Genet. Res., Camb. (1975), **26**, *pp.* 113–125
With 2 text-figures
Printed in Great Britain

A factor on a wild third chromosome (III^{Ra}) that modifies the Segregation Distortion phenomenon in *Drosophila melanogaster*

By G. TRIPPA and A. LOVERRE
Istituto di Genetica, Università di Roma, Rome, Italy

(*Received* 12 *September* 1974)

SUMMARY

III^{Ra} is a genetic modifier of Segregation Distortion (SD) in *Drosophila melanogaster*, which was discovered in the same natural population from Ranna (Sicily) that carried SD^{Ra}. It is located at $49{\cdot}7 \pm 0{\cdot}8$ on chromosome III. III^{Ra} was found to have a dominant effect on segregation distortion which varied with the origin of the SD chromosome tested. Thus it enhanced the level of distortion caused by 14 SD chromosomes from seven natural populations in Southern Italy and Sicily, but decreased the level of distortion caused by SD^{R-1}, a chromosome from a natural population near Rome. Moreover, III^{Ra} determined or enhanced the distorting effect of SD^{Ra} in males heterozygous for SD^{Ra} and various SD^{+} wild chromosomes differently sensitive to SD^{Ra}. The frequency of chromosomes having an effect like III^{Ra} chromosome was very high (around 70%) in samples from two natural populations of Southern Italy tested-those of Ranna and Corato. No effects of III^{Ra} other than its ability to modify SD have been detected.

1. INTRODUCTION

Examples of meiotic drive, as defined by Zimmering, Sandler & Nicoletti (1970), are found in maize, wheat, rye, mice, cattle and man. Factors which modify meiotic drive are also known, e.g. enhancing and suppressing elements in *Drosophila* (see Zimmering *et al.* 1970; Peacock & Miklos, 1973), so that some cases of meiotic drive appear to be the result of the action of complex genetic systems rather than a single gene.

The Segregation Distortion phenomenon in *Drosophila melanogaster* (Sandler *et al.* 1959) was recently analysed by Miklos (1972*a*, *b*) and Peacock & Miklos (1973), who showed that the system consists essentially of the SD gene, acting in the male line only. The effect of the SD factor (mapped on the second chromosome at locus $52{\cdot}9 \pm 1$, Tanzarella *et al.* 1972) is to cause the degeneration of SD^{+} gametes in heterozygous SD/SD^{+} males (Nicoletti, 1968; Tokuyasu, Peacock & Hardy, 1972) and consequently the preferential recovery of gametes carrying the SD chromosome (Nicoletti, Trippa & De Marco, 1967; Hartl, Hiraizumi & Crow, 1967). The existence of other factors which influence the Segregation Distorter system, such as $St(SD)$ = Stabilizer of SD and $Ac(SD)$ = Activator of SD, was

proposed by Sandler & Hiraizumi (1960*a*, *b*) on the basis of the analysis of their data on distortion in terms of *k* values ($k = SD/(SD + SD^+)$, the proportion of *SD* individuals recovered among the progeny of SD/SD^+ heterozygous males). These authors interpreted the Stabilizer as a gene which controls the degree of mutability of the *SD* locus and the Activator as a gene which controls the mechanism causing the *SD* gene to operate. Data collected by Sandler & Hiraizumi (1960*b*) and Hiraizumi & Nakazima (1967) have recently been brilliantly re-analysed by Miklos (1972*a*, *b*) and Peacock & Miklos (1973), in terms of standard deviation units in addition to *k* values. This has permitted interpretation of the data in terms of the presence or absence of simple modifiers of *SD* action rather than of *SD* Activator or Stabilizer effects, as defined above.

It has also been shown that Segregation Distortion can be modified by various factors: for instance, temperature (Mange, 1968; Hihara, 1971) and irradiation (Murnik, 1971) among environmental factors; and ageing of the SD/SD^+ male (Sandler & Hiraizumi, 1961; Hiraizumi & Watanabe, 1969; Nicoletti & Micheli, 1970) among physiological factors.

The following genetic factors affect Segregation Distortion:

1. The genetic factor responsible for differences in sensitivity of SD^+ second chromosomes to the action of *SD*; it has been mapped at or close to the SD^+ locus. According to Trippa & Loverre (1972) this factor is the SD^+ locus itself (as a series of different SD^+ alleles) whereas Sandler & Carpenter (1972) consider it more likely to be a different locus.

2. A series of modifiers of distortion located on the second chromosome between cn^+ and c^+, and between c^+ and px^+ (Miklos, 1972*a*).

