labiduridae. The parasitoids were represented by 6 species under the order Diptera families Tachnidae (5 spp.) and Sarcophogidae (1sp.) and 5 species under the order Hymenoptera families Ichneumonidae (1 sp.), Braconidae (2 spp.), Eulophidae (1sp.) and Encyrtidae subfamily encyrtinae (1sp.). The entomopathogenic fungus was tentatively placed under the genus Akanthomyces. The bioecology of these natural enemies in relation to *P. separata* and other rice pest is being investigated further.

Keywords: worm, rice eating caterpillar, rice predator, parasitoids, fungus, natural enemies

29. BIODIVERSITY CONSERVATION IN PHILIPPINE MANGIFERAS

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Several species of *Mangifera* and a rich germplasm resources of these species occur in a varied ecosystem in the Philippines. In 1976, a nation-wide biodiversity conservation program to collect these valuable plant resource for long-term safekeeping and for future use was started. To date, 5 *Mangifera* species, namely *M. altissima* (paho), *M. caesia* (bauno), *M. indica* (mango), *M. odorata* (huani), and *M. monandra* (apali). *M. altissima* and *M. monandra* are endemic species. Some 265 access of the mango, the country's third most important fruit, has been collected all over the country.

The Carabao, the premier mango cultivar, is represented by 115 accessions. Of the total accession, 124 were documented for tree and leaf characters and 68 for their fruit characters. Wide variations in tree, leaf and fruit characters were observed among the accessions. Work is continuing to collect 'Carabao' and other local mango strains in other parts of the country. The long-term goal is to keep a representative 'Carabao' mango strain from each of the country's municipalities.

Keywords: biodiversity conservation, mangiferas, germplasm resources, field gene bank, 'Carabao' mango

30. CONSERVATION OF NATIVE PHILIPPINE ORCHIDS

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Ongoing are efforts to help conserve the floral genetic heritage of the Philippines, specifically native Philippine orchids. Five main projects comprise the conservation program: collection of the native orchids from different provenances, embryo and tissue culture of endangered Philippine orchids, detemination and optimization of tissue culture conditions for each native species, development of in vitro storage techniques, and identification of DNA markers for native orchids. On the short-term, the program aims to: source and document nursery and herbarium specimens of endangered Philippine orchids; propagate these native species through embryo and tissue culture: determination Optimization of Tissue Culture Conditions for Each Native Species; Development of *In vitro* Storage Techniques, and identification of DNA Markers for Native Orchids. The long-term objectives set are as follows: establish a nursery for and maintain a herbarium collection of endangered Philippine orchids: establish tissue culture as a useful technology for plant diversity conservation; establish a gene bank of Philippine orchids for research and eventually for commercial purposes; and develop a rapid and accurate orchid identification procedure for regulatory purpose. Ultimately, it is envisioned that the program will replenish the native orchid species back to their habitats.

31. DIVERSITY WITHIN PHILIPPINE IMPROVED RICE VARIETIES AND THEIR PROGENITORS: A MULTIVARIATE ANALYSIS OF PHENOTYPE TRAITS

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Germplasm characterization enhance the efficiency of varietal improvement towards broadening the genetic base of improved cultivars. The study analyzed the diversity for phenotypic traits of 78 improved rice varieties released from 1965 to 1995 and their 81 ancestral lines. Data on morpho-agronomic traits obtained from field evaluation were analyzed by multivariate analysis. Ancestral lines were found more variable than their cultivated descendants. A total of 41 traits contributed to the total variation in ancestral lines Euclidean distance ranging from 3.970 to 17.389, while only 33 traits contributed to the total variation in improved varieties with Euclidean distances ranging from 2.228 to 16.706. Principal component analysis revealed that 6 qualitative characters significantly influence the variation in released varieties. Parental separation was strongly affected by variation in quantitative characters. Cluster analysis permitted separation of improved varieties into 2 major cluster: cluster 1 consisted of 72 (92%) varieties and cluster 2 consisted of 6 (8%) varieties having purple-colored plant parts. Among ancestral lines, *O. nivara* formed a different cluster from the rest of the *O. sativa* group. Results showed that rice breeders selected phenotypic divergence in improved varieties.

