

The Presence of Male Determining Factor
in
Aphiochaeta xanthina Speiser

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CONTENTS

1. Introduction.
2. The origin, character and expressivity of *short arista*.
3. The reverse mutation from *short arista*.
4. Genetic peculiarity of the reverted wild-type male.
5. Hypothesis concerning the sex determination and the chromosomal constitution of the reverted wild-type male.
6. Analysis of the III-Y chromosome of the reverted wild-type male.
 - (a) *Sa* gene in the reverted wild-type male.
 - (b) The III-Y chromosome and three genes on the third chromosome.
7. Crossing over between X and Y chromosome in male.
8. The III-Y chromosome in the male of *occhi chiari* stock from Naples strain.
9. Discussion.
10. Summary.
11. Literature cited.

Fig. 1

Aphiochaeta xanthina Speiser.

A : Female B : Male (×10)

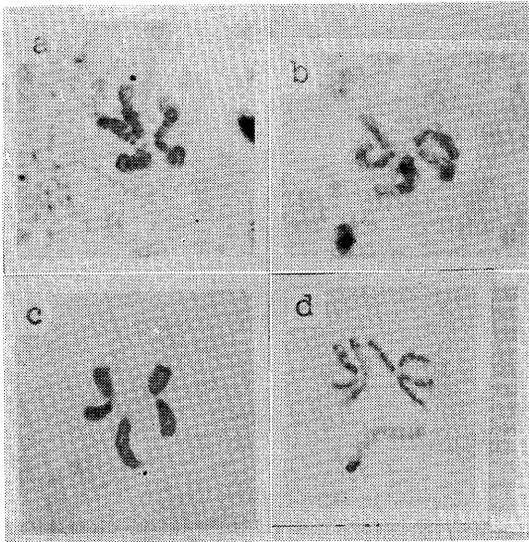
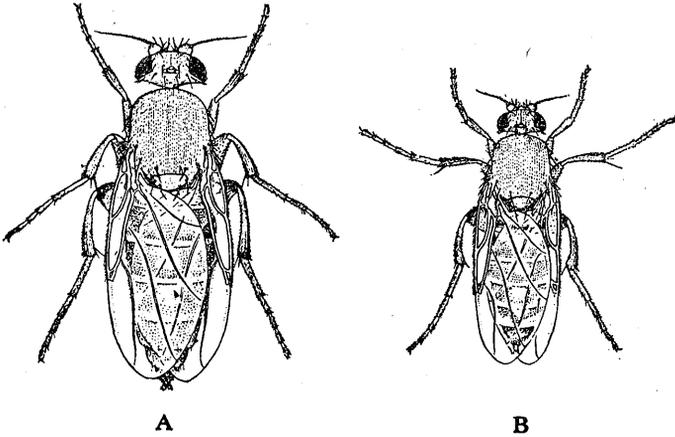


Fig. 2

Metaphase chromosome of *Aphiochaeta xanthina* Speiser.

(Consisted of two pairs of V shaped and one pair of rod shaped chromosome in mitosis.)

a, b : First meiotic metaphase in male (Naples strain).

c : The same (Okinawa strain).

d : Mitotic metaphase in larval ganglion cell (Naples strain).

Scale: 10/6 μ

Table 1. List of mutants in *Aphiochaeta xanthina* Speiser from Okinawa.

Mutant	Symbol	Chromosome	Appearance	Characteristics	Inheritance	Fecundity
<i>Abrupt</i>	<i>Ab</i>	I	Spontaneously	2nd longitudinal vein does not branch out, wing veins absent in various degrees except 1st and 2nd long. vein. At times show abnormality of head bristles and antenna.	Dominant, lethal in homo. Partially sex-linked.	Normal
<i>abrupt-4</i>	<i>ab⁴</i>	I	Spont. in <i>t</i> cross	End of 6th long. wing vein disappears. By low expressivity, in some individuals this appears only in one wing or phenotypically normal in homo.	Recessive, expressivity low. Partially sex-linked.	Slightly low
<i>Abrupt-low</i>	<i>Ab^l</i>		Spont.	Branch of 2nd long. wing vein does not extend to wing margin. A very slight wing vein deviation from normal. Individuals showing similar character appeared in wild-type stock and in cross experiments.	Dominant, low expressivity and penetrance.	Normal
<i>bar</i>	<i>b</i>	II	Spont.	Number of ommatidia of compound eye decreases and their arrangement become irregular.	Recessive	Normal
<i>brown</i>	<i>bw</i>	III	Spont. in <i>sa</i> cross	Changes body color especially of the thorax and legs to reddish brown instead of normal greyish yellow.	Recessive	Normal
<i>coarse</i>	<i>c</i>	III	Spont. in <i>b</i> stock	Causes irregular distribution and roughness of bristles on face and legs, especially on femur. Also causes in wing a tendency of fusing between 1st and 2nd long. vein at the point near proximal portion.	Recessive, semi-lethal in homo.	Low
<i>Delta</i>	<i>D</i>	III	Spont. in <i>M</i> cross	Wing margin uneven and veins thicker. Branch of 2nd long. vein is rare. In rare cases accompanied by <i>b</i> like eyes.	Dominant, lethal in homo.	Normal
<i>Delta-low 1</i>	<i>Dl¹</i>		Spont.	Similar to <i>D</i> but showed some flies whose 2nd long. wing vein branched out. Never accompanied by <i>b</i> like eyes.	Dominant, lethal in homo, penetrance is lower than <i>D</i> .	Normal
<i>Delta-low 2</i>	<i>Dl²</i>		Spont.	Similar to <i>D</i> but showed in most of individuals whose 2nd long. veins branched out. <i>b</i> like eyes do not appear.	Dominant, lethal in homo, penetrance and expressivity are lower than in <i>Dl¹</i> .	Normal
<i>Extra vein</i>	<i>Ex</i>		Spont. in <i>t</i> and <i>D</i> cross	Extra vein appearing from 3rd long. vein to what would correspond to the location for anterior cross vein in <i>Drosophila</i> . In some cases it extends to the location for posterior cross vein in <i>Drosophila</i> .	Dominant, expressivity and penetrance low.	Low
<i>Forked</i>	<i>F</i>		Spont.	Scutellum bristles forked.	Dominant with irregular expressivity, higher in female than in male.	Slightly low
<i>Missing</i>	<i>Ms</i>		Spont.	Head bristles mainly post verticals missing.	Dominant.	Slightly low
<i>naked</i>	<i>nk</i>		Spont. in <i>F</i> cross	Part of bristles, especially on thorax, missing.	Recessive, irregular in penetrance and expressivity.	Extremely low
<i>naked-2</i>	<i>nk²</i>		X-ray irradiation to pupa.	Similar to <i>nk</i> .	Similar to <i>nk</i> .	Similar to <i>nk</i>
<i>purple</i>	<i>p</i>		Spont. in <i>sa</i>	Eye color is purple, by strengthening of reddish of normal black with slight reddish.	Recessive.	Extremely low
<i>short arista</i>	<i>sa</i>	III	Spont. in <i>t</i> .	Arista become short in various degrees. Some show reduction of post vertical bristles. In low temperature the degree of abnormality is slight.	Recessive.	Normal
<i>Supernumerary</i>	<i>Sp</i>		Spont.	Show 3 or 4 pairs of scutellum bristles instead of normal 2 pairs. Some show abnormality in one side only.	Dominant, expressivity and penetrance low.	Low
<i>truncate</i>	<i>t</i>	II	Spont.	Wing margin between 2nd and 4th long. vein show truncation in various degrees.	Recessive, irregular in penetrance and expressivity in the presence of modifiers.	Slightly low
<i>twilight</i>	<i>tw</i>	I	Spont. in <i>bw</i> and <i>sa</i> cross	Wings are spread, semi-transparent, show smoky appearance. Sometimes a part of wing swells. Wing length is short by shortening of 1st and 2nd long. veins, making wing curved instead of flat. Sometimes accompanied by partial disappearance of a part of wing veins as in <i>Ab</i> .	Recessive. Partially sex-linked.	Low
<i>united</i>	<i>un</i>		Spont. in <i>t</i> cross	1st and 2nd long. veins unite at a point near proximal portion. Bristles on the marginal vein partly missing and arrangement irregular. Tip of 2nd long. vein does not branch out. Accompanied by partial disappearance of veins like <i>Ab</i> in many cases.	Incomplete recessive.	Low
<i>vestigial</i>	<i>vg</i>		Spont. in <i>Ab</i>	In some, wing completely lacking, others show short truncated wings.	Incomplete recessive, penetrance and expressivity are extremely low.	Extremely low
<i>yellow</i>	<i>y</i>	I	Spont. in <i>sa</i>	Changes color of body and bristles to light yellow.	Recessive, semi-lethal in homo. Partially sex-linked.	Slightly low