3. A series of suppressor genes which greatly reduce the action of *SD* designated *Su*(*SD*) = Suppressor of *SD*, identified on different chromosomes as follows: (*a*) on the proximal region of a laboratory *X* chromosome (Sandler, 1962); (*b*) on a standard *Muller-5 X* chromosome (Sandler & Rosenfeld, 1962); (*c*) on a laboratory *FM6 X* chromosome (Nicoletti & Trippa, 1967); (*d*) on *X* chromosomes from natural populations collected in Odate, Japan (Hiraizumi & Kataoka, 1965; Kataoka, 1967); (*e*) on second chromosomes from a natural population collected near Madison, Wisconsin (Hiraizumi, Sandler & Crow, 1960); (*f*) on *X* and second chromosomes from a natural population collected in Madison, Wisconsin (Hartl, 1970).

All the genetic factors described so far are elements that modify the action of *SD* and are located on either the *X* or the second chromosome. This paper describes a factor located on a wild third chromosome which is able to modify the level of segregation distortion in males heterozygous for different *SD* chromosomes and different second SD^+ chromosomes. Data are also supplied on the frequency of analogous third chromosomes modifying the SD effect in two Italian natural populations.

2. MATERIALS AND METHODS

The following *SD* second chromosomes were used:

(1) SD^{Ra}, isolated from the natural population obtained from Ranna, Sicily (Trippa *et al.* 1972). This chromosome contains a paracentric inversion on the left arm, a recessive gene *fs* $(2)^{TL}$ responsible for sterility in the female line only, located at locus 89·7 (Loverre *et al.* 1972), and a recessive mutation at locus *bw* or a small deficiency at the same locus, not recognizable in the salivary chromosomes analysis, which when heterozygous with *bw* exhibits a characteristic eye colour phenotype. The chromosome is homozygous viable.

(2) SD^{R-1}, isolated from a natural population from Rome (Nicoletti & Trippa, 1967; Sandler *et al.* 1968). This chromosome does not appear to be associated either with inversions detectable by salivary chromosome analysis or with recessive lethals. The *k* analysis of several recombinants between SD^{R-1} and a second multimarked chromosome did not reveal the presence of any kind of Stabilizer or Activator factors. The $\bar{k}$ value for $SD^{R-1}/bw\text{-}5$ males is $0{\cdot}988 \pm 0{\cdot}002$.

(3) A series of 14 *SD* chromosomes isolated from samples of 7 natural populations of Southern Italy (Trippa *et al.* 1972) and designated: *Ca 148*, *Ca 230* (Castellaneta); *Ra 88*, *Ra 126* (Ranna); *Sa 262* (Sambiase); *Pe 6*, *Pe 122* (Pedalino); *Ar 249*, *Ar 38* (Archi); *Ot 1* (Otranto); *Co 17*, *Co 64*, *Co 100*, *Co IV* (Corato).

The following lines and chromosomes were used for the construction of suitable genotypes, for mapping the modifying gene and for calculating the *k* values in the progeny of SD/SD^{+} males (for a more detailed description of the mutant genes and balancer chromosomes, see Lindsley & Grell, 1968):

(1) A series of eight second chromosomes derived from a sample of 291 SD^{+} chromosomes from the Ranna and Corato populations, which were maintained in stocks either as homozygotes or heterozygous with *SM5*. These second chromosomes had previously been shown (Trippa *et al.* 1973) to be moderately sensitive ($\bar{k} = 0{\cdot}63$) to the distorting action of two *SD* chromosomes derived by recombination from SD^{R-1} (referred as *SD cn L Pin* and *SD L*, whose $\bar{k}$ in males heterozygous for sensitive chromosomes was, respectively, 0·95 and 0·90).

(2) Chromosome III^{Ra}: derived from the Ranna natural population isolated from the same male that carried SD^{Ra}. This chromosome segregated normally in $III^{Ra}/st\text{-}5$ heterozygous males ($\bar{k} = 0{\cdot}540 \pm 0{\cdot}007$).

(3) Fifty-seven third chromosomes derived from samples of the same (geographic) populations of Ranna (47 chromosomes) and Corato (10 chromosomes), collected one year after the isolation of the *SD* and III^{Ra} chromosomes (October 1972) and balanced against *TM2*.

(4) *y; bw-5; st-5:* an isogenic line selected from a *bw*; *st* stock for high sensitivity to SD^{R-1} chromosome, by using the *y*; *SM5*; *TM2*/*T*(*2; 3*) *S 9*, *bw e* strain. The sensitivity of this line to the SD^{R-1} chromosome does not depend on the third chromosome because $SD^{R-1}/bw\text{-}5$; *st-5*/*st-5*, $SD^{R-1}/bw\text{-}5$; $+/st\text{-}5$ and $SD^{R-1}/bw\text{-}5$; $+/+$ males yield $\bar{k}$ values of $0{\cdot}988 \pm 0{\cdot}002$, $0{\cdot}994 \pm 0{\cdot}001$ and $0{\cdot}984 \pm 0{\cdot}003$, respectively.