Keywords: improved rice varieties, progenitors, multivariate analysis, phenotype traits

32. SOMATIC EMBRYOGENESIS IN BANANA (*Musa SPP.*) C. V. LAKATAN AND LATUNDAN

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Somatic embryos of banana cv Lakatan were initiated on half strength Murashige and Skoogs (MS) basal medium supplemented with 2,4-dichlorophenoxy acetic acid (5*u*M), proline (20 *u*M), casein hydrolysate (200 mg/l), ascorbic acid (10 mg/l) inositol (100 mg/i) and sucrose (40 g/l). Direct and indirect pathways of somatic embryogenies were observed from two different types of tissue explains. Regeneration of plants were obtained by transfer of embryos onto MSA medium supplemented with Zeatin (lu M), ascorbic acid (10 mg/l) and (40 mg/l)

Keywords: somatic embryogenesis, Lakatan, Latundan, tissue explants, regeneration

33. PRELIMINARY STUDIES ON SOMATIC HYBRIDIZATION BETWEEN *Carica papaya* AND *Carica* SPECIES

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Protoplast fusion is an alternative method employed in wide hybridization to effect the transfer of useful gene(s) from the wild to the cultivated species. *Carica caulifora, C. quercifolia* and *C. stipulata* are sources of resistance to papaya ringspot virus but they are incompatible with *C. papaya*. Protoplast were isolated from somatic embryos of 2 papaya cultivars (2001 and EM 6) and mesophyll cells of 3 *Carica* species by enzymatic digestion of the cell walls. Papaya protoplast were fused with mesophyll protoplast of the wild species with polyethylene glycol as fusogen. Fusion products were monitored for cell wall development and cell growth.

Keywords: *Carica papaya, cauliflora, C. pubescens, C. stipulata*, fusogen, protoplast fusion

34. PURIFICATION AND ANTISERUM PRODUCTION TO PAPAYA RINGSPOT POTYVIRUS

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Papaya ringspot caused by papaya ringspot potyvirus (PRSV) is a serious threat to the papaya industry. Its destructive nature necessitates test and accurate diagnosis. This paper reports the purification and production of antiserum to PRSV the prerequisites for the application of antibody-based diagnosis and in development of PRSV resistant varieties.

Biologically pure IPB-PRSV isolate was propagated and maintained in *Zucchini Blackjack* (ZBJ). Two purification protocols were modified to produce the purified virus particles. Antiserum to the virus was prepared by injecting the virus emulsified with Freund's adjuvant into a rabbit. The antiserum produced reacted to its homologous antigen in ELISA and Western blot.

Keywords: antiserum, antigen, ELISA, immunology, papaya, potyvirus, serology Western blot

35. COMPETITIVE INTERACTION OF RICE (*Oryza sativa*) AND *Echinochloa glabrescens* AS A FUNCTION OF PLANTING DENSITY UNDER ELEVATED CO_2 AND HIGH TEMPERATURE

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Potential competition between rice and *Echinochloa glabrescens* in terms of their vegetative and reproductive characteristics were examined at different planting densities at different CO_2 levels (ambient) Ambient + 200) and temperature regimens (27/221°C; 37/26°C). Increased CO_2 concentration promoted greater biomass, tiller number, grain yield, panicle weight and percentage filled spikelets for yield, panicle weight and percentage filled spikelets for rice relative to *E. glabrescens*. Comparison between the two species showed that the ratio of rice/ for total above ground biomass, leaf area, tiller number and grain yield increased with increasing CO_2 concentration indicating a potential competitive advantage for rice under elevated CO_2. However, if CO_2 and temperature increased simultaneously the increased in rice biomass declined ralative to the elevated CO_2 and condition alone. It was also observed that with increasing CO_2 and temperature for rice either CO_2 concentrations. In contrast, grain yield for *E. glabrescens*, while reduced was still significant at either CO_2 concentrations. Overall, this experiment suggests that relative effect of increasing atmospheric CO_2 and high temperature on reproduction could still C_4 over C_3 with global climate change.