1. Introduction

Aphiochaeta xanthina Speiser (Fig. 1) belonging to Phoridae was collected in Okinawa in 1941 and was inbred in stock for two years at Kyoto University. Genetic studies were begun with this material because of the easiness of culture, the small number of chromosomes ($2n=6$, $n=3$) and also of the interest the author had in comparing the genetical difference between this family and *Drosophilidae*.

Some twenty mutants appeared in this stock (Table 1). The mode of inheritance is more or less irregular in most cases. Some of these mutated genes have been definitely located in the chromosome, such as *short arista*, *brown*, *coarse*, and *Delta* on the third chromosome, *bar* and *truncate* on the second, and *yellow*, *twilight*, *abrupt-4* and *Abrupt* on the X chromosome.

In the course of study of the reverse mutation found in *short arista* mutant, it became clear that the mechanism of the sex determination in this species is unusual. After several years study of this problem, the author has come to believe the following hypothesis: In this fly the male has strong male determining factor in the normal Y chromosome, and the male sex is determined by the presence of this factor. At times this factor translocates to the third chromosome.

After World War II, the author learned unexpectedly that cytological and genetic studies have been done by several workers in Europe with the same species which were collected at Naples in Italy. Both Okinawa and Naples strains were identified as the same species by Dr. E. Séguy. However, Dr. C. Barigozzi and L. Semenza (1952) of Milan University reported that the chromosome number of the Naples strain is ten in diploid and five in male meiotic metaphase. Later, Dr. H. Ondraschek (1953), Vienna University, reported that the chromosome number of Naples strain in somatic cell is six and ascertained the strong somatic pairing which agreed with the description of the Okinawa strain by the author (1951), but she did not study the meiotic division. Dr. F. Mainx, Vienna University, kindly sent the author the Naples strain, wild and mutant "*occhi chiari*" stocks

exchanging with Okinawa stocks. The author studied larval ganglionic mitosis and male meiosis of the wild and "oc" mutant of Naples strain and ascertained that the chromosome number and shape were absolutely the same with the Okinawa strain (Fig. 2). Morphologically both strains did not show any differences, both can be crossed easily. Then the author conducted genetic experiments with wild and oc mutant of Naples strain, and discovered that the same sex determining hypothesis is working on the Naples strain too.

In this fly, most of the mutants which belong to high rank show complicated genetic behaviour from time to time, and the cause of these phenomena is still obscure. These factors provide the main difficulties to an elucidation on the sex determination mechanism through genetical studies. However, the data show the presence of the above mentioned sex determining mechanism in this fly which differs totally from that known in *Drosophila*.

In this paper the complicated genetic behaviour of this fly together with a working hypothesis concerning sex determination will be presented.

The first half of this study was done at the Zoological Institute of Kyoto University under the guidance of Dr. T. Komai. The rest of this work has been accomplished at the Atomic Bomb Casualty Commission and in Kobe College. The author wishes to express her special appreciation to Dr. T. Komai, National Institute of Genetics in Mishima, and also to Dr. S. Fujii, Prof. of Kobe Univ., and Dr. H. Kikkawa, Prof. of Osaka Univ., for their many helpful suggestions during the course of this study.

2. Origin, character and expressivity of *short arista*.

Short arista (*sa*) appeared during selection experiments with the mutant *truncate* (*t*). From these *sa* individuals a pure stock was prepared and has been maintained for a number of generations. *Sa* is characterized by the shortening of arista. The expressivity of *sa*

gene has been found to be variable, and *sa* individuals have been classified according to different expressivities of this gene into three groups, namely, those with very short arista (H *sa*), those with intermediate arista (M *sa*) and those with almost normal ones (L *sa*). Sometimes individuals appear which will be referred to as asymmetrical (Asym.) *sa*.

Table 2.

Relation between the parents offspring *short arista* expressivity.

H *sa* – high-grade arista,

M *sa* – medium-grade arista,

L *sa* – low-grade arista.

Asym *sa* – asymmetrical arista.

P ₁ cross	Case	F ₁			
		H <i>sa</i>	M <i>sa</i>	L <i>sa</i>	Asym. <i>sa</i>
H <i>sa</i> × H <i>sa</i>	18	1339	96	7	35
M <i>sa</i> × M <i>sa</i>	25	1119	347	32	73
L <i>sa</i> × L <i>sa</i>	11	358	223	228	55

As shown in Table 2, when crosses are made between homozygous *sa*, all these classes of *sa* individuals appear in F₁, H *sa* class being greatest in number, M *sa* class being less than H *sa*, and L *sa* being least of all. H *sa* × H *sa* crosses have been found to give rise to a higher percentage of H *sa* flies in F₁ than M *sa* × M *sa* or L *sa* × L *sa* crosses. On the other hand crosses between lower classes (L *sa* × L *sa* or M *sa* × M *sa*) produce in F₁ a greater number of lower class individuals. χ^2 tests were applied to the data presented in Table 2 in order to find out correlation in the *sa* expressivity between parents and F₁ brood, and it was found that the probability is smaller than 1×10^{-4} . This seems to indicate existence of some modifiers for the *sa* gene.

Table 4.

Details of the 19 cases which had reverted wild-types in the F₁ brood from P₁ homozygous *short arista* crosses.

(* indicates pair mating). The others are all mass culture cases containing less than three females in one culture.)