(5) *y; bw-7; st-7:* an isogenic line isolated as above from the same *bw*; *st* stock and selected for average sensitivity to the SD^{R-1} chromosome ($SD^{R-1}/bw\text{-}7$; *st-7/st-7* males show $\bar{k} = 0{\cdot}710 \pm 0{\cdot}007$ and $SD^{R-1}/bw\text{-}7$; $+/+$ males yield $\bar{k} = 0{\cdot}716 \pm 0{\cdot}013$).

(6) *SM5:* a balancer for chromosome 2; homozygous lethal.

(7) *TM2:* a balancer for chromosome 3; homozygous lethal.

(8) *GlSb/TM2:* balanced lethals stock where the *Gl Sb* chromosome carries the same modifying factor present on the III^{Ra} chromosome.

In all crosses for calculating *k* values, females of the *y; bw-5; st-5* stock were used. In all experiments matings were set up with one male and two virgin females in single vials with standard corn-meal-agar medium. The *k* values were calculated within ten days after eclosion. All work was performed under standard conditions at 24 ± 1 °C.

3. RESULTS AND DISCUSSION

(i) *Recovery and characterization of the* SD^{Ra} *and* III^{Ra} *chromosomes*

During a search performed to assess the frequency of *SD* chromosomes in natural populations of *Drosophila melanogaster* from Southern Italy (Trippa *et al.* 1972), a second and a third chromosome were isolated by crossing a wild-type male from the Ranna population with females of the *y; bw-5; st-5* stock.

The *k* values exhibited by F_2 males of $+/bw\text{-}5$; $+/st\text{-}5$ and $+/bw\text{-}5$; $st\text{-}5/st\text{-}5$ genetic composition were then measured. Their relative distribution is reported in Fig. 1, which shows that the wild second chromosome behaves as an *SD* chromosome, altering the segregation of the two second chromosome homologues. This second chromosome is designated SD^{Ra} (for description, see Materials and Methods). The data also show that there exists a significant difference ($P \ll 0{\cdot}001$) in the *k* values of the males of the two genotypes and that this difference stems from the presence of the wild third chromosome designated III^{Ra}, which enhances the distortion caused by SD^{Ra}. In a series of parallel crosses it has been ascertained that III^{Ra} has an equal enhancing effect when heterozygous and homozygous, indicating that the factor(s) present on the III^{Ra} chromosome is dominant.

(ii) *Genetic localization of the Segregation Distortion modifier*

To localize the modifier on III^{Ra}, $bw^+/bw\text{-}5$; $Gl\ Sb/III^{Ra}$ females were crossed with $SD^{Ra}/bw\text{-}5$; $st\text{-}5/st\text{-}5$ males. Since all the SD^{Ra} male progeny carrying a third recombinant chromosome (about 100 males) yielded a *k* value of 1·00, it was concluded that the *Gl Sb* chromosome was carrying the same modifier as the III^{Ra} chromosome. This was confirmed by testing $SD^{Ra}/bw\text{-}5$; $Gl\ Sb/st\text{-}5$ males, which yielded a *k* value of 1·00; and on the basis of these results, $bw^+/bw\text{-}5$; $Gl\ st^+\ Sb/Gl^+\ st\text{-}5\ Sb^+$ females were crossed with $SD^{Ra}/bw\text{-}5$; $Gl^+\ st\text{-}5\ Sb^+/Gl^+\ st\text{-}5\ Sb^+$ males to localize the modifier on the *Gl Sb* chromosome. It was then possible to map the modifier factor by using the *k* values shown by the various types of $SD^{Ra}/bw\text{-}5$; *third recombinant chromosome/st-5* males.

