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CROP IMPROVEMENT

1. Sorghum

KHATRI, R. S., S. K. PAHUJA, R. AVTAR AND D. S. PHOGAT 2001. INHERITANCE OF LEAFINESS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH. Forage Res., 27 (1) : pp. 35-38. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India.

Generation mean analysis comprising four genetically diverse genotypes was carried out to study the inheritance of leafiness (leaf length, breadth and its number) in forage sorghum [*Sorghum bicolor* (L.) Moench]. The additive-dominance model was found to be adequate for leaf breadth, while it was complete failure in case of leaf number and leaf length in all the six crosses studied. Both additive (d) and dominance (h) gene effects were observed to be significant with preponderance of former for leaf breadth, whereas for leaf length and number of leaves non-additive gene effects were found to be important. Duplicate type of epistasis was found to be responsible for the inheritance of leaf number and leaf length in crosses viz., G 71 x HC 171, G 71 x HC 260 and SSG 59-3 x HC 171. Appropriate breeding methodology for the improvement of leafiness in sorghum has been discussed.

450. KHATRI, R. S., G. P., LODHI, R. P. S. GREWAL AND S. K. PAHUJA, 2001. INHERITENCE OF REGROWTH IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH. Forage Res., 27 (2): pp. 147-148. Forage section, CCS HAU, Hisar.

An experiment was conducted to study the Inheritance of regrowth in forage sorghum at Forage section, CCS HAU, Hisar. It was observed that both additive and dominance component of variation were important for regrowth in forage sorghum and high heritability for narrow sense was also observed for regroth in sorghum.

451. AGARWAL, M., RAMESHWAR SINGH AND A. SHUKLA 2002. MULTIVARIATE CLASSIFICATION OF ELITE LINES IN SORGHUM. Forage Res., 27 (4): pp. 243-246. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263 145 (U. P.), India.

Genetic divergence using non-hierarchical Euclidean cluster analysis was done. Among 41 genotypes of sorghum, 25 "tillering types" and 16 "non-tillering" types with 14 component characters were chosen. The genotypes were grouped into five non-overlapping clusters. Six genotypes were included in cluster 1, 12 in cluster 2, eight in cluster 3, eight in cluster 4 and seven in cluster 5. Maximum and minimum inter cluster distances were observed between clusters 1 and 4, and 2 and 4, respectively.

452. SUNKU, S. S. K., M. BALAKRISHNA REDDY AND P. RAGHU RAM REDDY 2002. CHARACTER ASSOCIATION AND PATH ANALYSIS IN GRAIN SORGHUM [SORGHUM BICOLOR (L.) MOENCH] VIS-À-VIS THE SUDAN GRASSES(S. SUDANENSE). Forage Res., 28 (1) : pp. 42-45. Rajendranagar, Hyderabad (A. P.)

A field experiment was conducted at the college Farm, Rajendranagar, Hyderabad (A.P.) to study the character association and path analysis in grain sorghum [Sorghum bicolor(L.) Moench] vis-à-vis the sudan grasses(S. sudanense). Almost all the characters except crude protein had direct effect on dry matter yield in grain sorghum.Sudan grasses have high direct effect of number of leaves, dry matter content, leaf length and green fodder yield on dry matter yield.

453. SANKARAPANDIAN, R. 2002. **VARIABILITY STUDIES IN TWO GROUPS OF HYBRIDS POPULATION IN SORGHUM.** *Forage Res.*, **28** (1) : **pp. 46-48.** TNAU,Agricultural Research Station, Kovilpatti.

Variability studies in two groups of hybrids population in sorghum wascarried out at TNAU, Agricultural Research Station, Kovilpatti. The single cross hybids showed genetic advance for fodder and grain yield and crude fibre indicating predominance of additive gene effects.

454. BOORA, K. S. 2003. MOLECULAR MARKERS OF THREE FOLIAR DISEASES OF SORGHUM FOR MARKER-ASSISTED BREEDING. *Forage Res.*, 29 (1): pp. 44-48. Department of Biotechnology & Molecular Biology, CCS Haryana Agricultural University, Hisar-125 004, India.

Marker based breeding can be useful to expedite introgression of specific genetic material from a donor parent into the background of an elite variety through backcrossing. The promise of marker assisted selection (MAS) provides the opportunity to select desirable lines based on genotype rather than phenotype. Analyzing plants at seedling stage, screening multiple characters that would normally be epistatic with one another, deterministically minimizing linkage drag and rapidly recovering a recurrent parent's genotype were just a few of the attractions of MAS. As newer and simpler DNA marker systems like RAPDs and SSRs were used to tag resistance genes in sorghum to pathogens, Colletotrichum graminicola (anthracnose), Exerohilum turcicum (leaf blight) and Ramulispora sorghicola (oval leaf spot). Using bulked segregant analysis of F₂ derived F₃ gentoypes and recombinant lines derived from the crosses of resistant and susceptible parents for the respective disease, SSR and RAPD markers have been identified that segregated with the gene for resistance to anthracnose, leaf blight and oval leaf spot in sorghum. Four RAPD markers were found to be closely linked (< 10 cM) to the locus for anthracnose. RAPD marker OPA12, OPJ01, OP110 and OPD12 amplified a fragment of approximately 0.5, 1.0, 1.5 and 2.2 kbp, respectively. SSR marker Xtxp212 was found to be closely linked to the resistance gene and located at 6 cM away from the locus for anthracnose. This SSR marker was mapped on linkage group D of sorghum SSR and RFLP linkage map. Xtxp212 had a high degree of homology to an expressed sequence tag derived from a putative protein gene of Arabidopsis thaliana. Three RAPD markers were found to be closely linked (<10 cM) to the locus for leaf blight. RAPD marker OP109, OPC02 and OPB10 amplified a fragment of approximately 0.6, 1.1 and 2.0 kbp, respectively. SSR marker Xtxp274 was found to be closely linked to the resistance gene and located at 9.8 cM away from the resistance allele for leaf blight. SSR marker Xtxp309 was also found to be linked to the susceptible allele and located at 13.7 cM away from the allele for leaf blight. This SSR marker Xtxp274 was mapped on linkage group I of sorghum SSR and RFLP linkage map. Three RAPD markers were found to be closely linked (<10 cM) to the locus for oval leaf spot. RAPD marker OPC04, OPC16 and OPH07 amplified a fragment of approximately 0.9, 1.5 and 1.9 kbp, respectively. SSR marker Xtxp105 was found to be closely linked to the resistance gene and located at 8.0 cM away from the resistance allele for oval leaf spot. This SSR marker (Xtxp105) was mapped on linkage group H of sorghum SSR and RFLP linkage map.

455. YADAV, R., S. K. PAHUJA AND R. P. S. GREWAL 2003. EVALUATION OF PHENOTYPIC VARIABILITY IN FORAGE SORGHUM GENOTYPES COLLECTED FROM WESTERN UTTAR PRADESH USING MULTIVARIATE ANALYSIS. Forage Res., 29 (3) : pp. 123-128. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Fifty-five genotypes of forage sorghum collected from western Uttar Pradesh were grown in augmented design in 1999, 2000 and 2001. The observations were recorded on 16 characters related to fodder yield and head dimensions. Pooled analyses of data were done using Principal Component Analysis and Hierarchical Cluster Analysis. The first five Principal Components (PC) having eigen value > 1 accounted for 76.22 per cent variability. The first PC accounted for growth rate related characters, second PC accounted for the characters of fodder yield, third for leaf characters, fourth for earhead characters and fifth for number of tillers and stem borer attack. The principal factor scores were calculated for all the genotypes in these five PCs. On this basis the genotypes Bareilly-1, Harsherpur-3, Hapur-1, Pilqua-3 and Huzur Gurdar were found superior in PC 2 which accounted for fodder yield characters. The hierarchical cluster analysis resulted in formation of five clusters having 3 to 24 genotypes. The clustering pattern of genotypes revealed that geographical diversity did not necessarily represent genetic diversity. Maximum distance was observed between cluster 2 and cluster 4 and minimum distance between cluster 1 and cluster 5. Perusal of cluster means revealed that cluster 2 had better yield and related characters and also had least stem borer attack. This cluster comprised genotypes, namely, Huzur Gurdar, Bareilly-1 and 4, Harsherpur-3, Hapur-1 and Pilqua-3. These are the same genotypes which were found better through PC analysis hence the results of hierarchical cluster analysis and principal factor analysis confirm the findings of each other. The results of the

present study could be used as a stepping stone for evolving well defined approach based on evaluation and characterization of genetic variation in forage sorghum and could also be utilized in various breeding programmes depending on their specific objectives.

456. PAHUJA, S. K., RAJESH YADAV AND R. P. S. GREWAL. 2003. GENETICS OF FODDER YIELD AND ITS COMPONENTS IN MULTICUT X SINGLE CUT FORAGE SORGHUM CROSSES. Forage Res., 29 (3): pp. 139-141. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Six generations i. e. P_1 , P_2 , F_1 , F_2 , B_1 and B_2 of three crosses (SSG 59-3 x S 375, G 71 x HC 171 and G 71 x HC 260) involving two multicut (SSG 59-3 and G 71) and three single cut parents (S 375, HC 171 and HC 260) were raised in randomized block design. The observations were recorded on plant height, leaf length, leaf breadth, number of leaves/plant, number of tillers/plant, green fodder yield/plant and dry fodder yield/plant to carry out generation means analysis. Additive component was found significant for plant height, number of tillers/plant, leaf length and leaf breadth, whereas additive and dominance effects were found significant for number of leaves/plant, green fodder yield/plant. The epistatic gene effects were also present but the type and magnitude varied from character to characer and cross to cross. Estimates of gene effects in the present study revealed preponderance of additive gene effects for most of the component traits. Therefore, for further improvement in all these characters, simple pedigree selection based on progeny performance was suggested. However, for the number of leaves/plant, green fodder yield/plant the preponderance of additive as well as dominance gene effects suggested the usefulness of S_2 and reciprocal recurrent selection.

 457. GREWAL, R. P. S., RAJESH YADAV AND S. K. PAHUJA. 2003. INHERITANCE OF FODDER YIELD AND ITS COMPONENTS IN MULTICUT FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 29 (3) : pp. 142-144. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Six generations i. e. P_1 , P_2 , F_1 , F_2 , B_1 and B_2 of three forage sorghum crosses (SSG 59-3 x IS 3374, SSG 59-3 x G 71 and SSG 59-3 x G 73) involving four multicut parents were grown in randomized block design and observations were recorded on plant height, leaf length, leaf breadth, number of tillers/plant, number of leaves/plant, green fodder yield/plant and dry fodder yield/plant to carry out generation means analysis. Additive as well as dominance components were found significant for leaf length, leaf breadth, number of tillers/plant, green fodder yield/plant and dry fodder yield/plant, however, dominance effects were higher in magnitude for most of the characters. For plant height and number of leaves/plant preponderance of additive gene effects was observed. The epistatic gene effects were also present but their type and magnitude varied from character to character and cross to cross. For further improvement in plant height and number of leaves/plant simple pedigree selection based on progeny performance and for all other characters including fodder yield, S_2 and reciprocal recurrent selection were suggested for the desirable improvement.

458. MOHAN, M., S. K. PAHUJA AND RAJESH YADAV. 2003. HETEROSIS FOR MULTICUT TRAITS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 29 (3): pp. 145-149. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Seven male sterile lines, six testers alongwith 42 crosses were grown in randomized block design to study the heterosis over better parent, mid parent and standard check for number of tillers and regeneration percentage at two crop stages viz., crop without cut (C_1) and regenerated crop (C_2). The extent of heterosis was considerably high at C_1 than that of C_2 in most of the cases for the traits under study. It was interesting to note that the cross ICS 4A x SSG 59-3 showed maximum heterosis (over better parent or mid parent or standard check) for these traits at C_1 or C_2 or both in most of the cases. Therefore, this cross can be utilized at commercial level after proper testing at multi-locations and over large areas. From heterosis point of view, the other important crosses were ICS 4A x IS

699, ICS 95A x IS 3230, ICS 15A x IS 720, 2219A x IS 3230 and ICS 88020A x IS 3230. On the basis of the above study, it was concluded that these crosses could be commercially exploited after their proper testing.

459. PARMAR, H. P., J. R. PATEL AND P. C. PATEL. 2004. COMBINING ABILITY FOR QUANTITATIVE TRAITS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]*. Forage Res., 29 (4): pp. 170-172. Main Forage Research Station, Gujarat Agricultural University, Anand-388 110 (Gujarat), India

Heterosis and combining ability studies were made in a line x tester analysis in forage sorghum [*Sorghum bicolor* (L.) Moench] consisting of three lines and 15 testers with their 45 F_1 hybrids. The estimates of s^2 sca and s^2 gca revealed preponderance of additive genetic variance for days to 50 per cent flowering, plant height (cm), number of nodes/plant and leaf breadth, while non-additive genetic variance for number of tillers and leaves per plant. These results suggested that days to 50 per cent flowering, plant height, leaf breadth and pedigree nodes/plant can be improved by pedigree method of breeding in a desirable direction, whereas tillers and leaves can be improved through heterosis breeding method.

460. SHARMA, HEMLATA, G.S. SHARMAANDAMIT DADHEECH. 2004. COMBININGABILITYANALYSIS OVER ENVIRONMENTS FOR STOVER YIELD AND YIELD CONTRIBUTING CHARACTERS IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 29 (4): pp. 185-188. Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, MPUAT, Udaipur-313 001 (Rajasthan), India

Four male sterile lines and 20 restorers were crossed in a line x tester fashion to estimate the type of gene effects controlling stover yield and contributing traits. Estimates of variance due to general and specific combining ability indicated the preponderance of non-additive gene effect for all the characters except number of leaves per plant and number of green leaves per plant at physiological maturity. The lines 27A and 296 A among the females and SPV 1382, SPV 1201, SPV 1330, SU 562, SPV 1134, ICSV 298, SU 630 and SU 719 among the male parents were good general combiners for stover yield and contributing traits. Among the hybrids, 296A x SU 685 possessed the maximum sca effects for stover yield followed by 296A x ICSV 298, 27A x SU 562 and 2219A x SU 562. In view of greater role of non-additive gene effects for stover yield, heterosis breeding may be adapted for the development of hybrid.

461. AGARWAL, MEENU. 2004. STUDIES ON GENETIC VARIABILITY AND HERITABILITY IN FORAGE SORGHUM. *Forage Res.*, 30 (3) : pp. 163-164. G. B. P. U. A. &T., Pantnagar.

Studies on genetic variability and heritability in forage sorghum was done at G. B. P. U. A. &T., Pantnagar. High heritability was observed for days to50% flowering, shootly infestation, dry matter yield, green fodder yield, plant height, TSS per cent, stem diameter.

462. PARMAR, H. D., AND S. B. S. TIKKA 2005. HETEROSIS AND COMBINING ABILITY ANALYSIS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH] Forage Res., 30 (4) : pp. 209-212. Main Pulses Research Station, Gujarat Agricultural University, Sardar Krushinagar-385 506 (Gujarat), India

Estimates of heterosis, combining ability and nature of gene action were obtained in respect of fodder yield, protein content and yield components in forage sorghum. Significant heterotic effects were observed for all the characters under study; however, the expression of heterosis varied with the crosses and characters. Combining ability analysis showed that general as well as specific combining ability variances were significant for all the characters. The ratio of gca/sca variances suggested predominant role of additive type of gene action for all the characters under study. Specific combining ability effects revealed that $16 F_1$'s exhibited significant and positive sca effects for forage yield. Of these, SR 350-1 x FS 35, SR 350-1 x DR 15, DR 15 x FS 35 and DR 15 x FS 41 involved both good combining parents.

463. GREWAL, R. P. S. 2005. BREEDING FOR MULTICUT FORAGE SORGHUM–A REVIEW. Forage Res., 30 (4) : pp. 213-216. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Multicut varieties/hybrids are preferred over single cut in sorghum because of their higher fodder yield per unit area per unit time and availability of fodder for a longer period. Enough variability for multicut traits is present in forage sorghum [Sorghum bicolor (L.) Moench]. Yield is governed by more of dominance gene effects, whereas the component characters are governed by more of additive gene effects. High heterosis is present for green as well as dry fodder yield over better parent. The present article deals with a review on breeding multicut forage sorghum.

464. BHATT, ARUN AND VIKRAM SINGH 2005. GENETIC DIVERGENCE FOR QUANTITATIVE AND QUALITATIVE CHARACTERS IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 30 (4): pp. 231-234. Department of Genetics & Plant Breeding, G.B. P. U. A. & T., Pantnagar-263145.

On the basis of D^2 analysis, 40 genotypes were groped to eight clusters in the Department of Genetics & Plant Breeding, G.B. P. U. A. & T., Pantnagar. The most important characters contributing genetic divergence were days to 50% flowering, plant height, leaves/plant and 1000-grain weight.

465. BINI, K. AND D. I. SUMA BAI 2005. **CORRELATION AND PATH ANALYSIS IN FODDER SORGHUM.** *Forage Res.*, **30** (4) : pp. 238-239. Department of P.B. & Genet., CoA, Vellayani-695522(Kerala).

In the present study, green fodder yield had positive correlation with all the characters except leaf : stem ratio. Leaf weight per plant exhibited the maximum direct effect on green fodder yield. Moreover, both leaf weight per plant and leaf area index had high positive direct effect alongwith high genotypic correlation.

466. AGARWAL, MEENU, R. SINGH AND P. K. SHROTRIA. 2005 COMBINING ABILITY ANALYSIS FOR FORAGE YIELD AND QUALITY CHARACTERS IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 31 (1) : pp. 9-11. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttaranchal), India

Combining ability for forage yield and quality characters was studied using five CMS lines and 10 fertility restorer testers. Highly significant mean squares for lines and testers indicated the presence of sufficient variability in the parental lines. Ratio of general combining ability to specific combining ability variance indicated the presence of non-additive gene action for all the characters. The parents ICSA 84, ICSA 94 and SDSL 92111 were good general combiners for yield and quality characters. The crosses ICSA 84 x M 20, ICSA 84 x UPMC 504, ICSA 84 x Sel. 984, ICSA 94 x SDSL 92111, ICSA 95 x SDSL 92115, ICSA 95 x M 19, 296 A x Pant Chari-4 and 2219 A x UPMC 504 were identified as superior crosses having high sca effects for forage yield and quality traits and, therefore, these can be exploited at commercial level after proper testing in co-ordinated trials.

467. SUMALINI, K., J. S. DESALE AND S. K. GULIA 2005. GENETICS OF GRAIN AND FORAGE TRAITS IN SORGHUM BICOLOR (L.) MOENCH. Forage Res., 31 (1) : pp. 30-32. Department of Botany, Mahatma Phule Krishi Vidyapeeth, Rahuri-413 722 (Maharashtra), India

A line x tester mating set was obtained by crossing four male sterile lines with eight restorers of sorghum. Thirty-two F_1 's alongwith 12 parents including two checks were evaluated for 12 quantitative characters. The gca and sca variances revealed the predominant role of additive gene action for plant height, stem thickness, leaf breadth, days to 50 per cent flowering, panicle length, 1000-grain weight and dry fodder yield per plant and non-additive genetic effects in the inheritance of number of leaves per plant, leaf length, panicle breadth, grain weight per ear and green fodder yield per plant. The best general combiner identified for both gran and fodder yield were 18-3A and Ruchira.

468. CHAND, KARAM, R. P. S. GREWAL, YAGYA DUTT AND PADAM SINGH 2005. Combining ability analysis for fodder traits in sorghum [Sorghum bicolor (L.) Moench]. *Forage Res.*, 31 (2) : pp. 134-135. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana) India

The parent, S 250 was identified best as it recorded highest positive and significant gca effect for the green and dry fodder yield and also possessed good gca effects for most of other traits studied at Department of Plant Breeding, CCS Haryana Agricultural University, Hisar.

GREWAL, R. P. S., S. K. PAHUJA, RAJESH YADAV, Y. JINDAL, K. K. YADAV, D. S. RANA AND S. R. PUNDIR 2005. MULTICUT FORAGE SORGHUMS–WHERE DO WE STAND? Forage Res., 31 (3): pp. 170-184. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Development and cultivation of multicut forage sorghum varieties/hybrids is the only alternative to meet the fodder requirement of ever increasing livestock population in India. An effort has been made to review the progress done so far towards the development of multicut forage sorghums. Parameters of multicut traits identified and male sterility system in sorghum have been reported in detail. The studies on heterosis, combining ability and genetic architecture in sorghum have been reviewed. The major achievements in the field of multicut forage sorghum related to breeding, agronomy, quality, nutritional and resistance factors have been mentioned in this review alongwith the breeding methods and future strategies for the further progress.

470. SINGH, MONIKA AND K. S. BOORA 2006. **VARIETAL IDENTIFICATION IN FORAGE SORGHUM** (*SORGHUM BICOLOR*) USING MICROSATELLITE MARKERS. *Forage Res.*, **32** (1) : pp. 31-33. Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Sorghum bicolor is a highly diverse species belonging to the tribe Andropogonae and family Poaceae. It is grown mainly for fodder purpose during summer and kharif seasons in the northern states of India. Microsatellites or simple sequence repeats (SSRs) markers have been extensively utilized in the assessment of genetic diversity as they are codominant, highly informative and display high levels of polymorphism. In the present study, the SSR alleles specific to one or two genotypes were identified by performing the microsatellite analysis of 22 forage sorghum *(Sorghum bicolor)* lines using 40 SSR markers. Nineteen of the SSR markers produced specific alleles. Thirty-four of the amplified alleles discriminated one or two genotypes and hence, these alleles would be utilized in varietal or cultivar identification.

471. LAKSHYADEEPAND LATA CHAUDHARY. 2006. **STUDY OF HETEROSIS FOR FORAGE ATTRIBUTES IN SORGHUM.** *Forage Res.*, **32 (3) : pp. 133-143.** Department of Plant Breeding and Genetics, MPUA&T, Udaipure-313001.

In low plant density population environments (E_1 and E_2) cross S-300 x Raj-2 and in high plant density population environments cross GJ-39 x CSV-15, were having economic heterosis.

472. BOARD, V.P., GANGANI, M.K. AND PARMAR, H.P. 2007. CHARACTER ASSOCIATION IN FORAGE SORGHUM [BICOLOR (L.) MOENCH]. Forage Res., 32 (4) : pp. 213-215. Main Forage Research Station, AAU, Anand

A study undertaken with 49 sorghum types revealed high positive and significant association of stem girth, stem weight, leaf weight and crude protein yield with green fodder as well as dry matter yields both at phenotypic and genotypic levels. Among the inter-character correlations, stem girth, stem weight, leaf weight, dry matter yield and crude protein yield were significantly and positively associated with one another. Plant height, IVDMD per cent and HCN per cent had negative but non-significant association with most of the characters. Significant negative

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association was observed for IVDMD per cent with stem girth. The path coefficient analysis indicated significant contribution of stem weight and leaf weight to green fodder yield. The indirect effects of stem girth, crude protein yield and dry matter yield via stem weight and leaf weight further emphasized importance of these characters as main yield contributing characters.

473. YADAV, R. AND S. K. PAHUJA 2007. **COMBINING ABILITY FOR FODDER YIELD AND ITS COMPONENTS IN FORAGE SORGHUM.** *Forage Res.*, **32** (4) : pp. 220-223. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar

Combining ability effects were studied in forage sorghum using line x tester analysis consisting of 10 male sterile lines and five testers and their 50 hybrids. The estimates of 6 and 6 revealed preponderance of non-additive genetic variance for all the traits studied. Male sterile lines, namely, ICS 13A and ICS 10286A and pollinators S 241 and SSG 59-3 were found good combiners which can further be utilized in different cross combinations to get superior hybrids. The crosses AKMS 14A x IS 651 and ICS 2219A x S 241 exhibited higher sca effects for green and dry fodder yields and, therefore, can be utilized commercially after multi-location testing.

474. MUKESH MOHAN, S. K. PAHUJA AND R. YADAV 2007. COMBINING ABILITY STUDIES FOR MULTICUT TRAITS IN FORAGE SORGHUM INVOLVING MALE STERILE LINES AND TESTERS. *Forage Res.*, 32 (4) : pp. 249-253. Forage Section, CCS Haryana Agricultural University, Hisar

Combining ability effects were studied in seven male sterile lines viz., ICS 4A, ICS 15A, ICS 79A, ICS 95A, ICS 242A, 2219A and ICS 88020A; six pollinator parents viz., IS 699, IS 720, SSG 59-3, IS 3230, IS 3274 and IS 3289 and their 42 crosses. The estimates of variances due to specific combining ability (& sca) and general combining ability (a gca) and their ratio (a sca : a gca) indicated the importance of non- additive type of gene action for these characters. Male sterile lines viz., ICS 4A, ICS 79A and tester IS 3289 were good general combiners for most of the multicut traits which can further be utilized in different cross combinations to get superior hybrids. The crosses viz., ICS 88020A x SSG 59-3, ICS 15A xIS 3274, ICS 95A x IS 720, ICS 242A x IS 720, ICS 242A x IS 3289, 2219A xIS 3280 and ICS 4A x IS 699 exhibited higher sca effects for multicut traits.

475. MUKESH MOHAN, S. K. PAHUJA, R. YADAV AND R. AVTAR 2007. COMBINING ABILITY STUDIES FOR FODDER YIELD AND COMPONENTS IN FORAGE SORGHUM INVOLVING MALE STERILE LINES AND TESTERS Forage Res., 33 (1) : pp. 17-21. Forage Research Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Combining ability effects were studied in seven male sterile lines viz., ICS 4A, ICS 15A, ICS 79A, ICS 95A, ICS 242A, 2219A and ICS 88020A, six pollinator parents viz., IS 699, IS 720, SSG 59-3, IS 3230, IS 3274 and IS 3289 and their 42 crosses for fodder yield and component traits. The estimates of variances due to specific combining ability (s² sca) and general combining ability (s² gca) and their ratio (s² sca : s² gca) indicated the importance of non-additive type of gene action for all the characters. Male sterile lines viz., ICS 4A, ICS 79A and tester IS 3289 were good general combiners for most of the traits. The crosses viz., ICS 79A x IS 3274, ICS 79A x SSG 59-3, ICS 15A x IS 3289, ICS 95A x SSG 59-3, 2219A x IS 3230, 2219A x IS 720 and ICS 95A x IS 720 exhibited higher sca effects for most of the traits studied and these can be commercially utilized after multi-location testing over years.

476. WARKAD, Y. N., N. R. POTDUKHE, A. M. DETHE AND P. A. KAHATE 2008. ANALYSIS OF GENETIC VARIATION AND TRAIT INTER-RELATIONSHIP IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH] Forage Res., 33 (4) : pp. 199-202. Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola-444 104 (M. S.), India

The range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and the relationship between fodder yield and its components were estimated in 63 landraces and one improved sorghum variety viz.,

SPV 669. The collection of landraces showed considerable amount of variability for all the trials. High heritability estimates coupled with high genetic advance were observed for stem girth and dry fodder yield per plant indicating that heritability of these characters was most likely due to additive gene effects. Correlation studies showed that selection could be practised for days to 50 per cent flowering, days to maturity and plant height as these characters manifested positive significant correlation with dry fodder yield. Path coefficient analysis revealed that the number of leaves per plant was the main contributor for dry fodder yield followed by days to flowering, leaf breadth and number of internodes per plant. Hence, it was concluded that dry fodder as economic yield could be increased by improving plant height, days to flowering and maturity and might be considered as the important yield contributing components.

477. PAHUJA, S. K. AND RAJESH YADAV. 2008 FORAGE SORGHUM HYBRIDS : PROSPECTIVES AND CONSTRAINTS *Forage Res.*, 34 (1) : pp. 9-13. Forage Section, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Sorghum is a food, feed, fodder and fuel crop in different parts of the world and hence has achieved a special significance after wheat, rice and maize among cereals. It is impossible to increase the area under this crop due to various socio-economic reasons, therefore, increase in the production and productivity of sorghum can mainly be achieved through hybrid cultivation. For successful and economic hybrid production presence of male sterility, knowledge of genetic architecture, heterosis for various characters, good combining restorers for different economic traits are necessary. Commercial exploitation of heterosis in sorghum became possible after the discovery of cytoplasmic-genetic male sterility. The wide range of heterosis, the good combining and stable parents for yield and quality traits led to development of many grain and a few forage sorghum hybrids. However, still the productivity remained much below the world average. Therefore, exploitation of promising genetic stocks and evaluation of elite genetic stock and ms lines for quality, yield and resistance traits is required to meet out the objective. New trait specific ms lines with diverse cytoplasms are urgently required to be developed as most of the ms lines being utilized now-a-days are having milo cytoplasm for the development of sorghum hybrids.

