The F_2 pupae segregated according to the expected 3:1 ratio, and 154 wild pupae and 51 black pupae were obtained ($X^2=0.0016$). Only 32 black pupae were analyzed (table 1). These data seem to fit better in the hypothesis of linkage in only one of the sexes, and 50% recombination in the other. Imagos emerging from F_2 pupae confirmed the autosomal condition of the gene *niger:* 24 black males, 27 black females, 75 wild males and 79 wild females were found ($X^2=0.28$).

Table 1. Observed F_2 frequencies of esterase patterns among black pupae compared with expected frequencies in 3 alternative hypotheses

	Esterase pattern		
	1a/1a	1a/1b	1b/1b
Black F_2 pupae	14	18	0
Total linkage hypothesis	32.0	0	0
No linkage hypothesis	8.0	16.0	8.0
Linkage in only 1 sex	16.0	16.0	0

Esterase pattern 1a/1a = homozygote for *Est-1a* allele; 1b/1b homozygote for *Est-1b;* 1a/1b = heterozygote.

Table 2. Esterase pattern frequencies among backcross individuals

	Pupa color	Esterase pattern	
		1a/1a	1a/1b
♀ $F_1 \times \frac{nig\ 1a}{nig\ 1a}$	w	9	12
	n	9	11
♂ $F_1 \times \frac{nig\ 1a}{nig\ 1a}$	w	0	16
	n	16	0

Pupa color: n, *niger* homozygote; w, wild brown (heterozygote).

The results summarized in table 2 were obtained by backcrossing F_1 males and females with the maternal strain. It is evident that only parental type gametes (*nig Est-1a* and *+Est-1b*) are produced in F_1 males while the F_1 females produce all 4 types - 2 parentals and 2 recombinants (*nig Est-1b* or *+Est-1a*).

These results suggest that a) gene *Est-1* is probably in the same chromosome as gene *niger* but at nearly 50% recombination distance, and b) recombination does not occur in the male *C. capitata.* An alternative but somewhat queer explanation would be to assume that both genes are in separate chromosomes and that the centromeres of the same paternal origin tend to migrate to the same pole.

The apparent lack of agreement between cytological and genetical data now reported confirms that the occurrence of chiasmata during meiosis does not always indicate the existence of crossing over, i.e. the exchange of genetic material between homologous chromosomes, which means either that not all chiasmata are related to crossing over or that other pairing conditions can give rise to chromosomal configurations that simulate chiasmata.

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Germ cell chromosomes in two species of terrestrial isopods from India

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Summary. In 2 species of terrestrial isopods, namely *Porcellio assamensis* and *P. laevis,* the diploid and haploid numbers of chromosomes have been established to be 48 and 24 respectively for the former species and 50 and 25 respectively for the latter species. Female heterogamety of the ZW type has been found to exist in *P. laevis.*

Only a few sporadic references are available on the chromosomes of isopod crustaceans[2-16]. In fact, very little work has been done in India on the cytology of these isopods. So far there are only 3 species[14,15] on the cytological record. The present paper reports studies on the chromosomes of 2 more species of isopods belonging to the family Porcellionidae (suborder Oniscoidea).