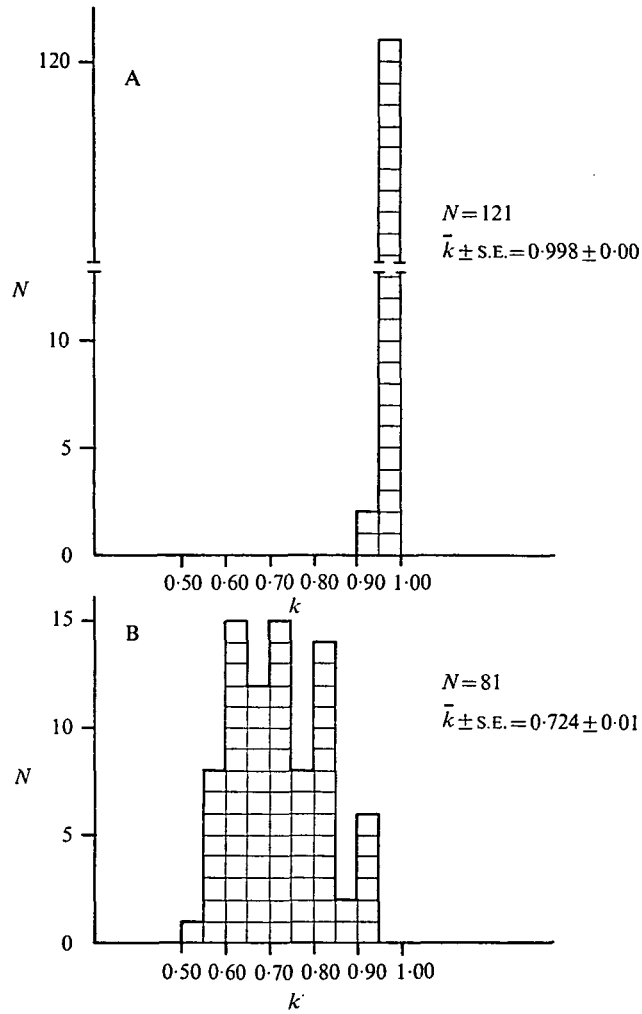

Fig. 1. Distribution of k values exhibited by $SD^{Ra}/bw\text{-}5$; $III^{Ra}/st\text{-}5$ (A) and $SD^{Ra}/bw\text{-}5$; $st\text{-}5/st\text{-}5$ (B) males. Each square represents the k value shown by one male.

Table 1. *Genetic localization of the* III^{Ra} *modifier*

Types of crossover	$\bar{k} \pm$ S.E. 0·76 ± 0·01 (modifier absent)	$\bar{k} \pm$ S.E. 1·00 ± 0·00 (modifier present)
Gl st Sb$^+$	13	—
Gl$^+$ st$^+$ Sb	1	12
Gl st$^+$ Sb$^+$	6	13
Gl$^+$ st Sb	35	26

(Distribution of the modifier among F_1 males of $SD^{Ra}/bw\text{-}5$; *different crossover*$/st\text{-}5$ genotypes. The parental cross was $bw^+/bw\text{-}5$; *Gl st*$^+$ *Sb* (carrying the modifier)$/Gl^+$ *st-5* Sb^+ females with $SD^{Ra}/bw\text{-}5$; Gl^+ *st-5* Sb^+/Gl^+ *st-5* Sb^+ males.)

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From a first analysis of the figures given in Table 1 it can be established that the modifier lies in the region between *st* and *Sb*. Moreover, since out of 80 crossovers between *st* and *Sb*, 32 were crossovers between *st* and the modifier and 48 between the modifier and the *Sb* locus, it was possible to locate the modifier at about 32 eightieths of the distance between the two markers (14·2 map units) from *st*. Using the standard gene locations (Lindsley & Grell, 1968) of *st* (44·0) and *Sb* (58·2), the locus of the modifier can be calculated at 49·7 ± 0·8.

(iii) *The* III^{Ra} *factor as modifier of the distortion caused by* SD *chromosomes*

An experiment was performed to ascertain the ability of the *III*^{Ra} factor to modify the amount of distortion exhibited by the various *SD* chromosomes listed under Materials and Methods. The *k* value of *SD/bw-5*; *III*^{Ra}/*st-5* males was thus

Table 2. *Reversal of the modifier effect of the* III^{Ra} *factor depending upon the source of the* SD *chromosomes*

Chromosome II tested	III^{Ra} absent* ($\bar{k}$ ± S.E.)	III^{Ra} present† ($\bar{k}$ ± S.E.)
SD from South Italy		
Ra-88	0·70 ± 0·02	0·996 ± 0·002
Ra-127	0·72 ± 0·03	0·969 ± 0·013
Ca-148	0·73 ± 0·02	1·000 ± 0·000
Ca-230	0·76 ± 0·02	0·999 ± 0·000
Ot-1	0·76 ± 0·03	0·994 ± 0·002
Co-17	0·81 ± 0·02	1·000 ± 0·000
Co-64	0·69 ± 0·01	1·000 ± 0·000
Co-100	0·65 ± 0·01	1·000 ± 0·000
Co-IV	0·69 ± 0·02	1·000 ± 0·000
Ar-38	0·67 ± 0·03	1·000 ± 0·000
Ar-249	0·74 ± 0·03	1·000 ± 0·000
Pe-6	0·76 ± 0·01	1·000 ± 0·000
Pe-122	0·73 ± 0·01	0·998 ± 0·000
Sa-262	0·75 ± 0·04	1·000 ± 0·000
SD from Rome		
R-1	0·99 ± 0·00	0·878 ± 0·020
SD^{+} chromosomes		
Sa-235	0·57 ± 0·03	0·535 ± 0·013
SM5	0·45 ± 0·02	0·466 ± 0·011