478. SINGH, RAJNEESH K. AND P. K. SHROTRIA 2008. COMBINING ABILITY ANALYSIS FOR FORAGE YIELD AND ITS COMPONENTS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH] Forage Res., 34 (2) : pp. 79-82. Department of Genetics & Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

Combining ability for various traits viz., plant height, stem diameter, number of leaves, leaf area, total soluble solids, crude protein content, dry matter digestibility, hydrocyanic acid content and green as well as dry fodder yield was studied through 7 x 7 diallel cross involving seven forage sorghum lines. Highly significant mean squares for gca and sca for most of the characters indicated that sufficient variability existed for gca effects in the parents and that for the sca effects in the crosses. Higher and significant sca variance suggested a higher non-additive gene action for these traits. Parent Pant Chari-5 proved to be the best general combiner followed by UTMC-523. The hybrids viz., UTMC-523 x UPFS-37, UTMC-523 x UPMC-6 and UTMC-523 x PC-23 were found to be the best specific crosses for all the traits and, therefore, these can be further exploited for selection of transgressive segregant.

479. SUKHCHAIN AND DARA SINGH. 2008. **HETEROSIS FOR VARIOUS CHARACTERS IN MULTICUT FORAGE SORGHUM.** *Forage Res.*, **34** (2) : **pp. 122-124.** Department of Plant Breeding and Genetics, PAU, Ludiana

It was observed the heterobeltiosis in crosses 94031A x SGL-98-9, 94031A x SGL-98-11, 94002A x SGL-98-M6 and 94031A x SGL-96 was respectively, 56.2,46.0,30.8 and 27.6 for fodder yield, 55.03, 37.38, 29.16 and 31.11 for dry matter yield and these crosses showed non-significant negative heterosis for leaf : steam ratio. Therefore, it is possible that some of the hybrids may have better forage quality.

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480. SINGH, RAJNEESH K AND P. K. SHROTRIA. 2008. HETEROSIS ANALYSIS FOR FORAGE YIELD IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH] Forage Res., 34 (3) : pp. 131-135. Department of Genetics & Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

Knowledge of heterosis helps in deciding the appropriate breeding methodology to be used for achieving higher yield levels. Twenty-one F_1 hybrids were evaluated to know the extent of heterosis over mid parent, better parent and two checks for yield as well as quality traits, viz. plant height, stem diameter, number of leaves, leaf area, total soluble solids, crude protein content, dry matter digestibility, hydrocyanic acid content and green and dry fodder yield. The magnitude of heterosis indicated sufficient diversity in the parents chosen for developing F_1 hybrids so as to exploit hybrid vigour as well as to select transgressive segregants F_2 onward. Crosses UTFS-45 x Pant Chari-6, UP Chari-2 x Pant Chari-6, UPFS-37 x Pant Chari-6, Pant Chari-5 x UTFS-45 and UPFS-34 x Pant Chari-5 exhibited presence of high positive heterosis for fodder yield and its components like plant height, stem diameter, leaf area and quality traits like TSS, protein content and digestibility per cent alongwith negative nature of heterosis for HCN content, thus strengthening the scope of heterosis breeding in forage sorghum.

481. JAIN, S.K., M. ELANGOVAN AND N.V. PATEL. 2009. GENETIC AND ENVIRONMENTAL VARIABILITY IN DUAL SORGHUM (SORGHUM BICOLOR (L) MOENCH) FOR YIELD AND RELATED TRAITS Forage Res., 34 (4): pp. 201-204. All India Sorghum Improvement Project, Sorghum Research Station, Sardarkrushinagar Dantiwada Agricultural University, Deesa-385535,BK (Gujrat),India Forage Res.

Genetic variability, correlation and path analysis were carried out in 48 genotypes of dual sorghum for yield and their contributing traits. Significant variation among all the genotypes was recorded for all the characters. Most of the characters had higher genotypic and phenotypic coefficient of variation. The genotypes also exhibited varying degrees of heritability and genetic advance. Characters such as grain yield per plant, dry fodder yield per plant and plant height responded positively to selection because of high broad sense heritability and high genetic advance. Leaf breadth was positively and significantly associated with grain yield per plant. Whereas plant height was positively and significantly associated with dry fodder yield per plant. Leaf breadth was positively and significantly associated with days to 50 per cent flowering and number of leaves per plant, whereas number of leaves per plant was positively and significantly correlated with plant height and leaf length. High direct effect of leaf breadth, plant height and leaf length was observed on grain yield plant. Plant height had a direct effect on dry fodder yield.

PANDEY, SUNEETA AND P. K. SHROTRIA. 2009. GENETIC PARAMETERS FOR HYDROCYANIC ACID CONTENT IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 35 (1): pp. 17-19. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

Six lines (ICSA 467, ICSA 276, 993100A, ICSA 271, SP 55609A and 11A₂) and nine testers (Pant Chari 5, Pant Chari 6, HC 260, UPMC 512, UTMC 523, UTMC 532, CSV 15, UPMC 8 and PMC-04 700R) were crossed in line x tester design to produce 54 hybrid combinations. These hybrids alongwith their 15 parents were grown in a randomized block design with three replications during 2007-08 and 2008-09. The samples for estimation of hydrocyanic acid content were taken 30 days after sowing (DAS) as per the appropriate protocol. All the genotypes showed significant differences for HCN content. The specific combining ability (sca) variance for HCN content was higher than general combining ability (gca) variance indicating that the trait is controlled by non-additive gene action. The parents ICSA 467, SP 55609A, PC 6, UTMC 523 and 11A₂ were found to be the best for low HCN content based on gca effects, while the hybrids viz., ICSA 467 x UTMC 523, 993100A x HC 260, 993100A x UPMC 512 and SP 55609 x UPMC 8 had substantially high negative sca effects for HCN content. Heterosis breeding, recurrent selection and other population improvement procedures were suggested for developing varieties with reduced HCN contents.

483. KUMAR, P. RAVI, C. V. SAMEER KUMAR, A. V. UMAKANTH AND TANMAY V. KOTASTHANE. 2009. GENETIC VARIABILITY AND CHARACTER ASSOCIATION FOR TRAITS OF IMPORTANCE IN SWEET SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 35 (2) : pp. 91-95. Directorate of Sorghum Research (DSR), Rajendranagar, Hyderabad-500 030 (A. P.), India.

The phenotypic and genotypic coefficients of variation, heritability, genetic advance and the relationship between green cane yield and related characters were estimated in 68 sweet sorghum genotypes. The analysis of genetic parameters revealed considerable amount of variability for all the traits and high GCV, PCV, heritability and genetic advance as per cent of mean were observed for juice volume, green cane yield and juice extraction per cent indicating that selection could be effective for improving these characters. Significant positive association of green cane yield was observed with juice volume followed by days to 50 per cent flowering, number of leaves per plant, stem girth and leaf length. The highest direct positive effect on green cane yield was exhibited by juice volume, followed by number of nodes per plant, days to 50 per cent flowering, grain yield and plant height

484. NARAYAN, ASHISH. 2009. GENOTYPIC RESPONSE UNDER DIFFERENT ENVIRONMENTS IN FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]*. Forage Res., 35 (2) : pp. 101-106. Department of Plant Breeding and Genetics, Rajendra Agricultural University, Pusa, Samastipur-848 125 (Bihar), India

The present investigation was carried out with 24 diverse genotypes of sorghum which were tested for their stability parameters (bi and S²di) in three different environments, namely, early, timely and late sowing. The yield, its component traits and quality characteristics exhibited variability in different genotypes and environments. Both grain and fodder yields are dependent traits being variously affected by different physiological and morphological traits throughout the growing period. The development of high yielding varieties adapted to different agro climatic conditions is the most important objective of any breeding programme. The genotypes showed variable response to different environments for expression of yield and contributing traits showed genotype × environment interaction. The stable varieties with bi equal to one and S²di equal to zero for different characters were observed in different genotypes of sorghum.

485. JADHAV, A. R., R. T. DESAI, K. N. CHAUDHARY, V. C. KODAPALLY AND D. A. SHINDE 2009. CORRELATION AND PATH ANALYSIS IN (SINGLE-CUT) FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 35 (3): pp. 175-179. Department of Agricultural Botany, Navsari Agricultural University, Navsari-396 450 (Gujarat), India.

A study was carried out using 62 diverse genotypes of forage sorghum. Correlation studies revealed that green fodder yield per plant had positive and significant association with days to 50 per cent flowering, plant height, leaves per plant, leaf length, leaf width, crude protein content and dry matter yield per plant. The correlation of green fodder yield per plant with number of tillers per metre row length was negative but significant. Hence, the emphasis should be given to the traits like tallness, late maturity, more leaves having broad and long leaf size, less number of tillers coupled with high dry matter yield and increased crude protein in developing the genotypes having high green fodder yield. Path coefficient analysis revealed that dry matter yield per plant exhibited highest positive direct effect on green fodder yield per plant indicating that direct selection for trait would be effective in improving green fodder yield. Dry matter (%) had high magnitude of negative and direct effect on green fodder yield per plant.

486. SAMEER KUMAR, C. V., CH. SREELAKSHMI AND D. SHIVANI. 2010 GENETIC ANALYSIS FOR QUALITATIVE TRAITS IN SWEET SORGHUM. *Forage Res.*, **36** (1) : pp. 1-3. ANGRAU Agricultural Research Station, Tandur-501 141, Rangareddy District (A. P.), India

The present study revealed significant variation for all the traits except cane yield and sucrose (%). Grain yield, plant height and TSS (%) recorded high estimates of genetic advance as percentage of mean, whereas moderate values were observed for stem girth and test weight. All the characters under study exhibited highly

significant positive correlation with cane yield except the correlation between reducing sugars with test weight and grain yield, purity percentage with plant height, stem girth, grain yield, brix (%) and reducing sugars. Direct positive effect on cane yield was exhibited by sucrose (%), TSS (%) and days to 50 per cent flowering.

487. SINGH, SHIVJI, V. K. DWIVEDI, P. K. SHROTRIA AND SUNEETA PANDEY 2010. COMBINING ABILITY ANALYSIS FOR FODDER YIELD AND ITS COMPONENTS IN FORAGE SORGHUM. Forage Res., 36 (1): pp. 4-8. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculure & Technology, Pantnagar-263 145 (U. P.), India

Combining ability estimates were computed using line x tester mating design between 10 sorghum type male sterile lines and five sudan grass type pollinator parents and their 50 hybrids. Preponderance of non-additive genetic variance for all the traits studied was observed. Male sterile lines, namely, HB 94004 A, SPA₂ 94012 and 993100 A and pollinators UTMC 532, Pant Chari 6 and PMC 03 1212 R were found as good combiners for yield and various components. The cross SPA₂ 94012 x Pant Chari 6 showed significantly highest sca effect for green and dry fodder yields and, therefore, can the utilized commercially after multi-location testing.

488. SAMEER KUMAR, C. V., CH. SREELAKSHMI AND D. SHIVANI 2010. STUDIES ON GENETIC DIVERSITY ANALYSIS FOR YIELD AND FODDER ATTRIBUTES IN RABI SORGHUM [SORGHUM BICOLOR (L.) MOENCH] GENOTYPES. Forage Res., 36 (1): pp. 45-47. Agricultural Research Station, Tandur-501 141, District Ranga Reddy (A. P.), India

Rabi sorghum genotypes (60) were evaluated for six yield and yield attributing characters to study the genetic diversity existing among them by using Mahalanobis D² statistics. The genotypes grouped in the various clusters revealed that there was no relationship between geographical distribution and genetic diversity. Maximum inter-cluster distance was observed between II and VI (1262.59), while lowest divergence was noticed between clusters I and V (188.87). Among the six characters studied, seed yield contributed maximum towards total genetic divergence (93.84%) followed by plant height (4.92%). Cluster VI exhibited highest means for seed yield followed by fodder yield, panicle length and days to maturity. Cluster II exhibited lowest mean for seed yield, fodder yield, panicle length and plant height. The genotypes from clusters VI and II, which have high and low cluster means for majority of the characters, are suggested as parents for hybridization programme to achieve novel recombinants.

489. SINGH, SHIVJI, V. K. DWIVEDI, P. K. SHROTRIA AND SUNEETA PANDEY 2010. GENETIC DIVERGENCE IN SORGHUM [SORGHUM BICOLOR (L.) MOENCH]. Forage Res., 36 (1): pp. 48-51. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (U. P.) India

A set of 40 genotypes of sorghum was used for estimating genetic diversity. On the basis of Mahalanobis's D^2 estimates, 40 genotypes were grouped into seven clusters. From the pattern of clustering, it could be concluded that sufficient divergence was present in the genotypes taken for the study, which enabled the formation of different clusters. The generalized intra-cluster distance ranged between 0.00 for cluster IV (with only one genotype) to 5.06 for cluster VII (with 14 genotypes). The highest inter-cluster D^2 value (5.87) was observed between clusters VII and II and lowest D^2 value (2.93) between clusters I and II. Desirable genotypes (with high mean value) from the clusters having inter-cluster distance more than the average inter-cluster distance, could be used for hybridization for evolving high yielding derivatives and selection of transgressive segregants with good yield potential and nutritional quality.

490. YADAV, R., S. K. PAHUJA, S. R. PUNDIR AND Y. JINDAL 2010. **RESPONSE OF FORAGE SORGHUM HYBRIDS IN VARYING ENVIRONMENTS.** *Forage Res.*, **36** (3) : pp. 133-136. Forage Section, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Multicut forage sorghum hybrids are the only alternative to meet the fodder requirement of ever increasing livestock population during summer and **kharif**. The new male-sterile lines with diverse genetic base may be used for successful and economical development of forage sorghum hybrids to fulfil this objective. Stability of these hybrids in different environments is main concern as the environments in forage sorghum hybrid growing areas fluctuate over the years. Sorghum selecting hybrids with stable performance and maximum yield potential, investigation is required that would stabilize the production over different environments. Many great workers in plant breeding have emphasized the role of G x E interactions for purposeful management of genetic variability.

491. YADAV, RAJESH AND S. K. PAHUJA 2011. EVALUATION, CHARACTERIZATION AND CATEGORIZATION OF EXOTIC SORGHUM GERMPLASM FOR FODDER ATTRIBUTES. Forage Res., 36 (4): pp. 214-219. Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Sorghum [Sorghum bicolor (L.) Moench] is grown worldwide for food, feed, fodder, fuel and industrial products. In India, it is one of the most important cereals for poor people in semi-arid zones; however, it is grown exclusively for fodder production in the states of Haryana, Punjab, Delhi, Western U. P. and in some parts of Uttrakhand, Gujarat, Bihar and Rajasthan. Sorghum is an ideal fodder crop due to its quick growing habit, high yielding ability, high dry matter content, better quality, good ratoonability, palatability, digestibility and its suitability in various forms of utilization such as green chop, silage and hay (*karbi*). The past research efforts in forage sorghum have resulted in development and release of numerous high yielding varieties and hybrids; however, a plateau has reached in the last few years as far as the production potential is concerned and it has become imperative to break it even with increasing livestock population as the availability of required quantity and quality of fodder has direct bearing on animal performance.

2. Oat

492. NEHVI, F. A., SHAFIQ A. WANI AND G. H. ZARGAR 2001. A STUDY OF COMPONENTS OF GENETIC VARIATION AND GENOTYPE X ENVIRONMENT INTERACTION IN OATS (AVENA SATIVA L.) Forage Res., 27 (3): pp. 177-184. Division of Plant Breeding and Genetics, S. K. University of Agricultural Sciences and Technology, Kashmir, India.

The components of genetic variation were studied in 72 TTC progenies over two environments for fodder yield and quality traits. The overall epistasis (i) type was present for green fodder yield per plant, dry fodder yield per plant and green fodder yield per hectare in both the environments. However, (j+l) type of epistasis was more pronounced than (i) type in both the environments for dry fodder yield per plant. Absence of significant (i) type epistasis for days to 50 per cent flowering, plant height and protein content in one environment indicated that overall epistasis was relatively a minor component of epistasis. Additive genetic component was relatively more important than dominance component for all the traits excepting plant height, and protein content. Additive genetic component was comparatively more sensitive to environmental influences.

493. GULIA, S. K., C. KISHOR, Y. KUMAR, A. SHARMAAND B. SANTHA 2001. GENETIC STUDIES OF FODDER YIELD AND ITS COMPONENT CHARACTERS IN OATS (AVENA SATIVA L.). Forage Res., 27 (1): pp. 21-24. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India.

The genetic study of green leaf weight, green stem weight, green fodder yield, dry leaf weight, dry stem weight and dry fodder yield comprising six generations of two crosses during **rabi** 1997-98 was conducted. Simple additive model was found to be adequate for all the above characters except dry leaf weight in cross I. Digenic interaction model revealed the presence of additive, dominance and all the three types of epistatic interactions viz., additive x additive, additive x dominance and dominance x dominance for most of the traits in both the crosses. Duplicate type of epistasis played a significant role in the inheritance of all the characters in both the crosses except green leaf weight in cross II and dry fodder yield in cross I where complementary type of epistasis was observed. Based upon the above findings, selective diallel mating and biparental crossing programme by adopting any of the NC mating design is suggested for genetic improvement in oats.

 494. GULIA, S. K., C. KISHOR, Y. KUMAR AND B. SANTHA 2001. GENETIC STUDIES OF CERTAIN QUANTITATIVE CHARACTERISTICS OF OATS (AVENA SATIVA L.). Forage Res., 27 (2): pp. 119-122. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

The quantitative genetic studies of days to panicle emergence, plant height, number of tillers and number of leaves were carried out in six generations and two crosses. The material was grown in compact family block design replicated thrice. Both additive and non-additive components of genetic variation were present in variable magnitude with majority of traits showing over dominance for most of the characteristics. For all the characters, duplicate types of epistasis played a significant role in inheritance of these characters. The magnitude of variability indicated that the improvement could be achieved by intercrossing of selected F_1 's and subjecting large F_2 population to recurrent selection, selective diallel mating and bi-parental crossing programme.

495. CHOUBEY, R. N., S. V. SAI PRASAD, S. N. ZADOO AND A. K. ROY 2001. ASSESSMENT OF GENETIC DIVERSITY AND INTER-RELATIONSHIPS AMONG YIELD CONTRIBUTING TRAITS IN FORAGE OAT GERMPLASM. Forage Res., 27 (3): pp. 149-154. Crop Improvement Division, Indian Grassland and Fodder Research Institute, Jhansi-284 003 (U. P), India

Genetic divergence using D² statistic of 300 oat germplasm lines of different eco-geographic origins revealed existence of considerable diversity. The cultivars were grouped into 14 clusters. The cluster III was the largest containing 39 genotypes followed by cluster V with 31 lines. Clusters X and XIV had nine genotypes each, whereas cluster XII, only two genotypes. The diversity among the genotypes measured by intercluster distance was adequate for improvement of forage oat by hybridization and selection. Tiller number, number of leaves and flag leaf length were the main traits for selection of high yielding types. The cultivars included in the diverse clusters can be used as promising parents for hybridization to obtain high heterotic response and thus better segregants in forage oat.

496. HET RAM, R. N. ARORAAND C. KISHOR 2001. **SEED VIGOUR STUDIES IN CULTIVATED AND WILD SPECIES OF OATS.** *Forage Res.*, **27** (3) : pp. 225-228. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

On the basis of average of two years' data, significant differences among different genotypes of five cultivated and wild species of oats, namely, *Avena sativa*, *A. sterillis*, *A. byzantina*, *A. fatua* and *A. nuda* were observed for fodder, grain, root and shoot length indicating substantial variability for these traits. Genotype OS 240 of species *A. sativa* was tallest and had longest panicle resulting in higher green fodder yield per plant as compared to other genotypes studied. Genotype Kent of *A. sativa* yielded higher grain yield per plant than other genotypes.

Differences in 100-seed weight, root and shoot length and number of tillers per plant of eight genotypes were also observed. Exploitation of this variability in oat breeding programme is suggested.

497. KUMAR, Y., HET RAM AND S. K. GULIA 2002. VARIETAL IDENTIFICATION IN OAT BASED ON FIELD PARAMETERS Forage Res., 28 (2): pp. 73-76. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

The present study was undertaken with a view to characterize oat varieties by field parameters in relation to varietal identification. The study of morphological characters revealed the plant growth habit, colour of stem, stem solidness, leaf type, colour of leaf sheath, flag leaf angle, shape of panicle, colour of panicle, hairiness of lowest joint of panicle, colour of node and hair above or below the node were found to be important diagnostic characters for varietal identification in oat. The flow chart was prepared on the basis of field parameters studied. An integrated approach using this flow chart for cultivar identification of oat has been developed which will be useful for plant breeders and seed certification organizations.

498. SHANKAR, S., P.B. JHA, J. GHOSH AND R. B. P. NIRALA 2002. VARIATION AND ASSOCIATION STUDIES IN OAT (AVENA SATIVA L.) Forage Res., 28 (2) : pp. 110-112. RAU, Pusa, Samastipur(Bihar).

Present study on variation and character association in oat (Avena sativa L.) was carried out at RAU, Pusa, Samastipur (Bihar).From the present study, it was obvious that grain yield in oat coul directly be improved on the based on NGP 1000GW, whereas GFY can be improved on basis of LSR and DMY

499. SHARMA, N. K. 2002. RELATIVE PERFORMANCE OF OAT AND BARLEY CULTIVARS FOR FORAGE YIELD. Forage Res., 28 (2) : pp. 113-114. Agricultural Research Station, Keshwana, Jalore (Raj.).

The performance of six oat and six barley cultivars was tested for forage yield at Agricultural Research Station, Keshwana, Jalore (Raj.). Regeneration capacity ,in general, was better in oat but varied from variety to variety ans best was registered in OS 7, followed by OL 9. Among barley varieties, RD 57, RD 2052 and RD 2053 performed comparatively better. Therefore, either crop grown for forage but due to higher biomass accumulation capacity during early growth period of barley, higher forage yield may be expected in early stage from barley.

500. SINGH, R. R., J. S. VERMA¹ AND I. S. AGRAWAL 2002. STUDIES ON FORAGE PRODUCTION POTENTIAL AND QUALITY OF DIFFERENT VARIETIES OF OATS (AVENA SATIVA L.) Forage Res., 28 (3): pp. 134-141. Department of Animal Science, G. B. Pant University of Agriculture and Technology, Pantnagar-263 145 (Uttaranchal), India

In a field trial comprising 24 strains of forage oat, conducted during **rabi** season of 1998-99, the morphological characters, production potential and forage quality were evaluated at 60 days after sowing (I cut) and at 50 per cent heading stage (II cut). The average plant height, leaf number/plant, tiller number/plant as well as leaf : stem ratio increased from 50.92 to 96.84, 17.47 to 26.85, 4.19 to 6.96 and 0.36 to 0.43 cm, respectively, with the increase in stage of maturity from I cut to II cut. The total yield of green forage, dry matter, crude protein and digestible dry matter from both the cuttings ranged from 278.19 to 724.24, 50.85 to 126.98, 3.42 to 7.67 and 25.92 to 62.89 q/ha, respectively. The average yield of green fodder and dry matter in I and II cuttings of these 24 strains was 122.90, 316.24, 16.98 and 62.58 q/ha, respectively, and was significantly higher in II cutting.

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501. KUMAR, Y., HET RAM AND S. K. GULIA 2002. IDENTIFICATION OF OAT VARIETIES BY LABORATORY TECHNIQUES Forage Res., 28 (3): pp. 142-146. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Study of laboratory parameters revealed that seed and seedling characters, namely, seed index, seed shape, seed colour, seed size, shoot and root length, colour of lemma and palea were useful in distinguishing oat varieties. The study of phenol and HCl test were found very effective in grouping all the 12 varieties as compared to florescence test. Treatment of these varieties with GA_3 and 2, 4-D separately differentiated them into responsive and non-responsive categories. In some varieties, the response was high, while some of them showed low to medium response. Two flow charts have been prepared on the basis of laboratory parameters studied for varietal identification. These charts will be useful for plant breeders, seed certification staff and seed testing laboratories.

502. PUNDIR, S. R., G. P. LODHI, PADAM SINGH AND YAGYA DUTT 2003.**STABILITY ANALYSIS FOR** GREEN AND DRY FODDER YIELD IN OAT (*AVENA SATIVA* L.) Forage Res., 28 (4) : pp. 215-217. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Stability of 36 oat genotypes was studied for green and dry fodder yield in four environments created by varying sowing dates. Genotypes x environment interaction was significant for both the traits under study. Partitioning of G x E interactions into heterogeneity between regression (linear) and remainder (non-linear) showed that mean squares due to these components were significant for both the traits under study. The magnitude (%) of linear and non-linear components of G x E interactions revealed that linear portion was more important for these traits. Genotypes viz., OS 6, OS 96, JHO 996, JHO 822 and UPO 238 performed well under wide range of environments. Therefore, these may be exploited for their yield and stability in future breeding programme.

 503. DAHIYA, O. S., R. C. PUNIAAND R. K. SINGH 2003. SEED QUALITY EVALUATION BY DIRECT AND INDIRECT LABORATORY PARAMETERS IN OATS (AVENA SATIVA) Forage Res., 29 (3) : pp. 107-109. Department of Seed Science & Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Seed is a vital ingredient in agriculture and it enhances productivity. The present study was planned to assess the seed quality of 15 genotypes through various laboratory and field tests. The observations were recorded on various direct (standard germination test, seedling length, vigour index and accelerated aging test) and indirect test (dehydrogenase activities, seed leachates conductivity and μ -amylase activities) of seed vigour. Seedling establishment showed significant and positive association with standard germination (0.92**) and μ -amylase activities (0.52*), whereas a negative association was observed with the seed leachates conductivity (-0.31). Seedling length had the significant and positive correlation with vigour index (0.89**). It was observed that standard germination (%) and μ -amylase activities were reliable predictor of seed vigour and quality in oats (*Avena sativa*).

504. A. K. THAKRAL AND J.S. VERMA 2003. HETEROSIS AND INBREEDING DEPRESSION IN FIVE CROSSES OF OAT (AVENA SATIVA L.) *Forage Res.*, 29 (3) : pp. 155-157. G. B. Pant University of Agriculture and Technology, Pantnagar.

Heterosis and inbreeding depression in five crosses of oat genotypes was studied at G.B. Pant University of Agriculture and Technology, Pantnagar. For grain yield in cross 1 and 4, the high estimates of better parent heterosis followed by comparatively low estimates of inbreeding depression in their F_2 indicating less reduction in the mean value of F_2 and F_1

505. DAR, Z. A., F. A. NEHVI, S.A. WANI, GUL ZAFFER AND M. A. RATHER 2004. GENETIC STUDIES IN RELATION TO GREEN FODDER YIELD AND QUALITY IMPROVEMENT IN OAT (AVENA SATIVA L.). Forage Res., 30 (1) : pp. 64-66. SKUAST(K).

Genetic studies in relation to green fodder yield and quality improvement in 50 genotypes of oat (*Avena sativa* L.) were carried out at SKUAST(K). Wide range of variability and very high heritability was reported.

506. BAHUGUNA, P. AND J. S. VERMA 2004. EFFICIENT SELECTION CRITERIA FOR GREEN FODDER YIELD IN OAT (AVENA SATIVA L.) Forage Res., 30 (2) : pp. 75-77. Department of Genetics & Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145, India

Selection indices were constructed and their efficiency assessed in terms of expected genetic advance using 30 genotypes of forage oat. Six characters viz., plant height, number of tillers and number of leaves per plant, growth rate (g/day/plot), dry matter and green fodder yield (kg/plot) were selected for the formulation of selection indices for green fodder yield. Efficacy of indices over direct selection in terms of relative selection efficiency ranged from 14.9 to 667.5 per cent, the highest efficiency being for the index score involving all the six traits. The efficiency of indices increased with increasing number of characters. The index score revealed 567.5 per cent higher efficiency over straight selection based on green fodder yield *per se*.

