GENETIC ASSOCIATION BETWEEN TWO PANICLE CHARACTERS IN SORGHUM

B. Y. KULLAISWAMY AND J. V. GOUD
Department of Agricultural Botany, College of Agriculture, Dharwad 580 005, India.

THE study of inheritance and linkage relationship of qualitative characters in sorghum is still in infancy. Eight of the possible ten linkage groups were reported in 1966 and only recently the other two (ninth and tenth) groups have been reported[1,2] but even in these, only two to three genes could be mapped. Hence the present study on the inheritance and interrelationship of two qualitative characters-panicle shape and panicle density is timely.

The parents IS8744 and IS1134 were selected from the germplasm collections, maintained by the Sorghum Breeder, Regional Research Station, Dharwad, for hybridization. The cross was effected in June 1978. The subsequent generations, F_1, F_2 and F_3 were raised at the College of Agriculture, Dharwad. 1438 plants comprised the F_2 population; out of these 72 plants were selfed at random, to advance for F_3 generation for confirmation of the F_2 ratios. The number of plants in F_3 progenies varied from 145-250. The recombination value was worked out by the direct method[8]

The segregation pattern (table 1) in the F_2 population revealed that both the characters under study were inherited monogenically which was confirmed by the F_3 breeding behaviour (table 2). Oval and loose panicles showed dominance over spindle and compact panicles, respectively. Ayyangar[3] found spindle-shaped panicle dominant over the oval shape. The gene symbol *Op* was later assigned[4] for the factor identified. Jayaramaiah and Goud[5] found the oval shape of the panicle dominant over the cylindrical as found in the present study in which the dominance relationship and the F_2 ratio obtained for panicle density agree with the reports of Ayyangar and Ayyar[6] and Ghawghawe *et al*[7], who

TABLE 1

Morphology of parents, F_1 and F_2 ratios

Characters	Parents IS8744	Parents IS1134	F_1	F_2 segregation			X^2	Probability with F_2 ratio
Panicle shape	Spindle	Oval	Oval		Oval	Spindle		
				Obs	1050	388	3.01	0.1–0.5 (3:1)
Panicle density	Compact	Loose	Loose		Loose	Compact		
				Obs	1066	372	0.58	0.5–0.3 (3:1)

TABLE 2

F_3 Breeding behaviour for two characters in the sorghum cross IS8744 × IS1134

Character		Number of families: Breeding true for	Segregating into 3:1	Breeding true for	X^2	Probability
Panicle shape		Oval		Spindle		
	O	20	30	22		
	E^1	18	36	18	2.11	0.50-0.30
Panicle density		Loose		Compact		
	O	16	34	22		
	E^1	18	36	18	1.22	0.70-0.50

O, observed; E^1, expected on 1:2:1 ratio.

TABLE 3

Joint segregation of panicle shape (3:1) with panicle density (3:1)

Joint ratio	Assumption	Obs/Exp	Phenotypes AB	Ab	aB	ab	X^2	Probability
9:3:3:1		Obs	752	298	314	74		
	Independence	Exp	808.9	269.6	269.6	89.9	17.1	< 0.01
	Linkage	Exp	783.7	294.7	294.8	64.7	3.9	0.3-0.2
	(Cross-over value 42.4%)							

gave gene symbol Pa_1 for the character concerned. The joint segregation (table 3), revealed that the factors Pa_1 (panicle density) and *Op* (panicle shape) were linked with a cross-over value of 42.43 Morgan Units. Two genes: Pa_1 and Z (pearly grains), were found to be linked by Ayyangar and Ayyar[6]. Ghawghawe *et al*[7] added another four factors, *Bs*, *Stp*, *Oy* and *Gh* to this group and termed this as fourth linkage group. The linear order was as follows:

Bs(25.8) *Z*(16.39) Pa_1? *Stp*(21.02) *Oy*(41.5)*Gh*.

The gene *Op* in the present study was found to be associated with Pa_1. As Pa_1 was located[7] in the fourth linkage group, it was inferred that the gene *Op* also belonged to the very group. The recombination value between *Op* and Pa_1 was 42.43 Morgan Units. The location of the gene *Op* with respect to other loci already mapped, could not be determined for want of the required contrasting characters in the cross studied. However, as the gene *Op* was located at a distance of 42.43 Morgan Units to Pa_1, it may be that the gene *Op* would lie beyond *Bs* or it may lie between *Stp* and *Oy* or *oy* and *Gh*. The exact location of the gene *Op* with respect to other loci, cannot be determined because Ghawghawe *et al*[7] did not indicate the distance between Pa_1 and *Stp*. The total mapped genes in this fourth linkage group of sorghum with the addition of *Op* from the present study would thus be seven.

15 July 1982; Revised 18 September 1982

1. Kullaiswamy, B. Y. and Goud, J. V., *Theor. Appl. Genet.*, 1982 (In press).
2. Kullaiswamy, B. Y. and Goud, J. V., *SABRAO.*, 1982 (In press).
3. Ayyangar, G. N. R., *J. Madras Univ.*, 1939, **11**, 131.
4. Schertz, K. F. and Stephens, J. C., *Tech. Mono. Texas. Agric.*, Exp. Stn., 1966, **3**, 42.
5. Jayaramaiah, H. and Goud, J. V., *Indian J. Genet.*, 1982 (In press).
6. Aygar, G. N. R. and Ayyar, M. A. S., *Proc. Indian Acad. Sci.*, 1938, **B8**, 100.
7. Ghawghawe, B. G., Bhale, N. L. and Shekar, V. B., *Indian J. Genet.*, 1966, **27**, 205.
8. Kolhe, A. K., *Indian J. Genet.*, 1972, **32**, 35.

A NEWLY INTROUDCED FODDER LEGUME (*HEDYSARUM CORONARIUM*—FAMILY LEGUMINOZAE JUSS)

V. ISWARAN, M. P. NUTI* AND S. CASELLA*
Division of Microbiology, Indian Agricultural Research Institute, New Delhi 110 012.
*University of Pisa, Institute of Microbiology, Agraria, Pisa, Italy.

HEDYSARUM Coronarium is a mediterranean forage legume able to grow, survive and give valuable fodder production, in extremely unfavourable conditions in clay/sandy soils upto pH 8.5-9, hot dry wet summers, etc. Its potential had been overlooked where nitrogen of chemical synthesis was not a limiting factor for crop production. Testing of rhizobia strains for the improved production of this crop was carried out by the senior author at the *Institue of Microbiology Agraria* Italy in 1981.

To determine symbiotic effectiveness, seeds of *H. coronarium* were grown in polythene pots 25 cm in dia containing substrate made from an equal mixture (V/V) of vermiculite and river sand. Surface sterilized germinated seeds were sown (30/pot) and inoculated wherever necessary with heavy suspensions prepared