Experiment Number	sa expressivity of P ₁	F ₁							
		sa				+			
		H sa	M sa	L sa	Asym sa	Reverted wild-types	% of reverted wild-types	Number of genetically analysed	Genotype of reverted wild-types
22	H sa	97	6	0	3	1	0.9	0	?
49	H sa *	25	3	0	0	14	33	10	sa/+
67	H sa	0	0	0	0	111	100	54	+/+
112	H sa. t♀ × H sa ♂*	0	0	0	0	66	100	49	+/+
123	H sa	79	5	0	1	2	3	0	?
319	H sa	88	69	2	9	5	2.8	3	sa/+
387	H sa	137	6	0	3	1	0.6	1	sa/+
1	M sa	0	0	0	0	67	100	34	+/, sa/+
9	M sa	10	18	2	4	1	2.8	0	?
10	M sa	1	6	12	0	34	64	12	sa/+
113	M sa	50	28	0	11	2	2	0	?
241	M sa	15	7	5	0	27	50	4	sa/+
313	M sa	10	3	5	1	19	50	8	sa/+
28	L sa	2	19	4	0	1	3.8	0	?
35	L sa	56	9	0	4	10	12.6	4	sa/+
307	H sa♀ × Asym sa ♂*	34	0	0	0	32	48	6	sa/+
317	L sa	26	24	0	3	74	58.2	8	+/, sa/+
388	L sa	147	29	18	12	2	0.9	2	sa/+
395	L sa♀ × H sa ♂*	12	7	4	0	17	43	7	sa/+

H sa females with t wing and H sa male were crossed and the F₁ offspring from this cross were all wild type, and F₂ as well as F₃ generations showed neither sa nor t individuals.

Inbreeding of these reverted wild-type flies gave rise to mutants such as *Abrupt-low*, *Abrupt*, *truncate*, *purple*, and *bar* in subsequent generations (Table 5). Sa also reappeared.

Table 5.

The appearance of mutants in the inbreeding strains of reverted wild-type.

Experiment number	Strain number	Mutants							
		F ₁	F ₂	F ₃	F ₄	F ₅	F ₆	F ₇	F ₈
10	40			<i>sa·t</i>			<i>Ab·t</i>		
10	44		<i>sa·t</i>						
10	74		<i>sa·t</i>		<i>t</i>		<i>Ab</i>		
1	38		<i>Ab</i>	<i>p</i>	<i>t</i>		<i>sa</i>		
1	41			<i>sa·t</i>					
1	45							<i>sa·t</i>	
1	53			<i>p</i>		<i>sa·t</i>			
1	58							<i>t</i> <i>Ab</i>	
1	59		<i>t</i>						
1	61		<i>t</i>				<i>Ab</i>		
1	65					<i>sa·t</i>			
1	75		<i>t</i>	<i>sa·p</i>					
1	79		<i>t</i>						
1	85		<i>t</i>						
1	94		<i>t</i>			<i>b</i>	<i>Ab</i>		
1	104		<i>t</i>						
1	105					<i>sa</i> <i>Ab</i> <i>p</i>			
67	178	<i>Ab</i>	<i>b</i>				<i>sa</i> <i>Ab</i>	<i>t</i> <i>Ab</i>	<i>t</i>
67	189		<i>t</i>	<i>p</i>				<i>Ab</i>	<i>sa</i>
67	197		<i>t</i>		<i>Ab</i>				

It is concluded from these data that the reverse mutation of *sa* mutant is due to mutation of *sa* gene to the wild gene and that the mutation of the other loci, *Ab*, *t*, *b* or *p*, also occurred. It is shown

that these reverted wild-type are genetically unstable. Furthermore, when the homozygous *sa* reverted to the heterozygous condition, the *sa* gene becomes unstable, and reverts to the wild allele in succeeding generations. This condition was encountered in three cases in Exp. No. 10.

4. Genetic peculiarity of the reverted wild-type male.

It has been found that the reverted wild-type individuals are genetically different from the normal flies of the wild stock, although they are alike in appearance. The genetic differences between the two are shown by the following genetic experiments with the reverted wild-type flies obtained from Exp. No. 10 and 67 in Table 4. These flies are indicated by symbol +¹⁰ (from Exp. No. 10) and +⁶⁷ (from Exp. No. 67). These two lines were selected for wild-type flies for several generations, and then the following experiments were made. (+^w indicates normal individuals of the wild stock).

When a reverted wild-type female is crossed to an ordinary *sa* male, *sa* character behaves as an autosomal recessive mutant, but when a reciprocal cross is made, *sa* character appears in F₁ and F₂ generations as sex-linked (Table 6).

Table 6.

Genetic relation between *short arista* and the reverted wild-type (+¹⁰ or +⁶⁷).

P ₁ cross	Case	F ₁		F ₁ cross	Case	F ₂	
		female	male			female	male
		+ <i>Ab</i> ^f	+ <i>sa</i>			+ <i>sa</i>	+ <i>sa</i>
+ ¹⁰ ♀ × <i>sa</i> ♂	1	30	0	F ₁ + × F ₁ +	2	90	30
		27	0	F ₁ + ♀ × <i>sa</i> ♂	2	20	26
<i>sa</i> ♀ × + ¹⁰ ♂	5	227	24	F ₁ + ♀ × F ₁ <i>sa</i> ♂	23	430	416
		1	265	F ₁ + ♀ × <i>sa</i> ♂	10	134	139
<i>sa</i> ♀ × + ⁶⁷ ♂	4	105	6	F ₁ + ♀ × F ₁ <i>sa</i> ♂	5	84	98
		0	109	F ₁ + ♀ × + ⁶⁷ ♂	3	239	0
						159	147

Table 7.

Genetic relations between *Delta* (*D*) and the reverted wild-type (+¹⁰ strain).

* In two of the crosses between $F_1 + \text{♀} \times F_1 D \text{♂}$ from P_1 cross $D \text{♀} \times +^{10} \text{♂}$, all the F_2 individuals were wild. From this pedigree *Delta* never appeared. These also are apparently due to reverse mutation.

** In this case, there appeared exceptional *sa* individuals. The original $P_1 +^{10}$ female is probably responsible for these exceptional progeny.

P ₁ cross	F ₁ cross	Case	F ₂					
			female			male		
			+	<i>D</i>	<i>sa</i>	+	<i>D</i>	<i>sa</i>
$D \text{♀} \times +W \text{♂}$	$F_1 + \text{♀} \times F_1 D \text{♂}$	2	40	32		37	37	
	$F_1 D \text{♀} \times F_1 D \text{♂}$	1	10	27		8	20	
$D \text{♀} \times +^{10} \text{♂}$	$F_1 + \text{♀} \times F_1 D \text{♂}$	16	0	550		583	0	
		2*	104	0		112	0	
	$F_1 D \text{♀} \times F_1 D \text{♂}$	4	0	72		88	72	
$+W \text{♀} \times D \text{♂}$	$F_1 + \text{♀} \times F_1 D \text{♂}$	6	113	113		151	139	
	$F_1 D \text{♀} \times F_1 D \text{♂}$	6	84	167		93	183	
$+^{10} \text{♀} \times D \text{♂}$	$F_1 + \text{♀} \times F_1 D \text{♂}$	12	300	350		300	281	
		1**	12	14	4	20	28	3
	$F_1 D \text{♀} \times F_1 D \text{♂}$	10	104	181		95	228	

Next, when a female from the stock of the autosomal mutant *Delta* (*D*) is crossed to a reverted wild male, *D* segregates as if it were sex-linked, whereas in the reciprocal cross it segregates normally (Table 7). These results, as will be indicated later, seem to show a difference in Y chromosome between the original wild male and the reverted wild-type male.