507. DAHIYA, O. S., R. C. PUNIA AND V. P. SANGWAN 2004. ELECTRICAL CONDUCTIVITY-A RELIABLE PREDICTOR OF SEED QUALITY IN OATS (AVENA SATIVA) Forage Res., 30 (3): pp. 131-133. Department of Seed Science & Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

For the present investigation, nine cultivars were taken for assessing the seed quality. Electrical conductivity showed significant and negative correlation with laboratory germination, vigour index, tetrazolium test, respiration rate and seedling establishment. Therefore, seed leachates measured by electrical conductivity meter gave precise information regarding seed quality in terms of viability, vigour and storability.

508. SOOD, V. K., SIMRANJEET SINGH, J. C. BHANDARI AND O. P. SOOD 2006. COMBINING ABILITY ANALYSIS FOR SOME FORAGE AND GRAIN CHARACTERISTICS IN OAT (AVENA SATIVA L.) Forage Res., 32 (1): pp. 4-7. Fodder Production & Grassland Management Centre, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (Himachal Pradesh), India

A line x tester analysis in oat indicated that non-additive genetic variances were higher for days to 50 per cent flowering, plant height, leaves per plant, tillers per plant, flag leaf area, fresh fodder yield per plant, dry matter yield per plant, crude protein content, crude protein yield per plant, grain yield per plant and harvest index, whereas both additive and non-additive variances were equally important for leaf : setm ratio and biological yield per plant. For 100-seed weight, additive variances were higher than the non-additive genetic variances. The parents JHO 822, UPO 130 and Kent were good general combiners for fresh fodder yield and its components, whereas Algerian, JHO 822, PO 26 and Palampur-1 were good combiners for grain yield and its component traits. Cross JHO 822 x HFO 114 was a potential hybrid for fodder yield, whereas Algerian x Palampur-1 was a potential cross for both fodder as well as grain yield.

509. ROY, S., D. K. DE AND P. BANDOPADHYAY 2006. CORRELATION AND PATH COEFFICIENT ANALYSIS OF FORAGE YIELD COMPONENTS IN OAT (AVENA SATIVAL.) Forage Res., 32 (1): pp. 51-55. Department of Genetics, BCKV, Mohanpur, Nanda (W.B.).

The mean. GCV, PCV, heritability and GA obtained for each cut and their respective total of two cuts in the Department of Genetics, BCKV, Mohanpur, Nanda (W.B.). revealed that the mean values increased in the second cut except for LSR.

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510. SHEKHAWAT, S. S., D. K. GARG AND J. S. VERMA 2006. CHARACTER ASSOCIATION AND VARIABILITY STUDY IN OATS (AVENA SATIVA L.) FOR GREEN FODDER YIELD AND RELATED TRAITS Forage Res., 32 (3) : pp. 163-168. AICRP on Forage Crops, Agricultural Research Station, Rajasthan Agricultural University, Beechwal, Bikaner-334 006, (Rajasthan), India

A study was done to know correlation, path coefficient, genetic divergence and variability in 69 genotypes of oats for green fodder yield and 11 related characters. The experiment was conducted in rabi season of 2004-05 in zone Ic of Rajasthan at Agricultural Research Station, Bikaner. The zone Ic is characterized by hyper arid condition having partial irrigation facility. Green fodder yield had significantly positive correlation with plant height and tillers per metre at genotypic level as well as at phenotypic level. Path coefficient analysis at phenotypic level showed that plant height, tillers/metre, leaf length, leaf width and stem girth had positive direct effect on green fodder yield. By genetic divergence analysis, the 69 genotypes could be grouped in six clusters according to Mahalanobis' D2 statistic. Cluster I was the largest including 39 genotypes followed by cluster IV (12 genotypes), cluster III (10 genotypes), cluster II (five genotypes), cluster V (two genotypes) and cluster VI (one genotype). Days to 50 per cent panicle emergence contributed the highest (21.78%) towards the divergence followed by panicle length (19.39%) and tillers/metre (13.90%). The range was 4.69 to 26.60 for GCV, 5.42 to 35.32 for PCV, 30.50 to 74.90 per cent for heritability (broad sense) and 8.36 to 46.78 per cent for genetic advance (as % of mean). The heritability was maximum (74.90%) for days to 50 per cent panicle emergence and the genetic advance as per cent of mean was maximum (46.78%) for leaf : stem ratio.

511. PUNDIR, S. R. AND V. P. SINGH 2007. [GENETIC VARIABILITY AND INTERRELATIONSHIP FOR VARIOUS SEEDLING AND FORAGE CHARACTERS IN OATS (AVENA SATIVA L.).] Forage Res., 32 (4) : pp. 254-256. Forage Section, CCS Haryana Agricultural University, Hisar

In the present study, high estimates of heritability accompanied by high genetic advance were observed for green fodder yield, dry fodder yield, number of leaves per plant, leaf length, leaf breadth, green leaf weight and dry leaf weight indicating the effectiveness of simple selection for the improvement of these traits. The strong and positive association of green fodder with all other characters such as green stem weight, dry stem weight, green leaf weight, dry leaf weight, dry fodder yield, leaf length, leaf breadth, stem girth, plant height, root length, fresh root weight, dry root weight and fresh shoot weight was observed(Table 2). All the character had large positive indirect effect on green fodder yield via green leaf weight and green stem weight.

512. BAHADUR, RAJAND R. N. CHOUBEY 2007. GENETIC DIVERSITY AND STABILITY IN FORAGE OAT (AVENA SATIVA L.) Forage Res., 33 (3): pp. 139-144. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

An attempt was made to study the genetic diversity and stability for 12 characters in 50 diverse genotypes of oat. Based on D² values, genotypes were grouped into 10 clusters. The intra-cluster distances ranged from 0.0 to 24.70. Inter-cluster distance was maximum between clusters IX and X, whereas closest proximity was observed between clusters IV and VI. Mean squares due to genotypes, environment and G x E interaction were highly significant for all the characters. Both linear and non-linear components were found significant. The genotypes, OS-7, OS-174, OS-237, HJ-8, JHO-99-6 and JHO-95-1 were found stable for green and dry fodder yield and suited to a wide range of environments, while JHO-889, OS-189, JHO-822, OL-805 and OS-242 were desirable and responsive to favourable environments. Therefore, these genotypes may be exploited in future breeding programmes aimed at improving overall forage production of oat.

513. SHARMA, MANMOHAN AND S. P. GUPTA 2007. GENOTYPE X ENVIRONMENT INTERACTIONS FOR FORAGE YIELD IN OATS (AVENA SATIVA L.) Forage Res., 33 (3) : pp. 149-151. S. K. University of Agricultural Sciences & Technology-Jammu, Regional Agricultural Research Station, Rajouri-185 131 (J & K), India

Stability parameters in 33 oats genotypes were studied to obtain information on the magnitude and nature of G x E interactions and stability for forage yield. These genotypes evaluated under three different environments depicted significant interaction with the environments for both green fodder and dry matter yields. OS 7, a high yielding genotype and responsive to favourable environment, was found to be the most unstable for both the characters. The high yielding genotypes which were stable over environments and responsive to favourable conditions included JHO-851, OS-297 and OS 293. The genotypes OS 311, OS 315, JHO 2000-6 and JHO 2000-2 were high yielding, responsive to poor environment and least deviating from regression, while UPO 271 was found to be high yielding, responsive to average environment and stable one.

514. PUNDIR, S. R., V. P. SINGH AND D. S. PHOGAT 2008. GENETIC VARIABILITY AND INTERRELATIONSHIPFOR VARIOUS GRAINAND SEEDLING CHARACTERS IN OATS (AVENA SATIVA L.) Forage Res., 33 (4): pp. 236-240. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Studies on genotypic and phenotypic coefficients of variation, heritability, expected genetic advance, correlation and path-analysis carried out in 36 genotypes of oats (*Avena sativa* L.) over four environments revealed moderate to high estimates of heritability coupled with high genetic advance for most of the traits. The correlation and path-analysis indicated the positive significance of harvest index, 100-grain weight as components of grain yield, traits; root length, dry root weight and dry shoot weight as important components of seedling traits. Among these traits, both dry root weight and dry shoot weight had positive direct association with grain yield in all the environments and indirect through biological yield. While the 100-grain weight, root length, shoot length, fresh root weight and fresh shoot weight had positive indirect association with grain yield through biological yield. Therefore, top priority should be given to these traits while selecting for high grain yield. However, higher growth rate of seedling traits associated with high grain yield would help in selecting grain genotypes with an improved yield in oats at early growth stage.

515. ARORA, R. N., S. S. BISHT AND B. S. JHORAR 2008. EVALUATION AND CHARACTERIZATION OF FODDER OAT GERMPLASM Forage Res., 34 (1): pp. 29-32. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Evaluation and characterization for some morphological traits was carried out in 554 germplasm accessions of oats. Moderate amount of genetic variability was recorded for green fodder yield and dry matter yield, while low for days to 50 per cent flowering. In all, 46 germplasm accessions were found significantly better in GFY and DMY as compared to the best check JHO 99-2, JO -1 for GFY and OS 7 for DMY. All the germplasm accessions were characterized and categorized on the basis of growth habit and foliage colour. Best accessions, namely, HFO 455, HFO 18 and HFO 442 can be utilized in oat varietal development programme.

516. MEHTA, A. K., S. K. BILAIYA AND G. S. RATHI 2008. GENETIC DIVERGENCE IN FODDER OAT (AVENA SATIVA L.) Forage Res., 34 (3): pp. 146-148. All India Coordinated Research Project on Forage Crops, Jawaharlal Nehru Krishi Vishva Vidyalaya, Jabalpur (M.P.), India

A set of 57 genotypes of oat was evaluated in randomized complete block design with three replications. The data were recorded on 10 competitive plants for 11 characters i. e. days to 50 per cent flowering, plant height, tillers per plant, leaf length, leaf width, leaf stem ratio, stem diameter, panicle length, green fodder yield (q/ha), dry matter yield (q/ha) and crude protein content. The genetic divergences were determined as per Mahalanobis' D^2

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method and were grouped in eight clusters. The cluster II had 16, while the cluster V had 1 genotype. The contribution of days to 50 per cent flowering towards genetic divergence was 27.12 per cent followed by tillers per plant (20.32%), leaf stem ratio (14.90%), panicle length (11.23%), crude protein content (7.92%), leaf width (4.23%), dry matter yield (4.13%), green fodder yield (3.86%), plant height (3.13%), leaf length (1.93%), and stem diameter (1.23%). Thus, the genotypes from clusters having high tillers per plant, leaf stem ratio and panicle length can be used in crossing programme to evolve transgressive segregants for better fodder yield and palatability.

517. BAGUL, R. S., P. P. SURANA, M. R. MANJARE, A. B. TAMBE AND V. L. AMOLIC 2008. PHULE HARITA (RO-19)–A NEW FORAGE MULTICUT OAT VARIETY Forage Res., 34 (3) : pp. 190-192. All India Co-ordinated Research Project on Forage Crops, Mahatma Phule Krishi Vidyapeeth, Rahuri-413 722 (M. S.), India

An improved multicut oat variety, Phule Harita has been developed under AICRP (FC) at Mahatma Phule Krishi Vidyapeeth, Rahuri based on mean performance of 49 multilocation test centres of the project. Phule Harita (RO-19) recorded higher mean green forage yield (532.03 q/ha), dry matter yield (96.39 q/ha) and crude protein yield (10.38 q/ha) which was 18.70, 16.98 and 14.82 per cent higher than the National check JHO-851 (GFY 448.20 q/ha, DMY 82.40 q/ha and CPY 9.04 q/ha). The variety also showed the superiority over the check Kent. Due to high green forage yield potential, better quality and resistance to major pest and diseases, the variety Phule Harita (RO-19) has been recommended for cultivation at all India level during the year 2006.

518. SHEKHAWAT, S. S., D. K. GARG, AND J. S. VERMA 2009. PHENOTYPIC STABILITY STUDY IN OATS (AVINA SATIVA L.) FOR GREEN FODDER YIELD AND RELATED TRAITS. Forage Res., 34(4): pp. 216-219. AICRP on Forage Crops, Agricultural Research Station, Rajasthan Agricultural University, Beechwal, Bikaner.334006(Raj.)

A study was under taken to find out phenotypic stability in 69 genotypes of oats for green fodder yield and 11related characters. The experiment was conducted in two rabi seasion (2003-04 and 2004-05) under three different sowing dates in early (last week of October), normal (mid-November) and late (mid-December) conditions in hyper arid zone 1c of Rajasthan. In each environment, the genotypes were growen in three replications. Each plot consisted of 3 m-row length with row-to –row spacing of 30 cm. In present study, average stability was showen by 49 genotypes for different charactera. The genotypes, which showed average stability for three or more than three characters were PA 03/02, PA 03/08, PA03/10, PA03/21, PA03/26, PA03/29, PA03/34, PA 033/39, OL9, OL529, OL1069, OL1221, JHO2001-02 and UPO 276. JHO 2001-02 showed average stability for green fodder yield and dry fodder yield.

519. BAHADUR, RAJ AND R.N. CHOUBEY 2009. **GENETIC DIVERGENCE IN FORAGE OAT** (*AVENA SATIVA* L.). *Forage Res.*, **34**(4) : **pp.225-229.** Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125004 (Haryana), India

Genetic divergence for fodder yield and quality characters among 50 diverse genotypes of forage oat under normal and late sown conditions was studied. Considerable variability existed for all the traits. The estimates of heritability were quite high for almost all the characters. Genetic advance was reasonably high for green as well as dry odder yield/ plant. Based on D values, eight clusters were formed in both of the environments. Clustering patter was random and independent. The intra-cluster distance varied from 0.00 to 34.50 and 0.00 to 35.40, whereas inter cluster distance varied from 55.00 to 1014.81 and 40.20 to 998.65 under normal late sown conditions, respectively. Diverse genotypes from varies clusters could be utilized in hybridization programme to create desired variability in forage oat.

520. ARORA, R. N., S. S. BIST, U. N. JOSHI, AND B. S. JHORAR 2009. EVALUATION AND CHARACTERIZATION OF OAT GERMPLASM FOR FODDER YIELD AND QUALITY UNDER DIFFERENT CUTTING REGIMES. Forage Res., 34 (4): pp.230-234. Forage Section, Department of Plant Breeding, CCSHAU, Hisar.

One hundred and eight germplasm accessions of oats collected from various sources were evaluated and characterized for some quantitative, qualitative and quality traits during rabi 2006-07 at CCSHAU,Hisar. Moderate to low amount of genetic variation was present in genetic stock for various traits studied. In both single cut as well as multi-cut system accession HFO278 was observed as the most early in flowering, while genotypes HFO446 was observed as the most late. The germplasm accessions, namely, HFO 106, 159 and 164 had high crude protein (10.5%) in single cut types, while in multi-cut type, the germplasm accession, namely, HFO 55 (17.5%), HFO 446 (17.0%) and HFO 257 (16.7%) had high crude protein content as compared to the best check OS-6 having 8.7 percent crude protein in single cut and 14.0 percent crude protein in multi-cut. The majority of the accessions were characterized as semi-erect in growth habit. Germplasm accessions, namely, HFO 407, 257, 289, 393 and 30 had high fodder yield in two-cut system. These accessions can be utilized in oat breeding programme for developing high yield and nutritive cultivars of oats.

521. SHARMA, V. K., RAI, H. K., DORJAI NAMGYALAND S. B. AHMED 2009. PERFORMANCE OF OAT GENOTYPES AS GREEN FODDER UNDER COLD ARID CONDITIONS OF LADAKH. Forage Res., 35 (2): pp. 124-125. Regional Research Station Stakna, SKUAST-Kashmir.

The experiment was conducted at regional research station Stakna farm of the SKUAST-K during May to September 2005 and 2006. The results indicated that Sabzar, SKO-12 and EC 529810 genotypes of oat should be used to get maximum green fodder yield from field under cold arid regions.

522. YOGESH RUWALI AND INDRA DEO 2009. ANALYSIS OF COMBINING ABILITY ESTIMATES, GENE ACTION AND HETEROSIS FOR VARIOUS QUANTITATIVE CHARACTERS IN OATS (AVENA SATIVA L.). Forage Res., 35 (3) : pp. 127-136. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

The present investigation involving 11 x 3 line-tester of oats (*Avena sativa* L.) including 33 F₁'s, 11 lines and three testers was undertaken with a view to estimate the general and specific combining ability effects, type of gene action and manifestation of heterosis. The observations were recorded on 16 quantitative characters, namely, plant height at 50 per cent heading, number of tillers per plant, number of spikelets per panicle, flag leaf area, leaf length, number of leaves per plant, panicle length, stem diameter, days to 50 per cent heading, days to maturity, 100-grain weight, grain yield, biological yield, straw yield, harvest index and growth rate. The experiment with F₁'s and parents was laid down in randomized block design with three replications at the Instructional Dairy Farm, G. B. Pant University of Agriculture & Technology, Pantnagar during **rabi** 2008-09. Kota, JHO-822 and UPO-271 were parents identified for good gca for many characters, while OL-125 x Kent and EC-246123 x Wright were among the crosses with good sca values for various characters. Lang, Wright and JHO-822 were among the parents showing higher significant better parent heterotic estimates for different characters viz., grain yield, 100-grain weight and growth rate, etc. Results on genetic components of variance showed the preponderance of non-additive genetic variance particularly for the yield related characters. Preponderance of dominance variance alongwith additive genetic variance for most of the traits needs to be exploited for the development of improved oat varieties.

523. ROY, C. AND J. S. VERMA 2011. RELATIVE EFFICIENCY OF SELECTION INDICES FOR GREEN FORAGE YIELD IN OAT (AVENA SATIVA L.) Forage Res., 36 (4) : pp. 242-244. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

Indices were constructed according to the procedure of Smith using 32 genotypes of forage oat and their efficiency was assessed in terms of expected genetic advance. Efficiency of indices over direct selection in terms of relative selection efficiency ranged from 25.30 to 503.40 per cent. Selection indices based on five traits combination of plant height, number of tillers, number of leaves per plant, dry matter percentage and green fodder yield per plot was most efficient index for selection with relative efficiency score 478.1 per cent. The score of this index revealed 378.1 per cent higher efficiency over straight selection based on green fodder yield *per se*.

524. ROY, C. AND J. S. VERMA 2011.GENETIC INTERRELATIONSHIPAMONG FODDER YIELD AND COMPONENT TRAITS IN OAT (AVENA SATIVA L.) Forage Res., 36 (4): pp. 245-249. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (Uttarakhand), India

The success of breeding programme depends on skills of breeders which in turn depends on the character expression indeed which the selection is acted upon. It was observed that days to 50 per cent heading, number of tillers, number of leaves per plant, leaf width, flag leaf width and dry matter yield had significant genetic correlation with green fodder yield which gave us a clue for indirect improvement of green fodder yield during selection. Path analysis revealed that dry matter percentage, number of tillers, number of leaves, leaf width and days to 50 per cent heading had high positive direct effect and ADF, NDF percentage had negative direct effect on green fodder yield.

3. Pearl Millet

525. SUKANYA, D. H., V. RAMAMURTHY AND C. R. RAMESH 2001. SELECTION OF PARENTS FOR LEAFINESS IN BAJRA X NAPIER HYBRIDS. Forage Res., 27 (2) : pp. 115-118. I. G. F. R. I. Regional Station, Dharwad-580 005, India

Thirty hybrids derived by crossing three **bajra** and 10 napier genotypes were evaluated for characters indicating leafiness viz., number of leaves per plant, leaf length, leaf breadth, leaf to stem ratio and green fodder yield. Significant variation existed for all the characters. Though, variation due to **bajra** and napier genotypes was significant, the contribution by specific combinations was more predominant. IP 6426 (**bajra**) and FD 439 (napier) were good general combiners for many characters. IP 6426 x FD 469 was the best performing hybrid for green fodder yield and leafiness and it could be tested for commercial cultivation.

526. SOLANKI, Y. P. S., I. S. KHAIRWAL¹ AND F. R. BIDINGER 2002. **GENETIC VARIABILITY IN SOME PRODUCTIVITY TRAITS OF PEARL MILLET COMPOSITES** *Forage Res.*, 27 (4) : pp. 273-276. CCSHAU Research Station, Rohtak-124 001 (Haryana), India

Estimates of genetic variability, heritability and genetic advance have been computed for five productivity traits in 24 experimental varieties of pearl millet. The genetic and phenotypic variability was highest for grain yield per m^2 and panicle number m^2 and lowest for days to 50 per cent flowering across the composites. High estimates of heritability coupled with high genetic advance as recorded for grain yield m^2 and panicle number m^2 should be considered as important parameters.

527. YADAV, H. P., P. S. SABHARWAL, C. R. BENIWALAND HANUMAN 2002. COMBINING ABILITY STUDY FOR SOME NEWLY DEVELOPED MALE STERILE LINES FOR FORAGE ATTRIBUTES IN PEARL MILLET Forage Res., 27 (4): pp. 277-280. Bajra Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

The experimental material was comprised of 77 F_1 hybrids developed by crossing seven male sterile lines with 11 testers (inbreds) in line x tester fashion. Variances due to lines, testers and their interaction were highly significant for all the characters. Estimates of sca variances were higher in magnitude for dry fodder yield and effective tillers indicating preponderance of non-additive gene effects for these traits. However, for plant height, additive component was higher as indicated by predictability ratio. Parents 92777A and 93111A among male sterile lines and ICR 161, 77/29-2, HP 8601 and HTP 91/32 among pollinators exhibited high gca effects for most of the traits. Among crosses 93111A x HTP 91/32, 95555A x 91/32, 95555A x ICR 161 and 95555A x 77/29-2 exhibited high sca effects and *per se* performance. The material could be best exploited following hybrid breeding programme and or reciprocal recurrent selection.

528. KARWASRA, R. S. AND R. S. MALIK 2002. COMPONENT ANALYSIS OF IMPROVED TECHNOLOGY FOR BAJRA (*PENNISETUM TYPHOIDES*) SEED PRODUCTION. *Forage Res.*, 28 (3) : pp. 156-158. Department of Agronomy, CCS Haryana Agricultural University, Hisar-125 004, India

An attempt was made to study the judicious use of the available limited money in optimising bajra (HHB-67) production. Experiments were conducted with local variety vs. HHB-67, no fertilizer vs. 60 kg N and 40 kg P_2O_5 per hectare and bullock drawn country plough vs. bullock drawn ridger seeder in randomised block design with four replications from 1988 to 1990. HHB-67 with ridger seeder sowing and fertilizer application gave significantly higher yield over rest of the treatments during 1988 and 1990. Whereas in 1989, this treatment was superior to local one in all conditions. The return from per rupee expenditure was highest (Rs. 19.68) from the improved variety (HHB-67) followed by ridger seeder planting (Rs. 2.80). The study indicated that split application of nitrogen doses from per rupee invested in fertilizer application increased the return.

529. DUTT, Y. AND C. R. BAINIWAL 2002. INTRA-POPULATION IMPROVEMENT PROCEDURES FOR FODDER TRAITS IN PEARL MILLET. *Forage Res.*, 28 (3) : pp. 162-164. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

The present study was conducted to compare the efficiency of three intra-population selection procedures i. e. half-sib (HS), full-sib (FS) and self generation (S_1) for improvement in fodder traits in pearl millet. To know the efficiency of these three progeny selection procedures, 55 HS, 55 FS and 55 S_1 progenies were derived from pearl millet composite, EC91 PCV5 during **kharif** 1998. These three types of progenies alongwith base population and checks were evaluated during **kharif** 1999 for dry fodder yield and plant height. Mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and expected genetic advance were worked out for two fodder traits i. e. dry fodder yield and plant height. The highest mean, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed in HS progeny selection followed by FS and S_1 progenies. Estimates of heritability and expected genetic advance were also recorded higher in HS progeny selection for dry fodder yield as well as plant height. Thus, among these three intra-population improvement selection procedures, HS selection procedure appears to be superior as compared to FS and S_1 progeny selection procedures for improvement in these fodder traits in composite EC91 PCV5.

530. SOLANKI, Y. P. S., I. S. KHAIRWAL AND F. R. BIDINGER 2002. GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN THREE PEARL MILLET COMPOSITES. Forage Res., 28 (3): pp. 174-176. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Genetic variability, heritability and genetic advance in three pearl millet composites was estimated. High PCV and GCV were observed for panicle surface area followed by grain yield. High heritability for grain number/panicle and 1000 grain weight was noticed. High genetic advance for 1000-grain weight and grain number/unit area was present.

531. SHUKLA, G. P. AND B. M. S. PARIHAR 2002. FERTILITY RESTORATION IN F₁ CROSSES INVOLVING MALE STERILES AND EXOTIC POLLINATORS IN FORAGE PEARL MILLET (*PENNISETUM TYPHOIDES* (BURM. F.) STAPF AND HUBB.)*. Forage Res., 29 (2) : pp. 79-81. Division of Crop Improvement, Indian Grassland, Fodder and Agro-forestry Research Institute, Jhansi-284 003 (U. P.), India

Twelve male sterile lines derived from A1 cytoplasmic source and ICMA 98777 derived from Ag cytoplasmic source were grown alongwith 40 exotic pollinators predominantly from African origin in the rainy season of the year 2001. The materials were grown in a single row of 4 m each. The agronomic practices were followed as per requirement of the crop. F, crosses were made with an objective to search for promising forage type non-restorer lines with a view to transfer their genome in an otherwise grain type male sterile through repeated backcross procedure in order to recover a forage type male sterile line for production of heterotic forage hybrids, secondly, to mark out restorer lines of forage value for an immediate use in the production of forage hybrids. The 312 F₁ crosses were recovered out of which 72 were grown in March 2002 and 240 in kharif 2002. The earheads of each cross were bagged to examine seed setting in the hybrid. Results indicated that there was no seed set in 30 out of 232 crosses on selfing with a percentage of 12.93. A group of 59 crosses was found to be fully fertile. The male sterile lines 89111A, 97333A, 90111A and 81A were found to interact with 6, 5, 6 and 4 pollinators showing fully sterile hybrids. 97111A, 91777A, 94444A, 95222A and 98777A interacted with maximum number of pollinators enumerating 10, 9, 6, 6 and 5 showing fully fertile hybrids. Rest of the 143 crosses showed mixed behaviour for fertility/sterility showing different status of fertility in a particular cross e. g. fertile and semi-fertile; fertile, semi-sterile and sterile; sterile and semi-sterile and so on. The information generated contained 19 pollinators out of 40 showing full restoration of fertility in 59 crosses with different male sterile lines. The 18 male parents involved in 30 crosses showing no seed set may, conclusively, be called fertility non-restorer lines. The fertility non-restorers may be utilized as a recurrent parent to convert an otherwise less productive cytoplasmic male sterile into a productive and vigorous forage type male sterile lines.

532. JINDAL, Y. AND PREM SAGAR 2003. HETEROTIC RELATIONSHIPS AMONG EARLY MATURING PEARL MILLLET (PENNISETUM GLAUCUM (L.) BR. EMEND STUNTZ) POPULATIONS. Forage Res., 29 (3): pp. 150-154. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Ten early maturing pearl millet populations collected from geographically diverse sources were used to study genetics and heterotic relationships. These populations were crossed in a population diallel and laid in 8 x 8 lattice design. Statistical analysis of design of experiment revealed significant differences among genotypes. These were studied using Variety Cross Diallel following Gardner and Eberhart (1966) Analysis II. Four traits viz., grain yield (q/ha), head weight (q/ha), head count and days to 50% flowering were kept under observation. For grain yield, out of the total heterosis (h_{kj}) 74.26%, maximum variation (70.25%) was contributed by population heterosis (h_k). The population effect (v_j) contributed for 25.74% variation of this important character. For days to 50% flowering, heterosis (h_{kj}) accounted for 55.57% variation out of which about 85% was due to specific heterosis (s_{ki}). A few important heterotic relationships were found viz., Pak LR 74 x LRE 128 and Pak LR 74 x EC II observed

for highest overall heterosis for grain yield, highest positive and significant s_{kj} values were shown for EC II x EC 87 and EC C6 x Hi Tip 89 for this trait. For days to 50% flowering, ESRC II x EC 89 and ESRC II x EC 87 revealed highest heterosis for earliness, while the specific heterosis values were best for EC 87 x ESRC II and EC C6 x W-Raj Pop C₂. These results can help pearl millet breeders engaged in population improvement programme.