36. *Desmanthus* AS HEDGEROWS IN AGROFORESTRY CROPPING SYSTEMS

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The potential of *Desmanthus virgatus*, DS 92803 hedgerows in agroforestry cropping systems in the-arid hillylands of Ilocos Norte was evaluated over a four year period. As hedgerows, the plants were set at 7, 10, and 20 plants linear m and lopped at a height of 50, 75, and 100 cm above the ground. The grain yield of agricultural crops planted in between the hedgerows were recorded every harvest period. *Desmanthus* hedgerows established at wider spacing were significantly taller and had larger stem diameter. The fresh biomass yields of the plants was not affected by plant density. However, lopping the hedgerows at 50 cm during the establishment period produced more biomass than those cut higher than 50 cm above the ground. Succeeding observations confirmed that biomass was not critically affected by intrarow spacing. Although cutting the plants at a height of 50, 70, and 100 cm above the ground produced more or less the same amount of biomass, these management regimes did not critically affect grain yield of corn, rice, and mungbean. Continuous lopping every 45 days and use of the fresh biomass as much in alleys contributed to a noticeable increase in the amount of soil organic matter over a four year period. The adaptability and high productivity of *Desmanthus* under very close or dense spacing as well as its long tap root and numerous secondary roots undoubtedly suggest its high potential for erosion control.

Keywords: *Desmanthus*, hedgerows, lopping, biomass, organic matter, alley crops, hilly lands, cutting height, grain yield, semi-arid.

37. DEVELOPMENT OF LOCATION-SPECIFIC TECHNOLOGIES IN MAJOR CORN GROWING AREAS OF LUZON

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To support the Gintong Ani Corn production Program of the Department of Agriculture, the On-farm Research and Outreach Project (OFRO-Corn) was implemented in major corn growing areas in Pangasinan, Tarlac, and Batangas utilizing the on-farm research methodology to test and generate technologies appropriate to unique requirements and circumstances of these areas. Eight to ten farmer-partners were requested to set aside a particular area in their farms to test two factors, namely variety and utilizer. Six to eight varieties of corn were tested through trials superimposed on cropping pattern (CP) plots. The fertilizer trial involved the use of various bio-organic (BOF) and inorganic (IOF) combinations. Irrigation management trial was implemented in one of the farmers' field in Tarlac site. Results of 1994-1995 and 1995-1996 dry season cropping showed that all hybrid varieties tested produced better yield and higher net benefit in the three key sites. Planting hybrid and application of combined BOF and IOF appeared to be promising in the three key sites. Application of six times irrigation for corn production after wetland-rice in Tarlac starting from 0 DAP to 70-75 DAP, gave better yield and higher net benefit. These technologies were disseminated through farmers' yield days, farmers, extension workers, researchers, and officials of private, non-government organizations and local government, thus, facilitating transfer of appropriate technologies.

Keywords: on-farm research and outreach, corn, bio-organic fertilizer

38. EFFECTIVE PLANTING TIME AND ARRANGEMENT OF TRAP CROPS AGAINST COTTON BOLLWORM

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The study was conducted at the Central Experiment Station, Cotton Research and Development Institute, Batac, Ilocos Norte to determine the best planting time and arrangement of promising trap crops that would give the most effective control for cotton bollworm. Native tomato and pigeon pea were found most in tomato at one plant per hill spaced 50 cm between hills, planted 14 days after planting cotton in 15 rows of cotton demonstrated a significant reduction of cotton bollworm population and ultimately a high net income of P 47,861.63 per hectare. On the other hand, planting two rows of pigeon pea at 2 plants per hill spaced 30 cm. between hills in every 10 rows of cotton also significantly reduced cotton bollworm population and consequently higher net income compared to single row cotton monoculture. Planting tomato or pigeon pea as trap crop against cotton bollworm significantly reduced spraying frequency from 7-8 to 3-4 times only during the cropping period.

Keywords: trap crops, cotton bollworm

39. RELAY CROPPING OF GARLIC WITH TOMATO FOR GARLIC FUNGAL DISEASE CONTROL

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An environment-friendly and effective control of Cercospora leaf spot and purple blotch of garlic was generated. This was done by relay-cropping with tomato. Tomato was planted one-month after planting garlic at a distance of 1.5 m between rows and 0.5 between hills. This practice reduced infection of Cercospora leaf spot and purple blotch by about 32 and 20%, respectively. Likewise, it significantly increased yield of garlic by 650 kg ha over that of the garlic monocrop. An additional net income of P58,704.54 ha^{-1} over that of garlic alone was derived from the garlic and tomato harvests.