Every $\bar{k}$ estimate was obtained from about 24* or 12† males, respectively. Each male was tested by examining a progeny of approximately 100 individuals. After having ascertained that the *n* *k*'s of different males of the same group were homogeneous, the $\bar{k}$ was calculated as their arithmetical mean and its S.E. by the following formula: $\sqrt{\frac{\sum_{i=1}^{n}(k_i-\bar{k})^2}{n(n-1)}}$.

calculated. Two control crosses were made: (1) to evaluate the amount of distortion caused by the *SD* chromosomes in the absence of the *III*^{Ra} chromosome; the *k* value yielded by *SD/bw-5*; *st-5/st-5* males was thus measured; (2) to ascertain whether the *III*^{Ra} factor modified the segregation of second chromosomes only when an *SD* chromosome was present in the male genotype, while not interfering

in the segregation of two SD^+ chromosomes. For this purpose, either a second chromosome extracted from the natural population of Sambiase, *Sa-235*, or the *SM5* balancer chromosome was used. The k values of *Sa-235/bw-5*; III^{Ra}/*st-5* and *SM5/bw-5*; III^{Ra}/*st-5* males were then measured.

Table 2 shows the amount of segregation distortion exhibited by males carrying different *SD* or SD^+ chromosomes when the III^{Ra} factor is present in their genotype and when it is absent. *SD/bw-5*; *st-5/st-5* males yield $\bar{k}$ values varying between 0·65 and 0·81, SD^{R-1}/*bw-5*; *st-5/st-5* males, by contrast, exhibit a $\bar{k}$ value of 0·99. When III^{Ra} is also present the k exhibited by all the Southern Italian *SD*-bearing males increases to values between 0·99 and 1·00, while that shown by SD^{R-1} males drops to $0{\cdot}88 \pm 0{\cdot}02$. Hence, from its behaviour in the laboratory, it would seem that the III^{Ra} factor should be regarded as a modifier of the Segregation Distortion phenomenon rather than specifically as an enhancer or a suppressor. Table 2 also shows that III^{Ra} did not alter the segregation of either the *Sa-235* or the *SM5* chromosome in comparison with a *bw-5* chromosome, indicating that it does not affect the segregation of second chromosomes when neither carries *SD*.

(iv) *The modification of* SD *factors induced by* III^{Ra} *is not heritable*

Sandler & Rosenfeld (1962) demonstrated that the *X*-chromosome balancer, *Muller-5*, has one or more modifiers (suppressors) of Segregation Distortion and that the inhibiting action of the modifier remains heritable for at least two generations after the *Muller-5* chromosome has been removed. These authors believed it reasonable to suppose that modification of *SD* activity involves changes at the *SD* locus itself and not in the products of *SD* activity.

To test whether the modifying action of III^{Ra} is heritable the distortion in the progeny of *SD/bw-5*; *st-5/st-5* males, derived from *SD/bw-5*; III^{Ra}/*st-5* males,

Table 3. *Testing the heritability of the modifying effect of* III^{Ra} *on* SD. $\bar{k}$ *values shown by* SD/bw-5; st-5/st-5 *males and* SD/bw-5; III^{Ra}/st-5 *parental males and* SD/bw-5; st-5/st-5 F_1 *males*

	Types of males		
SD chromosomes examined	With no III^{Ra} chromosome and derived from parents with no III^{Ra} chromosome ($\bar{k} \pm$ S.E.)	Carrying III^{Ra} chromosome ($\bar{k} \pm$ S.E.)	With no III^{Ra} chromosome but derived from parents with III^{Ra} chromosome ($\bar{k}^* \pm$ S.E.)
Ra	$0{\cdot}72 \pm 0{\cdot}01$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}70 \pm 0{\cdot}02$
Ra-88	$0{\cdot}70 \pm 0{\cdot}02$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}64 \pm 0{\cdot}02$
Ca-230	$0{\cdot}76 \pm 0{\cdot}02$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}69 \pm 0{\cdot}01$
Ot-1	$0{\cdot}76 \pm 0{\cdot}03$	$0{\cdot}99 \pm 0{\cdot}00$	$0{\cdot}67 \pm 0{\cdot}04$
Co-17	$0{\cdot}81 \pm 0{\cdot}02$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}80 \pm 0{\cdot}02$
Co-64	$0{\cdot}69 \pm 0{\cdot}01$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}60 \pm 0{\cdot}03$
Pe-122	$0{\cdot}73 \pm 0{\cdot}01$	$1{\cdot}00 \pm 0{\cdot}00$	$0{\cdot}75 \pm 0{\cdot}02$