533. YADAV, Y. P., D. KUMAR AND H. P. YADAV 2004. STUDIES ON COMBINING ABILITY AND HETEROSIS FOR DRY FODDER YIELD AND ITS CONTRIBUTING TRAITS IN PEARL MILLET. *Forage Res.*, 30 (1): pp. 55-58 (2004) RRS, Bawal (Haryana).

Study on combining ability and heterosis for dry fodder yield and its contributing traits in 42 pearl millet genotypes was carried out at RRS, Bawal (Hryana). The results revealed that parents, ICMA 95555, HMS 9A, HMS 22A, G 73-107 and H 77/833-2 possessd high gca effects and crosses ICMA 95555 x CSSC 46-2, HMS 9A x G 73-107 exhibited high heterosis for DFY.

534. PRAKASH, VED AND R. V. SINGH 2004. GENETIC STUDIES OF QUALITY CHARACTERS IN PEARL MILLET. *Forage Res.*, 30 (2) : pp. 99-100. RAU Agricultural Research Station, Durgapura, Jaipur.

Genetic studies of quality characters in pearl millet conducted at RAU Agricultural Research Station, Durgapura, Jaipur. There was no correspondence between the *per se* expression and sca effects.

535. CHAUDHARY, D. P., B. L. BHARDWAJ, MANOJ SREEVASTAVA AND AJAIB SINGH 2007. COMPARATIVE EVALUATION OF FORAGE PEARL MILLET [PENNISETUM GLAUCUM (L.) R. BR.] GENOTYPES FOR DRY MATTER AND FODDER QUALITY. Forage Res., 33 (2): pp. 111-113. Department of Plant Breeding, Genetics and Biotechnology, Punjab Agricultural University, Ludhiana-141 004 (Punjab), India

Ten genotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.] were evaluated for their dry matter content, nutritional quality and digestibility. The dry matter content ranged between 17.55-22.35 per cent, while crude protein 7.43-10.93 per cent, crude fibre 29.3-35.85 per cent, ether extract 1.7-2.0 per cent, total ash 9.25-13.1 per cent, nitrogen free extract 40.72-49.62 per cent and *in vitro* dry matter digestibility (IVDMD) from 54.4-67.3 per cent. Significant difference was found in dry matter content, crude protein, crude fibre, total ash, nitrogen free extract and IVDMD. The per cent NDF content ranged between 60.7-67.75, while ADF 30.7-35.6, ADL 5.0-6.85 and hemi-cellulose 28.1-34.40 per cent. Significant difference was found in oxalate content, which ranged between 1.9-2.5 per cent

536. ARYA, R. K., H. P. YADAV, ASHOK KUMAR YADAV AND DESH RAJ 2008. GENETICARCHITECTURE OF YIELD AND ITS CONTRIBUTING TRAITS IN WHITE AND GREY GRAIN COLOUR GENOTYPES IN PEARL MILLET. FORAGE RES., 34 (1) : PP. 33-38. Department of Plant Breeding (Bajra Section), CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Genetic analysis of six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of each of the three crosses viz. White × White (ICMA 94222 × HMS 36B), White × Grey (ICMA 94222×78/711) and Grey × Grey (ICMA 89111× G 73-107) was carried out to elucidate the inheritance pattern. The estimates of gene effects revealed the presence of additive gene action in all the three crosses for all the characters except for harvest index in cross I and dominance gene action in all the three crosses for most of the characters except ear length and grain yield in cross I, ear girth, ear weight, grain yield, biological yield and harvest index in cross II; and effective tillers and ear length in cross III. Most of the characters showed duplicate type of epistasis except grain yield and harvest index.

537. PATEL, M. A., J. P. YADAVENDRA, D. H. PATEL, N. V. UPADHYAY AND J. A. SHAIKH. 2008. STUDIES ON HETEROSIS FOR GREEN FODDER YIELD AND ITS CONTRIBUTING TRAITS IN PEARL MILLET [PENNISETUM GLAUCUM (L.) R. Br.]*. Forage Res., 34 (3) : pp. 149-155. Medicinal and Aromatic Plants Project, Anand Agricultural University, Anand-388 110 (Gujarat), India

Using Line x Tester mating design, 40 top cross hybrids were produced and evaluated to know the extent of heterosis over mid and better parent for 10 quantitative traits including green fodder yield in pearl millet. Top cross hybrids exhibited significant heterosis in desired direction for days to 50 per cent flowering, plant height, number of tillers per plant, number of leaves per plant, leaf length, leaf width, leaf stem ratio, stem diameter, internodal length and green fodder yield per plant. The four crosses ICMA 95222 x IP 22269, ICMA 00999 x IP 22269, ICMA 00999 x Giant Bajra and ICMA 94555 x AFB-2 depicted high heterosis over mid parent. These four hybrids also exhibited positive heterosis over better parent and were having high yielding ability. Hence, these crosses can be utilized in further breeding programme to isolate high yielding pure lines.

538. ARYA, R K., H P YADAV, M K SINGH AND S ARYA 2009. A COMPARATIVE STUDY OF WHITE AND GREY GRAIN COLOUR HYBRIDS IN PEARL MILLET [PENNISETUM TYPHOIDES (L.) R BR.]. Forage Res., 34(4) : pp. 220-224. Department of Plant Breeding, CCS HAU, Hisar-125004(Haryana), India.

The present investigation was carried out to study the comparative performance of white and grey grain colour hybrids. The experimental material was comprised of 16 white and 16 grey grain colour hybrids. The experiment was planed in RBD in three replications under four different environments and data were recorded on yield and its contributing traits as well as on quality parameters. The results of present investigation based on mean performance revealed that the white grain colour hybrids were early in flowering and found superior to grey ones for grain yield, ear girth, ear weight, dry fodder yield biological yield, 1000-grain weight and harvest index but comparable in quality parameters viz., protein, starch and fat content.

539. YADAV, A. K., M. S. NARWAL AND RAJESH KUMAR ARYA 2009. SCREENING FOR SUPRA-OPTIMAL TEMPERATURE TOLERANCE THROUGH MEMBRANE THERMO-STABILITY IN PEARL MILLET [PENNISETUM GLAUCUM (L.) R. BR.]. Forage Res., 35 (2) : pp. 85-90. Department of Plant Breeding (Bajra Section), CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Forty-six genotypes of pearl millet which included advanced inbred lines, elite pollinators, populations and hybrids were screened for supra-optimal temperature tolerance at the research area of Department of Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. On pooled basis, the membrane thermo-stability (MTS) values ranged from 52.35 to 75.05 with an average of 65.10. The genotype CVJ-2-5-3-1-3 showed highest value for membrane thermo-stability (MTS) followed by 99 HS-18, Togo-II, H 77/833-2 (77/371 × BSECT CP-1), G73-107 and 96AC-93. These genotypes were selected as the tolerant genotypes for heat stress. The genotype 1305 showed lowest value for membrane thermo-stability (MTS) followed by 77/245 and H 77/29-2 and these genotypes were selected as the susceptible for heat stress. On pooled basis, membrane thermo-stability (MTS) exhibited a significant positive correlation with germination (%), number of leaves/seedling, seedling fresh weight (g) and seedling dry weight (g).

540. ARYA, R. K., SUNDER ARYA AND S. K. PAHUJA 2009. GENETIC DISSECTION OF WHITE GRAIN PEARL MILLET [PENNISETUM TYPHOIDES (L.) R. BR.]. Forage Res., 35 (3) : pp. 169-174. RDS Seed Farm, Forage Section (P. B.), CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Superiority of white grain colour pearl millet hybrids for grain quality, grain yield and fodder yield has been proved. Development of white grain colour hybrid is easy as white grain colour in pearl millet is controlled by single dominant gene and sufficient white grain genetic stock is available. But its maintenance is difficult due to Xenia

effect in pearl millet. For majority of yield contributing traits both linear and non-linear type of G x E interaction was reported but magnitude of linear component was higher. The white grain colour hybrids i. e. ICMA 94222 x H77/833-2 and 94222 x 78/711 were ideal for all the test environments. White grain colour pearl millet responded to nitrogen application. Additive and dominance gene effects alongwith their interactions as well as duplicate type of epistasis were reported. Yield improvement was possible due to availability of wide variability accompanied with high heritability for yield contributing traits and grain yield showed significant and positive association with majority of yield contributing traits.

541. YADAV, D. K., A. K. CHHABRA, H. P. YADAV AND L. K. CHUGH 2010. STUDIES ON BIOCHEMICAL TRAITS FOR RANCIDITY IN PEARL MILLET [PENNISETUM GLAUCUM (L.) R. Br.]. Forage Res., 36 (1) : pp. 37-41. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana) India

In the present investigation, 20 pearl millet genotypes were tested in Biochemistry Laboratory of Bajra Section, in the Department of Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar for rancidity and biochemical traits related to fat content (%), total phenols (mg/100 g flour), C-glycosylflavones (μ mole/100 g flour), fat acidity (mg KOH/100 g flour), free fatty acid (% oleic acid), peroxide value (meq peroxide/kg fat) and peroxidase activity. Results of the present study revealed that the genotypes 94222A x 78/711 (4.13), Barmer Pop (4.20) and H77/833-2 (4.27) exhibited minimum score for rancidity. However, the genotypes HHB 67 (10.0), 97111A x HBL 11 (9.73) and HHB 67 (9.67) exhibited maximum score for rancidity alongwith high total phenols, C-glycosylflavones and peroxidase activity. But variable expression was observed for fat content, fat acidity, free faty acid and peroxide value in relation to rancidity. Therefore, it was revealed that the total phenols, C-glycosylflavones and peroxides activity were responsible for rancidity.

542. YADAV, A. K., M. S. NARWAL AND RAJESH KUMAR ARYA 2010. STABILITY STUDIES FOR SEEDLING TRAITS WITH SUPRA-OPTIMAL TEMPERATURE EXPOSURE IN PEARL MILLET (PENNISETUM GLAUCUM) Forage Res., 36 (2) : pp. 65-70. Department of Plant Breeding (Bajra Section), CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The supra-optimal temperatures at seedling stage in pearl millet are known to be the most important cause of poor crop stands at farmers' field which can only be managed through developing high temperature tolerant stable pearl millet varieties. Identification of the superior and stable parents for supra-optimal temperatures tolerance is essential for effective manipulation through breeding. The most profound effect of high temperature has been well documented on early growth stages of pearl millet. Indeed, development of varieties showing wide adaptability has received increasing attention in recent years. In this experiment, the stability effect of the genotypes was studied for seedling traits under supra-optimal temperature conditions. Ten parents alongwith 45 hybrids were tested for stability for germination, emergence rate, number of leaves/seedling, seedling height, fresh weight/seedling and dry weight/seedling. The simultaneous examination of three stability parameters i. e. mean, linear regression and S^2_{di} revealed that F_1 hybrid H77/29-2 \times Togo-II was found stable for most of the characters viz., germination, emergence rate, seedling fresh weight and seedling dry weight. The cross combination $H77/833-2 \times 1305$ exhibited stability for emergence rate (ER), number of leaves/seedling and seedling height, whereas H77/29-2 \times 1305 was stable for number of leaves/seedling and seedling height only. The parent CVJ-2-5-3-1-3 showed the highest mean performance as well as response to environmental changes and high stability for seed germination, whereas (77/371× BSECT CP-1) had the highest mean value for emergence rate (ER) and appeared to be the stable genotype. Both the genotypes were also tolerant to heat stress and also the good general combiners.

543. PATEL, M. A., J. P. YADAVENDRA, J. A. SHAIKH, D. H. PATELAND N. V. UPADHYAY 2010. STABILITY ANALYSIS FOR GREEN FODDER YIELD IN PEARL MILLET [PENNISETUM GLAUCUM (L.) R. BR.]. Forage Res., 36 (3) : pp. 150-153. Medicinal and Aromatic Plants Project, Anand Agricultural University, Anand-388 110 (Gujarat), India

The present study was carried out at Anand Agricultural University, Anand to identify stable genotypes that could perform more or less uniformly under different environmental conditions for various economic traits. This study included 40 hybrids with their 14 parents. These genotypes were evaluated in three different environments viz., 15th June, 2004 (E_1), 15th July, 2004 (E_2) and 15th August, 2004 (E_3). The mean sum of squares due to genotypes were highly significant for days to 50 per cent flowering, plant height, leaves per plant, leaf length, leaf width, stem diameter, internodal length, green forage yield per plant, crude protein content and crude protein yield per plant except tillers per plant, leaf : stem ratio and dry matter content indicated the presence of substantial variation in the material studied. For green forage yield per plant, Top cross (TC) hybrids 5054A x IP 22269, PN₆A x IP 22269 and L111 A x Giant *Bajra* were identified as stable with wider adaptability over environments. These hybrids were concluded as stable hybrids.

544. ARYA, R. K., H. P. YADAV, A. K. YADAV AND M. K. SINGH 2010. EFFECT OF ENVIRONMENT ON YIELD AND ITS CONTRIBUTING TRAITS IN PEARL MILLET. Forage Res., 36 (3) : pp. 176-180. Department of Plant Breeding (Bajra Section), CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Sixteen white and 16 grey grain colour hybrids of pearl millet alongwith check HHB 94 were evaluated under four environments to determine the effect of environment on yield and its contributing traits in pearl millet. Data were recorded for five yield related characters viz., days to 50 per cent flowering, plant height (cm), effective tillers/plant, ear weight (g/plant), grain yield (g/plant) and dry fodder yield (g/plant). In the present study, it was found that unfavourable environment at early stages of growth and development, effects were more dangerous than the later stages. Any kind of stress at early stages of plant growth reduced the number of tillering drastically and also provided stimulus to the plant for early flowering, resulting in reduction in plant's normal size which ultimately produced small earhead thus drastic reduction in grain yield alongwith fodder yield was noticed. However, highly favourable environmental conditions prevailing during early growth period which stimulated plant for profused tillering and more speedy plant growth delayed the flowering and more accumulation of biomass due to long life span of the plant. If favourable conditions also continue during the grain filling period, it will produce maximum yield both grain as well as fodder. But, if unfavourable conditions operate during grain filling period than there will be reduction in grain size and weight which results in reduction in grain yield.

545. ARYA, R. K., H. P. YADAV, Y. P. YADAV AND S. K. PAHUJA 2011. STUDIES ON HETEROSIS AMONG WHITE GRAIN COLOUR HYBRIDS OF PEARL MILLET. Forage Res., 36 (4) : pp. 197-199. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Fifteen white grain colour hybrids developed and evaluated for their standard heterosis over existing check hybrid HHB 94 for grain yield as well as for dry fodder yield at four different environments in CCS Haryana Agricultural University. Out of the 15 hybrids, only six hybrids for grain yield and only five hybrids for dry fodder exhibited the positive standard heterosis. Only four hybrids viz., HMS 36A x 1250, ICMA 94222 x ICR 161, HMS 36 A x 99 and ICMA 94222 x 98/711 revealed the high positive standard heterosis for both grain yield as well as for dry fodder yield under all the four test environments as well as over the environments. Therefore, these hybrids could be commercialized after further testing over time and space.

4. Berseem

546. ROY, A. K., DEVENDRA RAM MALAVIYA AND PANKAJ KAUSHAL 2002. CORRELATION COEFFICIENTS OF VARIOUS YIELD ATTRIBUTES AND THEIR HOMOGENEITY OVER A SERIES OF CUTS IN EGYPTIAN CLOVER. Forage Res., 28 (1): pp. 19-23. Division of Crop Improvement, Indian Grassland and Fodder Research Institute, Jhansi-284 003, India

Egyptian clover, a multicut fodder, is grown in India as a winter annual from November to April. Homogeneity test was conducted using z-transformation in correlation coefficient of various yield attributes during regeneration after successive cuts in nine diploid and six tetraploid lines. Morphological characters and yield were found to vary in regenerated plants after cuts probably because of differential response of genes with changing climate. Correlation coefficients of yield attributes after each cut were analysed to test their consistency over subsequent cuts. Some character correlations like plant height-stem diameter, stem diameter-number of nodes, stem diameter-leaf length and GFY-DMY were stable over the cuts in 4x lines, whereas plant height-GFY, plant height-DMY and GFY-DMY were stable in 2x lines. Path analysis revealed that plant height to have maximum direct contribution towards DMY in all cuts of 2x lines, while the same had maximum contribution only in 1st and 2nd cuts in 4x lines.

547. SINGH, GAJRAJ, O. P. S. RANA AND RAM AVTAR 2005. SOLE AND COMBINED EFFECTS OF EMS AND GAMMA RAYS ON GERMINATION AND SEEDLING TRAITS IN BERSEEM. Forage Res., 30 (4) : pp. 173-175. Department of Genetics, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Dry seeds of berseem variety Mescavi were treated with different doses of EMS, gamma rays and their combined treatments. Effects on germination percentage, root and shoot length, its ratio and mitotic index were studied. A concentration of 1.5 per cent EMS was found totally lethal. Germination percentage decreased with higher doses of both EMS and gamma rays. Effect was more drastic and steep by EMS than gamma rays for all the traits observed. There is possibility to create more genetic variability by EMS alongwith gamma rays.

548. AVATAR, R., USHA DALAL, S. K. PAHUJA AND B. S. JHORAR 2007. EFFECTS OF PHYSICALAND CHEMICAL MUTAGENS ON SEED GERMINATION, PLANT SURVIVALAND SEED FERTILITY IN BERSEEM. Forage Res., 33 (1): pp. 61-62. Forage Section, Department of plant Breeding, CCSHAU, Hisar-125004.

Different doses of physical and chemical mutagens caused significant reduction in all the three M1 parameters studied which indicated that mutagenesis was quite effective and it would further help in berseem breeding programmes by identifying plants with maximum genetic damage that are likely to exhibit micro-mutations in later generations with higher frequency.

549. AVTAR, R., B. S. JHORAR AND USHA DALAL 2007. GENETIC VARIABILITY AND TRAIT ASSOCIATION IN EXOTIC AND INDIGENOUS LINES OF BERSEEM GERMPLASM. *Forage Res.*, 33 (2): pp. 87-90. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Berseem germplasm comprising 221 indigenous and 27 exotic accessions was evaluated for 10 different traits of economic importance including green fodder yield. A wide range of variation was observed for different traits studied in the genetic stock. Estimates of GCV and PCV were highest for tillers/plant. High heritability coupled with high genetic advance was recorded for plant height, leaf breadth, green stem weight/plant and stem girth. Many accessions in the germplasm registered their superiority for more than two traits. Based upon correlation and path analysis, plant height, tillers/plant and leaves/plant were observed to be the main components of green fodder yield which should be taken into account in berseem breeding programmes aimed at higher fodder yields.

550. DALAL, USHA, O. P. S. RANA AND R. AVTAR 2007. MUTAGENIC AND TEMPERATURE EFFECTS ON SEED GERMINATION AND MITOTIC INDEX IN BERSEEM. *Forage Res.*, 33 (2) : pp. 98-100. Department of Genetics, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

One hundred seeds in triplicate of berseem variety Mescavi were got treated with three doses (50, 70 and 100 kR) of gamma rays and three doses (0.1, 0.3 and 0.6%) of DES, MMS and SA at three different treatment temperatures i. e. 0°, 18° and 35°C to study the effect on seed germination and mitotic index values. Both mutagenic doses and treatment temperatures had significant effects on both seed germination and mitotic index. Estimates of both the parameters were found to be highest at lowest doses which decreased further with the increasing doses of the mutagens. Treatment temperature also affected invariably both the parameters studied.

551. DALAL, USHA, O. P. S. RANAAND R. AVTAR 2007. MUTATION EFFECTS ON SEED GERMINATION, PLANT SURVIVALAND SEED FERTILITY IN EGYPTIAN CLOVER. Forage Res., 33 (3): pp. 188-189. Department of Genetics, CCSHAU, Hisar.

The different doses of physical and chemical mutagens caused significant reduction in all the three M1 parameters stuidied which indicate that mutagenesis was quite effective and it would further help in berseem breeding programmes by identifying plants with maximum genetic damage that are likely to exhibit micro-mutations in later generations with higher frequency.

552. BAKHEIT, BAHY R., MERVAT M. HASHAD AND TALAAT A. AHMED 2008. ASSESSMENT OF GENETIC RELATIONSHIP BETWEEN A NEW MULTIFOLIATE STRAIN AND SEVEN EGYPTIAN COMMERCIAL CULTIVARS OF BERSEEM CLOVER AS REVEALED BY PROTEIN AND RAPD MARKERS. Forage Res., 34 (1): pp. 1-8. Agronomy Department, Faculty of Agriculture, Assiut University, Egypt

A multicut multifoliate strain was developed by transferring the multifoliate gene (s) from a mutant of monocut Fahl cultivar to the multicut trifoliate cultivar Mescavi by crossing between them, followed by 12 generations of selection. The new multifoliate strain was subjected to field evaluation with seven Egyptian commercial cultivars (Serw 1, Giza 6, Sakha 3, Sakha 4, Gemmiza, Fahl and Helaly) for the two seasons of 2003-04 and 2004-05. The multifoliate strain gave significantly higher fresh and dry forage yield than all other commercial cultivars except Gemmiza and monocut Fahl cultivars in the first cut. In addition, the multifoliate strain gave significantly higher protein yield than all other commercial cultivars except Fahl. Protein and RAPD markers were used to identify and assess the phylogenetic relationship between the new mulifoliate strain and the other Egyptian commercial cultivars. A total of 31 protein bands were generated from the new multifoliate strain including five polymorphic bands. Seven protein bands disappeared in the new strain, while they appeared at least in one or more of the commercial cultivars. Analysis of relationship revealed genetic diversity between the new multifoliate strain and other commercial cultivars. The protein cluster showed three main cluster groups, while the new multifoliate strain took an independent position. The new multifoliate strain was very distinct and unique from all other commercial cultivars. Five primers amplified a total of 13 DNA bands from the new multifoliate strain. Four of these bands were unique DNA fragments of 402.35 bp in B7 primer, 505.45 and 610.47 bp in A 12 primer, and 708.30 bp in C 10 primer generated only from the new multifoliate strain, and thus they can be used as fingerprints to characterize and discriminate the new multifoliate strain among berseem clover genotypes.

553. LOHAN, SHIV K. AND O. S. DAHIYA 2008. **IMPROVEMENT IN BERSEEM SEED QUALITY THROUGH PROCESSING.** *Forage Res.*, 34 (2) : pp. 97-100. Department of Seed Science and Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana) India

Raw breeder seed of berseem was processed with various processing steps viz., cleaning, grading and separation. Seed quality parameters i.e. physical purity, 1000-seed mass (g), germination (%), seed vigour, seed

recovery (%) and seed rejection (%) were observed before and after each step of processing. After completing the processing, 83.59 per cent seed recovery and 16.41 per cent seed rejection was observed. Simultaneously, the quality of recovered seed lot was improved in respect of physical purity (15%), seed mass (16%), standard germination (70%) and seed vigour (133%) over the raw seed. The gravity separator was found most effective for enhancing the viability, vigour and seed mass, however, more increase in physical purity was observed after cleaning by precleaner. The cost of processing was calculated as Rs. 485/q.

554. DALAL, USHA, R. AVTAR, O.P.S. RANA AND GAJRAJ SINGH 2009. FREQUENCY AND SPECTRUM OF INDICED MACROMUTATIONS AND MUTAGENIC EFFECTIVENESS AND EFFICIENCY IN BERSEEM (TRIFOLIUM ALEXANDERINUM L.). Forage Res., 34 (4) : pp.208-211. Department of Genetics, CCS Haryana Agricultural University, Hisar-125004 (Haryana),India

Seeds of berseem variety Mescavi were got treated with three doses (50, 70 and 100 kR) of gamma rays and three doses (0.1, 0.3 and 0.6%) each of methyl methane sulphonate (MMS), diethyl sulphonate (DES) and sodium azide (SA) to study the frequency and spectrum of induced morphological was found to be highest with MMS (3.60%) followed by SA (3.25%), DES (2.53%) and gamma rays for chemical mutagens medium dose (0.3%) induced maximum frequency of such macromutants. Among the spectrum, leaf types appeared more frequently (62.75%) than other types of mutations. Mutagenic effectiveness was found maximum at lowest dose (0.1%) of chemical mutagens but in case of gamma rays medium dose (70 kR) was observed to be most effective. Order of both mutagenic effectiveness and efficiency was SA>MMS>DES>gamma rays.

555. DALAL, USHA AND RAM AVTAR 2011. **MUTAGENIC AND TEMPERATURE EFFECTS ON ROOT AND SHOOT LENGTH IN BERSEEM** *Forage Res.*, 36 (4) : pp. 236-238. Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

One hundred seeds in triplicate of berseem variety Mescavi were treated with 50, 70 and 100 kR doses of gamma rays and 0.1, 0.3 and 0.6% doses of chemical mutagens (DES, MMS and SA) at three different temperatures (0°, 18° and 35°) to study the effect of these mutagens on both root and shoot length. A dose dependent relationship of all the mutagens on both the parameters was recorded. Longest root and shoot lengths at all the three temperatures were observed with lowest doses of all the mutagens used and these decreased further with increasing doses. The treatment temperatures had invariable effects on both root and shoot lengths.

5. Guar

556. PATEL, B. V. AND F. P. CHAUDHARI 2001. COMPONENT ANALYSIS OF YIELD IN CLUSTERBEAN. *Forage Res.*, 27 (2) : pp. 123-126. Department of Plant Breeding & Genetics, Gujarat Agricultural University, Sardar Krushinagar-385 506, India.

A set of 40 clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] genotypes of diverse geographic origin was evaluated for 11 morphological traits. Correlation study revealed that in general the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Grain yield per plant was found to be positively and significantly associated with all characters except gum content and pod length. Number of seeds per pod, number of pods per plant and pod length were the most important component characters which directly contributed to seed yield. It is suggested that selection based on number of seeds per pod, and number of pods per plant is likely to be useful for improvement in the grain yield of clusterbean.

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557. SINGH, J. V., ANITA PUNIA, SUBHASH CHANDER AND VIVEK GUPTA 2002. CHARACTERIZATION AND EVALUATION OF CLUSTERBEAN [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.] GERMPLASM. Forage Res., 28 (3): pp. 130-133. Forage Research Section, CCS Haryana Agricultural University, Hisar-125 004, India

One hundred and sixty-six germplasm accessions of clusterbean were evaluated for yield and its contributing characters to study the extent of variation in different quantitative characters. Coefficient of variation was high for branches per plant, yield per plant, pods per plant and plant height. Promising germplasm lines were identified for different economic traits for use in future breeding programme.

558. SETH, RAKESH AND CH. PADMAVATHI 2003. EXPRESSION OF SEED VIGOUR AND HARD SEEDEDNESS IN RELATION TO SEED COAT COLOUR IN FODDER CLUSTERBEAN [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.] CULTIVARS. Forage Res., 28 (4) : pp. 185-189. Division of Seed Technology, Indian Grassland and Fodder Research Institute, Jhansi-284 003 (U. P.), India.

Seed quality alongwith the expression of seed vigour and hard seededness in relation to seed coat colour were monitored in three cultivars of fodder clusterbean viz., Bundel Guar-1, 2 and 3. The harvested seeds (after seven months storage) were stratified in three seed coat colour categories viz., (i) whitish grey (ii) greyish black and (iii) ungraded (control). The results revealed that the seed quality in terms of germination, germination energy and vigour was better in whitish grey seed coat colour category as compared to the other two categories in all the three cultivars. However, atypical trends (contrary to the trends indicated by laboratory tests) were observed in field emergence. Maximum number of hard seeds was observed in greyish black category (cat. II), as against other two categories. The impacts and implications of these findings for quality seed production of clusterbean are discussed.

559. SINGH, J. V., ANITA PUNIA, P.P. GUPTA AND ASHOK YADAV 2004. STANDARDISATION OF DNA EXTRACTION IN GUAR (CYAMOPSIS TETRAGONOLOBA) FOR MOLECULAR MARKER ANALYSIS. Forage Res., 30 (1): pp. 59 Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Standardisation of DNA extraction in guar (*Cyamopsis tetragonoloba*) for molecular marker analysis was done at CCSHAU, Hisar. It was observed that Phenol chloroform extraction method is better compared to CTAB for guar.

