

ADDITIONAL LINKAGES IN *SORGHUM*

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GHAWGHAWE, Bhale and Shekar (1966) have summarized eight linkage groups in *Sorghum vulgare* (Pers.) covering 38 gene loci. Confirmatory evidence regarding the relationship of some of these genes was gathered in the work which was carried out subsequently. This work also resulted in the identification of loci for three additional characters, coleoptile colour (red/green), basal spikelet colour (red/white) and seed shape (umbonate/round) in two of the eight linkage groups. The results of the study concerning the locations of the new genes are presented in this paper.

MATERIALS AND METHODS

Four crosses involving five varieties of *jowar* (*Sorghum vulgare* Pers.), A.S.158, *Redar*, *Dodania*, *Vidul* and MS.CK.-60, were utilized for this study. The total F₂ population of the four crosses grown comprised 1,000 individuals. Detailed observations were recorded adopting the standard method suggested by Rangaswamy Ayyangar (1943). In all, 24 different plant characters were studied, but only the data regarding the new characters and nine other characters which bear linkage relationship with them are included in the present paper.

As for gene symbols, Ayyangar, Rao and Nambiar (1935) have used **U u** to designate the allelic pair umbonate vs. round grain shape. For coleoptile colour and basal spikelet colour, the symbols **Rc rc** and **Bsr bsr** respectively are used.

RESULTS AND DISCUSSION

The F₂ data regarding the new characters of all the four crosses are given below. The results of the remaining characters were in agreement with monogenic segregation, already reported in the earlier paper. The new characters, studied independently, have also shown simple monohybrid type of inheritance.

Joint segregation of two characters taken together at each time in all possible combinations was studied. Linkage was detected in 49 combinations where the chi-square value exceeded the theoretical value at 5 per cent level. The dihybrid chi-squares in these cases were partitioned into two monohybrid chi-squares and a chi-square due to linkage. The latter was found to be

significant in all the cases. The cross-over values of the linked genes in such combinations were then computed by the product-ratio method. The results of these 49 combinations are given in Table 2.

TABLE 1
F₂ segregation for individual characters

Characters	Symbols	Total F ₂ popula- tion	Phenotypic class frequencies		χ ²	P
			Domi- nant	Reces- sive		
<i>MS. CK.60 × A.S. 158</i>						
Basal spikelet colour: Red/white	<i>Bsr bsr</i>	288	218	70	0.074	0.80 to 0.70
Sheed shape: Umbonate/round	<i>U u</i>	288	215	73	0.0185	0.90 to 0.80
<i>MS. CK. 60 × Dodania</i>						
Coleoptile colour: Red/green	<i>Rc rc</i>	218	173	45	2.2	0.20 to 0.10
<i>MS. CK. 60 × Vidul</i>						
Coleoptile colour: Red/green	<i>Rc rc</i>	210	159	51	0.05	0.90 to 0.80
<i>MS. CK. 60 × Redar</i>						
Coleoptile colour: Red/green	<i>Rc rc</i>	284	217	67	0.075	0.80 to 0.70
Basal spikelet colour: Red/white	<i>Bsr bsr</i>	284	215	69	0.075	0.80 to 0.70

TABLE 2
Linked characters with their cross-over values

Linkage between pair of genes	Observed frequency under				χ ² Linkage for 1 D.F.	P	Cross-over value
	AB	Ab	aB	ab			
1	2	3	4	5	6	7	8
<i>MS. CK.60 × A.S. 158</i>							
Wmd wmd-D d	206	0	0	82	343.80	above 0.001	Nil
Wmd wmd-P p	168	38	38	44	43.55	—do—	29.07 ± 2.21

TABLE 2—Contd.