Keywords: relay cropping, tomato, garlic, fungal disease control, Cercospora leaf spot, purple blotch

40. SYSTEM APPROACH IN THE EXTRAPOLATION OF RICE PRODUCTION ENVIRONMENTS

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The study dealt with the assessment and agroecological zonation of rice suitability of an environment, documentation of soil and water management practices in rainfed lowland rice watershed as well as risk assessment and sensitivity analysis of rice productivity based on qualitative and quantitative approaches. It was an attempt to contribute to the long-felt need to strategically extrapolate and zonify rice environments in the country. A case study was conducted in the agroecological environment of the municipality of Batac, Ilocos Norte athe northern part of the Philippines to characterize, describe and extrapolate rice production environments using GIS, simulation modeling, and optimization. A strategic rice on-sit (SRO) area of 5, 132 ha or 33% of the total land area of Batac was classified as suitable for rice production by overlaying physical maps of land use/land cover, soil type, erosion, slope and agroclimate using the Computer-Aided Mapping Program (CAMP). The contiguous 19-ha rainfed lowland rice growing watershed studied had no access to irrigation systems. However, rainfed farmers performed approved soil and water management practices to provide rain-water conservation facilities and structures to sustain the growth of rainfed rice. Simulated yields of rainfed lowland rice from 1984 to 1995 ranged from 2, 7 to 9.2 t/ha using crop growth simulation model Oryza W under water-limited condition. Risk analysis of the different land evaluation units (LEUs) showed variation of alternative cropping patterns (rice and diversified crops) using the optimization minimization of total absolute deviations (MOTAD). The study demonstrated that the use of systems research tools such as crop growth simulation models and optimization linked with GIS proved useful to farmers, researchers, extensionists, and planners for land use planning.

Keywords: System approach, simulation modelling, geographic information systems, environment, optimization, land use planning, rice, extrapolation, Oryza W. MOTAD

41. YIELD AND QUALITY COMPONENTS OF CORN HYBRIDS FOR SILAGE

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Corn producers face many interacting factors such as hybrid selection, planting date, fertilization, among others, for each crop they grow. However, in corn grown for silage, consideration of feed quality is also important in establishing its contribution towards meeting an animals needs. This was conducted to independently determine the effects of hybrid and plant population on yield and yield components, nutritive value, dry matter partitioning and N% of corn hybrids grown for silage under New Zealand conditions.

Hybrids CF1 achieved the highest (20,046 kg/ha) whole crop DM yield at final harvest while Janna produced the lowest (15,776 kg/ha) yield. The 75,000 plant population yielded significantly less than 100,000 and 140,000 plants/ha. There was no difference between the 100,000 and 140,000 plant populations. Dry matter partitioning at final harvest revealed the highest proportion in the grain component, followed by the stem, husk and leaf. Total metabolizable energy (ME) content ranged from 11.3 MJME/kg DM to 10.28 MJME/kg. DM. The ME content of of CF1 was significantly higher than all other hybrids. There were no significant hybrid differences in whole crop N% which ranged from 1.07 to 1.16%.

Keywords: silage, corn hybrids, plant population, feed quality, metabolizable energy, nutritive value, dry matter yield, dry matter partitioning, nitrogen percentage, yield and yield components

42. EFFECTS OF VESICULAR-ARBUSCULAR MYCORRHIZA INOCULATION ON COTTON GROWN IN NUTRIENT DEFICIENT SOIL

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The study was conducted at the Cotton Research and Development Institute, Batac, Ilocos Norte to detemine the effects of inoculating vesicular-arbuscular mycorrhiza on cotton (var. CRDI-1) grown in nutrient-deficient soil. The pot experiment was laid out in Completely Randomized Design (CRD) with four replications with the following treatments; Control; VA mycorrhiza alone; VA mycorrhiza + 50% recommended $NP_2O_5K_2O$; VA mycorrhiza + 100% recommended $NP_2O_5K_2O$; and 100% recommended $NP_2O_2K_2O$. Mycorrhiza (Mycovam) from National Institutes of Technology and Applied Microbiology was applied at 5g per seed placed at 1 inch below the cotton seed. Results showed that the addition of VA mycorrhiza to inorganic $NP_2O_5K_2O$ fertilizer increased the growth and development of the cotton plant up to the reproductive stage. Plants inoculated with VA mycorrhiza + Inorganic $NP_2O_5K_2O$ fertilizer were generally taller, and had higher drymatter yield, and had higher number of bolls per plant resulting to higher seedcotton yield. The addition of VA mycorrhiza to only one-half of the recommended inorganic $NP_2O_5K_2O$ fertilizer gave the highest seedcotton yield. This indicates that inorganic $NP_2O_5K_2O$ fertilizer inputs can be lessened by as much as 50% and the cost of production may be lowered without altering the natural soil composition and structure.