 560. SINGH, J. V., Y. KUMAR AND SUDHIR SHARMA 2004. INTERRELATION BETWEEN YIELD AND ITS COMPONENTS IN CLUSTERBEAN (CYAMOPSIS TETRAGONOLOBA(L.)TAUB.). Forage Res., 30 (1): pp. 60-61 Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Interrelation between yield and its components in 42 lines of clusterbean was studied at CCSHAU, Hisar. Possitive correlation between number of pods/plant and seed yield was mainly due to positive direct effect of pods/ plant.

561. SAINI, M. L., PUNEET JAIN AND J. V. SINGH 2004. GENETIC DIVERSITY IN A GERMPLASM COLLECTION OF GUAR [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.]. Forage Res., 30 (2) : pp. 92-95. CCSHAU Regional Research Station, Bawal-123 501, Rewari (Haryana), India

Classification studies in germplasm collections lead to proper management and utilization of genetic stocks. Two hundred and twenty-seven genotypes of guar [*Cyamopsis tetragonoloba* (L.) Taub.] were assessed for genetic divergence using Mahalanobis D^2 technique. The germplasm lines exhibited wide genetic diversity for all the 15 characters investigated. With the help of multi-variate analysis strains were grouped in 10 clusters. Cluster I consisted of maximum number of genotypes (97) followed by 38 genotypes in cluster II, 31 in cluster III, 30 in cluster VI, 13 in cluster IV, 10 in cluster V, 5 in cluster VIII and clusters VII, IX and X had one genotype each. The inter-cluster distance between clusters I and VII was the highest, whereas the intra-cluster distance was maximum in cluster III. The genotypes belonging to these clusters may be useful in multiple breeding programme to recover transgressive segregants with the desirable combinations of yield components.

562. SEKHAWAT, S. S. AND D. L. SINGHANIA 2004. PHENOTYPIC STABILITY OF SEED YIELD AND QUALITY TRAITS IN CLUSTERBEAN. *Forage Res.*, 30 (2) : pp. 101-103 RAU SKN College of Agriculture, Jobner(Raj.).

Phenotypic stability of seed yield and quality traits in clusterbean was studied at RAU SKN College of Agriculture, Jobner(Raj.). RGC-1010 and rgc-1018 were identified as stable genotypes having high seed yield potential.

563. SAHARAN, M. S., G. S. SAHARAN AND J. V. SINGH 2004. INHERITANCE OF BRANCHING BEHAVIOUR IN CLUSTERBEAN [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.] Forage Res., 30 (2): pp. 107-108. IGFRI, Jhansi (U. P.), India

Inheritance of branching behaviour in clusterbean [Cyamopsis tetragonoloba (L.) Taub.] was done at IGFRI, Jhansi. It was observed that single dominant gene was responsible for branched character.

564. SHEKHAWAT, S. S. AND D. L. SINGHANIA 2005. CORRELATION AND PATH ANALYSIS IN CLUSTERBEAN. Forage Res., 30 (4): pp. 196-199. Department of Plant Breeding & Genetics, RAU Agricultural Research Station, Durgapura-302 018, Jaipur (Rajasthan), India

Clusterbean, popularly known as guar, is an important **kharif** legume crop of the semi-arid and arid regions. The experimental material consisted of 50 clusterbean genotypes of diverse geographic origin. Correlation study revealed that in general the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Seed yield per plant showed significant and positive correlation with all the characters studied except days to 50 per cent flowering, days to maturity and plant height. The path coefficient analysis at genotypic level showed that days to maturity, branches/plant, clusters/plant, pods/cluster, pods/plant, gum content, 100-seed weight and plant height had direct positive effect on seed yield. It is suggested that in semi-arid tract selection based on days to maturity, branches/plant, clusters/plant, pods/cluster, gum content and 100-seed weight is likely to be useful for improvement in the seed yield of clusterbean.

565. SAINI, M. L., PUNEET JAIN AND J. V. SINGH 2006. GENETIC DIVERGENCE IN CLUSTERBEAN [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.]. Forage Res., 32 (2) : pp. 89-92. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India.

Two hundred and eleven genotypes of guar [*Cyamopsis tetragonoloba* (L.) Taub.] were assessed for genetic divergence using Mahalanobis D² technique. The germplasm lines exhibited wide genetic diversity for all the 15 characters studied. Based on D²-values, 211 genotypes of guar were grouped into 10 clusters. Maximum number of genotypes was grouped in cluster I (45) followed by clusters II (42), III (30), IV (27), V (23), VI (15), VII (14), VIII (10) and IX (4). There was only one genotype in cluster X. The maximum inter-cluster distance was observed between the clusters I and IX, whereas cluster IX exhibited maximum intra-cluster distance. Crossing between their lines may result in the development of useful progenies.
566. LOHAN, SHIV K. AND SURJEET JAIN 2007. IMPROVEMENT IN COLOUR PURITY AND SEED QUALITY OF CLUSTERBEAN SEED LOT BY DIGITAL COLOUR SORTER. Forage Res., 33 (2): pp. 91-94. Department of Seed Science and Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India.

The study was conducted to sort out the off coloured seed from the clusterbean seed lot by digital colour sorter for improving the colour purity as well as seed quality. The seeds were sorted out at different intensity of black colour (55, 60, 65, 70, 75, 80, 85 and 90) adjustments of digital colour sorter. Seed quality was assessed through germination test, seed vigour index and electrical conductivity to compare the difference in accepted good white and rejected poor off coloured black seed. It was observed that the maximum rejection of black coloured seed by digital colour sorter was 94 per cent. About 6 per cent of white good seed went in the rejection lot alongwith the black seed and about 8 per cent of black seed remained in good accepted seed lot at black colour intensity of 75. The white fraction resulted in significantly higher germination and vigour than the black coloured seed, therefore, the seeds with off coloured seed coats were found of poor quality. Little difference in electrical conductivity was observed in white and off coloured seed.

6. Cowpea

567. VISWANATHA, K. P., M. K. JAYASHREEAND P. ARUNACHALAM 2001. HETEROSIS AND INBREEDING DEPRESSION IN PHYSIOLOGICAL TRAITS OF COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 27 (2) : pp. 83-86. AICRP on Arid Legumes, GKVK, University of Agricultural Sciences, Bangalore-560 065 (Karnataka), India

Heterosis and inbreeding depression were estimated for seed yield and physiological traits in three intervarietal crosses of cowpea. The characters under study exhibited significant heterosis over mid parent and better parent either in positive or negative magnitude. In general, crosses showed high heterosis, where also exhibited high inbreeding depression for most of the characters with some exceptions. Such a close relationship between heterosis and inbreeding depression would reveal predominance of non-additive gene action in cowpea.

568. RAMESH KUMAR, R. S. SANGWAN AND V. P. SINGH 2001. CORRELATIONS AND PATHANALYSIS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 27 (1) : pp. 25-28. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Correlations and path analysis were studied for grain yield and its related eight traits in 72 diverse genotypes of cowpea. Genotypic correlations were higher than their corresponding phenotypic correlations. The grain yield per plant was positively correlated with all the traits except days to maturity and seeds per pod. 100-seed weight had the maximum direct and indirect effect on grain yield of cowpea. Most of the component traits had positive association among themselves and with grain yield of cowpea.

569. VISWANATHA, K. P. AND M. K. JAYASHREE 2001. INHERITANCE OF THREE QUALITATIVE CHARACTERS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 27 (1): pp. 11-14. AICRP on Arid Legumes, University of Agricultural Sciences, G. K. V. K. Farm, Bangalore-560 065 (Karnataka), India

Inheritance of three qualitative characters viz., flower colour, presence or absence of tendril and growth habit was studied in cowpea cross (PS 42 x CO-1). Two to three genes were found to control the inheritance of the characters under investigation. Pleiotropy and differential expression were noticed between genes controlling tendril and growth habit.

570. DAHIYA, O. S., R. C. PUNIA, R. S. SANGWAN, V. P. SANGWAN AND C. RAM. 2001. SEEDLING VIGOUR AND ITS ASSOCIATED CHARACTERS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.] GENOTYPES. Forage Res., 27 (2) : pp. 127-130. Seed Technology Center, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

An experiment was conducted on nine genotypes of cowpea to assess the seed quality by various laboratory and field vigour parameters. Simple correlations between various vigour parameters showed that seedling establishment was significantly and positively associated with standard germination (%), respiration rate (ulo_2 /seed/h), accelerated ageing, vigour index-I and vigour index-II. Therefore, a combination of these vigour tests would serve as a reliable predictor of seedling vigour and seedling establishment in the laboratory as well as in the field.

571. DAHIYA, O. S., R. C. PUNIA, D. P. DESWAL AND R. P. S. KHARB 2001. PREDICTION OF GERMINABILITY OF COWPEA SEED LOTS-A BIOCHEMICAL CRITERIA. Forage Res., 27 (3): pp. 213-216. Seed Technology Centre, CCS Haryana Agricultural University, Hisar-125 004, India

Nine cowpea [*Vigna unguiculata* (L.) Walp.] genotypes were taken for conducting the biochemical study in the laboratory. The results revealed that standard germination had significant association with tetrazolium test and dehydrogenase activity but negative and significant association with electrical conductivity test. It was concluded that these biochemical tests in the laboratory would be an effective means of predicting standard germination. The combination of these three tests could predict standard germination to a reliable level (R^2 =0.99). The importance and implications of these tests have been discussed in relation to seed testing and marketing.

572. SINGH, M. K. AND J. S. VERMA 2002. VARIATION AND CHARACTER ASSOCIATION FOR CERTAIN QUANTITATIVE TRAITS IN COWPEA GERMPLASM. Forage Res., 27 (4): pp. 251-254. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture & Technology, Pantnagar-263 145 (U. P.), India

A total of 600 cowpea germplasm lines were evaluated in augmented randomized block design. A wide spectrum of variability was observed for all the characteristics except for days to maturity and number of seeds per pod which exhibited moderate variability. Seed yield, plant height, 100-seed weight and pods per peduncle showed high coefficient of variation ranging from 20 to 25 per cent. Seed yield showed positive correlation with 100-seed weight and pod length. While positive association of 100-seed weight with pod length and plant height revealed that taller plants, in general, had longer pods with bold seeds resulting in higher seed yield. The negative correlation of number of pods per peduncle with 100-seed weight and seed yield indicated that high yielding genotypes had longer pods and higher test weight yet with less number of pods per peduncle. Negative association of 100-seed weight with days to 50 per cent flowering and maturity revealed that in early flowering genotypes dry matter accumulation in seed was at a faster rate than in late flowering genotypes. Several promising donors were identified.

573. SANGWAN, R. S. AND G. P. LODHI 2002. HETEROSIS AND INBREEDING DEPRESSION IN FODDER COWPEA Forage Res., 28 (1): pp. 35-37. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Heterosis and inbreeding depression for six characters in five crosses of cowpea [*Vigna unguiculata* (L.) Walp.] were studied. Maximum heterosis over mid parent and better parent was observed for green fodder yield (GFY) and dry matter yield (DMY), whereas it was lowest for leaf length and leaf breadth. Inbreeding depression in F_2 generation was observed in most of the crosses. Two crosses, namely, CS 39 x GC 2 and HFC 42-1 x GC 2 were found most promising as these had high heterosis and less inbreeding depression for GFY and DMY per plant.

574. SANGWAN, R. S. V. P. SANGWAN AND R. N. ARORA 2003. PHENOTYPIC STABILITY FOR GRAIN YIELD IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. *Forage Res.*, 29 (2): pp. 105. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Phenotypic stability for grain yield of 21 cowpea genotypes was carried out at CCSHAU, Hisar. The genotypes, HC 98-52, HC98-30, HC 98-60 and HC 98-45 gave high grain yield, above average response and were stable also.

575. SAGWAN, V. P. AND R. S. SANGWAN 2003. HETEROSIS AND INBREEDING DEPRESSION IN FODDER COWPEA. Forage Res., 29 (3) : pp. 107-109. CCSHAU, Hisar

An experiment was conducted at CCSHAU, Hisar to study the heterosis and inbreeding depression in five crosses of fodder cowpea. On the basis of high heterosis and low depression for green fodder and dry matter yield, the crosses, CS 39 X GC 2 and HFC 42-1 X GC 2 appeared to be most promising.

576. KAVITA, R., R. S. KHATRI, R. S. SAGWAN AND ATTAR SINGH 2004. STABILITY ANALYSIS FOR PODS PER PLANT IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 29 (4) : pp. 212-213. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Stability analysis for pods per plant in cowpea was conducted at Hisar. Five genotypes HC 98-40, TC 99-1, HC 99-33, GC9210 and HC 98-50 can be used as a stable source for number of pods per plant in future cowpea breeding programme.

577. BHARDWAJ, B. L. AND THOUNAJAM RAJEN SINGH 2004. GENOTYPE X ENVIRONMENT INTERACTION FOR FODDER YIELD AND ITS COMPONENTS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 30 (1) : pp. 1-2. Department of Plant Breeding,Punjab Agricultural University, Ludhiana-141 004 (Punjab), India

Thirty-four genotypes of cowpea were evaluated under six dates of sowing starting from March to July. In general, genotypic variance was predominant for stem girth, plant height, leaf weight, green fodder yield and number of branches. Genotype x environment interaction was important for all the characters studied indicating the importance of testing in large number of environments. Heritability estimates were high for plant height and stem girth and were comparatively low for other characters.

578. RADHIKA, V. S., D. I. SUMA BAI AND P. SARASWATHI 2004. **COMBINING ABILITY AND GENE ACTION IN FODDER COWPEA.** *Forage Res.*, **30** (3) : pp. 134-136. Department of Plant Breeding & Genetics, College of Agriculture, Vellayani, Thiruvananathapuram-695 522, India

Combining ability analysis was done in fodder cowpea for 10 yield and quantitative traits including crude protein content, calcium and phosphorus contents. Predominance of sca variance was observed in all characters except number of primary branches per plant. The lines IFC 8401 and IFC 95102 were good general combiners for fodder yield. The crosses HES 82 x EC 241044 and EC 241021 x UPC 953 exhibited superior values for most of the characters.

 579. SAINI, M. L., PUNEET JAIN AND R. N. ARORA 2004. GENETIC DIVERGENCE STUDIES FOR QUANTITATIVE CHARACTERS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 30 (3): pp. 152-154. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

One hundred and fifty-five cowpea germplasm lines were evaluated for their genetic divergence by D^2 analysis for a set of eight quantitative characters. The D^2 -analysis revealed that gentoypes exhibited considerable

diversity and were grouped in 10 clusters. Cluster I exhibited maximum number of germplasm lines. Inter-cluster distance was maximum between clusters IV and X followed by clusters IX and X. Cluster IX recorded highest mean seed yield per plant, 100-seed weight and also the intra-cluster distance. The genotypes belonging to these clusters viz., GC 3 and DCP 10 may be useful in multiple breeding programme to recover transgressive segregants with the desirable combinations of yield components.

580. KUMARI, VINEETA, R. N. ARORAAND U. N. JOSHI 2005. GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR QUALITY TRAITS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 30 (4): pp. 200-202. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Fifty genotypes of cowpea grown during **kharif** 2001 under rainfed conditions at Dryland Research Area, CCS Haryana Agricultural University, Hisar were evaluated for tannin content, crude protein and *in vitro* protein digestibility. Results revealed that tannin content varied from 0.45 to 24.49 mg/g seed. It was interesting to note that the genotypes (HC 98-66 and GP 34) having black coloured seed had more tannin content as compared to the genotype (HC 98-45) having white coloured seed. Crude protein was maximum (27.57%) in genotype HC 98-64 and minimum (21.15%) in genotype TCM 77-4. The maximum *in vitro* protein digestibility (61.40%) was recorded in the genotype GC-3 and the minimum (45.00%) in the genotype CAZC-10. Substantial amount of variability for tannin content was present in the existing material, while it was meagre for protein and IVPD. High estimates of heritability coupled with high estimates of genetic advance were recorded for tannin content only. No significant association among the tannin content, crude protein and *in vitro* protein digestibility was observed. However, tannin and IVPD had negative direct effect and crude protein had positive direct effect on seed yield.

581. VERMA, J. S. AND M. M. MISHRA 2005. METROGLYPHAND INDEX SCORE ANALYSIS IN EXOTIC LINES OF COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 31 (1): pp. 45-47. Department of Genetics & Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263 145 (Uttaranchal), India

The present study was conducted to classify a collection of 39 exotic cowpea lines, introducted from IITA, Nigeria, into morphologically distinct complexes based on metroglyph and index score analysis. The clustering pattern recognized eight distinct broad groups particularly on the basis of number of pods/plant and seed yield/plant. The highest yielding group (cluster IV) contained two genotypes (IT 86D-715 and IT 89KD-374-57) with high values for pods/peduncle, dry matter/plant, reproductive phase, 100-seed weight, pods/plant and seed yield/plant. Within-group variations were generally low. The index score of five top-yielding genotypes revealed the importance of pods/plant, reproductive phase, dry matter/plant and 100-seed weight for yield improvement in cowpea.

582. KUMAR, D., V. P. SAGWAN AND R. N. ARORA 2005. GENETIC COMPONENTS OF VARIATION IN COWPEA. Forage Res., 31 (2): pp. 138-139. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana) India

Present study revealed average degree of dominance for days to 50 per cent flowering, days to maturity and seed yield/plant. The coefficient of inbreeding (F) value was positive and significant for pods/cluster indicating the presence of dominant genes. In majority of characters an excess of dominant genes was noticed.

583. AVTAR, R., R. YADAV AND S. K. PAHUJA 2005. PRINCIPAL FACTOR AND CLUSTER ANALYSES IN FODDER COWPEA GERMPLASM. Forage Res., 31 (4): pp. 221-227. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Principal factor and hierarchical cluster analyses were carried out with 87 accessions of fodder cowpea. The study was undertaken on 15 quantitative and eight qualitative traits which identified nine principal components

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explaining 76% variability altogether. Genotypes GPF 308, GPF 297, GPF 401, GPF 404 B, GPF 267, GPF 274, GPF 523 and GPF 289 were found to be better performers with regard to fodder yield and its component traits when all the principal factors were considered simultaneously. These genotypes can further be utilized in breeding programmes for improving fodder yield. Hierarchical cluster analysis (UPGMA with city block distances) classified these genotypes into 10 clusters having 1 to 41 genotypes. The results of principal factor analysis were corroborated with hierarchical cluster analysis with regard to grouping of genotypes.

584. JAIN, PUNEET, M. L. SAINI AND R. N. ARORA 2006. GENETIC DIVERGENCE IN COWPEA. Forage Res., 32 (1): pp. 12-14. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

One hundred and twenty-seven cowpea germplasm lines were grouped into 10 clusters on the basis of D^2 analysis. Cluster I exhibited maximum number of genotypes. Inter-cluster distance was maximum between clusters VIII and X followed by clusters IV and VIII. Intra-cluster distance was maximum in cluster VIII. The observed distances showed the genetic diversity among and within the clusters and clustering was useful to identify the diverse genotypes. Cluster IX registered the highest mean value for plant height (88.74 cm), seed yield per plant (35.69 g) and 100-seed weight (14.93 g). Divergent parents from various clusters can be used in hybridization programme to get transgressive recombinants for grain yield and its component traits.

585. MITTAL, V. P., B. L. BHARDWAJ AND MANOJ SRIVASTAVA 2006. CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS IN FORAGE COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 32 (1): pp. 57-59. Department of Plant Breeding, Genetics and Biotechnology, PAU, Ludhiana.

It was observed that forage yield in cowpea can be improved by selecting plants with greater stem diameter and length in the segregating populations of the cross studied at Department of Plant Breeding, Genetics and Biotechnology, PAU, Ludhiana.

586. DEEPAK KUMAR AND V. P. SAGWAN. 2006. COMBINING ABILITY ANALYSIS FOR GRAIN YIELD AND ITS COMPONENTS IN COWPEA.]. *Forage Res.*, 32 (1): pp. 59-60. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India.

The cross FS-68 x TC 99-1 exhibited significantly positive sca effect for seed yield/plant, cluster/plant also to some extent for seed yield. Hence, this cross could throw desirable recombinants in subsequent generations having high seed yield per plant.

587. VISWANATHA, K. P., H. O. BHUSHANA, L. N. YOGEESHAND K. DEVARAJU 2006. HETEROSIS STUDIES FOR YIELD AND YIELD ATTRIBUTING TRAITS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 32 (3) : pp. 148-151. AICRP on Arid Legumes, GKVK Farm, University of Agricultural Sciences, Bangalore - 560 065 (Karnataka), India

The utility of heterosis *per se* may not be of much use, but cross combinations showing excellent hybrid vigour can be used in developing high yielding pure lines in cowpea. The 36 F1 hybrids were produced and evaluated to know the extent of heterosis over mid parent and better parent for 10 quantative traits including seed yield. Hybrids exhibited significant heterosis in desired direction for days to 50 per cent flowering, number of primary branches, number of pods per plant, 100 seed weight, pod length, number of seeds per pod and seed yield per plant. The highest number of seeds per pod was observed in the hybrid TVX-944 x APC-1452. The two crosses KBC-1 x APC-714 and KBC-2 x APC-1452 exhibited high heterosis for seed yield. Four hybrids having high yielding ability compared to check were suggested for carrying them forward to advanced generations where in, the chance of getting homozygous selections for high yielding were high.

588. GIRISH, G., K. P. VISWANATHA AND L. N. YOGEESH 2006. CLUSTER ANALYSIS IN COWPEA GERMPLASM FOR SEED YIELD AND FORAGE YIELD. Forage Res., 32 (3): pp. 185-187. AICRP on Arid Legumes, GKVK Farm, University of Agricultural Sciences, Bangalore-560 065 (Karnataka), India

One hundred cowpea genotypes were evaluated for 11 quantitative characters to quantify the genetic diversity existed among them by using Mahalanois D2 statistics. The genotypes fell into 11 clusters. Among the 11 quantitative characters studied, fodder yield contributed highest (75.73%) towards the divergence followed by plant height (8.28%) and seed yield (6.3%). Cluster VI had minimum days to first flower opening and days to maturity, and also had maximum number of pods per plant, pod length, number of seeds per pod and seed yield. Cluster IX exhibited lowest means for seed yield, fodder yield, pod length, number of seeds per pod, primary branches and plant height. The genotypes from clusters VI and IX, which have high and low cluster means for majority of the characters are suggested as promising parents for hybridization.

589. SINGH J. AND B. L. BHARDWAJ 2007. GENOTYPE X ENVIRONMENT INTERACTION FOR FODDER YIELD AND COMPONENT CHARACTERS IN COWPEA. Forage Res., 33 (2): pp. 107-110. Department of Plant Breeding, Genetics and Biotechnology, Punjab Agricultural University, Ludhiana-141 004 (Punjab), India

Forty genotypes of cowpea were evaluated in six diverse environmental conditions comprising three different dates of sowing and two locations in Punjab during 2006. The pooled analysis of variance revealed significant differences among the genotypes and the testing environments and significant genotype by environment interaction for the characters such as plant height, number of branches, leaf stem ratio, green fodder yield, dry matter yield and crude protein content. The genotype x environment (linear) interaction was significant for all the characters except leaflet length and crude protein content. The pooled deviations were significant for all the characters. The genotypes FOS 1 and L 196 were found most stable in green fodder yield across the environment.

590. BHANDARI, M. S. AND J. S. VERMA 2007. GENETIC DIVERGENCE AND CORRELATION STUDIES IN FORAGE COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 33 (3) : pp. 133-138. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263 145 (Uttarakhand), India

Twenty advanced generation forage cowpea genotypes alongwith two released varieties were evaluated for genetic divergence and correlation analysis. Based on divergence analysis of pooled data, the 22 genotypes were grouped into seven clusters. Cluster 1 had maximum number of genotypes (10), clusters II and III had five and three genotypes, respectively. Maximum intra-cluster distance was in cluster III and maximum inter-cluster distance was between clusters V and VII. Crude protein content, dry matter digestibility, dry matter yield and number of leaves per plant were major contributors towards genetic divergence. Correlation analysis revealed that plant height, number of leaves per plant, leaf : stem ratio, crude protein content and dry matter digestibility had major contribution in determining quantity and quality of green and dry forage yield.

591. VIVEKANANDA, B. S., R. S. KHATRI AND J. V. SINGH 2007. VARIETAL IDENTIFICATION IN COWPEA USING MORPHOLOGICAL CHARACTERS Forage Res., 33 (3) : pp. 145-148. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The present investigation was carried out during **kharif** 2006 to characterize 22 cowpea genotypes on the basis of morphological traits. Varietal identification was carried out on different morphological traits viz., terminal leaflet shape, leaf surface, plant habit, stem colour, flower colour, immature pod colour, mature pod colour, seed shape, seed crowding and seed eye pattern. Flow chart for cowpea genotype identification on the basis of different morphological traits was also constructed. This study revealed that cowpea genotypes could safely be identified on a set of morphological traits.

592. SAHAY, G.A. CHANDRA, R. B. BHASKAR AND G. P. SHUKLA 2008. GENETIC RELATIONSHIP AMONG ELITE LINES OF COWPEA BASED ON ISOZYME AND RAPD MARKERS. *Forage Res.*, 33 (4) : pp. 193-198. Crop Improvement Division, Indian Grassland and Fodder Research Institute, Jhansi-284 003 (U. P.), India

Genetic relationships among elite lines of cowpea were assessed using four enzyme systems and 10 random oligonucleotide primers. Multimeric isozyme profile and polymorphic RAPD markers reflected presence of considerable amount of genetic variability among the genotypes. Keeping in view the need for developing varieties with early maturity, determinate growth habit and high yield, 22 selected genotypes with following characteristics i. e. 30-32 days to flowering, maturity 60-65 days, compact erect growth habit and root rot disease (*Rhizoctonia solani*) resistant and susceptible lines were used in the present investigation to assess their genetic relationships. This may be of great importance to initiate an effective breeding programme in future. Except superoxide dismutase (SOD), other three-isozyme systems, peroxidase (PRX), esterase (EST) and polyphenol oxidase (PPO) yielded polymorphic bands. The cluster analysis showed that genotypes could be grouped into three main clusters. The level of polymorphism observed with both RAPD and isozyme indicated diversity in genotypes for root rot resistance. RAPD analysis indicated that amongst the released varieties, Bundel lobia-1 was most distinct. Its similarity coefficients with Bundel lobia-2, Kohinoor and UPC-5286 were 79, 78 and 75 per cent, respectively.

593. BHANDARI, M. S. AND J. S. VERMA 2008. GENETIC ANALYSIS OF FORAGE YIELDAND QUALITY TRAITS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 33 (4) : pp. 203-205. Department of Genetics and Plant Breeding, G. B. Pant University of Agriculture and Technology, Pantnagar-263 145 (Uttarakhand), India

Twenty advanced generation cowpea lines alongwith two standard check varieties were evaluated for coefficient of variation, heritability and genetic advance estimation. Analysis of variance revealed adequate genetic variability among genotypes for most of the characters studied over the years. Based on pooled analysis, heritability estimates were high and coupled with high to moderate genetic advance for plant height, days to 50 per cent flowering, number of leaves per plant, crude protein content and green forage yield indicating predominance of additive gene effects for these characters.

 594. SAHAY, G, AMRESH CHANDRA, R. B. BHASKAR AND G. P. SHUKLA 2008. IDENTIFICATION OF PUTATIVE HYBRIDS OF COWPEA AND THEIR GENETIC EVALUATION. Forage Res., 34 (2) : pp. 73-78. Division of Crop Improvement, Indian Grassland and Fodder Research Institute, Jhansi-284 003 (M. P.), India

Putative hybrids have to be identified/confirmed before their further utilization. In the present study, RAPD markers have been employed for putative hybrid identification, IGFRI-95-1 parent was used as a repeating female parent, while IL-14, Local-1, Local-2, Local-3, RAJL-2 and RAJL-16 as male parent, respectively, in Line x Tester design. The six F_1 hybrids and seven parents of the above were used in the present study. A total of 727 DNA fragments were amplified by the 17 primers. Among them, there were 262 fragments polymorphic between the parents, and almost all the fragments observed in the hybrids established the hybridity. Altogether, male-specific fragments (U-01) and female-specific fragments (G-08) were identified and were all found to be present in the hybrid progeny also. On confirming the hybridity, the morphological data of F_1 hybrids and parents evaluation in RBD with two replications were analysed using INDOSTAT package software for genetic evaluation i. e. combining ability and heterosis. It was concluded that Local-2 x IGFRI-95-1, Local-3 x IGFRI-95-1 and IL-14 x IGFRI-95-1 could be selected as the best crosses amongst the six crosses evaluated. The above results conform to the similarity coefficient analysis.