1	2	3	4	5	6	7	8
Dd-Pp	168	38	38	44	43.55	above 0.001	20.07 ± 2.21
Yag ysg-Rsg rsg	215	3	6	64	225.19	—do—	4.09 ± 0.71
Yag ysg-Ra ra	205	13	11	59	170.09	—do—	9.0 ± 1.23
Yag ysg-Bsr bsr	212	6	6	64	214.47	—do—	4.64 ± 0.82
Yag ysg-Lr lr	212	6	6	64	214.47	—do—	4.64 ± 0.82
Yag ysg-R r	206	12	4	66	214.47	—do—	5.45 ± 1.02
Rsg rsg-Ra ra	209	12	7	60	184.74	—do—	6.97 ± 1.13
Rsg rsg-Bsr bsr	204	7	4	63	210.12	—do—	4.19 ± 0.79
Rsg rsg-Lr lr	209	12	3	64	211.26	—do—	4.91 ± 0.93
Rsg rsg-R r	207	14	3	64	206.72	—do—	4.96 ± 0.92
Ra ra -Bsr bsr	208	8	10	62	195.58	—do—	6.41 ± 1.004
Ra ra -Lr lr	200	16	12	60	166.02	—do—	10.00 ± 1.27
Ra ra - R r	196	20	14	58	146.39	—do—	12.47 ± 1.44
Bsr bsr - Lr lr	208	10	4	66	222.83	—do—	4.47 ± 0.84
Bsr bsr - R r	206	12	4	66	214.47	—do—	5.001 ± 0.89
Lr lr - R r	206	6	4	72	261.95	—do—	3.53 ± 0.75
R r - U u	165	45	50	28	6.72	0.01- 0.001	40.4 ± 2.65
					<i>MS. CK. 60 × Dodania</i>		
Rc rc - P p	161	12	10	35	85.67	above 0.001	11.36 ± 1.54
					<i>MS. CK.60 × Vidul</i>		
Rc rc - Wmd wmd	134	25	20	31	40.89	—do—	23.36 ± 2.25
Rc rc - D d	134	25	20	31	40.89	—do—	23.36 ± 2.25
Rc rc - P p	152	7	11	40	110.98	—do—	9.028 ± 1.41
Wmd wmd - D d	154	0	0	56	229.08	—do—	Nil
Wmd wmd - Gep gep	130	24	25	31	36.31	—do—	26.37 ± 2.47
Wmd wmd - P p	132	22	31	25	20.74	—do—	29.90 ± 2.64
D d - Gep gep	130	24	25	31	36.31	—do—	26.37 ± 2.47
D d - P p	132	22	31	25	20.74	—do—	29.90 ± 2.64
					<i>MS. CK. 60 × Redar</i>		
Rc rc - Wmd wmd	184	33	29	38	45.22	—do—	25.45 ± 2.07

TABLE 2—Contd.

	1	2	3	4	5	6	7	8
Rc rc - D d		184	33	29	38	45.22	above 0.001	25.45±2.07
Rc rc - P p		205	12	10	57	166.31	—do—	7.82±1.08
Wmd wmd - D d		213	0	0	71	284.00	—do—	Nil
Wmd wmd - P p		175	38	40	31	18.93	—do—	32.57±2.33
D d - P p		175	38	40	31	18.93	—do—	32.57±2.33
Ysg ysg - Rsg rsg		208	4	5	67	240.47	—do—	3.41±0.79
Ysg yst - Ra ra		196	16	7	65	198.33	—do—	7.72±1.12
Ysg ysg - Lr lr		204	5	4	68	245.40	—do—	3.92±0.79
Ysg ysg - Bsr bsr		208	4	7	65	225.97	—do—	4.12±0.89
Ysg ysg - R r		205	7	4	68	234.38	—do—	4.21±0.87
Rsg rsg - Ra ra		199	14	4	67	218.89	—do—	5.78±1.04
Rsg rsg - Lr lr		204	9	7	64	209.63	—do—	5.99±1.02
Rsg rsg - Bsr bsr		208	5	7	64	218.89	—do—	4.60±0.02
Rsg rsg - R r		201	12	8	63	196.11	—do—	7.20±1.09
Ra ra - Lr lr		192	11	19	62	170.42	—do—	10.45±1.30
Ra ra - Bsr bsr		198	5	17	64	196.11	—do—	6.92±1.12
Ra ra - R r		189	14	20	61	158.21	—do—	12.29±1.43
Lr lr - Bsr bsr		203	8	12	61	187.74	—do—	7.36±1.12
Lr lr - R r		205	6	4	69	247.89	—do—	4.03±0.93
Bsr bsr - R r		201	14	8	61	183.04	—do—	8.03±1.18

(Phase of linkage in all cases : coupling)

By grouping together the loci showing mutual association, it is possible to recognize two discrete linkage groups. 1. **P, Wmd, D, Gep** and **Rc**; 2. **Ra, Rsg, Ysg, Lr, R, Bsr** and **U**.

These correspond to the 3rd and 8th linkage groups described by Ghawghawe *et al.* (1966).

The new gene **Rc** is therefore located in the 3rd linkage group while the other two genes **Bsr** and **U** are in the 8th linkage group.