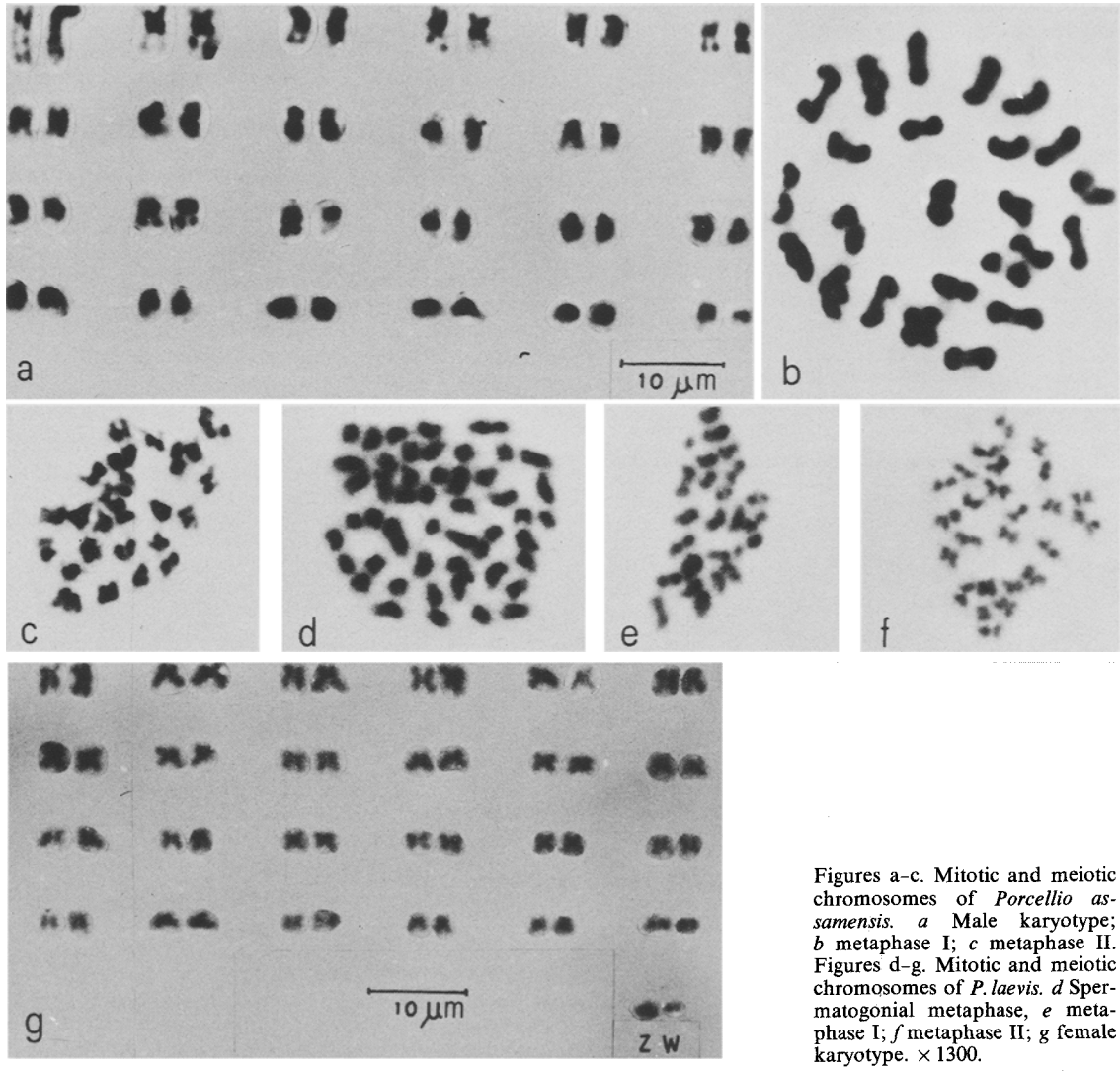
Materials and methods. The male and female individuals of *Porcellio assamensis* and *P. laevis* were collected at Raigarh (M.P.) and Chandigarh, from underneath débris lying in moist places. Whereas in the case of *P. assamensis* only the testicular material was utilized, for *P. laevis* both the testicular and ovarian tissues were used for the chromosomal studies. The chromosome preparations were made by employing the air drying technique[17] and stained in Carbol Fuchsin.