595. MITTAL, V. P., PARAMJIT SINGH AND K. S. BRAR 2009. ASSOCIATION ANALYSIS FOR FORAGE YIELD COMPONENTS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.] Forage Res., 34(4) : pp.246-248. PAU Regional Research Station, Bathinda-151001.

A correlation and path coefficient analysis in forage cowpea indicated that dry matter yield as well as green fodder yield had significant positive association with stem length, primary branches per plant, leaflet length, and leaflet breadth. Significant positive association to the extent of 0.99 was observed between dry matter yield and green fodder yield indicting that moisture content did not differently influence different genotypes. High positive genotypic correlation of dry matter as well as green fodder yield was observed with primary branches per plant, leaflet length and leaflet breadth. Path analysis showed high positive direct contribution of stem length and leaflet breadth while indirect contribution of primary branches per plant and leaflet length.

596. MITTAL, V. P., K. S. BRAR AND PARAMJIT SINGH 2009. TRIPLE TEST CROSS ANALYSIS IN FORAGE COWPEA [VIGNA UNGUICULATA (L.) WALP]. Forage Res., 35 (1): pp. 20-22. PAU Regional Research Station, Bathinda-151 001 (Punjab), India

Triple test cross analysis in cowpea indicated the presence of epistasis in the inheritance of different forage characters. It was found that additive genetic variance was more important than dominance variance for stem diameter, stem length, leaflet length, leaflet breadth, green fodder yield and dry matter yield. For primary branches per plant and leaf : stem ratio, dominance variance was more important than additive variance. In view of preponderance of additive genetic variance for most of the characters, simple breeding procedures like single seed descent and bulk methods were suggested. It was cautioned that the estimates of only additive, dominance gene effects and formulating breeding procedures, presuming the absence of epistasis will be misleading.

597. MALHOTRA, SURUCHI, PUSHPA KHARB, K. S. BOORA AND SANTOSH DHILLON 2009. GENETIC DIVERSITY IN COWPEA [VIGNA UNGUICULATA (L.) WALP.] AS DETERMINED BY RAPD MARKERS. Forage Res., 35 (2): pp. 67-72. Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Randomly amplified polymorphic DNA (RAPD) markers were used to assess the genetic diversity among selected genotypes of *Vigna unguiculata*. Out of 35 RAPD primers tested, 14 allowed amplifications of random polymorphic (RAPD) loci. A total of 113 amplified products were obtained out of which 16 were monomorphic and 97 were polymorphic. Average polymorphism across 24 genotypes was found to be 79.87 per cent. For the genotypes tested, 2 to 14 bands were obtained, with an average of 8.007 bands per primer. Analysis of this polymorphism profile, generated by using suitable statistical programmes, grouped the 24 genotypes into two major clusters at a similarity coefficient of 0.50. Genotype DCP-15 was outgrouped and formed the 1st sub-cluster of major cluster. Genetic similarity matrices of the genotypes ranged from 0.3462 to 0.8681, indicating a high genetic variability among the genotypes. Genotypes CPD-90 and CPD-91 were genetically most similar with genetic similarity value of 0.8681 and so could not be distinguished by the dendrogram. Similarity value for all other genotypes varied between the two extreme values. The results indicated that RAPD markers were efficient for the identification of *V. unguiculata* genotypes and for the determination of genetic relationships among them. Fingerprint data obtained in this study can be further utilized in the identification and development of improved cowpea varieties.

598. MITTAL, V. P., PARAMJIT SINGH AND K. S. BRAR. 2009. ANALYSIS STUDIES ON GENE EFFECTS IN FORAGE COWPEA [VIGNA UNGUICULATA (L.) WALP]. Forage Res., 35 (3): pp. 143-146 PAU Regional Research Station, Bathinda-151 001 (Punjab), India

Analysis of mean values of seven generations in a varietal cross of cowpea indicated the presence of epistasis in the inheritance of different forage characters, revealing that estimation of only additive-dominance gene effects and formulating breeding procedures presuming the absence of epistasis will be misleading. Presence of

additive genetic variance for stem diameter, primary branches per plant, leaflet length, leaflet breadth and leaf : stem ratio and of additive x additive variance for stem length, leaflet length and leaflet breadth suggested that simple breeding procedures like single seed descent, bulk method, etc. which do not involve any progeny evaluation in early generations, should be fruitful in deriving high forage yielding lines from the cross studied.

599. MITTAL, V. P., PARAMJIT SINGH AND K. S. BRAR. 2010. GENETIC VARIATION IN FORAGE COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 35 (4) : pp. 206-208. PAU Regional Research Station, Bathinda-151 001 (Punjab), India

Genetic analysis of triple test cross in cowpea indicated the presence of epistasis in the inheritance of stem diameter, stem length, primary branches per plant, leaflet length and leaf : stem ratio. It was found that additive genetic variance was more important than dominance variance for stem diameter, stem length, leaflet breadth, leaf : stem ratio, green fodder yield and dry matter yield. For primary branches per plant and leaflet length, dominance variance was more important than additive variance. In view of preponderance of additive genetic variance for most of the characters, simple breeding procedures like single seed descent and bulk methods were suggested. It was concluded that the estimation of only additive, dominance components of variation and formulating breeding procedures, presuming the absence of epistasis will be misleading.

600. ARORA, R. N., B. S. JHORAR AND S. S. BISHT 2010. EVALUATION OF RELEASED CULTIVARS OF COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 35 (4) : pp. 219-222. Forage Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Evaluation for some morphological traits was carried out in 23 cultivars of cowpea released in India for various purposes. The results revealed that the magnitude of genotypic and phenotypic coefficients of variation was high for seed yield/plant, moderate for pods/plant, plant height and clusters/plant, while these were low for seeds/ pod, pod length, branches/plant, days to 50 per cent flowering and days to maturity. High heritability estimates accompanied with high genetic advance were observed for seed yield/plant, pods/plant, plant height, clusters/plant and days to maturity. The correlation and path coefficient analysis revealed that seed yield/plant had significantly positive association with number of pods/plant and number of clusters/plant, while it showed significantly negative association with days to 50 per cent flowering, days to maturity, plant height, number of branches/plant and pod length. The direct and indirect effect of nine characters on seed yield/plant indicated that number of seeds/pod and number of pods/plant followed by 100-seed weight had the maximum direct positive effect on seed yield/plant, while among the indirect effects, number of seeds/pod had the maximum effect via pod length, plant height, days to maturity and days to 50 per cent flowering, respectively. On the basis of these results it is suggested that selection based on number of seeds/pod which is having high positive direct effect as well as indirect effect on seed yield/plant may result in improvement of this trait in cowpea.

MITTAL, V. P., PARAMJIT SINGH, PRITPAL SINGH AND K. S. BRAR 2010. GENERATION MEANS ANALYSIS FOR FORAGE YIELD COMPONENTS IN COWPEA [VIGNA UNGUICULATA (L.) WALP.]. Forage Res., 36 (2): pp. 71-73. PAU Regional Research Station, Bathinda-151 001 (Punjab), India

Generation means analysis in a varietal cross of cowpea indicated the presence of epistasis in the inheritance of different forage characters. Besides digenic epistasis, higher order interactions were also detected revealing that estimation of only additive-dominance gene effects and formulating breeding procedures presuming the absence of epistasis will be misleading. Presence of additive genetic variance for leaflet length, leaflet breadth, green fodder as well as dry matter yield and of additivexadditive variance for stem diameter, stem length, primary branches per plant and leaflet breadth suggested that simple breeding procedures like single seed descent, bulk method, etc. which do not involve any progeny evaluation in early generations should be fruitful in deriving high forage yielding lines from the cross studied.

7. Maize

602. KATIYAR, P.K., SINGH, U.P. AND CHOUBEY, R.N. 2001. COLLECTING STAY GREEN MAIZE FROM CENTRAL UTTAR PREDESH REGION OF INDIA. *Forage res.*, 27 (3) : pp. 233-236.

The exploration trip was undertaken to collect stay green types of maize from Central U.P. part of India. In total 221 collections were made from selected sites viz., Etawah. Auraiya, Mainpuri, Kannauj and Kanpur. Sufficient genetic variability for almost all the traits was observed in the collected material.

603. JHA, P. B., D. N. SINGH AND J. GHOSH 2002. HETEROSIS AND GENE ACTION FOR FODDER YIEL IN MAIZE. Forage Res., 28 (1): pp. 49-51. RAU, Pusa, Samastipur (Bihar), India

In the present study, 30 crosses and 11parents were evaluated at RAU, Pusa, Samastipur (Bihar). Both additive and non-additive variances were present and standard heterosis was also high for GFY and DMY. It is therefore suggested that reciprocal recurrent selection, the improved population may be used as source of composite or hybrid varieties.

604. SHARMA, SUDHIR, M. S. NARWAL, RAKESH KUMAR AND SAIN DASS 2004. LINE X TESTER ANALYSIS IN MAIZE (ZEA MAYS L.). Forage Res., 30 (1): pp. 28-30. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The gene action and combining ability for important yield components in maize were analyzed through line x tester mating design involving 12 lines and five testers. This study revealed that both additive and non-additive gene effects were involved in the inheritance of grain yield and its component traits. The inbred line HKI 31 was the best general combiner followed by HKI 220 and HKI 430 for grain yield/plant. Hybrids HKI 76 x POP 590-5, HKI 620 x HKI 498 and HKI 620 x HKI 355 exhibited high sca effects for grain yield and also for days to maturity, plant height and cob length.

605. PATEL, D. A., G. C. JADEJA, D. B. PATEL AND J. S. PATEL 2004. HETEROSIS FOR FORAGE YIELD AND ITS COMPONENTS IN MAIZE x TEOSINTE HYBRIDS. Forage Res., 30 (3): pp. 145-148. Department of Agricultural Botany, Gujarat Agricultural University, Anand-388 110 (Gujarat), India

Forty-two F_1 hybrids derived from hybridization between four *Zea* species were evaluated with their parents for heterotic manifestation of fodder yield and its component characters. Good amount of heterosis was observed for dry matter yield, green fodder yield and stem girth. Relatively low magnitude of heterosis was recorded for number of leaves per plant. The range of heterosis for green fodder yield and dry matter yield was observed to be -51.74 to 47.91 and -48.22 to 48.66 per cent over better parent, respectively. Two crosses viz., *Zea mays* cv. IC-77101 x *Z. mexicana* and *Zea mays* cv. African tall x *Z. diploperennis* showed the maximum heterobeltiosis (BP) and high *per se* performance for green fodder yield, dry matter yield and most of the yield components. These crosses could be exploited in breeding programme in order to develop high fodder yielding varieties in maize.

606. MACWANA, SNEHA, J. P. YADVENDRA, S. K. DIXIT, J. S. PATEL AND R. S. PARMAR 2005. CLUSTERING OF GENOTYPES BASED ON GENOTYPE X ENVIRONMENT INTERACTION MEAN SQUARES IN FORAGE MAIZE (ZEA MAYS L.). Forage Res., 31 (2): pp. 88-90. Main Forage Research StationAnand Agricultural University, Anand-388 110 (Gujarat), India

To facilitate the interpretation of data from a genotype by environment (G x E) experiment when the G x E interaction is large the stability analysis is used (Eberhart and Russell, 1966). A cluster method is proposed to group genotypes according to their response to environments in which genotypes with similar intercepts and slopes

can be grouped into clusters. Forty-two forage maize genotypes were evaluated for three seasons. The genotype x environment interactions for green forage, dry matter yield and crude protein content were significant. Thus, these characters were subjected to clustering analysis based on G x E interaction mean squares. The genotypes belonging to a cluster will have no G x E interaction among them and they will not deviate from a common linear regression line and intercept. They will also have same response to environment. All 42 genotypes were clustered in nine groups for green fodder yield, five clusters for dry matter yield and eight clusters for crude protein content. Such information will be useful to breeders in selection of genotypes from different clusters.

607. SNEHA MACWANA, J. P. YADVENDRA AND J. S. PATEL 2005. CORRELATION AND PATHANALYSIS IN FORAGE MAIZE. Forage Res., 31 (2): pp. 140-141. Main Forage Restation Station, GAU, Anand-388110.

The present investigation revealed that the characters viz., plant height, leaf length and leaf width had high positive association with forage yield and also showed higher direct positive contribution in forage yield inforage maize.

608. AHMED, S., D. R. MALAVIYA AND A. B. MAJUMDAR 2010. **GENETIC DIVERGENCE AND VARIABILITY IN FODDER MAIZE.** *Forage Res.*, **35** (4) : pp. 223-226. Crop Improvement Division, Indian Grassland and Fodder Research Institute, Jhansi-284 003 (U. P.), India

Genetic diversity, clustering pattern and variability were studied in 10 lines of maize for fodder yield and contributing traits. Clustering pattern divided the lines into three different clusters. Cluster I occupied the eight lines and clusters II and III with one line each. On mean basis, cluster I was characterized for having prominent traits like plant height, number of leaves, days to 50 per cent flowering, leaf length, leaf breadth, dry matter and green fodder yield. Such clustering helps in selecting desirable lines and traits for future crossing programme. PCA revealed that informative components accounted for 93.70 per cent variance. Most of the important traits with higher weightings were days to 50 per cent flowering, plant height, leaf length and stem girth in PCI and days to 50 per cent flowering, dry matter and green fodder yield in PCII and days to 50 per cent flowering and dry matter in PCIII.

8. Ricebean

609. DESWAL, D. P., U. CHAND, B. S. DAHIYA AND R. P. S. KHARB 2002. PREDICTION OF FIELD EMERGENCE THROUGH SEED VIGOUR AND VIABILITY TESTS IN RICEBEAN. Forage Res., 27 (4): pp. 255-262. Department of Seed Science & Technology, CCS Haryana Agricultural University, Hisar-125 004, India

The association between the field emergence and different vigour and viability parameters was worked out. The tetrazolium test (Tz), accelerated ageing test (24 and 48 h), standard germination and speed of germination index exhibited highly significant correlation with field emergence. Seed weight and DHA tests positively while the E. C. negatively were found correlated with the field emergence. The strongest association (r=0.67) was observed between field emergence and standard germination. Among the various tests, the highest association (r=0.66) was observed between E. C. and seed weight.

610. DESWAL, D. P., U. CHAND AND B. S. DAHIYA 2002. STANDARDIZATION OF GERMINATION TEST IN RICEBEAN [VIGNA UMBELLATE(THUNB) OHWAI AND OHASHI]. *Forage Res.*, 28 (2) : pp. 106-109. Seed Science Center, CCS Haryana Agricultural University, Hisar-125 004, India

Standardization of germination test in ricebean was carried out at CCSHAU, Hisar. The seeds of ricebean can be tested for standard germination in B. P. method at 30°C and seedlings may be evaluated for first count on 5th day and 8th day. At present, there does not exist any standard for germination test in ISTA rules or AOSA rules.

Therefore, the germination can be carried out as per the present findings in the testing laboratories and research programmes.

611. SHUKLA, G. P., N. P. MELKANIA, K. SINGH, S. K. RAJPAL AND O. N. ARYA. 2003. GENOTYPE X LOCATION ENVIRONMENT INTERACTION IN RICEBEAN [VIGNA UMBELLATA (THUNB) OHWI AND OHASHI] WITH SPECIAL REFERENCE TO ACIDIC SOIL. Forage Res., 28 (4) : pp. 194-200. All India Coordinated Project for Research on Forage Crops (ICAR), Indian Grassland and Fodder Research Institute, Jhansi-284 003 (U. P.), India

A set of eight elite lines of ricebean [*Vigna umbellata* (Thunb.) Ohwi and Ohashi], which included a recently released national variety Bidhan-1 (or K-1) as a check, was tested in multilocational trial during **kharif** (rainy season) 2000 at three diverse environments in randomized block design with three replications. The three environments are sparsely situated in North-Eastern Indian Zone with a distance over 500 km apart having dissimilar topography and agroclimatic conditions. Genotype (G) x Environment (E) interactions leading to stability were worked out for green forage and dry matter yield and plant height. Results indicated variance due to environments and deviations to be significant. The G x E interactions in gross and G x E interactions (linear) were also significant when tested against pooled error. The variances showed a rational uniformity for the characters studied. As a cross check of the character resemblances, the correlation coefficients were found to be significant. Essence of inferences considering three parameters of stability *viz.*, mean, regression coefficients and deviation components indicated strain KRB-2 to be the best stable for general environment, KRB-5 for the enriched environment and KRB-13 for the poorer environment.

612. LOKESH, P. K. VERMA, S. N. GUPTA AND R. K. BEHL 2004. GENOTYPIC VARIATION FOR IMPORTANT MORPHOLOGICAL CHARACTERS AND SEED YIELD ATTRIBUTES IN RICE BEAN. *Forage Res.*, 29 (4) : pp. 189-191. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Wide range of variability was recorded for different morphological and yield characters in rice bean. High PCV and GCV were found for pods per plant, clusters per plant, plant height, seed yield per plant, days to flower and pods per cluster. High heritability followed by high genetic advance as per cent of mean was recorded for pods per plant, plant height, seed yield per plant and clusters per plant. Genotypes YS 99-8, YS 99-21, GS 99-6 and AS 99-43 appeared to be promising.

613. LOKESH, P. K. VERMA AND R. K. BEHL. 2004. CORRELATION COEFFICIENTS STUDY BETWEEN DIFFERENT QUALITY CHARACTERS IN RICE BEAN. Forage Res., 30 (3): pp. 149-151. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Genotypic and phenotypic correlation coefficients for different quality characters were recorded. Positive and highly significant association was present viz., manganese with potassium, sodium and iron, calcium with zinc, starch with sodium and copper, lipids with sodium and copper, respectively. Highly significant and negative correlation was recorded between calcium and magnesium only.

614. DE, D. K., P. BANDOPADHYAY AND D. MAZUMDAR 2004. GENETIC VARIABILITY OF DIFFERENT LEAF MEASUREMNTS IN RICE BEAN(VIGNA CALCARATUS ROXB.). Forage Res., 30 (3) : pp. 159-162. BCKV, Kalyani

Genetic variability of different leaf measuremnts in rice bean(vigna calcaratus roxb.) was studies at BCKV, Kalyani. The 12th leaf registered high degree of all the genetic parameters. Therefore, this leaf alone could be relied upon for selection of better genotype with higher fodder yield.

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615. REDDY, S. R. R., S. N. GUPTA AND P. K. VERMA. 2005. G X E INTERACTION FOR SEED YIELD AND ITS COMPONENTS IN FABA BEAN (*VICIA FABA L.*). Forage Res., 31 (1): pp. 21-25. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana) India

Sixty genotypes of faba bean were evaluated for stability by growin in four environments, created by manipulating two dates of sowing (normal and late) and two fertilizer doses of nitrogen (20 and 40 kg/ha) and phosphorus (30 and 60 kg/ha). The results indicated that the environments were varying for all the genotypes in respect of all the characters studied, indicating thereby that the performance of genotypes varied in different environmental conditions and the presence of genotype x environment (G x E) interaction for seed yield per plant and its components. Both the linear as well as non-linear components significantly contributed to the total G x E interaction for the expression of characters under study. There was preponderance of linear component for branches per plant, seeds per pod, 100-seed weight, shelling percentage and seed yield per plant. However, the substantial amount of non-linear portion of G x E interaction content. Based on mean performance (X), regression (bi) and least deviation from regression (Sdi), eight genotypes were desirable for seeds per pod and pod length; six for 100-seed weight; four for shelling per cent and only one genotype for seed yield per plant. For seed yield per plant, genotype EC 329683 was suitable for unfavourable environment (b_i<1); genotype IC 243770 for general adaptability (b_i=1); and genotypes HB 188, IC 243726 and IC 243835 for favourable environments (bi>1). These five genotypes were also stable for most of the yield contributing characters.

616. DE, D. K., P. BANDOPADHYAY, D. MAZUMDAR AND B. N. PANJA 2007. ESTIMATION OF AREA OF RICEBEAN (VIGNA UMBELLATA) LEAF BY LINEAR MEASUREMENTS. Forage Res., 33 (1): pp. 9-12. Department of Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia (W. B.), India

Five genotypes of ricebean were grown at the University Research Farm during **kharif** 2003 and 2004. Correlation coefficients between (i) length of side leaflet, (ii) breadth of side leaflet, (iii) length of top leaflet, (iv) breadth of top leaflet, (v) area of side leaflet, (vi) area of top leaflet and (vii) total area obtained from two years' data were highly significant and positive. Regression equations and their respective R^2 values worked out for each genotype and over the genotypes for the estimation of leaflet area (side or top) or total leaf area using measurements for i-iv revealed a highly reasonable accuracy with the actual area obtained from leaf area meter (Systronics-321). Equation obtained following full model multiple regression was : vii=14.11+5.68 (i)+5.68 (i)+9.38 (ii)+0.40 (i x ii)-9.77 (iii)-4.16 (iv)+1.28 (iii x iv). Length x breadth of side leaflet and breadth of top leaflet appeared most.

617. SARKAR, A. AND S. BHATTACHARYA 2007. METROGLYPH AND INDEX SCORE ANALYSIS IN GERMPLASMS OF RICE BEAN (VIGNA UMBELLATA (THUNB.) OHWI AND OHASHI]. Forage Res., 33 (1): pp. 44-47. Department of Genetics and Plant Breeding, Uttar Banga Krishi Vishvavidyalaya, Pundibari, Coochbehar, India

The present study was carried out with 26 germplasms of rice bean collected from different sources with a view to classify them into morphologically distinct classes based on metroglyph and index score analysis. The analysis revealed seven distinct groups based on the two highly variable characters viz., plant height (cm) and pods per plant. The largest group contained 12 genotypes with low to high values for seeds per pod, 100-seed weight and pod length. Within the group the genetic variation among the genotypes was also noticed thus offering another scope for selection within the cluster. The index score of seven promising genotypes revealed the importance of clusters per plant, seeds per pod and 100-seed weight as the characters to be considered for selection for crop improvement in rice bean. It significant predictor variables as both R^2 and adjustable R^2 values were 0.99. The equation there would be : vii=- 14.03+1.38 (i x ii)+6.57 (iv).

618. KATOCH, R. SALEJ SOOD, NAVEEN KUMAR AND J. C. BANDHARI 2007. FODDER PRODUCTION POTENTIALAND NODULATION EFFICIENCY OF DIFFERENT RICEBEAN GENOTYPES. Forage Res., 33 (2): pp. 73-77. Fodder Production & Grassland Management Centre, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (H. P.), India

Fodder yield and nodulation efficiency of 30 diverse rice bean genotypes were recorded under mid-hill conditions of Himachal Pradesh. The plant height and days to 50 per cent flowering were found to have direct influence on fresh fodder yield. The genotypes IC-137200 (U. P.), IC-137190 (Sikkim) and IC-137195 (U. P.) gave higher fodder yield of 138.33, 123.89q/ha and 121.67, respectively. The local genotypes were of lesser height and early in flowering. The germplasm lines with more height and late flowering appeared to have higher fresh fodder yield than early flowering and short genotypes. The maximum number of nodules per plant and nodule weight were recorded in genotype IC-137194 (U. P.) and the values for nodule weight generally paralleled the observations for nodule number per plant.

619. SARKAR, A. AND S. BHATTACHARYA 2007. CLUSTER ANALYSIS IN RICE BEAN [VIGNA UMBELLATA (THUNB.) OHWI AND OHASHI] GERMPLASMS FOR SEED YIELD UNDER TERAI REGION OF WEST BENGAL. Forage Res., 33 (2) : pp. 118-121. Department of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar-736 165 (West Bengal), India

Twenty-six rice bean genotypes were evaluated for 11 quantitative characters to assess the extent of their genetic diversity by Mahalanobis D^2 statistics. The cluster analysis separated the germplasms into six distinct clusters with cluster I containing the maximum number of genotypes. Among the 11 characters studied, seed yield contributed the highest towards total divergence followed by plant height, while the character pods per cluster contributed the least towards the same. Cluster III had the maximum plant height and also had the minimum clusters per plant. Cluster V showed the maximum mean for primary branches and clusters per plant and had the lowest means for 100-seed weight. The genotypes from clusters with high and low mean values for majority of the characters were considered as promising parents for hybridization.

KARWASRA, R. S., Y. KUMAR, V. KUMAR AND A. KUMAR 2007. RESPONSE OF RICEBEAN (VIGNA UMBELLATE) GENOTYPES TO VARYING UNDER RAINY SEASON OF HARYANA. *Forage Res.*, 33 (3): pp. 190-191. Department of Plant Breeding, CCSHAU, Hisar.

The response of ricebean (*vigna umbellate*) genotypes to varying under rainy season of Haryana were studied in the Department of Plant Breeding, CCSHAU, Hisar. It is concluded that genotype RBL-9 is the best amongst the genotypes studied and 40 x10 cm spacing may be used to obtain higher yield of ricebean in rainy (kharif) season.

621. KATOCH, R. UTTAM CHAND, NAVEEN KUMAR AND J. C. BANDHARI 2008. A STUDY ON ASYNCHRONY IN POD MATURITY AND PRODUCTION POTENTIAL IN RICE BEAN. Forage Res., 33 (4): pp. 255-257 (2008) FPTGMC, Department of Plant Breeding, CSK Himachal Pradesh Krishi Vishvavisyalaya, Palampur-176062(H.P.).

The present study presents morpho-physiological characteristics of genotypes which would help in selection of genotypes for particular agroclimatic zones that would reduce yield losses of crop by shattering. Selection of genotypes with short maturity period would lessen the expenditure on the harvest of the crop.

622. BHATTACHARYA, N. M., G. RAMA PRASHAT AND S. BHATTACHARYA 2008. SCREENING OF RICE BEAN [VIGNA UMBELLATA (THUNB) OHWI & OHASI] GERMPLASM FOR SALT TOLERANCE AT EMERGENCE STAGE AND THEIR RAPD-BASED DNAANALYSIS. Forage Res., 34 (2) : pp. 65-72. Department of Genetics, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia (West Bengal), India

Ten rice bean genotypes, which included two released varieties (Bidhan-1 and Bidhan-2) and eight other promising lines (KRB-5, KRB-6, KRB-7, KRB-9, KRB-10, KRB-12, KRB-14 and KRB-18), were evaluated for their tolerance to different salinity levels. Seed germination and seedling growth have been used as a marker to screen salt tolerance in the present study. The genotypes (KRB-7 and Bidhan-1) which performed significantly better at higher NaCl concentrations of 100, 120 and 140 mM at germination have been considered as salt stress tolerant genotypes. RAPD reaction was performed using 17 primers, out of which only seven primers gave reproducible banding pattern. The genotype KRB-7, which is the most salt tolerant line, showed only 64 per cent similarities to the least salt tolerant variety Bidhan-2. Bidhan-1, the second most tolerant variety, showed 88 per cent similarity to the variety Bidhan-2. In other words, RAPD results revealed 36 per cent dissimilarity between KRB-7 and Bidhan-2 and 22 per cent between Bidhan-1 and Bidhan-2. This genetic diversity may account for the observed salinity tolerance in KRB-7. Also, the few bands, which are present in the line KRB-7 but are absent in Bidhan-2 and Bidhan-1, may be interpreted as collinear for the salinity tolerance.

623. ROY, S. AND DILIP KUMAR DE. 2009. STUDY OF SEED PROTEIN AND ISOZYME DIVERSITY IN RICE BEAN (VIGNA UMBELLATA L.) GENOTYPES. Forage Res., 35 (1): pp. 1-4. Department of Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia-741 252 (West Bengal), India

A study was performed with 11 diverse rice bean germplasm lines to estimate the genetic variability through isozyme (peroxidase and esterase) and seed protein analysis. Eight bands were observed in case of esterase, which demonstrated polymorphism in band number, intensity and width and the Rm values ranged from 0.095 to 0.568. Polymorphism was also noticed in peroxidase, which on staining revealed nine bands and the Rm values ranged from 0.083 to 0.754. Twenty bands were visible on staining the SDS-Polyacrylamide gel with Commasie blue, which revealed that the expression of seed protein to be controlled by the multigene families. The study clearly indicated the importance of isozyme and seed protein studies in varietal identification of fodder legumes. Isozyme and seed protein studies might also be used to identify the superior parents for the future breeding programmes.

