

A provisional map of the yellow chromosome of *Pharbitis Nil*

by

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With 1 Text-figure

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The yellow linkage group was established in 1928 (IMAI 1929). At that time this group was known as containing only two genes, yellow and dusky. Two years later, it developed in this way: "The yellow linkage group is composed of five genes, yellow (y), dusky (dy), light-1 (lt1), deformed (de) and speckled-reduced (sp-r). The frequency of recombination for y and dy is 1.0 per cent, Light-1 is linked rather closely with y and dy. Speckled-reduced is linked with y at about 28.5 per cent of recombination, and y with de at about 15 per cent of recombination" (IMAI 1931b). The genes constituting the yellow linkage group are regarded as arranged in the yellow chromosome. Owing to the incomplete knowledge with regard to their linkage relations, the drawing of the chromosome map of this group was not attempted as yet; and in this paper is presented a provisional map of the chromosome. By a recent investigation, IMAI (1933) adds a new gene bushy (bs) to this linkage group. The description of the characters of the genes is referred to IMAI's publication (1930).

MIYAZAWA (1918) first pointed out the dependent segregation of yellow and dusky, and later the recombination frequency was calculated to be 1.0 per cent by IMAI (1925). The calculation was made from the F_2 and F_3 data obtained by crossing normal with yellow dusky, which will give a coupling segregation. In Table 1 are shown their available data obtained by the writers recently, including those given by IMAI (1925).

Table 1. F_2 of cross, normal \times yellow dusky

Cross	+	y	dy	y dy	Total
IMAI's data	2873	20	18	867	3778
L25 \times YK	193	0	1	61	255
T32W \times YK	166	3	4	66	239
410 \times YKS	131	1	1	27	160
YK \times RF	711	5	4	241	961
YK \times 455	234	2	1	76	313
YK \times 9T	304	2	2	94	402
Total	4612	33	31	1432	6108

From the available coupling data the recombination frequency is calculated to be 1.1 per cent. Conducting backcross experiments, the writers, however, obtained a more reliable figure. Table 2 contains those data recorded last summer.

Table 2. Backcross, (normal \times yellow dusky) \times yellow dusky

Backcross	+	y	dy	y dy	Total
(410 \times YK) \times YK	54	0	0	51	105
YK \times (L25 \times YK)	275	4	4	223	506
(L25 \times YK) \times YK	47	1	0	74	122
Total	376	5	4	348	733

The data represent the gametic distribution of the linked assortment, and the estimation of recombination frequency can be made directly from the observed numbers. Thus the recombination percentage for y and dy is determined to be 1.3, which is the most reliable figure at present. The data segregating yellow and light-1 were given by IMAI (1931a). In Table 3, they are listed including new data.

Table 3. F_2 of cross, yellow \times lighth-1

Cross	+	y	lt1	y lt1	Total
421 \times 430 ¹	93	45	31	1	170
422 \times 435 ²	94	45	34	0	173
L25 \times YK	150	61	44	0	255
Total	337	151	109	1	598

¹ Segregation occurred into y^1 : y: y^1 lt1: y lt1, and ² into +: y^1 : lt1: y^1 lt1.

On account of the deficit of light-1 segregates, the calculation is made from the observed numbers of classes lt1:y lt1, giving 9.6 per cent of recombination. Owing to repulsion, the recombination frequency obtained is not very reliable, only indicating a rough value. For the relation between dusky and light-1 we have the data indicated in Table 4.

Table 4. F_2 of cross, dusky \times light-1

Cross	+	dy	lt1	dy lt1	Total
L25 \times YK	149	62	44	0	255

The segregation is also of repulsion of rather high intensity, and contains no double recessives. With these facts, the three genes, yellow, dusky and light-1, are linked each other rather closely; so that they are considered as grouping their loci in the chromosome with rather a short distance.

The linked segregation for yellow and deformed was shown by the data, which were some of F_2 from the cross of yellow by normal heterozygous for deformed (IMAI 1931a). Thirty-seven normal F_2 were selfed, and their progeny was examined, the summary of the observations being shown in Table 5.

Table 5. F_3 from F_2 having constitution, y +/+ de

No. of families	+	y	de	y de	Total
10	1076	298	—	—	1374
5	637	—	164	—	801
22	1840	739	656	30	3265

Owing to repulsion with about 15 per cent recombination, no homozygous families were observed in this examination. All families segregating for y and de were of repulsion and there were observed no coupling pedigrees. In Table 6 are collected available data for linkage of y and de.

Table 6. Available data of linkage for yellow and deformed

Origin	+	y	de	y de	Total
Previous F_2	431	217	128	3	779
New F_2	277	121	48	2	448
F_3	1840	739	656	30	3265
Total	2548	1077	832	35	4492

As the result of the low viability of deformed, a great deficit of its segregates was observed. Calculating on the basis of the observed numbers of the classes *de* and *y*, the recombination frequency is 20.1 per cent. The relation of deformed to dusky is found by the data in Table 7.