Abrupt (*Ab*) is a partially sex-linked gene. When an *Ab* female is crossed to a reverted wild-type male or a male which has the Y chromosome of the reverted wild-type male, the *Ab* character segregates as if it is an autosomal mutant. The following experiments

show this fact. *Ab* was combined with *bar* (*b*). *Ab. b* females were crossed with reverted wild-type males, and in the F_2 segregations from the crosses between F_1+ or $F_1 Ab$ female and $F_1 Ab$ male indicate that *Ab* behaves as an autosomal mutant. *Bar* behaves normally as an autosomal recessive gene. From among the F_2 generation of these crosses, *Ab. b* males were selected. These *Ab. b* males can be thought of as having the Y chromosome of the reverted wild-type male. Therefore they may be indicated as *Ab. b* male (Y^{10}) or (Y^{67}), according to the line of the reverted wild-type male used in the P_1 cross. Then cross was made between the *Ab. b*(Y^{10}) or *Ab. b*(Y^{67}) male and *sa* female. The F_1 segregation of these crosses is shown in Table 8. In 45 of all the 46 crosses, *sa* segregated

Table 8.

The F_1 segregations of the P_1 cross between short arista or wild-type female and *Ab. b* male bearing the III-Y chromosome.

P ₁ cross	Case	F ₁								
		female				male				
		+	<i>Ab</i>	<i>sa</i>	<i>Ab.sa</i>	+	<i>Ab</i>	<i>sa</i>	<i>Ab.sa</i> - mosaic- like	<i>Ab.sa</i>
<i>sa</i> ♀ × <i>Ab. b</i> ♂ (Y^{10}) or <i>Ab. b</i> ♂ (Y^{67})	45	383	397	3	4			400		319
	1		29					42		
+ ^w ♀ × <i>Ab. b</i> ♂ (Y^{10})	13	209	232			224	161		21	28

as if it were sex-linked and *Ab* segregated as if it were no longer sex-linked, though the F_1 segregation as a whole appears somewhat unusual. In one cross the F_1 brood consisted of 29 *Ab* females and 42 wild-type males. Back crosses between this F_1 wild-type male and *sa* female gave rise, in the next generation, to +20, *sa* 23 females and +20, *sa* 16 males. Thus in this single case, *sa* and *Ab* character apparently behaved normally, except that the sex ratio in F_1 was rather abnormal. Next, when cross was made between the +^w female and *Ab. b*(Y^{10}) male, the *Ab* character segregated in the F_1 as if *Ab* were an autosomal mutant as shown in the last line in Table 8.

5. Hypothesis concerning the sex determination and the chromosomal constitution of the reverted wild-type male.

The genetic peculiarity seen in the reverted wild-type male mentioned above could be explained on the basis of the following assumptions. 1. The Y chromosome in this species bears a strong male determining factor (M)*, and male sex is determined by the presence of this factor. 2. A translocation between the Y and the third chromosome gave rise to a third chromosome combined with a part of the Y bearing this male determining factor. The reverted wild-type male has such a III-Y (including M) chromosome instead of the normal Y chromosome. *sa* gene locates on the third chromosome of this III-Y chromosome. In the course of the selection of the reverted wild strain the Y-III chromosome (if the translocation were reciprocal) or the rest of normal Y chromosome which no longer has M (if the translocation were single) was lost, and the reverted wild male acquired another X chromosome. This hypothesis concerning the origin of the reverted wild male is diagrammatically presented in Fig. 3.

In the cross with such a male the third chromosome behaves as a sex chromosome and the X behaves as an autosome.

Fig. 3

Diagram illustrating the hypothesis concerning the origin of sex-linkage of *sa* gene and the reversion to wild-type gene. (II-chromosomes are not shown.)

a : *sa* male

b : Translocation between the third and Y chromosome.

Simultaneously with this change, *sa* gene on the other third chromosome reverts to *sa*⁺ allele.

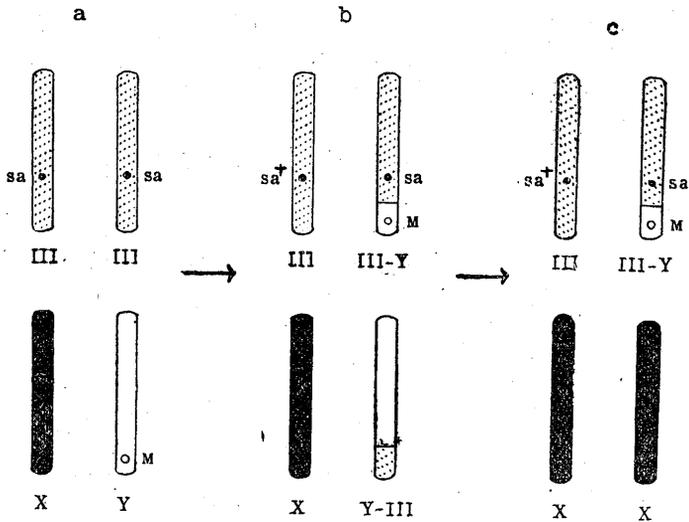
c : In the course of selection the Y-III chromosome is lost and the reverted wild-type male acquires another X chromosome.

M: Male determining factor.

Black portion : X chromosome, White portion : Y chromosome,

Dotted portion : Third chromosome.

* At the present stage of this study, it is difficult to say if this is the male determining gene or male determining part. The author will use the word factor with symbol M until the details can be cleared up in the future.



6. Analysis of the III-Y chromosome of the reverted wild-type male.

(a) *Sa* gene in the reverted wild-type male.

From the cross between sa female and the reverted wild-type male, a few exceptional sa females and wild-type males occasionally appear in F_1 (for instance, see Table 6, 8). When this exceptional wild-type male was back-crossed to sa female, all males in the next generation were wild-type except for the occasional appearance of some sa males. When, on the other hand, the above exceptional sa female was crossed with sa male from the sa stock, all individuals in the following generations were sa . Thus the exceptional females were presumably homozygous for sa gene. The chromosomes of the larval ganglion of the offspring of these exceptional sa females were examined by aceto-orcein smear method, but no difference was detected between these and the wild-type individuals. It is clear from

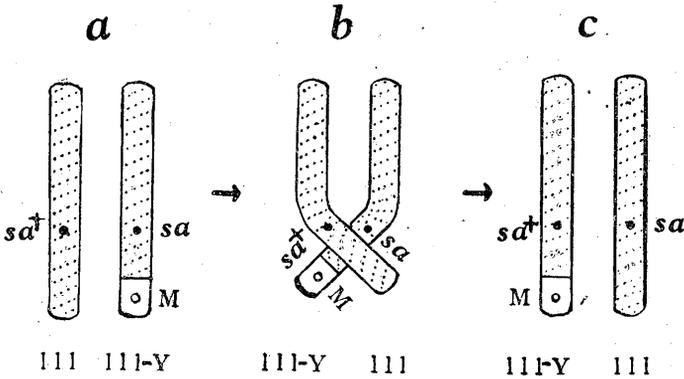
this fact that these exceptional *sa* females are not due to the non-disjunction of the chromosome which has *sa* gene.