624. KATOCH, R. AND SALEJ SOOD 2009. A STUDY ON THE FIELD PERFORMANCE OF DIFFERENT RICE BEAN [VIGNA UMBELLATA (THUNB.) OHWI AND OHASHI] GENOTYPES. Forage Res., 35 (2): pp. 80-84. Department of Crop Improvement, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (H. P.), India.

The rice bean genotypes under study showed variations in different traits. All the genotypes showed fast initial growth except local genotypes which showed increase in height only upto 50 DAS and afterwards their growth became static. Sharp increase in height was observed for IC-137194 (U. P.), IC-137195 (U. P.), IC-140805 (Punjab), IC-140808 (Punjab) and IC-140796 (Punjab) after 70 to 115 DAS. Local genotypes were earlier in flowering and maturity, whereas exotic lines EC-48223-B (China), IC-140803 (Punjab), IC-137190 (Sikkim) and IC-140805 (Punjab) were late both in flowering and maturity. Pod traits were observed to have direct effect on seed yield. The variations from 44.0 g in EC-48223-B (China) to 274.27 g in IC-137195 (U. P.) were recorded in seed yield per plot. The genotypes IC-137195 (U. P.), IC-140795 (Punjab) and IC-019352 (Orissa) showed high seed production potential, which could be due to comparatively longer pods and large number of seeds per pod in these genotypes.

9. Miscellaneous

625. JAYASHREE, M. K., K. P. VISWANATHA AND P. RUDRASWAMY 2001. ISOLATION OF USEFUL MUTANTS IN LITTLE MILLET (PANICUM MILLIARE LAM.). Forage Res., 27 (3): pp. 163-166. Department of Genetics and Plant Breeding, University of Agricultural Sciences, G. K. V. K., Bangalore-560 065 (Karnataka), India

Three varieties of little millet viz., IPM 1006, DPI 1213 and PRC-9 were exposed to five doses of gamma rays and four concentrations of ethylmethane sulphonate and their M_1 and M_2 generations were studied. Agronomically important mutations for earliness in DPI 1213, high tillering types in IPM 1006 and grassy types for fodder purpose in PRC 9 and DPI 1213 were isolated in M_2 generation, which could be utilized directly or indirectly in the breeding programme.

626. BANGARWA, K. S. AND V. P. SINGH. 2001. PROVENANCE VARIATION FOR SEED AND POD CHARACTERS IN DALBERGIA SISSOO ROXB. Forage Res., 27 (3): pp. 207-212 (2001). Department of Forestry, CCS Haryana Agricultural University, Hisar-125 004, India

Seed pods were collected from five randomly taken trees of *Dalbergia sissoo* Roxb. from 20 diverse sites (provenances) of Uttar Pradesh, Punjab, Haryana and Rajasthan in India. Data on pod and seed characters were recorded from each site. Significant variation was observed among provenances for seed and pod characters. Variation was higher for seed and pod weight in comparison to seeds per pod, seed length, seed breadth, pod length and pod breadth. Among 1-4 seeded pods, single seeded pods were 60 to 90 per cent. Pod length and breadth had no association with seeds per pod, seed length and 100-seed weight. Seed breadth had positive association with all the seed and pod parameters.

627. CHANDAGI RAM, ANITA MANN AND R. C. PUNIA 2001. DISTINCTNESS, UNIFORMITY AND STABILITY (DUS) TESTING AND TECHNIQUES FOR TESTING GUIDELINES OF VARIETIES BY LABORATORY AND FIELD TECHNIQUES. Forage Res., 27 (3) : pp. 239-242. Seed Technology Centre, Haryana Agricultural University, Hisar-125 004, India

Dostinctness, Uniformity and stability (DUS) testing and techniques for testing guidelines of varieties by laboratory and field techniques. Various laboratory and field techniques for DUS testing have been given in this communication.

628. AVTAR, R., D. S. JATASRAAND B. S. JHORAR 2002. ANALYSIS OF GENE EFFECTS FOR SOME IMPORTANT YIELD COMPONENTS IN FENUGREEK (*TRIGONELLA FOENUM-GRAECUM L.*). *Forage Res.*, 28 (2) : pp. 59-62. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Generation mean analysis was carried out for plant height, branches/plant, pods/plant and seeds/pod using four crosses of fenugreek in inoculated (E_1) and natural (E_2) environments. Additive-dominance model was found to be adequate for seeds/pod, whereas it was inadequate for plant height, branches/plant and pods/plant. Dominance gene effects and dominance x dominance interaction played an important role in the inheritance of these traits, although additive type of effects were also present. Duplicate type of epistasis was evident in the inheritance of all the traits exhibiting interactions. Biparental mating has been suggested for further genetic improvement in these traits.

629. REDDY, S. R. R., S. N. GUPTA, P. K. VERMA AND LAJPAT RAI 2002. GENETIC VARIATION, CORRELATION AND PATH COEFFICIENT ANALYSIS UNDER NORMAL SOWN CONDITIONS IN VICIA FABA L. Forage Res., 28 (2): pp. 63-66. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Fababean (*Vicia faba* L.) is an underutilized leguminous crop having very high seed yield potential and used as food and feed by human beings and animals, respectively. Sixty genotypes were studied for variability, correlations and path coefficients for seed yield and its component characters. To improve seed yield, number of pods for plant was found most important trait followed by plant height and number of branches per plant. Pod length, though, had high direct effect on seed yield but the same was diluted by negative high indirect effects contributed via number of seeds per pod and 100-seed weight.

630. YADAV, B. D., S. P. SINGH AND RAMESH CHAND 2002. EVALUATION OF SOME NEW BARLEY VARIETIES FOR THEIR YIELD POTENTIALAND RESISTANCE TO CEREAL CYST NEMATODE, HETERODERA AVENAE IN RAJASTHAN, INDIA. Forage Res., 28 (2) : pp. 115-116. Rajasthan.

In the present study new barley varieties for their yield potential and resistance to cereal cyst nematode, Heterodera avenae in Rajasthan. RD 2052, RD 2035 and RD 2049 give significantly higher yield over all other varieties and stood 1st, 2nd, 3rd in performance. RD 103 allowed CCN multiplication to a maximum extent, while other varieties being resistant or moderately resistant reduced the CCN final population as compared to initial soil population.

631. SRIMATHI, P., R. GEETHA AND K. MALARKODI 2002. PHYSICAL MANAGEMENT FOR HIGHER SEED QUALITY IN LUCERNE CV. CO1. Forage Res., 28 (3) : pp. 153-155. Department of Seed Science and Technology, Tamil Nadu Agricultural University, Coimbatore-641 003 (Tamil Nadu), India.

Studies were made to enhance the seed quality of lucerne cv. CO 1 through physical seed management. Seed were size graded using 12, 14, 16, 18, 20 and 22 sieve number of British Standard Sieves (BSS). The seeds were also separated into three colour grades viz., yellow, light brown and dark brown, based on the availability of colours in the seed lot. Graded seeds were evaluated for seed quality characters *viz.*, germinability and vigour parameters. The study revealed that the seeds recorded a positive association within the size grades. However, based on higher recovery combined with higher quality, the seeds should be graded with BSS 14 x 14 size sieve. Among the colour grades, yellow coloured seeds should be selected for better seed quality performance than other colours.

632. REDDY, S. R. R., S. N. GUPTA AND P. K. VERMA. 2002. GENETIC VARIABILITY, ASSOCIATION AND PATH ANALYSIS IN *VICIA FABA* L. UNDER HIGH FERTILITY CONDITIONS. *Forage Res.*, 28 (3): pp. 169-173. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

Sixty genotypes of fababean (*Vicia faba* L.) were studied for variability, correlation and path coefficients for seed yield parameters and protein content. Pods per plant was found to be the most important character, followed by plant height and branches per plant. 100-seed weight had very poor correlation with seed yield, but its direct effect was positive and substantial which was nullified by its indirect negative effect through pods per plant.

633. DESALE, J. S., R. L. BHILARE, V. S. PATILAND A. G. HIRAY 2002. INFLUENCE OF AGE OF MOTHER CROP AT SEED HARVEST ON FORAGE YIELD AND LONGEVITY OF PROGENY CROP OF LUCERNE. Forage Res., 28 (3): pp. 177-178. Forage Crops Research Project, MPKV, Rahuri.

The experiment was carried out at Forage Crops Research Project, MPKV, Rahuri. No adverse effect on its forage yield as well as longevity of crop because of seed collected at any age of mother crop.

634. DAHIYA, B. S. AND R. P. S. KHARB 2003. FODDER SEED PRODUCTION–CONSTRAINTS AND STRATEGIES *Forage Res.*, 29 (1): pp. 10-17. Department of Seed Science and Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Inadequate availability of quality seed of improved varieties of fodder crops is the single most important constraint in increasing the production and productivity of these crops. As such they are shy seeders with low seed productivity. There are many genetical, physiological, environmental and organisational problems/constraints associated with low seed productivity. In addition, the appropriate crop management practices greatly help in enhancing the seed production potential. In this article, strategies are discussed for development of an effective and viable seed production programme from maintenance breeding to certified seed. Through systematic efforts at all levels, the forage seed production problem could be resolved to a reasonable level.

635. DHILLON, R. S., M. S. HOODA, D. CHOPRA AND S. ARYA 2003. STUDIES ON FLORAL BIOLOGY AND BREEDING BEHAVIOUR OF *PROSOPIS CINERARIA* (L.) DRUCE (KHEJRI) *Forage Res.*, 29 (2): pp. 71-75. Department of Forestry, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Defoliation started during the month of November and continued till end of January. The new leaves started appearing in February. The floral buds began to open from first week of April. The peak period of flowering was noticed from mid April to mid May. Flowering pattern was observed asynchronous and the flowers were small in size, yellow and creamy white in colour. Stigma receptivity was recorded between 8-11 a. m. Natural pod setting started in last week of April and it was ready to harvest in first week of June. Per cent pod set varied from 0.19 for selfing/bagging to 1.58 for natural open pollination during 1999 and 0.15 to 1.84 per cent during 2000. Apomixis was found to be totally absent.

636. BASSI, GEETA, SUKHCHAIN, J. S. SAMRA AND MALKIT SINGH 2003. DETERMINATION OF OPTIMUM PERIOD OF MATURITY AND PERIOD OF STORAGE IN GUINEA GRASS. *Forage Res.*, 29 (2) : pp. 82-83. Seed Technology Centre, Punjab Agricultural University, Ludhiana-141 004 (Punjab), India

Guinea grass (*Panicum maximum* Jacq.) is primarily a pasture grass grown in tropical and sub-tropical areas of the world. One of the major problems in this crop is seed shattering which leads to significant reduction in seed yield. In order to determine the optimum stage of harvesting, seeds were collected from 15, 20 and 25 days old panicles days after their emergence. Besides, seeds harvested during end October from the crop produced during **kharif** 2001 and stored under ambient conditions were collected from Forage Section, Department of Plant Breeding, PAU, Ludhiana. The data on seed germination and seed vigour in terms of seedling length were recorded for 6 and 9-month old seeds of the same lot. Germination in 6-month old seeds was higher than that in 9-month old seeds. However, period of storage had no effect on seed vigour since there was non-significant difference in terms of seedling length in 6 and 9-month old seeds. However, number of seeds in the panicles harvested 15 and 20 days after emergence was higher than that in the panicles harvested 25 days after emergence. Thus, 25 days old panicles appeared to be the optimum stage for harvesting.

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637. ARORA, R. N. 2004. COMPARISON OF SEED AND SEEDLING VIGOUR IN SOME FORAGE LEGUME SPECIES. *Forage Res.*, 29 (4) : pp. 214-216. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Comparison of seed and seedling vigour in some forage legume species was done at CCSHAU, Hisar. Wide variation for various parameters of seed and seedling vigour was observed among various legumes species.

 638. RAO, V. SATYANARAYANA 2004. FORAGE AND FORAGE SEED PRODUCTION–PERSPECTIVES, RESOURCES AND STRATEGIES FOR THE TELENGANA REGION OF ANDHRA PRADESH. Forage Res., 29 (4) : pp. 163-169. AICRP on Forage Crops, Livestock Research Institute, Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad (A. P.), India

The bovine population of Andhra Pradesh, though remained almost constant during the last four decades 1961-99, has undergone significant structural changes. Male cattle population remained constant during the period indicating that agriculture is still dependent on animal power. Shift in cow population to buffalo population indicated the preference for buffalo milk. There was a phenominal increase in ovine population between 1993-96. The area under cultivated fodder crops in the State, 2.04 lakh hectare was less than 1 per cent of the geographical area of the State. The grazing pressure of the State was 3.49 ACU/ha and the availability of grazing area in ha/ACU was 0.29. The shortage of fodder in Telengana region was 115.01 lakh tonnes. Seed production of forage crops in the State is yet to start. Breeder seed requirement of this region is approximately 2163 kg.

639. SHARMA, N. K. 2004. COLLECTION AND SCREENING OF GERMPLASM OF CENCHRUS CILIARIS L. FOR FORAGE YIELD. *Forage Res.*, 30 (1) : pp. 53-54. ARS, Keshwana, Jalore

Collection and screening of germplasm of Cenchrus ciliais L. for forage yield was done ARS, Keshwana, Jalore. The vast exploitable genetic potential was noticed in this grass species as reflected by the variation in overall green forage yield in different genotypes collected through exploratory survey of natural habitat.

640. ARORA, R. N. 2004. A SHORT NOTE ON SPONTANEOUS OCCURRENCE OF "BROAD LEAF MUTANT" IN FENUGREEK. *Forage Res.*, 30 (2) : pp. 106 (2004) Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

At CCSHAU, Hisar a spontaneous occurrence of "Broad Leaf Mutant" in fenugreek was observed. It possessing morphological marker traits can be of immense importance.

641. SAINI, M. L., U. N. JOSHI AND PUNEET JAIN 2005. VARIABILITY IN MORPHOLOGICALAND QUALITY PARAMETERS IN DIFFERENT GRASS SPECIES UNDER SEMI-ARID ECOSYSTEM. *Forage Res.*, 30 (4): pp. 217-223. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

An experiment was conducted in different grass species for forage production at CCS Haryana Agricultural University Regional Research Station, Bawal (Rewari) during 2003-04 and 2004-05. Four cuttings were taken in the months of September and November in both the years. The data were recorded on various morphological characters, namely, plant height (cm), number of tillers per clump, leaf length (cm), leaf width (cm), weight per clump (g), green fodder yield (q/ha), dry matter yield (q/ha) and quality characters i. e. crude protein (%) and IVDMD (%). Protein yield (q/ha) and digestible dry matter (q/ha) were calculated by multiplication of protein content and IVDMD with dry matter yield, respectively. The analysis of variance revealed considerable genetic variability for green fodder and dry matter yield in all the four cuttings. The total green fodder yield was maximum in Napier-bajra hybrid cvs. Co 3 and NB 21 during 2003-04 and 2004-05, respectively. Total dry matter yield was maximum in Napier-

bajra hybrid cv. NB 21 during 2003-04 and *P. antidotale* cv. RDS-2 during 2004-05. Crude protein yield and digestible dry matter were maximum in Napier-bajra hybrid cv. NB 21 during 2003-04 and *P. antidotale* cv. RDS-2 during 2004-05. It was concluded that Napier-bajra hybrid cv. NB 21 and *P. antidotale* cv. RDS-2 were best among the studied grasses because they yielded maximum dry matter yield, protein yield and digestible dry matter. So, these genotypes are recommended in the arid and semi-arid regions for green fodder production and quality parameters.

642. YADAV, R., S. K. PAHUJA AND J. V. SINGH 2005. HIERACHICAL CLUSTER ANALYSIS-A CLASSIFICATORY TOOL FOR GERMPLASM EVALUATION. *Forage Res.*, 30 (4) : pp. 240-245 CCSHAU, Hisar-125004

This procedure attempts to identify relatively homogeneous groups of cases based on selected characteristics, using an algorithm that starts with each (or variable) in a separate cluster and combines clusters until only one left.

643. KANT, SHRI AND K. P. SINGH 2005. STABILITY PARAMETERS FOR YIELD AND ITS COMPONENTS IN MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK]*. *Forage Res.*, 31 (2) : pp. 85-87. Amar Singh (P. G.) College, Lakhaoti, Bulandshahr-245 407 (U. P.), India

Mungbean is a major crop in Asia and Africa. Mungbean varieties show a wide range of fluctuations in their performance when grown under varied agro-climatic conditions. Some genotypes perform well over a wide range of environments, while others require specific environmental conditions to express their full genetic potential. Significant improvement in crop productivity may be possible by breeding stable varieties. Although studies have been made on the released cultivators, the information is scanty on the stability of promising genotype in advance generations. A successful evaluation of stable genotype, which could be used in future breeding programme to develop stable and promising genotypes, can be done through the study of genotype x environment interactions. Many stability parameters were suggested by various authors. Earlier studies in mungbean for grain yield and harvest index indicating the different genotypes behave differently under varying environmental conditions. Thus, the present investigation has been undertaken with a view to study the phenotyic stability of different genotypes in mungbean for biological yield, grain yield and harvest index. Genotype x environment interaction for biological yield, grain yield and harvest index in mungbean [Vigna radiata (L.) Wilczek] was studied by growing 44 genotypes in four environments over two years. All the genotypes showed significant interactions with the environment for biological yield/plant and grain yield/plant and a large portion of these interactions was accounted for by the linear regression on the environmental index for biological yield and grain yield, whereas reverse was the case for harvest index. The genotype L-38 was most stable with high yield and unit regression coefficient for both the traits studied.

KUMAR, MUKESH, K. P. SINGH, B. S. CHAUDHARY AND J. B. SINGH 2006. GENETIC ARCHITECTURE OF YIELD AND ITS COMPONENTS IN GOBHI SARSON (BRASSICA NAPUS L.). Forage Res., 32 (3) : pp. 178-180. Department of Agricultural Botany, Janta Vadic (PG) College, Baraut-250611, Baghpat (Uttar Pradesh), India

Forty-five F_1 hybrids from a 10-parent diallel mating design in gobhi sarson (*Brassica napus*) were analysed to study genetic architecture of seed yield and its components. Out of 45 crosses studied, 11 showed superior performance. Only five cross combinations were the result ant of good x good gca parent cross for seed yield and its components, whereas another five such crosses came out of good x poor combinations. Only one cross (*B. napus*-1 x EC-400802) was the combination from poor x poor gca parents which indicated the presence of non-additive gene action. Therefore, it was noticed that poor general combine could also produce superior cross combination for metric traits. Significant variances for different attributes and predominance of non-additive gene action were observed for all the traits. In addition, flow of alleles was symmetrical but dominant genes were distributed more frequently than the recessive genes.

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545. JAIN, PUNEET, U. N. JOSHI, M. L. SAINI AND NARESH VERMA 2007. NUTRITIVE VALUE AND GENETIC PERFORMANCE OF SOME GRASS SPECIES IN AN ARID REGION OF HARYANA. *Forage Res.*, 32 (4) pp. 224-228. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar

An experiment was conducted on eight grass species at CCS Haryana Agricultural University Regional Research Station, Bawal, District Rewari, Haryana during the year 2004. Two cuttings were taken in the months of September and November in 2004. Cultivars CAZRI 347 and Forage of Panicum antidotale exhibited the maximum green fodder and dry matter yield, respectively, while it was minimum in Bothrichloa inrermedia in both the cuttings. P. antidotale cv. RDS-1 exhibited the maximum protein content (21.88%) and minimum IVDMD (50.20%) in both the cuttings. The highest protein yield (18.77 q/ha) was exhibited in P. antidotale cv. Forage and digestible dry matter (57.26 q/ha) in Urochloa masambicinensis, while B. intermedia exhibited minimum protein yield (4.74 qfha) and digestible dry matter (19.65 q/ha). High magnitude of heritability coupled with high to moderate genetic advance was observed for number of tillers/clump, weight/clump, leaf width, green fodder yield and dry matter yield suggested thereby simple selection for their improvement: It was concluded that P. antidotale cv. Forage can be recommended as the one with the most potential among the studied grassess for use in the arid regions of south-west Haryana, India.

646. PATEL, K. V., J. P. YADAVENDRA, H. P. PARMAR, M. K. GANGANI AND P. C. PATEL 2007. ESTIMATES OF VARIABILITY IN CENCHRUS CILIARIS L. *Forage Res.*, 32 (4) : pp. 229-232. Main Forage Research Station, AAU, Anand

The present experiment comprising 26 genotypes of Anjan grass was conducted in randomized block design with three replications at Anand to study the variability and correlation of green fodder yield with its contributing characters. The results were based on pooled data of five cuttings. The significant difference was found for mean of all the characters. All the characters under study showed high heritability. Heritability and genetic advance were high for green fodder yield (GFY) and dry matter yield (DMY), indicating that straight selection is effective for its improvement. The estimation of genetic correlation coefficient was higher than their corresponding phenotypic correlation coefficient for all characters. It was observed that dry matter yield per plant, leaf width, leaf length, plant height, tiller number per plant and days to 50 per cent flowering were found the most important characters for making enhancement of green fodder yield. Path coefficient analysis based on genotypic correlation coefficients showed that tiller number per plant, leaf length, leaf width and days to 50 per cent flowering were the major characters which exerted considerable direct effect on green fodder yield per plant, revealing scope for considering the selection programme.

647. KATOCH, R., UTTAM CHAND AND BANDANA. 2007. **RED CLOVER : PRESENT STATUS AND FUTURE NEEDS.** *Forage Res.*, 33 (1) : pp.1-8. FPGMC, Department of Plant Breeding and Genetics. CSK Himachal Pradesh Krishi Vishwavidyalaya, Palampur-176 062 (H. P.), India

Red clover (Trifolium pratense L.) is an important forage legume widely cultivated in most temperate regions because of its characteristics of high seedling vigour, rapid growth and tolerance to acidic and humid conditions. It is also used as a green manure crop because of its high nutrient content resulting partly from symbiosis with nitrogen fixing bacteria of the genus Rhizobium. Highest hay yields of red clover about 8-12 t dry matter/ha could be obtained in the year after seeding. Hybridisation between species of the genus Trifolium under natural conditions is very improbable even in closely related species. The high level of heterozygosity has hampered intensive genetic and genomic analyses of red clover. Recently, the first genetic linkage map with 256 restriction fragment length polymorphism (RFLP) markers has been constructed (Isobe et al., 2003). Study of pre-fertilization barriers of crosses has shown that red clover plants at a tetraploid level were more effective for fertilization in comparison with diploid ones. Various in vitro methods such as protoplast fusion and in vitro pollination (Taylor and Quesenberry, 1996) are necessary for the crop improvement. The incorporation of foreign genes by genetic transformation by

means of Agrobacterium tumefaciens has proved successful. Red clover is also a rich source of isoflavonoid phytoestrogens including biochanin A, formononetin, daidzein and genisten, which have promising results in the treatment of number of conditions associated with menopause. Because of excellent forage quality and medicinal properties, research on red clover needs to be continued and expanded, especially in the areas that relate to human and animal utilization.

648. PUNIA, R. C., R. P. S. KHARB AND R. S. KHATRI. 2007. SEED VIGOUR STUDIES IN HORSEGRAM *Forage Res.*, 33 (1) : pp. 37-39. Department of Seed Science & Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The study was conducted on 10 genotypes of horsegram for evaluation of seed quality. The genotypes 8B, CRIDA-1-9R and CRIDA-2-18R were found highly vigorous, while the genotypes AK 42 and AK 44 were found to have low vigour on the basis of average performance of various parameters studied. The laboratory tests viz., standard germination, vigour index, accelerating ageing, electrical conductivity and tetrazolium test were found to be reliable predictors of the seedling establishment.

649. LOHAN, SHIV K. AND S. S. JAKHAR 2007. FEASIBILITY PERFORMANCE EVALUATION OF VERTICAL ROTOR SEED PLANTER IN FORAGE CROPS *Forage Res.*, 33 (1): pp. 40-43. Department of Seed Science & Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The evaluation of vertical rotor seed planter having vertical rotor seed metering mechanism was done on emergence of forage crops i. e. clusterbean, sorghum and oat under laboratory as well as field conditions. Under laboratory and field condition, the seed germination was observed as 74.0 and 62.5 per cent in clusterbean, 76.0 and 64.4 per cent in sorghum and 85.0 and 73.6 per cent in oat, respectively. The effective field capacity was observed higher in oat crop (0.68 ha/h) followed by clusterbean (0.65 ha/h) and sorghum crops (0.62 ha/h). The operational cost for sowing of clusterbean, sorghum and oat crops was calculated as Rs. 460, 484 and 442/ha, respectively. The energy consumption was observed to be higher in oat (1770 MJ/ha) followed by sorghum (842.4 MJ/ha) and clusterbean (468.2 MJ/ha). The fuel consumption of 5.15 to 5.65 litre per hectare was measured in all the selected crops.

650. SOOD, V. K., J. C. BHANDARI, NAVEEN KUMAR AND RAJAN KATOCH 2008. EVALUATION OF SETARIA GENOTYPES FOR FODDER YIELD AND QUALITY TRAITS UNDER COOL SUB-TROPICALAND SUB-TEMPERATE HIMALAYAN REGION. Forage Res., 34 (1): pp. 25-28. Fodder Production and Grassland Management Centre, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (H. P.), India

Setaria grass (*Setaria anceps* Stapf ex Massey) has long vegetative growth period (April-December), quick regeneration capacity and frost tolerance and is suitable for grasslands, pastures and wastelands of mid-hill cool sub-tropical conditions of Himalayan region. In order to identify superior genotypes of Setaria with high yield potential, better nutritional status and other desirable traits, 12 clonal selections were evaluated alongwith two checks for three years (2004-06). Analysis of variance indicated sufficient variation for fodder yields (q/ha), plant height (cm) and crude protein content (%). On the basis of three years' data, two genotypes S-18 and S-20 were at par with the best check PSS-1 for fodder yields. Oxalate content in these two clonal selections was quite low as compared to the best check, S-92. However, on the basis of frost reaction, fodder yields and quality traits, only one genotype S-20 was overall superior and suitable for grasslands and wastelands in cool sub-tropical and sub-temperate Himalayan region.

651. PATHAN, S. H. AND R. L. BHILARE 2008. EVALUATION OF SUGARCANE GENOTYPES WITH HYBRID NAPIER FOR GREEN FORAGE YIELD. Forage Res., 34 (1) : pp. 58-59. Forage Crops Research Poject, Mahatma Phule Krishi Vidyapeeth, Rahuri-413722 (Maharashtra).

The genotype RBN-9 of hybrid Napier recorded significantly higher green forage, dry matter yield, and crude protein yield as compared to all other genotypes of sugarcane. However, among the genotypes of sugarcane, genotype Arenthesis spp. being at par with CoM-9810 and CoM-0251.

652. SUKHCHAIN AND D. P. CHAUDHARY. 2009. INTER-RELATIONSHIPAMONG DIFFERENT QUALITY TRAITS IN LEAVES AND CLUMES OF FORAGE BARLEY. *Forage Res.*, 34(4) : pp.235-238. Department of Plant Breeding, PAU, Ludhiana-141004 (Punjab),India.

Correlation coefficients of leaf dry matter yield (LDMY) and clum dry matter yield (CDMY) with crude protein, either extract, ash content, in vitro dry matter digestibility (IVDMD), cellulose, hemicellulose (HC), leaf : stem ratio (LSR) and plant height revealed that LDMY was positively correlated with IVDMD and plant height and CDMY were positively correlated with ether extract and also with plant height. Cellulose and hemicellulose were negatively correlated in leaf, correlation between these traits in culm was non-significant. Plant height, IVDMD, HC, cellulose and LSR had positive moderate directs, while ash content had negative moderate direct effects, crude protein and ether extract had low positive direct effects, on LDMY. On the other hand, plant height and ether excract had positive moderate direct effects, cellulose and LSR had negative moderate direct effects and IVDMD, ash content, hemicellulose and crude protein had low negative direct effects on CDMY. Selection for plant with higher LSR may not only improve cellulose and IVDMD but also LDMY. Likewise, selection for plants may improve ether extract alongwith CDMY.