Table 7. F_2 from F_1 having constitution, *dy* +/+ *de*

Cross	+	<i>dy</i>	<i>de</i>	<i>dy de</i>	Total
T32 W × YK	136	68	33	2	239

The recombination frequency for *dy* and *de* is 23.9 per cent¹. The data from which this figure is obtained are rather small in number and we cannot attach much importance to it. However, if we compare it (23.9%) with that (20.1%) for *y* and *de*, the former is a little more than the latter. This shows, if reliable, the fact that the locus *de* is situated nearer to *y* than *dy*, the order of arrangement in the chromosome being *de—y—dy*. The difference 3.8 (= 23.9-20.1) may correspond to the recombination (1.3) of *y* and *dy*. The linkage between *lt1* and *de* is indicated by the data in Table 8.

Table 8. F_2 from F_1 having constitution, *lt1* +/+ *de*

Cross	+	<i>lt1</i>	<i>de</i>	<i>lt1 de</i>	Total
T30 × L25	147	47	14	1	209

The recombination frequency is 25.8 per cent. From this figure, if reliable, the order of the linear arrangement of the genes in the chromosome may be *de—y—dy—lt1*.

Speckled-reduced is a modifier working on speckled. The recombination frequency of *y* and *sp-r* was 28.5 per cent. The data from which the calculation was made were 124 + : 51 *y* : 57 *sp-r* : 5 *y sp-r*, all having the gene speckled (IMAI 1931a, Table 13). New data showing the same segregation are presented in Table 9.

¹ Owing to the low viability of deformed, the calculation is made on the basis of the observed numbers of the two *de* classes, as previously made. The same method is applied to those data given in Tables 8, 14 and 15. In Tables 14 and 15, the deficit, however, occurs in the willow segregates.

Table 9. F_2 of cross, yellow (speckled) \times speckled-reduced (speckled)

Cross	+	y	sp-r	y sp-r	Total
410 \times YKS	87	24	45	4	160

On account of the simultaneous segregation of one or more modifiers affecting the quantity of spots on the corollas, nearly continuous gradations occurred in the speckled flowers. Those with the smallest quantity of spots have a close connection with speckled-reduced flowers having the largest quantity of spots. On this condition, the discrimination of speckled and speckled-reduced segregates is difficult at times. The data listed in Table 9 and also in the following tables were taken with such a handicap, which may result in unbalanced distribution of the segregates. Therefore, the recombination frequency is calculated on the basis of the observed numbers of the two sp-r classes, giving 28.6 per cent¹, which is practically the same with the figure formerly calculated. The same cross showed also the linked segregation of dy and sp-r, the data of which are indicated in Table 10.

Table 10. F_2 of cross, dusky (speckled) \times speckled-reduced (speckled)

Cross	+	dy	sp-r	dy sp-r	Total
410 \times YKS	86	25	46	3	160

The recombination frequency is 24.8 per cent, presenting probably a proof for the relative loci of dy and y in the chromosome, or y—dy—lt1—sp-r. Crosses were made between speckled speckled-reduced and normal heterozygous for deformed; and in some of F_2 , a trihybrid segregation occurred. The first observation was made at the seedling stage, the results obtained being shown in Table 11.

Table 11. F_2 seedlings from F_1 having constitution, + sp sp-r/de + +

Cross	+	sp	de	de sp	Total
T32a \times 410	114	27	31	7	179
T32b \times 410	112	45	25	10	192
T32c \times 410	198	60	40	16	314
Total	424	132	96	33	685

¹ The same method is applied to the case of Table 10.

In these crosses, the majority of green-stemmed seedlings had no spots on their hypocotyls, only a few of them being speckled. This fact seems to have some connections with the occurrence of modifiers affecting the quantity of the speckles of the flower. Therefore we had no clue to distinguish sp and sp sp-r segregates at their seedling stage, and we were obliged to grow further the green-stemmed seedlings for this purpose. In summer a second observation was made on their flowers, the actual data being shown in Table 12.

Table 12. Later observation on green-stemmed seedlings from Table 11

Observed	sp	sp sp-r	de sp	de sp sp-r	Total
	94	36	8	4	

Although the data are much incomplete for several reasons, they show roughly an independent relation between de and sp-r. The locus sp-r is considered to be situated on the other side of de in the chromosome, the order of arrangement being de—y—dy—lt1—sp-r. In this arrangement, the relation of sp-r and de is expected to be nearly independent, as actually the case was.

Maple (m) was known to be independent of the genes of the known ten linkage groups, including y and dy of the yellow linkage group; therefore it was regarded as to constitute another linkage group (IMAI 1931b). In a recent observation¹, however, m shows linkage with y, dy and other genes of the yellow linkage group, and maple is now determined to be gathered under this group. HAGIWARA's data (1932) also include linkage of y and m. In Table 13 are collected the results indicating linkage between y and m.

Table 13. F₂ of cross, yellow × maple

Cross	+	y	m	y m	Total
ML × H70	73	26	27	2	128
ML × YK	180	82	80	8	350
D110 × W315	118	50	51	2	221
Total	371	158	158	12	699

¹ The former data were rather fragmental.