This phenomenon could be interpreted as follows: The reverted wild type male has the III-Y chromosome which bears a *sa* gene in the III part. The F₁ exceptional *sa* females and wild-type males are derived from crossing over in the P₁ reverted wild-type male between the third chromosome and the III-Y chromosome, in such a manner that, the third chromosome receives the *sa* gene and the III-Y chromosome receives the *sa*⁺ allele, producing, as the result, the F₁ wild-type male having the *sa*⁺ allele linked to the M factor. This assumption is diagrammatically shown in Fig. 4.

Fig. 4

Diagram illustrating the cause of appearance of a few exceptional + male and *sa* female in the F₁ of the P₁ cross between *sa* female and reverted wild-type male.

- a : The third chromosome pair of the reverted wild-type male.
- b : Crossing over between the third chromosome and the III-Y chromosome.
- c : The resulting chromosome.
- M : Male determining factor.



- (b) The III-Y chromosome and three genes on the third chromosome.

As mentioned before, if the hypothesis concerning the reverted

wild-type male, especially the III-Y chromosome which has male determining factor in the Y part is true, the third chromosome genes might behave like sex-linked genes or partial sex-linked genes by the cross with this male. To confirm this, the following experiments were made with the other mutants belonging to the third chromosome.

Coarse (*c*) appeared in the *bar* (*b*) stock. The F₁ individuals from the P₁ crosses in *sa*♀ × *b.c*♂, *b.c*♀ × +^w♂ and *b.c*♀ × +¹⁰♂, all show wild phenotype. As shown in Table 9, the F₂ segregations

Table 9.

Genetic test of coarse mutant with *short arista* (III), *bar* (II) and the reverted wild-type male bearing III-Y chromosome.

(*b.c* male and +^w male has a normal Y chromosome, +¹⁰ male has the III-Y chromosome.)

P ₁ cross	F ₁ cross	Case	F ₂							
			female							
			+	<i>t</i>	<i>sa</i>	<i>b</i>	<i>c</i>	<i>b.sa</i>	<i>b.c</i>	<i>bt.c.</i>
<i>sa</i> ♀ × <i>b.c</i> ♂	F ₁ +♀ × F ₁ +♂	23	459		134	138	95	29	23	
	F ₁ +♀ × <i>b.c</i> ♂	3	40			42	8		9	
<i>b.c</i> ♀ × + ^w ♂	F ₁ +♀ × F ₁ +♂	5	100			15	17		1	
	F ₁ +♀ × F ₁ +♂	22	308			61	91		7	
<i>b.c</i> ♀ × + ¹⁰ ♂	F ₁ +♀ × F ₁ +♂	27	316	1		265	148		95	2

F ₂							
male							
+	<i>sa</i>	<i>sa</i> mosaic like	<i>b</i>	<i>c</i>	<i>b.sa</i>	<i>b.c</i>	<i>bt.c.</i>
549	141		161	138	47	37	
31			26	14		11	
66			15	5			
696	11	14	136	4			
255			250	106		90	1

except that of F_1 brother-sister mating of the $P_1 \text{ } b.c \text{ } \varphi \times +^{10} \text{ } \delta$ cross, indicate that c is linked to sa on the third chromosome. These F_2 segregations, however, did not match well with the expectation, which fact may be accounted for by semi-lethality of the homozygous *coarse*. The F_2 segregation of the F_1 brother-sister mating from the $P_1 \text{ } b.c \text{ } \varphi \times +^{10} \text{ } \delta$ cross may be explained by supposing that the c locus is on the homologous part of the III part of the III-Y chromosome. According to this interpretation, c male could not have appeared in the pedigree of the $b.c \text{ } \varphi \times +^{10} \text{ } \delta$ cross. However, there appeared four c males in the F_2 brood. The appearance of these exceptional c males may be explained by the same assumption as in the previously mentioned sa case (see Fig.4), namely, the results of the crossing over between the third chromosome which has c gene and the III-Y chromosome which has c^+ allele in the F_1 male. In the F_2 male, there appeared also several exceptional sa and sa mosaic-like males. These sa males were crossed with homozygous sa female, and it became clear that these exceptional sa and sa mosaic-like characters were only phenotypical. The occurrence of these exceptional sa phenotype still can not be explained but it may have some relation with the III-Y chromosome which has sa gene in the III part.

The mutant *brown* (bw) appeared spontaneously in one female in a series of crossing experiments with sa , reverted wild-type female and reverted sa male. This mutant was purified by inbreeding, then it was made into a pure stock of which male has the III-Y chromosome. In this bw stock, all females show bw , and males, wild phenotype, except for a few + females and bw males. When cross is made between these exceptional bw male and sister bw , all individuals in the next generation become bw . This suggests that the bw gene is on the third chromosome part of the III-Y chromosome as *coarse* locus is suggested to be. The occurrence of exceptional + female and bw male seems to be due to the crossing over between

the third chromosome which has *bw* gene on it and the III-Y chromosome which has *bw*⁺ allele. Then the *bw* gene came to be linked with the male determining factor in the Y part of the III-Y chromosome. These assumptions have been confirmed by several cross experiments shown in Table 10, though the F₂ segregation does not satisfy the expectation very well.

Table 10.

Genetic test of *brown* mutant.

(+ male of *bw* stock has *bw* gene on the third chromosome and *bw*⁺ allele on his III-Y chromosome. d : deformed individual)

P ₁ cross	F ₁ cross	Case	F ₂					
			female			male		
			+	<i>bw</i>	<i>Ab d</i>	+	<i>bw</i>	<i>sa Ab.sa d</i>
<i>bw</i> ♀ × + ^W ♂	F ₁ + × F ₁ +	22	685	270		829	255	
		1	39	16	10	59	12	4
	<i>bw</i> ♀ × F ₁ + ♂	18	176	100	1	199	155	1
	F ₁ + ♀ × + ♂ (from <i>bw</i> stock)	8	209	227		372		3
		1	39	8		52	10	1
<i>bw</i> ♀ × + ¹⁰ ♂	F ₁ + × F ₁ +	9	178	149		299	1	27
		13	1	234		206		26
	F ₁ + ♀ × + ♂ (from <i>bw</i> stock)	6	134	112		251		19

Delta (*D*) is another mutant on the third chromosome. With this mutant also the crossing over between the third chromosome with *D* gene and the III-Y chromosome has been demonstrated as the following experiments show. From the pedigree of the cross between *D* female and reverted wild-type male of the +¹⁰ strain, *D* male(Y¹⁰) is selected, which is supposed to have *D* gene on the third chromosome and a III-Y chromosome. *D* male(Y¹⁰) are crossed with +^W or +¹⁰ female. In the F₁ about 0.4% were exceptional individuals, namely *D* males and + females (Table 11).

Table 11.

Crossing over between *Delta* and male determining factor in the III-Y chromosome.

(*D* male(Y¹⁰): This male has *D* gene on the third chromosome and the III-Y chromosome.)