For each *SD* chromosome the $\bar{k}$ values in columns two and four are not statistically different. The S.E.s were calculated as in Table 2.

* About eight males, each with a progeny of approximately 100 individuals, were tested.

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was measured (Table 3). It appears that the fact of being derived from a male parent carrying III^{Ra} does not alter the segregation distortion caused by any of the seven natural SD chromosomes examined. Thus III^{Ra} does not induce any hereditary modification of the SD gene.

(v) *Action of* III^{Ra} *in males heterozygous for* SD *and second chromosomes moderately sensitive to* SD

A series of experiments was performed to check whether III^{Ra} was capable of modifying the segregation distortion even when the SD^{Ra} chromosome was heterozygous with second chromosomes of different sensitivity to SD^{Ra}. These second chromosomes were derived from Ranna and Corato populations and the

Table 4. *The dependence of the segregation ratio observed upon the* SD$^+$ *and* SD *chromosomes, the presence of the* III^{Ra} *modifier, and the provenience of all these chromosomes relative to each other*

	Male genotypes						
		SD^{Ra}/SD^+; $III^+/st\text{-}5$			SD^{Ra}/SD^+; $III^{Ra}/st\text{-}5$		
SD$^+$ second chromosome examined	SD^{R-1}/SD^+ ($\bar{k}$)	No. of males tested	Total progeny examined	$\bar{k} \pm$ S.E.	No. of males tested	Total progeny examined	$\bar{k} \pm$ S.E.
Chromosomes from nature							
Ra-39	0·67	4	434	0·54 ± 0·05	8	885	0·74 ± 0·04
Ra-67	0·65	12	825	0·50 ± 0·02	19	1878	0·61 ± 0·02
Ra-64	0·62	8	718	0·52 ± 0·01	7	522	0·63 ± 0·02
Ra-144	0·69	20	1986	0·58 ± 0·01	12	1350	0·75 ± 0·02
Co-5	0·68	7	865	0·76 ± 0·03	10	1503	0·97 ± 0·01
Co-11	0·60	7	497	0·78 ± 0·02	7	427	0·94 ± 0·03
Co-23	0·60	8	832	0·88 ± 0·04	8	680	1·00 ± 0·00
Co-50	0·60	12	1476	0·64 ± 0·03	18	2163	0·92 ± 0·02
Chromosome from the laboratory							
bw-7	0·71	30	2414	0·77 ± 0·01	26	3117	1·00 ± 0·00

For each SD^+ chromosome the $\bar{k}$ values in columns five and eight are statistically different ($P < 0{\cdot}01$). The S.E.s were calculated as explained in Table 2.

laboratory strain *bw-7*, and were all selected on the basis of their moderate response to SD^{R-1} (column 2, Table 4). Table 4 gives the average k values exhibited by males heterozygous for the SD^{Ra} chromosome and, in turn, these second chromosomes, with and without the III^{Ra} modifier. The results shown in Table 4 allow the following observations to be made: (*a*) the SD^{R-1} and SD^{Ra} factors show different distorting effects when heterozygous with the same second SD^+ chromosomes (columns 2 and 5), (*b*) the two groups of second SD^+ chromosomes from Ranna and Corato respond differently to the same SD^{Ra} chromosome (column 5), (*c*) the III^{Ra} chromosome induces or enhances segregation distortion when in-

sensitive second chromosomes (Ranna, $\bar{k} = 0{\cdot}54$) are present and also when rather sensitive second chromosomes (Corato and *bw-7*, $\bar{k} = 0{\cdot}77$) are present in heterozygosis with SD^{Ra}. The increase in k values in both cases is the same, being about 0·8 (the ratio between the mean k's obtained without and with III^{Ra}).