Results. Each spermatogonial metaphase of *P. assamensis* reveals the diploid number of 48 chromosomes which form 24 homologous pairs (figure, a) according to their size and shape. Of them, 13 pairs are metacentric, 5 are submetacentric and the remaining 6 are acrocentric. The largest pair in the karyotype is submetacentric and measures about 6.46 µm. The 2nd and 3rd pairs measure about 5.23 µm and 4.13 µm respectively. However, the rest of the chromosomes reveal a gradual decrease in their size from 4.08 µm to 1.41 µm. Each of the metaphase I plates (figure, b) carries 24 bivalents showing a rather low frequency of chiasmata. The chiasma frequency per cell, at this stage, has been calculated to be 24.28 ± 0.45. Metaphase II (figure, c), again shows 24 chromosomes.

After scanning a number of spermatogonial metaphase plates of *P. laevis* (figure, d) a diploid number of 50 chromosomes has been established for this species. Of these, 42 are metacentric, 6 are submetacentric and the remaining 2 are acrocentric chromosomes. The last 2 might be the ZZ chromosomes corresponding to the acrocentric Z of the female. Metaphase I (figure, e) carries 25 bivalents of different configurations. However, most of them are dumbbell-shaped. Metaphase II (figure, f) again shows 25 chromosomes, each displaying its chromatids quite distinctly.

The oogonial metaphase chromosomes of this species can be sorted out into 24 homologous pairs (figure, g) and the remaining 2 unequal chromosomes can be designated as ZW chromosomes, thus indicating the existence of female heterogamety. The female karyotype consists of 42 metacentric, 6 submetacentric, 1 acrocentric Z and 1 metacentric W chromosome. The chromosomes range in length from 3.64 µm to 0.90 µm with a gradual decrease in their size from the largest to the smallest pair.

Discussion. General: In the family Porcellionidae, the chro-



Figures a–c. Mitotic and meiotic chromosomes of *Porcellio assamensis*. *a* Male karyotype; *b* metaphase I; *c* metaphase II. Figures d–g. Mitotic and meiotic chromosomes of *P. laevis*. *d* Spermatogonial metaphase, *e* metaphase I; *f* metaphase II; g female karyotype. × 1300.

List of chromosome numbers in the cytologically known species of the family Porcellionidae

Species	Chromosome number 2n	n	Authors
Porcellio assamensis	48s	24 ♂ (I, II)	Present studies
P. dilatatus	50s	25 ♂ (I)	Teichmann[9]
P. gallicus	–	28 ♀ (I)	Vandel[3]
P. laevis (loevis)	–	28 ♀ (I)	Vandel[3]
	50s	25 ♂ (I)	Teichmann[9]
	50s, o	25 ♂ (I, II)	Present studies
P. pictus	–	25 ♂ (?)	Teichmann[9]
P. rathkei	50s, o	25 ♂ (I, II)	Mittal and Pahwa[14]
P. scaber	56s	28 ♂ (I, II)	Imai and Makino[4]
	–	28 ♀ (I)	Vandel[3]
	50s, m	25 ♂ (I)	Teichmann[9]
Proporcellio quadristriatus	–	25 ♂ (I)	Teichmann[9]
Metoponorthus sexfasciatus	50s, m	25 ♂ (I)	Teichmann[9]
Nagara modesta	34–36o, m	34 ♀ (I) Parth.	Hill[5]
Leptotrichus naupliensis	50s	25 ♂ (I)	Teichmann[9]

Note: s, o and m stand for spermatogonial, oogonial and somatic cells respectively.

mosomes of 11 species[2-5,8,9,14] are on record (table). The present observations on *P. laevis*, i.e. 2n = 50 (n = 25) are quite in conformity with those of Teichmann[9]. However, during the present studies female heterogamety of the ZW type has been found to exist, whereas Teichmann[9] could not establish the sex mechanism in this species. Moreover, she has reported 2 types of chromosomes, i.e., metacentric and submetacentric, in the diploid garniture of this species, whereas during the present investigations its karyotype was found to consist of 3 types of chromosomes, i.e. metacentric, submetacentric and acrocentric. The chromosome architecture of *P. assamensis* cannot be compared with that of any other species as no cytologically known species of the family Porcellionidae (table) possesses this chromosome number. From the table it becomes evident that a large majority of species exhibit n = 25 which, therefore, can be taken as the 'modal haploid number' for the family Porcellionidae.