P ₁ cross	Case	F ₁			
		female		male	
		+	<i>D</i>	+	<i>D</i>
+ ^W ♀ × <i>D</i> ♂ (Y ¹⁰)	16	3	507	529	1
+ ¹⁰ ♀ × <i>D</i> ♂ (Y ¹⁰)	60	7	1201	1377	3
F ₁ cross	Case	F ₂			
		female		male	
		+	<i>D</i>	+	<i>D</i>
+ ^W ♀ × F ₁ <i>D</i> ♂	1	49	1	0	43
+ ¹⁰ ♀ × F ₁ <i>D</i> ♂	1	22	1	0	22
F ₁ +♀ × <i>D</i> ♂ (Y ¹⁰)	1	3	44	55	0
F ₁ +♀ × + ¹⁰ ♂ (Y ¹⁰)	1	24	0	25	0
F ₂ cross	Case	F ₃			
		female		male	
		+	<i>D</i>	+	<i>D</i>
+ ^W ♀ × F ₂ <i>D</i> ♂	8	208	3	0	218
+ ¹⁰ ♀ × F ₂ <i>D</i> ♂	6	108	1	0	101
F ₂ +♀ × F ₂ <i>D</i> ♂	13	467	3	1	504

These exceptional *D* males were back crossed to +^W or +¹⁰ females; in the next generation the males were all *D*, while females were all wild-type except for a few *D* females. These results indicate that the F₁ *D* male came to receive *D* gene on the third chromosome part of his III-Y chromosome. This would mean that the *D* gene of this F₁ *D* male came to be linked with the male determining factor, by a crossing over between the third chromosome which has *D* gene and the III-Y chromosome which has *D*⁺ allele in the P₁ *D* male.

F₂ segregation of the crosses with these exceptional F₁ + females and F₁ *D* males agrees with this assumption as shown in Table II. In the F₂ segregation, as shown in this table, exceptional individuals appeared again. This is also due to crossing over between the third and the III-Y chromosome. *D* males in the F₂ brood are crossed with +^w, +¹⁰ and sister + females. Similar results were obtained in the next generation. In these cases the crossing over value between *D* and the male determining factor (M) varied from 0.4 to 0.7% as shown in Table II.

These results indicate the presence of the male determining factor on the Y part of the III-Y chromosome, the presence of the alleles of above mentioned three known mutants on the third chromosome part of the III-Y chromosome and also the presence of the crossing over between the third and the III-Y chromosome in the male. The recombination values between M in the III-Y chromosome and four genes on the third chromosome as they appeared in the experiments can be summarized as follows :

<i>sa</i> - M	: 0.8 % ± 0.18%	(total 2373 individuals, 32 pair matings)
<i>D</i> - M	: 0.38% ± 0.06%	(total 10266 individuals, 175 pair matings)
<i>bw</i> - M	: 0.35% ± 0.09%	(total 3940 individuals, 70 pair matings)
<i>c</i> - M	: 0.30% ± 0.11%	(total 2320 individuals, 64 pair matings)

7. Crossing over between X and Y chromosome in male.

To explain the results, the author suggested the presence of crossing over between the third chromosome and the III-Y chromosome in male. In the normal male between X and Y chromosome, there exist crossing over with rather high frequencies comparing with the case in the male of *Drosophila*. This is demonstrated by using known mutants locating on the X chromosome as will be described below.

There are four mutants, *abrupt-4* (*ab*⁴), *Abrupt* (*Ab*), *yellow*

(*y*) and *twilight* (*tw*), locating on the X chromosome in Okinawa strain. Ondraschek (1953) described two partial sex-linked genes, *occhi chiari* and *r4 reduced* in Naples strain. All of these mutants show partial sex-linkage. This means that in the normal Y chromosome of this fly, there is a part homologous with the X

Table 12.

Crossing over experiment between X with *Ab* gene and Y with *Ab*⁺ allele: F₁ segregation of the P₁ cross between wild-type female and *Ab* male.

* Three wing deformed individuals included. This deformity was not inherited.

*1, *2: See text.

	Case	Experiment number	F ₁					
			female		male			
			+	<i>Ab</i>	<i>Ab</i> .sex- abnormal	+	<i>Ab</i>	<i>Ab</i> .sex abnormal
Normal cases	127		5129		5269*			
Exceptional cases	A	1	No. 21	1*1	10	13		
		1	No. 43	1*1	17	20		
		1	No. 46	1*1	52	32		
		1	No. 48	1*1	42	35		
		1	No. 73	1	16	23		
		1	No. 79	1	21	13		
		1	No. 84	1*1	58	46		
		1	No. 325		52	62	1*2	
		1	No. 20		58	55	1	
		1	No. 22	1	71	90	1	
	B	1	No. 12		40	48	1	
		1	No. 336		37	37	1	
		1	No. 323		44	25	20	
		1	No. 44		51	36		

chromosome and on this part are located wild alleles of these genes.

Table 12 shows the F_1 segregation of Ab gene by the P_1 cross between wild female and Ab male. In 127 cases of the total 141 pair mating cases, Ab gene segregated as expected. In the remaining 14 cases were produced exceptional individuals in F_1 brood. Exceptional + females and Ab males which appeared in 10 cases which are included in A group in the table are considered as the products of the crossing over between X with Ab gene and Y with wild allele of Ab gene. Five + females with *1 mark in this table were tested genetically, and did not show any Ab gene. One of the three Ab males (Exp. No. 325, marked *2 in this table) produced offspring by the test cross and showed that Ab gene of this male is linked with Y chromosome. This is shown in Table 13. The other

Table 13.

Test cross with the F_1 Ab male in Exp. No. 325 shown in Table 12.

Cross	Case	Offspring			
		female		male	
		+	Ab	+	Ab
No. 325 wild ♀ × F_1Ab ♂	1	39	8	2	57
F_2+ ♀ × F_2Ab ♂	8	344	9	0	217
wild ♀ × F_2Ab ♂	7	328	45	15	339
F_3+ ♀ × F_3Ab ♂	6	135	6	3	128
F_4+ ♀ × F_4Ab ♂	4	102	2	0	102

two Ab males failed to produce offspring but probably those might be the same as the one mentioned above. In three of the remaining four cases included in B group of Table 12 are the cases in which Ab individuals with sex abnormality appeared. F_1 Ab male from Exp. No. 12 and 336, each having rather large body size, incomplete

clasper, and testes, were sterile. Though they could not be submitted to the test cross, these *Ab* males with sex abnormality probably may be due to the crossing over between X and Y. In the Exp. No. 323 case, there appeared sex abnormality in 25 individuals with *Ab* character. Of these six have female-like appearance and nineteen have body size rather larger than normal male, but have incomplete clasper and male-like appearance. Four of the six female-like and fifteen of the nineteen male-like individuals were tested cytologically and demonstrated that all had ovaries. Further study is needed to clear up the cause of the origin of these sex abnormality. The F_1 segregation of one case shown in the last line of B group in Table 12 (Exp. No. 44) is peculiar. All F_1 female were wild-type and showed no *Ab* gene by the test cross with ten of them. The same explanation as in the case of the reverse mutation of *short arista* mentioned before and the case of the disappearance of *D* gene shown in Table 7 (in the case with * mark) may be applied to this case as an interpretation.