PLACEMENT OF THE NEW GENES

The data collected in the present paper fully support the linear order of genes in the 3rd and 8th linkage groups previously reported. The positions of the new genes in the linkage groups are discussed below :

Rc rc—*Coleoptile (Red/green)*.—The cross-over percentage between the genes **P** and **Rc**, ascertained in F_2 of three different crosses, MS.CK.-60 \times *Vidul*, MS.CK.-60 \times *Dodania* and MS.CK.-60 \times *Redar*, were 9.08, 11.36 and 7.82 respectively with an average of 9.40. The cross-over between the genes **Rc** and **D** as observed in two crosses, MS.CK.60 \times *Vidul* and MS.CK.60 \times *Redar* were 23.36 per cent. and 25.46 per cent. respectively with an average of 24.41 per cent., whereas between **P** and **D** these values were 29.90 per cent. and 32.57 per cent. respectively with an average of 31.23 per cent. It is evident therefore that the factor **Rc** lies between **P** and **D** and at a distance of 9.40 map units from **P**.

Stephens and Quinby (1939) have reported the location of the gene, **Rs** (Red stem colour) in between the genes, **P** and **D**, at a distance of 16.4 map units from **P**. The new gene **Rc** lies, at a distance of 9.4 map units from **P**. It is inferred, therefore, that the new gene **Rc** lies in between **P** and **Rs**. The arrangement of the four genes and the distances between them would, therefore, be **P** (9.40) **Rc** (7.0) **Rs** (14.83) **D**.

Bsr bsr—*Basal spikelet (coloured/colourless)*.—The cross-over values observed in two crosses MS.CK.-60 \times A.S.158 and MS.CK.-60 \times *Redar*, clearly point out that the two loci **Bsr** and **Rsg** lie in between **Ra** and **Ysg**. It is not quite clear, however, whether the order should be **Ra**, **Bsr**, **Rsg**, **Ysg** or **Ra**, **Rsg**, **Bsr**, **Ysg**. Since evidence in support of the former arrangement is strong, it has been provisionally adopted in the present paper.

The cross-over values between the genes **Ra** and **Bsr** were observed to be 6.41 per cent. and 6.92 per cent. respectively with an average of 6.66 per cent. and between **Bsr** and **Rsg** to be 4.19 per cent. and 4.60 per cent. with an average of 4.39 per cent. The above two averages were exceeded by the cross-over value between **Ra** and **Rsg** (6.97) in the cross—MS.CK.-60 \times A.S.518. This suggests placement of **Bsr** in between **Ra** and **Rsg**, so that the three loci are in the linear order of **Ra**, **Bsr**, **Rsg**, so that the three loci are in the linear order of **Ra**, **Bsr**, **Rsg**. In the same cross the cross-over values between **Bsr** **Rsg** and **Rsg** **Ysg** were found to be 4.19 per cent. and 4.09 per cent. respectively. Both the values were exceeded by the cross-over between **Bsr**—**Ysg** (4.64%). This indicates that the linear arrangement of these genes is **Bsr**, **Rsg**, **Ysg**. In the other cross, MS.CK.-60 \times *Redar*, the observed value between **Ysg** and **Bsr** (4.12%) is greater than that of **Ysg**—**Rsg** (3.41%) and these two values are exceeded by the cross-over between **Ra**—**Ysg** (7.72%). This lends further support to the placement of **Bsr** between the loci **Ra** and **Rsg**. The genes therefore, with their distances lie in the order of **Ra** (6.66) **Bsr** (4.39) **Rsg** (3.75) **Ysg**.

U u—*Grain (umbonate/round)*.—The cross-over value between **U** and **R** in the cross MS.CK.-60 \times A.S.158 was observed to be 40.4 per cent. whereas **U** showed independent assortment with **Ra**, **Ysg**, **Lr**, etc. It is evident therefore that the distance of **U** from the latter loci is greater than its distance from **R**. This leads to the placing of **U** at a distance of 40.4 per cent. from **R** but away from **Ra**.

With the addition of the new genes the two groups can now be summarized as :

Group 3: **P** (9.40) **Rc** (7.0) **Rs** (14.83) **D** (0.0) **Wmd** (26.37) **Gep** (43.1)
Mu.

Group 8 : **Ra** (6.66) **Bsr** (4.39) **Rsg** (3.75) **Ysg** (3.90) **Lr** (3.78) **R** (40.4) **U**.

SUMMARY

Study of linkage was carried out in the F_2 population of four crosses involving five parents, A.S.158, *Dodania*, *Vidul*, *Redar* and male sterile CK-60.

Three new gene loci, **Rc rc** (coleoptile colour red/green) **Bsr bsr** (basal spikelet colour red/white) and **U u** (Grain shape-umbonate/round) were indentified for the first time. The locus **Rc** was placed in between **P** and **Rs** at a distance of 9.40 from **P** in linkage group No. 3.

The remaining two loci, **Bsr** and **U**, were found to be in linkage group No. 8, the position of the **Bsr** being in between **Ra** and **Rsg** at a distance of 6.66 from **Ra**. **U** was observed to lie at a distance of 40.4 from **R** but away from **Ra**.

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