Keywords: mycorrhiza, vesicular, arbiscular, inoculation, cotton

43. POLLUTION POTENTIAL OF AGRICULTURAL PESTICIDES IN WATER

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The possible contamination of pesticides in ground water and lakes were determined both in the field and in semi-field model ecosystem. Insecticides were applied in rice paddy 15 and 45 days after transplanting at recommended rates. Horizontal movement of the pesticides was monitored by allowing the paddy water to overflow up to 100 m away from the treated field simulating an actual flood condition.

A 100% fish *T.mossambicus* and frog (*Bufo marinus*) mortality was observed after hours of exposure to BPMC +chlorpyrifos treated run off paddy water at 10 and 25 m distance, respectively. However, there were no fish mortalities observed in methyl parathion and monocrotophos treated paddy water exposed at the same condition. Downward movement of monocrotophos was traced in paddy soil packed in PVC pipes. Movement of monocrotophos reached 490 cm layer depth in 30 days and went down further to 60 cm depth in 60 days. The concentration peaked in 270 days but declined in 360 days. This supported the results obtained in ground waters within the treated rice field. Monitoring of well waters within the vicinity of the treated rice fields showed contamination with monocrotophos, chlorpyrifos and endosulfan residues but at levels within tolerable limits based on actual consumption of glasses of water daily. Actual monitoring of pesticide residues in the lakes (Laguna de Bay and Manila Bay) revealed some residues of DDT, DDE, DDD, HCB and TCB atppb levels (1980-1994) inspite of the rapid dissipation rate of persistent organochlorines in tropical climate with half line of 8 months (DDT) compared to 10 years in temperature countries. Residues of these organochlorines were not accumulated in oyster and mussles.

Keywords: pollution, pesticides, water growthwater, lakes

44. UTILIZATION OF *Trichogramma chilonis* IN COTTON PRODUCTION

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Studies on the use of *Trichogramma chilonis* were undertaken to derive maximum benefits for cotton pest control. From 1986 to 1995, different methods of releasing the parasitoids were evaluated and the appropriate stage when to release and the time and schedule of releases were determined. Six techniques of release were evaluated. Pupae and adults were released at different hous starting in the morning until afternoon. Different parasitoid density and schedule of releases were also evaluated. One release station was composed of halved empty coconut shell tied it with a string suspended from a bamboo pole at least 30 cm above the cotton plants. A paper clip tied inside the halved coconut shell was used to hang the strip containing *Trichogramma*. At other times the strip was clipped on the undersides of at leaf located on the upper one third of the plant. These methods protected the parasitoids from intense sunlight and excessive moisture. The study showed that the parasitoids could be released using the pupal stage (about to emerge) in the late afternoon or the newly emerged adults morning. *T. chilonis* parasitized 84.60% of *H.armigera* eggs when released at 49,000/ ha per release at 2 days interval under field cage conditions while 33.65% parasitization

was observed when released at 67,500hs release starting at 50 DAE and weekly thereafter.

Keywords: cotton, *Trichogramma chilonis* pest control

45. PROCESSING OF A TRIPOLIATE YAM, GAMAT (*Dioscorea* sp.) FROM CATANDUANES

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A trifoliate yam, (Dioscorea sp.) locally known as Gamat in Catanduanes, Bicol Region was processed into flour. Snack items were prepared and evaluated. Results of the objective evaluation showed that the processed products were acceptable to a wide range of consumers in the province. Preliminary results of the nutritive analysis of carbohydrates, fats and proteins were also included.