Through the experiments shown in Table 12, the exceptional F_1 individuals may be thought of as the results of the crossing over which occurred between X with *Ab* gene and Y with the wild allele of *Ab* gene in P_1 *Ab* male, except two cases, Exp. No. 323 and 44. The frequency is $0.112 \pm 0.031\%$, which means the recombination value between *Ab* gene and male determining factor in Y chromosome. The *Ab* gene which came to be linked with Y chromosome comes back to X chromosome for several successive generations with relatively high frequencies as seen in Table 13. This may suggest that the crossing over which the author has been dealing with in this fly may include some unknown mechanism which is not encountered in crossing over cases of *Drosophila*.

Yellow gene (*y*) is recessive, locating on the X chromosome and showing partial sex-linkage. Nearly half of the homozygous *y* flies die. Pure stock of this mutant consist of *y* females and wild-type

males which have y gene on the X and the wild allele in the Y chromosome. Sometimes a few exceptional + females and y males appear, which can be explained by the assumption of the result of crossing over between X with y gene and Y with the wild allele. By crossing this exceptional y male with normal y female, the stock is established having females and males in y character. To see the frequency of this crossing over, pair mating experiments shown in Table 14 were carried out. Of the eight cases which produced

Table 14.

Crossing over experiment between X with y gene and Y with y^+ allele. : F_1 segregations of P_1 cross $y.sa$ female ($y/y.sa/sa$) \times sa male ($y/y^+.M.sa/sa$).

		Case	Experiment number	F_1			
				female		male	
				sa	$y.sa$	sa	$y.sa$
Normal cases		95		1055	2461		
Exceptional cases	A	1	No. 138		11	36	1
		1	No. 551		5	39	1
		1	No. 555	1	22	53	
		1	No. 557	1	14	50	1
		1	No. 604	1	9	32	
	B	1	No. 179	9	13	36	
		1	No. 567	19	8	34	
		1	No. 569	19	3	20	

exceptional individuals in the F_1 brood, five cases which are included in the A group in this table can be explained by the above mentioned assumption. But the remaining three cases, which are included in B group, cannot be explained by the same assumption. These need some other explanation and suggest the complexity of the genetics of this fly. Therefore, to see the recombination frequency between

y in X and M in Y, the three cases in B group are excluded, and also considering the mortality of about the half of homozygous y , the author calculated double the number of y individuals as compensation. Through these treatments the recombination value becomes approximately $0.18 \pm 0.06\%$ from these experiments.

Twilight gene (tw) shows the same partial sex-linkage as the y gene. This gene at times transfers to the Y chromosome by the crossing over between X with tw and Y with the wild allele. Because the viability of this mutant fly is low, the ratio of success of the pair mating is very low, and although the experiment to test the recombination frequency is still incomplete, the data indicated that the recombination frequency between tw and M may be the order of 0.1%. (One cross-over appeared in 724 individuals in 17 pair mating cases).

The remaining partial sex-linked gene *abrupt-4* (ab^4) was not suitable for use in this experiment because of the low expressivity in homozygous condition.

According to the paper by Ondraschek (1953), the recombination value between oc gene on the X and Y chromosome in Naples strain is $1.12 \pm 0.25\%$. This seems rather high compared with the above mentioned value in the cases of three partially sex-linked genes of Okinawa strain. The recombination value on another partial sex-linked mutant $r4$ *reduced* has not yet been reported.

8. The III-Y chromosome in the male of *occhi chiari* stock from Naples strain.

In the *occhi chiari* (oc) stock, the author found another case of the translocation of Y to the third chromosome similar to the case in the reverted wild male mentioned earlier.

When oc stock reached here last May from Vienna by the courtesy of Dr. F. Mainx, both female and male had oc character. It was thought that this pure stock might be established by the cross between homozygous oc female and oc male which has oc gene in Y

chromosome, originated by the crossing over between X with *oc* and Y with the wild allele in the male ancestor. However, this did not seem to be the case. After undertaking several experiments with this mutant stock, it appeared that the male of this stock has III-Y chromosome instead of having one of the normal third chromosome, and to have two X chromosomes each having *oc* gene on it instead of having one normal X and Y chromosome. This assumption is based on the experiments described below.

F₁ *Ab* male from the cross between *Ab* female and *oc* male was back crossed with *oc* female. As shown in Table 15 the F₂ segregation shows that *Ab* and *oc* gene behaves as an autosomal gene.

Table 15.

F₂ segregation of the F₁ cross between *oc* female and F₁*Ab* male from the P₁ cross between *Ab* female and *oc* male.

Case	F ₂										
	<i>oc</i>	<i>oc</i> deformed wing	<i>oc</i> def.- head	<i>oc</i> sex ab- normal	<i>Ab</i>	<i>Ab</i> def.- head	<i>Ab</i> sex- abn.	Mosaic wing (<i>Ab</i> ·+)	+	+ sex- abn.	<i>Ab</i> · <i>oc</i>
122	♀ 1690	1	2	3	1860	2			18	1	33
	♂						1	1			
	♂ 1698	4		1	1940	5	1		48	1	48

This immediately called attention to the supposition that the male determining factor may be transferred to another chromosome, as in the case of the reverted wild-type male mentioned before. The exceptional + and *Ab*·*oc* individuals are thought of as the result of crossing over between *Ab* on one X and *oc* on another X in F₁ *Ab* male. These individuals occupy $2.03 \pm 0.16\%$ in this table. However, a few of the tested exceptional + individuals showed *Ab* character in the next generation; this value may be rather higher than the true recombination value. It is notable that by the cross with *Ab* and *oc*, there appear some sex abnormal and deformed individuals. Some of these are shown in Table 15. Most of the deformities are of the

head, the characteristic being the reduction of the head portion in greater or lesser degree. The slightly deformed shows the narrowing of the face part. In the next degree the face disappeared and only two compound eyes which fuse in one, plus mouth parts constitute the head. Then, occurred a reduction in the number of ommatidia of the fused compound eye. Finally in the extremely deformed, the head, consisting only of degenerated mouth parts and a tiny slice of tissue on which we can hardly recognize ommatidia, was attached to the head stalk. This fly looks at a glance as if it has no head. These deformed flies can cross and yield offspring except in the extremely deformed and showed that this deformity is not inherited.

Through the above mentioned experiments, it becomes clear that the male determining factor of *oc* male might be transferred to another chromosome from the normal Y chromosome. It was ascertained by several experiments with genes on the second and third chromosome that this factor translocated to the third chromosome. For instance, from the P₁ cross between *D.sa* female and *oc* male, F₁ *D* male was crossed with *sa* female. Then F₂ brood consisted of 385 *D.sa* females and 412 + males in 16 pair mating cases. From the reciprocal P₁ cross, *oc* ♀ × *D.sa* ♂, F₁ *D* male was crossed with *sa* female. In the F₂ brood, there were 384 + and 315 *D.sa* females and + 431 and 335 *D.sa* males, in total with 19 pair mating cases. In the former cross F₁ *D* male has III-Y chromosome, then by the cross with this male, *D* and *sa* behaved as if they are partially sex-linked genes. On the contrary in the latter case F₁ *D* male has normal Y chromosome from the P₁ *D.sa* male, then by the cross with this male, *D* and *sa* behaved normally. The III-Y chromosome in *oc* male are supposed to have *sa*⁺ allele in the III part because in the F₁ by the *D.sa* female and *oc* male cross, there appeared only + and *D* individuals.