Considering (*a*) and (*b*) it may be concluded that the best hypothesis to explain the occurrence of the Segregation Distortion phenomenon is one which involves the interaction of SD and SD^{+} factors (as suggested in an earlier paper, Trippa *et al.* 1974). Thus the sensitivity of the SD^{+} chromosome is not a peculiar property of itself. The classification of a second SD^{+} chromosome as more or less sensitive would, in fact, depend on the type of SD chromosome with which it is paired in the male. In particular, as far as the sensitivity of SD^{+} wild chromosomes examined is concerned, the presence of SD^{+} Ranna chromosomes in SD^{Ra}/SD^{+} males causes a reduction in the amount of distortion to quite normal values compared with the distortion in SD^{R-1}/SD^{+} males (from $\bar{k} = 0{\cdot}66$ to $\bar{k} = 0{\cdot}54$), while SD^{+} Corato and *bw-7* chromosomes in SD^{Ra}/SD^{+} males exhibit an increase in the segregation distortion (from $\bar{k} = 0{\cdot}64$ to $\bar{k} = 0{\cdot}77$; columns 2 and 5). Thus the SD^{+} Ranna chromosomes appear to be insensitive to an SD chromosome derived from the same population (SD^{Ra}), while those from Corato and the *bw-7* line are as sensitive to an SD chromosome derived from another population, as to SD^{Ra}.

Finally, as far as the explanation of the findings reported in (*c*) is concerned, two different models may equally well account for them: (1) III^{Ra} factor may increase the distorting action of SD^{Ra}; (2) III^{Ra} may increase the sensitivity of the second SD^{+} chromosomes. The results do not enable us to choose between the two models.

(vi) *Diffusion of third chromosomes carrying modifiers of the SD phenomenon similar to* III^{Ra} *in the natural populations of Ranna and Corato*

To estimate the frequency in nature of third chromosomes with behaviour similar to that of the III^{Ra} chromosome, 57 third chromosomes of the two populations of Ranna and Corato were tested. The amount of distortion shown by SD^{Ra}/*bw-5*; III^{+}/*st-5* males was calculated. Four males for each wild third chromosome sampled were tested in individual matings.

The distribution of $\bar{k}$ values is given in Fig. 2. Of the sample of 47 third Ranna chromosomes, 31 (i.e. 66%) have a $\bar{k}$ value greater than 0·90 with a mean $k = 0{\cdot}99$; the remaining 16 chromosomes (34%) have a $\bar{k}$ value between 0·66 and 0·85 with a mean $k = 0{\cdot}78$. Of the ten Corato chromosomes, seven have a $\bar{k}$ value higher than 0·90 with a mean $\bar{k} = 0{\cdot}98$, while three have a $\bar{k}$ between 0·75 and 0·85 with a mean $k = 0{\cdot}80$. The frequency of third SD-modifier chromosomes (of the kind that enhances the amount of distortion caused by SD^{Ra}) thus seems very high among third chromosomes of the Ranna and Corato populations. Around 70% of the third chromosomes in the samples of the two natural populations tested show the ability to modify the k value from 0·72 (which represents the 'normal' distortion value of the SD^{Ra} factor alone) to about 1·00.

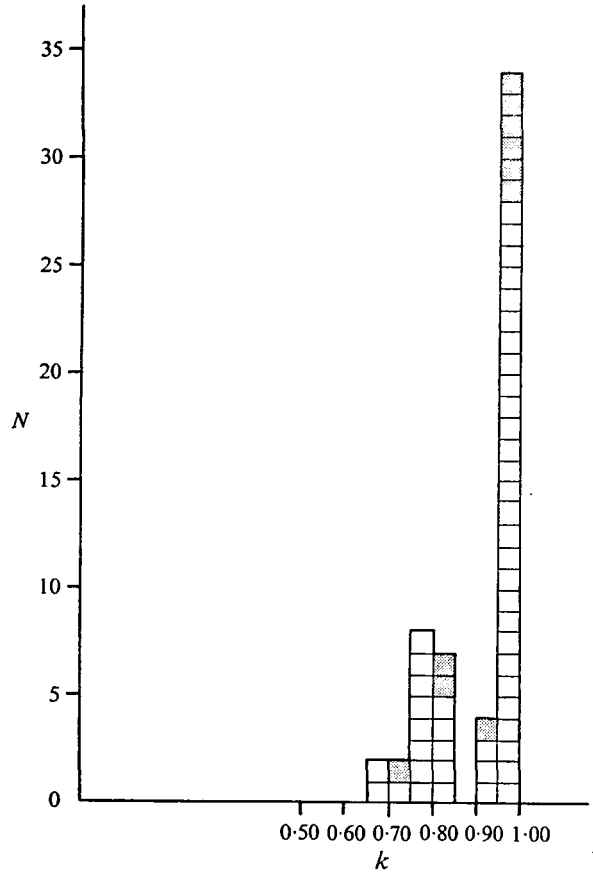

Fig. 2. Distribution of $\bar{k}$ values of $SD^{Ra}/bw\text{-}5$ males carrying, in turn, each one of the 47 III^{+} chromosomes of the Ranna population (□) or one of the ten III^{+} chromosomes of the Corato population (▦). Each square represents the $\bar{k}$ value exhibited by four males of identical genotype.