653. GILL, A. S. 2009. TREE PERFORMANCE FOR FORAGE YIELD UNDER RAINFED SEMI-ARID SUB-TROPICS. *Forage Res.*, 34(4) : pp. 239-243. IGFRI, Jhansi-284003 (U.P.), India.

Studies were initiated with four tree species under agro forestry system in rainfed semi-arid sub-tropics at Indian Grassland and Fodder Research, Jhansi(U.P.) to evaluate their foliage yield. The tree, namely, Siris (*Albizia lebbeck*), Neem (*Azadirachta indica*), Shisham (*Dalbergia sissoo*) and Babul (*Acacia nilotica*) plant saplings were planted during **kharif** 1998 in 6 x 12 m spacing. The trees were planted under sole planting, with barley and chickpea crops. In all three were 14 treatments including two treatments of sole planting of crops. On six years basis (on average) shisham gave the best growth characters followed by babul, siris and neem. For foliage production (green and dry) the trend was identical as achieved with the growth charactera. However, for crude protein yield, highest production was achieved with babul followed by shishim, siris and neem. In case of intercrops, best performance (on an average) for green and dry foliage was registered with sole planting of trees followed by chickpea and barley. But for quality forage, higher crude protein yield was recorded with trees in association with chickpea. Thus, planting shisham/babul with chickpea in the inter spaces gave the best performance for quality forage yield under semi-arid sub-tropics.

654. SOOD, V. K., J. C. BHANDARI, RAJAN KATOCH AND VINEETA KAILA. 2009. COMBINING ABILITY FOR SOME FORAGE TRAITS THROUGH POLYCROSS PROGENY ANALYSIS IN TALL FESCUE. Forage Res., 35 (1): pp. 9-11. Department of Crop Improvement, Forages & Grassland Management, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176 062 (Himachal Pradesh), India

Polycross progeny test of 10 diverse genotypes of Tall Fescue (Festuca arundinacea Schreb.) was undertaken with the objective of identifying superior parents on the basis of their general combining ability (gca) for development of synthetic variety(s). The gca was studied for seven fodder traits viz., green fodder yield, dry matter yield, tillers per plant, plant height, leaf : stem ratio, crude protein (%) and crude protein yield. Analysis of variance revealed significant differences for gca among the genotypes for all the traits studied. The genotype EC 178188 had good gca

for five characters viz., green fodder yield, dry matter yield, plant height, tillers per plant and crude protein yield, while genotype EC 178185 was good general combiner for green fodder yield, dry matter yield and tillers per plant. Genotype EC 178182 was good general combiner for tillers per plant and for per cent crude protein, while Hima 4 had good gca effects for tillers/plant. Hence, genotypes viz., EC 178188, EC 178185, EC 178182 and Hima 4 were found suitable and may be used for the development of a synthetic variety for increased fodder yield in Tall Fescue.

655. ARORA, R. N., B. S. JHORAR AND S. S. BISHT 2010. GENETIC VARIABILITY AND PATH ANALYSIS FOR FODDER AND GRAIN YIELD IN DUAL PURPOSE BARLEY. Forage Res., 36 (1): pp. 26-31. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Twenty genotypes of barley (*Hordeum vulgare* L.) were evaluated for fodder and grain yield traits to estimate the variability, heritability, genetic advance, correlation and path coefficients for four traits at fodder harvest stage and for eight traits at grain harvest stage during **rabi** 2004-05 at CCS Haryana Agricultural University, Hisar. Maximum range of variation was noted for number of tillers/metre at fodder and grain harvest stage, respectively, followed by biological yield and green fodder yield. GCV and PCV values were highest for dry matter yield followed by green fodder yield, respectively, at fodder harvest stage and for grain yield at grain harvest stage. High heritability coupled with high genetic advance was observed for dry matter yield, number of tillers/metre and green fodder yield at fodder harvest stage. Path analysis studies at fodder harvest stage revealed that green fodder yield had the maximum and desirable direct and indirect effect on dry matter yield, while at grain harvest stage; biological yield followed by harvest index had the maximum direct as well as indirect effect on grain yield. The combined path analysis studies considering all the traits of fodder as well as grain yield, all the three components i. e. biological yield, green fodder yield and harvest index had the maximum positive direct effects on grain yield. The results of the present investigation suggested that the selection based on the above three characters might bring simultaneous genetic improvement in fodder as well as grain yield in dual purpose barley.

656. DEEN MK, HOODA, J. S. AND YADAV, I. S. 2010. STUDIES ON PERFORMANCE OF FABABEAN GERMPLASM LINES. *Forage Res.*, 36 (1) : pp. 52-56. Department of Genetics & Plant Breeding, CCS HAU, Hisar.

A study on 37 germplasm lines of fababean was conducted at Research farm of Department of Genetics & Plant Breeding, CCS HAU, Hisar. It was observed that the lines EC 329637, EC 267639, EC 117784, EC 2435 88 were found promising for various morphological and quality traits studied.

657. ROY, S. AND DILIP KUMAR DE. 2010. THE ACTION OF CHICORY (CICHORIUM INTYBUS L.) ROOT EXTRACT ON BACTERIA. Forage Res., 36 (2) : pp. 118-120. Department of Biotechnology, Burdwan University, Burdwan-713 104 (West Bengal), India

The present investigation was conducted to assess the inhibitory activity of the solvent extract of chicory root powder (commercially available) on gram-positive and gram-negative bacteria. Distilled water, ethyl alcohol, methyl alcohol and ethyl acetate were used as solvent and their antibacterial activities were tested using the agar well diffusion method. Ethyl acetate extract exhibited the best inhibitory activity at all the concentrations used i. e. 2-10 mg/ml in *Staphylococcus aureus*. *E. coli* showed the least activity. The inulin content in the roots was found to be around 28 per cent. The OD values obtained in the UV-VIS range of the ethyl extract sowed a single peak at 414 nm. The other solvent extracts did not demonstrate satisfactory results in respect to the inhibitory properties.

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658. SURYA PRAKASH AND C. S. MAHTO 2010. GENOTYPE-ENVIRONMENT INTERACTION AND PHENOTYPIC STABILITY ANALYSIS FOR FODDER YIELD IN GUINEA GRASS (PANICUM MAXIMUM JACQ.) Forage Res., 36 (3) : pp. 142-145. Department of Plant Breeding & Genetics, Birsa Agricultural University, Ranchi-834 006 (Bihar), India

Six promising genotypes of Guinea grass were studied for three seasons (2006-2008) at Birsa Agricultural University, Ranchi to evaluate their phenotypic stability for five important fodder yield attributing characters. Significant mean square of genotypes (G) and environments for the characters green fodder yield (GFY) and dry matter yield (DMY) indicated the differences within genotypes and environments. Highly significant pooled deviation was observed for GFY indicating significant differences among genotypes for non-linear response to environments (stability). Linear component of G x E interaction was predominant for the characters dry atter (%) and L : S ratio, while non-linear component for green fodder yield. Both linear and non-linear components were equally important for dry matter yield. Genotype JHGG-05-2 was the most stable and consistent genotype for most of the traits studied over the environments.

659. ABHAY BADOLAY, J. S. HOODA, B. P. S. MALIK AND I. S. YADAV 2011. GENETIC DIVERGENCE IN FABABEAN (VICIA FABA LINN.) Forage Res., 36 (4): pp. 229-232. Department of Genetics & Plant Breeding CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

On the basis of non-hierarchical Euclidean cluster analysis, 100 genotypes were grouped into VIII clusters. The maximum genetic distance existed between clusters VI and IV. The maximum intra-cluster distance was in cluster VI. The genotypes. RED MUTANT-2, HB-7, IC-331571, IC-243634, HB-45, EC-5873, EC-251014 and HB-38 were identified as most divergent genotypes for seed yield and its component traits. Hence, on the basis of ongoing results there are some genotypes in the cluster that can be exploited in future hybridization programme for achieving desirable segregants for the improvement of *Vicia faba* crop.

660. ADITI GULATI, P. BOORA, S. DHILLON AND K. S. BOORA 2011. GENETIC DIVERGENCE IN SOME MOTHBEAN [VIGNA ACONITIFOLIA (JACQ.) MARECHAL] GENOTYPES BY SSR ANALYSIS. Forage Res., 36 (4) : pp. 210-213. Forage Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

In the present investigation, genetic diversity was assessed using 68 SSR (simple sequence repeats) primer pairs in 50 mothbean genotypes. Out of 68 SSR primers used, 12 yielded polymorphic banding pattern. The polymorphism was scored and used in allele sharing analysis to identify genetic relationship. Cluster analysis based on Jaccard's similarity coefficient using UPGMA grouped all the genotypes into two major groups at a similarity coefficient of 0.58. The genotypes IC-14148 and IC-402292 had maximum distance of 0.81, while the genotypes IC-415132 and IC-402287 had minimum distance of 0.35. The UPGMA cluster tree identified two major clusters with 13 genotypes in one cluster and 36 genotypes in the other. The genotype Jadia was different and so it outgrouped from the rest 49 genotypes of mothbean.

10. Plant Physiology

(i) Sorghum

661. ARORA, R. N., N. K. THAKRAL, U. N. JOSHI AND S. K. PAHUJA 2001. IMBIBITION AND DRY MATTERACCUMULATION IN THE GERMINATING SEEDS OF FORAGE SORGHUM [SORGHUM BICOLOR (L.) MOENCH. Forage Res., 27 (1): pp. 39-42. Department of Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, India

A study was undertaken on seven varieties of forage sorghum and eight soaking periods during 1992-93. The observations on imbibition and dry matter utilization indicated that variety MP Chari had the maximum water uptake as well as dry matter utilization, whereas the variety S 241 showed minimum imbibition rate and dry matter accumulation. The maximum rate of imbibition and dry matter accumulation was observed after 48 h of soaking. The interaction of genotypes and soaking periods revealed that the variety MP Chari had higher imbibition rate and dry matter accumulation at 48 h of soaking.

(ii) Oat

662. PAL, A. K., S. HAJRA AND D. K. DE 2008. EFFECT OF GROWTH REGULATORS ON LEAF GROWTH, PHOTOSYNTHETIC PIGMENTS, DRY MATTER PARTITIONING AND GRAIN YIELD OF OAT (AVENA SATIVA L.) UNDER SINGLE CUT MANAGEMENT Forage Res., 33 (4) : pp. 216-218. Department of Plant Physiology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur-741 252, Nadia (West Bengal), India

Field experiment was conducted at Gayeshpur, West Bengal, during **rabi** season of 2005-06 to study the effects of different concentrations of NAA and GA on flag leaf characters, plant growth, assimilate translocation and grain yield in oat after forage cut at 50 DAS. Foliar spray of 50 ppm GA resulted in highest increase in area, dry matter accumulation and chlorophyll content of flag leaf at 50 per cent flowering over untreated control plants. GA-treatment also significantly increased leaf number and dry matter content of plants alongwith its partitioning towards sink, but reduced plant height. There was a substantial increase in sink size that ultimately led to higher grain yield in GA-treated and thereafter regenerated plants after forage cut. Application of 50 ppm concentration of GA was found to be the best in the present study.

(iii) Guar

663. GARG, B. K. AND UDAY BURMAN 2001. PHYSIOLOGICALASPECTS OF DROUGHT AND SALT TOLERANCE IN CLUSTERBEAN. Forage Res., 27 (1): pp. 1-10. Division of Soil-Water Plant Relationship, C. A. Z. R. I., Jodhpur-342 003, India

Clusterbean (*Cyamopsis tetragonoloba*) is one of the major **kharif** crops of drylands and is grown for vegetable, cattle feed, green manure, fodder and various industrial uses because of the occurrence of gum in its endosperm. The available information on physiological aspects of drought and salt tolerance of this crop has been reviewed in view of its wide cultivation in arid and semi-arid areas which are also highly prone to salinity stress.

ABSTRACTS OF PUBLISHED WORKS

Although clusterbean has been found to be highly drought tolerant crop but significant genotypic difference at the germination and other growth stages indicates the prospects of improvement of its drought tolerance capacity. Among many yield components affected by water stress, number of pods per plant appears most important trait for yield. Maintenance of adequate potassium in soil improves plant water relations, photosynthesis and yield of clusterbean. Early genotypes of clusterbean performed better under low rainfall conditions, while late genotypes outyielded the early type under good rainfall condition. However, planting of early and late genotypes in 1 : 1 ratio in alternate rows was found most appropriate for obtaining sustainable yields under diverse rainfall situations. Clusterbean has also been found to be moderately tolerant to salinity and a significant reduction in yield occurs only after a threshold level of salinity (6 dSm⁻¹) is reached. Reduction in number of pods and weight per seed are the primary factors responsible for decrease in yield under saline conditions. Flowering stage has been found to be most sensitive to salinity. Salt stress depressed the concentrations of N, Mg, K and P, whereas those of Ca, Na and Cl were significantly increased. Supplemental calcium alleviated the detrimental effects of NaCl salinity by decreasing Na absorption, enhancing Ca and K uptake and favourably influencing nitrogen metabolism. Tolerant genotypes of clusterbean experienced less metabolic alterations than sensitive genotypes. Several management practices have also been discussed for improvement of clusterbean production under drought and salinity stresses.

664. CHAMPA, R. AND K. SWARAJ 2004. QUALITATIVE CHANGES IN NODULE PROTEINS OF CLUSTERBEAN (CYAMOPSIS TETRAGONOLOBA TAUB.) WITH PROGRESS IN SENESCENCE Forage Res., 30 (3) : pp. 113-117. Department of Botany and Plant Physiology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

The qualitative changes in nodule proteins on senescence were carried out on 50 days old plants of clusterbean. Nodules of 3-8 mm diameter were selected for the purpose, as leghaemoglobin and protein content were found maximum in these nodules. Nodules were sliced under dissecting microscope into distal, middle and proximal portions. Leghaemoglobin and total nodule soluble protein contents were maximum in red/distal portion of nodule and minimum in green/proximal senescent portion. In order to identify proteins associated with nodule greening, proteins from different portions of the nodule were resolved by SDS-PAGE (5-20% acrylamide concentration gradient). Nineteen protein bands with molecular weight ranging from 5 kD to 56 kD were detected. Protein bands with molecular weight 43, 38, 34 and 22 kD were absent from green portion of nodules. However, two protein bands with molecular weight 25 and 24 kD appeared only in green portion of nodules.

665. SHUBHRA AND J. DAYAL 2005. IMPACT OF PHOSPHORUS APPLICATION ON LEAF CHARACTERISTICS, NODULE GROWTH AND PLANT NITROGEN CONTENT UNDER WATER DEFICIT IN CLUSTERBEAN Forage Res., 31 (3) : pp. 212-214. Department of Botany and Plant Physiology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Clusterbean, being a rainfed crop, is subjected to water stress at various stages and this water deficit affects foliage development, leaf area index and nitrogen content. Phosphorus, being an important macronutrient, plays an important role in plant growth and development. Therefore, present investigation in clusterbean genotype HG-365 was conducted to observe the effects of phosphorus on leaf characteristics, nodule growth and nitrogen content under water conditions. Water stress was created by withholding irrigation at three growth stages of the plant i. e. vegetative, flowering and pod-filling stage. Phosphorus was supplied as 75, 150 and 300 mg/pot in two

split doses at weekly interval in the form of KH_2PO_4 . Leaf number, leaf area and nodule growth (fresh and dry weight) declined under water stress and improved by phosphorus application at successive growth stages. Both number of leaves and leaf area increased with the age of plant. Nodule growth (nodule fresh and dry weight) was maximum at flowering stage. Nitrogen content of plant (leaf, stem and root) declined under water stress and improved by phosphorus application. Nitrogen content of leaf and root was maximum at flowering stage. On the contrary, maximum nitrogen content of stem occurred at pod-filling stage. The present investigation revealed that phosphorus treatment proved effective to some extent alleviating the effect of water deficit in clusterbean.

666. PUNIA, R. C., R. P. S. KHARB AND O. S. DAHIYA 2006. SEED DEVELOPMENT AND PHYSIOLOGICAL MATURITY IN CLUSTERBEAN [CYAMOPSIS TETRAGONOLOBA (L.) TAUB.]. Forage Res., 32 (2): pp. 118-121. Department of Seed Science and Technology, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Three clusterbean varieties attained the ability to germinate in about 19 days of pod development period. The physiological maturity attained in 40 days (HG 365) and 47 days (HG 75 and FS 277) after the mean time to 50 per cent flowering. The harvestable maturity occurred after two weeks of the physiological maturity in all the varieties. The characters like change in seed and pod colour over different stages of development and maturation were found reliable indicators of the physiological and harvestable maturity.

 PAWAR, A. B., U. S. GAIKWAD, A. D. KADLAG AND B. D. TAMBOLI 2010. NUTRITIONAL STATUS OF FODDER TREE LEAVES AND SHRUBS OF SCARCITY ZONE OF MAHARASHTRA. Forage Res., 36 (3): pp. 125-127. National Agricultural Research Project, Zonal Agricultural Research Station, Krishak-Bhavan, Solapur-413 002 (M. S.), India

The intent of this experiment was to figure out the nutritive value of fodder tree leaves and shrubs of dryland area in Solapur district, Maharashtra. The climate of this region is characterized by a relatively low annual rainfall (594.8 mm) and it varies from 594.8 to 655.6 mm from year to year. Temperature during winter is 22.5° C and summer 40.1°C. The average annual total evaporation is 2817.7 mm. Leaves of fodder trees and shrubs were selected and analyzed for dry matter, organic matter, ash, crude protein, neutral detergent fiber, acid detergent fiber, hemicelluloses and proximate composition. The mean per cent values for dry matter, crude fiber, crude protein, neutral detergent fiber, acid detergent fiber and hemicelluloses were 32.66, 22.60, 4.79, 55.75, 47.97 and 7.81 per cent, respectively. The average per cent of ash, calcium and phosphorus in fodder tree leaves and shrubs was 8.28, 2.18 and 0.235, respectively. Whereas iron, zinc and manganese were 3419, 51 and 252 μ g/g, respectively. The fodder tree leaves and shrubs are good source of protein, fiber and minerals.

(iv) Miscellanious

668. BISHT, J. K., PRAMOD KUMAR, S. CHANDRA, R. D. SINGH AND V. P. MANI 2002. EFFECT OF GIBBERELLIC ACID ON GROWTH, PHOTOSYNTHESIS AND FORAGE PRODUCTION OF BHIMAL (GREWIA OPTIVA J. R.) Forage Res., 27 (4) : pp. 247-250. Vivekananda Parvatiya Krishi Anusandhan Sansthan (ICAR), Almora-263 601 (U. P.), India

In the present study, one year old saplings of *Grewia optiva* (Syn. *G. oppositifolia* Buch Ham. Ex. D. Dun) were sprayed with three concentrations of GA_3 (100, 200 and 300 ppm) and water as a control. Foliar application of GA_3 resulted in an increase in shoot length, stem girth, leaf area, green/dry forage, rates of photosynthesis and transpiration in *G. optiva*. Foliar spray of GA_3 @ 200 ppm was found the best among the different concentrations. GA_3 has been reported beneficial in hastening plant growth, forage production and photosynthesis in *G. optiva*.

669. ANITA, M. R., S. LAKSHMI, S. JANARDANAN PILLAI AND P. SARASWATHI 2003. NUTRIENT UPTAKE BY GUINEA GRASS (*PANICUM MAXIMUM J.*) UNDER VARYING LIGHT INTENSITIES *Forage Res.*, 29 (3) : pp. 107-109. Department of Agronomy, College of Agriculture, Vellayani, Kerala-695 522 (Kerala), India

An investigation was undertaken in the Instructional Farm, College of Agriculture, Vellayani to find out the nutrient uptake by guinea grass varieties under varying shade levels during 2001-02. It was found that there was a significant increase in uptake of N, P and K with decrease in shade levels. Higher nutrient uptake was recorded at zero per cent shade level. Among the varieties hamil recorded the highest nutrient uptake compared to haritha. Higher doses of potassium (150 kg/ha) resulted in higher uptake of nitrogen, phosphorus and potassium by the plant.

670. KRISHNA, V., B. C. CHANNAKESHAVA AND K. P. VISWANATHA 2006. INFLUENCE OF GROWTH REGULATORS, MICRONUTRIENTS AND PHEROMONE ON CROP GROWTH, FLOWERING BEHAVIOUR AND SEED YIELD IN LUCERNE. Forage Res., 32 (2): pp. 98-100. Department of Seed Science and Technology, University of Agricultural Sciences, GKVK, Bangalore-560 065 (Karnataka), India

An experiment was carried out in lucerne cv. T-9 to study the effect of growth regulating chemicals, GA3 (0.005 per cent)+IAA (0.001 per cent) micronutrients Bo (3 ppm)+Mo (5 ppm) and pheromones Bee-Q (0.175 per cent) + Jaggery solution (1 : 2) at bud formation stage, 50 per cent flowering stage and both the stages on crop growth and flowering behaviour and in turn their effect on seed yield in lucerne. The treatments were imposed after first cut (45 days after sowing). The results of field experiment conducted at main Research Station, Hebbal, Bangalore revealed that spraying of GA3 (0.005 per cent) + IAA (0.001 per cent) at both bud formation and 50 per cent of flowering stage (T3) influenced the crop growth and flowering behavior of the crop. The highest plant height (91.3 cm) were number of flowers (342), number of pods (62.0) and number of branches were recorded. All these treatments showed significantly higher seed yield (253 kg/ha) compared to control (145 kg/ha). Plants sprayed with Bo (3 ppm) + Mo (5 ppm) at both bud formation and 50 per cent flowering recorded the highest seed yield (290 kg/ha).

671. PAL, A. K., S. SINGH AND D. K. DE 2008. EVALUATION OF REGROWTH POTENTIALITY UNDER CUTTING MANAGEMENT IN RICEBEAN AND ITS PHYSIOLOGICAL INDICATORS Forage Res., 34 (3): pp. 136-140. Department of Plant Physiology, Bidhan Chandra Krishi Viswavidyalaya,, Mohanpur-741 252, Nadia (West Bengal), India

A field experiment was conducted at Gayeshpur, West Bengal during **kharif** 2006 to assess the regrowth potentiality and seed yield after forage harvest at 65 days after sowing in six genotypes of ricebean. Bidhan 1 and KRB 233 registered highest green fodder and dry matter yield. Genotype KRB 106 exhibited highest regrowth index (0.73) alongwith highest percentage (75.00) of plants surviving after forage cut and had substantial range of seed yield with early flowering habit. KRB 247 and KRB 105 with moderate regrowth index (0.60) featured in highest seed yielding ability after forage harvest. Correlation studies indicated greater impact of residual root dry matter and leaf area than above-ground dry matter in determining biomass of regenerated plants at the end of defoliation-regrowth cycle. Nitrogen reserve in root emerged to be the primary nutrient contributor of regrowth, while carbohydrate reserve did not seem to have any significant role in sink activity of regrowing shoot.

672. PAL, A. K., D. RAI AND D. K. DE 2009. EVALUATION OF RICEBEAN GENOTYPES FOR SALT TOLERANCE DURING EARLY SEEDLING GROWTH AND PHYSIOLOGICAL BASIS OF TOLERANCE. Forage Res., 35 (2): pp. 73-79. Department of Plant Physiology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur-741 252, Nadia (West Bengal), India

Fifteen genotypes of ricebean were screened for salt tolerance at germination and early seedling stage at a salinity level of 12 dS/m imposed by a mixture of NaCl and CaCl₂. The genotypes showed wide ranges of variation for germination percentage, salt tolerance index as well as reduction in seedling length, fresh and dry weight under stress over non-stressed control. Clustering of genotypes on the basis of principal component vectors (PC 1 and PC 2) and genetic similarity (Euclidean distance) revealed three groups. Bidhan 1, Bidhan 2 and KRB 8 constituted the most tolerant group with salt tolerance index ranging from 65.43-73.46 per cent, KRB 9, KRB 19, KRB 105 and KRB 106 showing values of tolerance index between 34.31 to 39.26 per cent were found to be most susceptible genotypes. The remaining genotypes exhibited moderate to low salt tolerance. Further physiological studies indicated that KRB 106 (most susceptible) had much higher value of membrane injury but lower value of chlorophyll stability index at 12 dS/m than Bidhan 1 (most tolerant). Higher accumulation of proline and sugar in the leaves of Bidhan 1 at salinity helped the genotype in better maintenance of turgor in comparison with the susceptible genotype. Of the three antioxidative enzymes studied here, activity of peroxidase and superoxide dismutase increased at salinity stress in both the genotypes, while that of catalase decreased as compared with non-saline environment. Salinity adversely affected the level of nitrate reductase in leaves of 7-day old seedling in the present experiment. In contrast, the amylase enzyme in the germinating seeds registered enhanced activity at 24 h of germination at 12 dS/m in comparison to control and then declined gradually. The extent of increase was much higher in tolerant genotype than the susceptible one.

673. KAPIL, A. K., N. K. BANSAL AND SATYAWAN ARYA 2010. WHEAT STRAW RETRIEVAL FROM COMBINE HARVESTED FIELD FOR USE AS CATTLE FEED. Forage Res., 36 (3) : pp. 146-149. Department of Farm Machinery and Power Engineering, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

Wheat is the major crop of India. It is estimated that more than 50 per cent area under wheat is harvested with combine harvester in Harvana and it is increasing continuously due to shortage of farm labour in the state. Combine harvesting leaves behind enormous quantity of straw which is either burnt in the field or requires a lot of energy in straw management. There is about 47 per cent shortage of cattle fodder in India. Therefore, it is necessary to conserve the straw for cattle feed to ensure the milk production and animal power. With the introduction of straw combines, the problem of wheat straw is managed and comparable quality of wheat straw is obtained. It also increases their farm income. Keeping this in view, a study was carried out at farmers' field in Karnal district to check the performance evaluation and economic feasibility of straw combine in wheat variety PBW 343. The field capacity of the straw combine was found to be 0.48 ha/h with a forward speed of 3.4 km/h and width of the cutter bar was 2.02 m. The efficiency of the straw combine was found to be 70 per cent. The fuel consumption was found to be 4.97 l/h or 9.74 l/ha. Straw recovery was found to be 28 g/ha and average straw recovery was 54 per cent. The average length of bhusa was 2.3 cm. The moisture content of the straw was 8.5 per cent on wet basis. The average height of cut was 52 mm. The average straw split was found to be 91.50 per cent. During operation of straw, reaping the grain recovery was found to be 100 kg/ha (grain collected in the pan). The cost of operation was found to be Rs. 1150/ha when farmer used his own machine and Rs. 1500/ha when used on custom hire basis. The net return from one hectare of wheat straw was Rs. 8450 and 8100 when farmer used his own machine and on rent, respectively, when the rate of *bhusa* was Rs. 300/q. The total straw availability by using straw combine in the state was around 2.75 million tonnes and additional 0.7 million tonnes straw may be collected if leftover 20 per cent area is also covered by the machine which is presently burnt by the farmers and this chopped straw is used for cattle feed.

 674. URMILA DEVI AND SHASHI KANTA VARMA 2011.CONSTRAINTS FACED BY FARM WOMEN IN GETTING TECHNOLOGICAL INFORMATION FOR FODDER CROP. Forage Res., 36 (4): pp. 239-241. Department of Home Science Extension Education and Communication Management, CCS Haryana Agricultural University, Hisar-125 004 (Haryana), India

A study on various constraints faced by the farm women in utilizing the technical information regarding different fodder crops was conducted in two districts of Haryana. Further one block from each district and two villages from each block were selected purposively. Thus, four villages from two districts were selected purposively. So, proportionate random samples were drawn from each village comprising 165 rural women who were selected purposively. The results of the study showed that among all the constraints, in Jind district most serious constraints faced by berseem and sorghum growers were lack of technical expertise, physical and time constraints and in wheat cultivation physical and time constraints were perceived most serious constraints by the respondents.

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- 2. To disseminate the knowledge of scientific agriculture and technology in the production of forages.
- 3. To provide facilities for association and conference among forage research scientists and for the encouragement of close relationship between the scientists, cultivators, industrialists and traders of feeds and fodders.

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