46. AQUACULTURE ENGINEERING DESIGN OF TILAPIA HATCHERY IN A FRESHWATER RECIRCULATING SYSTEM

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Production of all male tilapia using hormone has become increasingly popular in the aquaculture industry but its effect on human health has not been known. Waste from traditional fry production in fishponds and cages can affect the quality of the water thereby affecting fry production supply. The tilapia hatchery system was designed and constructed to produce an all-male tilapia fry. The system consisted of an all-male compartment, all-female compartment, fry compartment and fry collectors. The emphasis of the design was the reproduction of handling of breeders and fry to improve qualtiy and survival. The system used recycled water making it environment friendly. The system redesigning and re-engineering could be considered a potential household backyard fry production component of the industry to supply the requirement of the traditional grow-out production system in natural waters.

Keywords: aquaculture engineering, tilapia, hatchery system

47. LIVESTOCK-AGROFORESTRY PRODUCTION SYSTEM

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In an existing agroforesty production system, the abundance of by-products and crop residues such as shrub/tree fodder, corn stover, soybean/mungbean stover, necessitates more effective utilization aside from the traditional practice of enriching soil quality through mulching. Incorporation of livestock, particularly luminants, which can effectively utilize such resources for conversion into an existing agroforestry production system. The study assessed the quantity and quality of available livestock feed resources and determined animal performance in the system. Feed conservation strategies were developed that would fit into the livestock-crop production system module. Limited area entails an efficient use of the available resource and the incorporation of small ruminants were found to be most suitable in the existing system. The loose-pasture and feathering system were not suitable due to the cost of fencing and the limitedd open area such that complete confinement is recommended. The animals performed well under such management scheme exhibiting positive average daily gains. Available forage for ruminants were identified as follow, Kakawate (*Gliricidia sepium*), Napier grass (*Pennisetum purpureum*), Vetiber (*Vetiveria zizanioides*), Flemingia (*Flemingia macrophylla*), Rensonni (*Desmodium rensonni*), Atsoan Dilaw (*Cassia spectabilis*), Sesbian (*Sesbania sesban*), Katuray (*Sesbania grandiflora*), Sitaw (*Vigna a unguiculuta*) and Corn (*Zea mays*). The most suitable silage materials in terms of biomass yield and quality were found to be Napier and Kakawate (with a pH of about 5.03) which could be harvested within 3 weeks of ensiling. Quality analysis such as dry matter yield, ash content, % CP and %IVDMD showed variability within the year and these were incorporated into the livestock-crop production model.

Keywords: agroforestry, goats, livestock, napier, silage

48. PLANNING FOR AGROFORESTRY FARM DEVELOPMENT THROUGH ALCAM

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Agroforestry, a land-use management system which utilizes the simultaneous or sequential raising of forest trees, agricultural crops, livestock and/or other resources in the same area, is now recognized globally as one of the best technologies for the cultivated uplands. The study aimed to develop a scheme that will enable the farmers to assess an area's capability for agroforestry using slope, existing vegetation and soil fertility as parameters. The factors enumerated can specify the area's potential for erosion, adaptability to trees and other crops, and capacity for sustainable production levels. The study resolved to the Agroforestry Land Capability Mapping Scheme. The scheme classified the areas into the following classes: I-highly capable for agroforestry; II-marginally capable; III-conditionally capable; and IV-not for agroforestry use.

Keywords: agroforestry, farm development, cultivated uplands, and capability mapping

49. LOW-FAT-SALT PROBOTIC CHEESE FOR HEALTH-CONSCIOUS CONSUMERS

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A soft cheese with the probiotic yogurt starter bacterian *S. thermophilus* and *bulgaricus* was developed to meet the increasing consumers demand for value-added low fat and low salt dairy products which are perceived to lessen the consumers' risk to cardiovascular disorders. Its proximate composition, sensory quality, consumers acceptability, shelflife and yield were assessed. Result gave high acceptable probiotic-containing soft cheese having 50.775 and 43.55% lower fat and salt contents, respectively. It also had a longer shelf life that the conventional soft cheese. Its sensory quality improved on storage. Cheese yield and other components were comparable. Scanning electron microscopy showed that the health promoting yogurt starter bacteria were embedded in the cheese matrix and therfore available when the cheese was eaten.

Keywords: cheese, probiotic, low-fat, low-salt