The frequency of recombination for *y* and *m* is 28.1 per cent. The maple locus includes another recessive variant willow (*m^w*). Willow, therefore, is expected also to be linked with *y*. Table 14 contains data showing this relation.

Table 14
F₂ from F₁ having constitution, *y* +/+ *m^w*

Cross	+	<i>y</i>	<i>m^w</i>	<i>y m^w</i>	Total
T32 W × YK ¹	134	65	36	4	239
YK × LW	257	82	65	6	410
Total	391	147	101	10	649

Notwithstanding the fact that the low viability of willow gave a deficit of its segregates, the data show linkage between *y* and *m^w* with 30.0 per cent of recombination, as expected. Nearly the same percentage of recombination was observed between *dy* and *m^w*, as indicated by the data in Table 15.

Table 15
F₂ from F₁ having constitution, *dy* +/+ *m^w*

Cross	+	<i>dy</i>	<i>m^w</i>	<i>dy m^w</i>	Total
T32 W × YK	133	66	36	4	239

The recombination frequency is 31.6 per cent. For the relation of willow to deformed, the writers obtained nearly an independent segregation, as presented by the data in Table 16.

The low viability of the recessives, especially the double recessive, results in an unbalanced distribution of the data. The segregation being nearly independent, the location of maple may be on the other side of deformed in the chromosome. On the same arm of the chromosome speckled-reduced is also situated. The distance of *sp-r* to *y* is 28.5²

¹ The data were obtained by selfing F₁, having a constitution of *y* +/+ *m^w*, which was given by crossing yellow with normal heterozygous for willow.

² This formerly calculated figure may be more reliable than the newly estimated one (28.6).

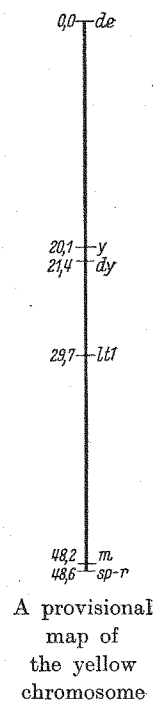
and that of *m* to the same is 28.1¹, *sp-r* and *m* being expected to be arranged very closely in the chromosome.

Table 16. F₂ from F₁ having constitution *de m^w / ++*

Cross	+	<i>de</i>	<i>m^w</i>	<i>de m^w</i>	Total
T30a × 410	45	20	12	3	80
T30 Wa × L25	65	17	17	3	102
T30 Wa × YK	53	28	16	2	99
T30 Wb × L25	59	16	19	3	97
T30 Wb × YK	58	15	19	7	99
T30 Wc × L25	28	11	6	2	47
T30 Wd × L25	37	12	11	2	62
T30 We × L25	39	12	8	2	61
T32 W × YK	164	35	40	0	239
T32 Wa × 410	66	22	21	4	113
T32 Wa × YK	191	66	77	11	345
T32 Wb × YK	187	57	49	18	311
Total	992	311	295	57	1655

Conclusion

The linkage relations of the known six genes, deformed, yellow, dusky, light-1, speckled-reduced and maple, are as follows: The recombination percentage of *de* is 20.1 with *y*, 23.9 with *dy*, 25.8 with *lt1* and nearly independent of *sp-r* and *m*; *y* is linked with *dy* at 1.3 per cent of recombination, with *lt1* at 9.6, with *sp-r* at 28.5 and with *m* at 28.1; *dy* is linked with *lt1* rather closely, with *sp-r* at 24.8 and with *m* at 31.6. Adopting the figures written in gothic, a provisional map of the yellow chromosome may be drawn, as presented in the accompanying diagram, with the following loci: *de* (0), *y* (20.1), *dy* (21.4), *lt1* (29.7), *m* (48.2) and *sp-r* (48.6).



Literature cited

HAGIWARA, TOKIO, 1932. Genetic studies of flower-colours in Japanese morning glories. IV. Botanical Magazine, Tokyo 44, 573—580 (Japanese).
 IMAI, YOSHITAKA, 1925. Two cases of close linkage in the Japanese morning-glory. Genetics 10, 456—469.

¹ This figure may be more reliable than 30.0.

- IMAI, YOSHITAKA, 1929. Linkage groups of the Japanese morning-glory. *Genetics* **14**, 223—255.
- , 1930. Description of the genes found in *Pharbitis Nil*. *Genetica* **12**, 297—318.
- , 1931a. Linkage studies in *Pharbitis Nil*. I. *Genetics* **16**, 26—41.
- , 1931b. Linkage studies in *Pharbitis Nil*. II. *Zeitschr. f. ind. Abst.- u. Vererbungsl.* **58**, 317—331.
- , 1933. Linkage studies in *Pharbitis Nil*. III. *Zeitschr. f. ind. Abst.- u. Vererbungsl.* **66**, 219—235.
- MIYAZAWA, BUNGO, 1918. Studies of inheritance in the Japanese *Convolvulus*. *Journ. Genetics* **8**, 59—82.
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