9. Discussion

During the study of reverse mutation of *short arista* mutant, it becomes clear that the reverted wild-type male causes the reversion of the manner of inheritance of sex-linked mutant to autosomal and the third chromosome mutant to sex-linked. This cannot be explained by supposing that the sex in this fly is determined by the balance between X chromosomes and autosomes, as in the case of *Drosophila*. To explain this peculiar phenomenon another sex-determining mechanism must be applied to this fly. The author proposed a hypothesis, that in this fly there is a strong male determining factor and male sex is determined by the presence of this factor. In the reverted wild-type male, this factor is translocated to one of the third chromosomes and this III-Y chromosome behaves as a normal Y chromosome, and also suggested that there might be two X chromosomes instead of having one X and Y chromosome. This hypothesis was borne out by the results of experiments with the first and third chromosomal mutants as shown in this paper. And also it appeared that crossing over occurred between the III-Y chromosome and the third chromosome, the resulting genes on the third chromosome being transferred to the III-Y chromosome. As the result of these experiments the recombination values between these third chromosomal mutants and M factor were obtained. Yet to decide immediately this value means the distance between the mutant and M factor or not, needs more study. This and the study to elaborate on the mutual local correlations between these mutants and M factor, for the purpose of analysing the III-Y chromosome are still being continued.

As mentioned before, the known genes locating on the X chromosome are six, four from Okinawa, two from Naples strain. All of them show partially sex-linked inheritance which means that the normal Y has a homologous part with X chromosome and as a result, genes on the X become linked with Y chromosome. In the normal Y chromosome the arrangement of the differentiated Y part

which includes the male determining factor, and the homologous part with X chromosome is now under study through observing crossing over between X and Y using the sex-linked genes. As for the X chromosome, there are still no data through genetic and cytological study which show the presence of the differentiated X part at the present stage of progress. A further elucidation on this part depends on future study and this is necessary in clearing up the whole sex determination mechanism of this fly.

Another case in which the male determining factor translocated to the third chromosome was detected in the male of the pure *oc* stock from Naples strain by the author. The author does not know the manner of occurrence of the III-Y chromosome of this male, however, this might be caused by the same mechanism as in the case of the reverted wild-type male occurred at the time when the *sa* mutant reverted to the wild-type. The reverse mutation phenomena of *sa* were complicated as mentioned in this paper, and appeared to include many changes. One of them being the reversion of *sa* gene to the wild allele, another the occurrence of other mutants and deformed individuals, simultaneously with the reversion of *sa* gene or in the successive generations. The occurrence of III-Y chromosome is another distinct change. For several generations after the occurrence of these complicated reversion, the reverted strain showed genetically unstable conditions. In some strain the reverted wild-type male which had had III-Y chromosome came to lose the peculiarity of the III-Y chromosome. In many, several mutants appeared including *sa*. This occurrence of *sa* individuals in the reverted wild-type strain is demonstrated by the experiments as the result of the crossing over between the third chromosome which has *sa*⁺ gene and the III-Y chromosome having *sa* gene on the third chromosome part. The author has been keeping in stock two of the reverted wild-type strains which have III-Y chromosome in male. After several years one (+¹⁰ strain) showed the disappearance of this characteristic and another (+⁶⁷ strain) still shows the same characteristic.

In various species of *Drosophilidae*, reverse mutation phenomena induced spontaneously or artificially have been found by various investigators. Spontaneous reverse mutations are rather rare. The best analysed cases are the cases of unstable genes in *Drosophila virilis* found by Demerec and the cases of the *px-bl* and its derivatives in *D. melanogaster* studied by Goldschmidt et al. The latter case involves reverse mutations which were found by Goldschmidt in 1935 and studied genetically and cytologically for several years by him and his collaborators. Goldschmidt has concluded from these studies that, "mutation does not entail a chemical change in a gene molecule but mechanical disturbances of the serial order of the material which constitute the decisive part of chromosome, including those below the level of one salivary band." (Goldschmidt et al, '45).

The reverse mutation phenomena found in *short arista* mutant resembles the case of *px-bl* stock in *D. melanogaster*. This case is supposed to involve point mutation and some chromosomal rearrangements such as III-Y translocation may be involved.

The occurrence of the III-Y chromosome is distinct in this reverse mutation case and the fact that in the male of *oc* stock the similar translocation from Y to the third chromosome occurred independently of the reverse mutation in *sa*, suggests that there might be some underlying factor which causes the translocation from Y to the third chromosome. This underlying factor probably may be considered as follows: There is some homologous portion in the normal Y and the third chromosome. This portion might be euchromatic but is probably heterochromatic or a nucleolar-like substance. At times Y chromosome and the third chromosome pair at this part, and as the result, a part of Y containing M factor translocates to the third chromosome.

In this fly, the author encountered some complicated genetic phenomena other than the *sa* reverse mutation. For instance, the disappearance of *Delta* gene or *Abrupt* gene in some crosses, abnormal segregation in some mutants in some cases, or appearance of

deformed or abnormally sexed individuals in some crosses. The author is led to think that these phenomena might have some correlation with some chromosomal rearrangement. As for the cause of the rather frequent occurrence of these chromosomal rearrangements an explanation involving the similar underlying factor as were suggested in the case of III-Y translocation may be considered.

Intense cytological studies have been made in an attempt to find if chromosomal aberrations are present in *sa* stock, reverted wild-type strain and *sa* derivatives. Unfortunately salivary gland chromosomes were totally unusable in this fly, and therefore chromosomes of larval ganglion and of the gonad were studied. Although no aberration was detected by this test, it is highly possible that undetectable chromosomal rearrangements exist.

In this paper the author has attempted to present the strong peculiarity in sex determination mechanism and also the complicated genetic behaviour shown by this fly which are considered by the author as due to more or less minute rearrangements of the chromosomes, perhaps caused by an unknown special chromosomal constitution in this fly.

10. Summary

1. Two strains of *Aphiochaeta xanthina* Speiser, one collected at Okinawa, the other in Naples, show no difference by cytological and morphological tests.
2. Genetic behaviour of *short. avista* mutant is described. The complicated reverse mutation phenomena of this mutant which occurred during several generations after this mutant stock was established is described.
3. The reverted wild-type male caused the reversion of the manner of inheritance between the mutants belonging to the third and first chromosome. To explain this fact the author proposes a hypothesis concerning the sex determining mechanism in this fly and the chromosomal constitution of the reverted wild-type male.

4. The same genetic characteristics as in the reverted wild-type male are found in the male of *occhi chiari* mutant stock from Naples strain.
5. Crossing over between normal X and Y chromosome, and between the III-Y of the reverted wild-type male and third chromosome are demonstrated. The frequency is considerably higher than in male *Drosophila*.
6. Sex determining mechanism and the complicated genetic behaviour found in this species, including the reverse mutation phenomena of *short arista*, is discussed.

11. Literature cited

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