4. CONCLUSIONS

The III^{Ra} factor is the first gene modifying Segregation Distortion found on the third chromosome. We consider it as a modifier since with the SD chromosomes derived from Southern Italian populations it acts as a k enhancer but with the SD^{R-1} chromosome it behaves like a k reducer (see Table 2).

Recently the Segregation Distortion phenomenon has been clarified somewhat. Nicoletti (1968), by analysing testes of SD/SD^{+} males with the electron microscope, found several cysts with degenerating spermatids that could account for the abnormal recovery of SD^{+} sperms. Tokuyasu *et al.* (1972) by the same kind of analysis, were able to show the dysfunction of one half of the spermatozoa (probably the SD^{+}) together with the failure of the spermatid individualization phase during spermiogenesis. However, the precise mechanism through which this dysfunction occurs is still unknown (Peacock & Miklos, 1973). This fact makes

it even more difficult to interpret how the III^{Ra} factor intervenes in such a puzzling mechanism.

As regards the sensitivity of SD^+ chromosomes to SD, for the first time it has been possible to measure the amount of distortion exhibited by males carrying an original SD chromosome (SD^{Ra}) and original SD^+ second chromosomes extracted from the same natural population (Ranna). Previously it had always been necessary to use a marker either on the SD or on the SD^+ chromosome and in so doing crossovers were always obtained, thus jeopardizing in some way the SD-SD^+ system that was operating in nature. If it is considered, too, that some males tested also carried the III^{Ra} chromosome, it can be said that for these males it has been possible to re-establish in the laboratory to a great extent the genetic composition of the males of the natural population of Ranna.

The data of Table 4 reveal that the second SD^+ Ranna chromosomes are virtually all insensitive to SD^{Ra}, while the SD^+ Corato chromosomes appear to be quite sensitive. This result thus seems to confirm the hypothesis put forward by Hiraizumi *et al.* (1960) on the basis of data obtained from laboratory populations, of a spontaneous occurrence and successive diffusion of second SD^+ chromosomes insensitive to the SD factors present in the same population. Hence the different levels of sensitivity of the SD^+ chromosomes in the populations would appear to depend closely on the presence of the SD factors and the distorting power of these factors and the time-length of their interaction with the SD^+ chromosomes. The average level of sensitivity to SD^{Ra} of the SD^+ chromosomes from the Corato population may be interpreted as indirect evidence of the unique nature of the SD-SD^+ system as regards the occurrence of insensitivity in the SD^+ chromosomes.

The occurrence, in the Ranna population, of SD^+ chromosomes insensitive to the SD^{Ra} action, could be interpreted as a force that would rapidly lead to the disappearance of the SD phenomenon. On the other hand, the simultaneous presence in the Ranna population of enhancer chromosomes of the III^{Ra} type with the observed high value (see Fig. 2) must be considered as a counteracting factor in favour of SD^{Ra}.

This series of observations enables us to interpret the SD phenomenon in the populations as the outcome of the interaction of opposite selective forces that result in maintaining the frequency of SD genes at the generally observed values of 0·01–0·10 (Sandler, Hiraizumi & Sandler, 1959; Hiraizumi *et al.* 1960; Mange, 1961; Greenberg, 1962; Hiraizumi & Nakazima, 1965; Watanabe, 1967; Trippa *et al.* 1972). Particularly in the Ranna population, the maintenance of SD chromosomes might be due to an equilibrium among factors that tend to spread the SD chromosomes in the population (the SD factors themselves and the III^{Ra} enhancer) and factors that, on the other hand, tend to limit this spread: the low distortion power of the SD chromosomes (Trippa *et al.* 1973), the presence of insensitive SD^+ chromosomes, the complete sterility of SD^{Ra}/SD^{Ra} males and females, and the semisterility of SD/SD^+ males.

Nothing is yet known as to the biological significance of keeping SD chromosomes at the frequencies observed in natural populations. It is, however, known

that with the mechanism of the preferential segregation of a chromosome it is possible to diffuse clusters of genes rapidly in populations, thus accelerating changes of gene frequency.

The authors express their thanks to Professor B. Nicoletti for critical reading of the manuscript.

This work was supported by a grant from The National Research Council (CNR).

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