Sex-chromosomes. Though there is a good deal of discussion on the question of sex mechanisms in Isopoda, only a few workers[6-8,14,16] have dealt with its cytological demonstration in this group. Female heterogamety of the ZW_1W_2-type has been recorded in 5 species of the marine superspecies *Jaera marina*[6,7] belonging to the family Janiridae and of the ZW-type in another isopod, *P. rathkei*[14], belonging to the family Porcellionidae. During the present studies, the same type of sex mechanism, i.e., ZW-type, demonstrating female heterogamety, has been found to exist in the isopod *P. laevis*, belonging to the same family, Porcellionidae. On the other hand, male heterogamety of the XO-type has been established in the isopod, *Tecticeps japonicus*[8] (family Sphaeromatidae), whereas the same of the XX-type has been demonstrated in the isopod, *Armadillidium nasatum*[16]. Thus, it is seen that heterogamety both in the male and female has been reported in a few of the cytologically worked out species of isopods, while most of the forms studied do not show any evidence of sex-chromosomes. It seems that morphologically differentiable sex-chromosomes have not evolved to a considerable extent in the isopods.

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A spontaneous tandem duplication in a *Drosophila* chromosome[1]

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Summary. A unique long tandem duplication was discovered in salivary gland chromosome arm 3L of *Drosophila kikkawai*. It occurred spontaneously under laboratory conditions.

We report here the case of a long tandem duplication which occurred spontaneously. It was discovered in a larval female of *Drosophila kikkawai* during salivary gland chromosome analysis for gene arrangements.

Materials and methods. A culture stock of *D. kikkawai* has recently been established from a wild-caught female collected from Tananarive, Madagascar (stock No. J9) by Dr O. Kitagawa. It has been maintained in the laboratory at 25 ± 1 °C. A male of this stock was allowed to mate, in a vial of normal medium, with a virgin female of standard stock from Samut Songkhram, Thailand. Salivary gland chromosomes were prepared from 3rd stage larvae using standard aceto-orcein squash preparation[2].

Results and discussion. A total of 30 F_1 larvae were routinely examined and scored for gene arrangements in comparison with the standard gene sequence[2,3]. All the chromosome arms showed standard gene order. Surprisingly, 1 of the larvae manifested, in heterozygous condition, the long tandem duplication in chromosome arm 3L, which is the subject of this note. The repeated segment was remarkably long, involving about 62% of the chromosome length. The 2 break points were at 62B and 73B (figure, a). It may be noted that the region of duplicated segments was completely synapsed, in general (figure, b). However, an asynapsed triplo was occasionally observed in some cells.

The origin of this unusually long tandem duplication may be attributed to unequal crossing-over of the non-sister chromatids. The duplicated chromosome survived during the meiotic process while the chromosome with deficiency for a long segment was probably lost due to the expected severe lethal effect. However, a chromosome with such a long repeated segment is not expected to be retained in the population, because of strongly unfavorable selection. Therefore, it is difficult to envisage that it arose in the wild population. It seems more likely that such event took place spontaneously in the laboratory population. Moreover, there is no evidence indicating that the tandem duplication has ever been established in our laboratory population despite a search which was carefully made ever since it was first detected.

A tandem duplication involving a short portion of a chromosome is not an uncommon event in various organisms[4]. The first case of a naturally occurring tandem duplication associated with the bar eye phenotype was discovered in *D. melanogaster*[5]. Generally, the effects of duplication of a small region of a chromosome are not lethal. In fact, duplication appears to be much less deleterious than a deficiency. Nevertheless, a more severe phenotypic effect could result if the portion of duplication is so large that it approaches a condition similar to trisomy. Unfortunately, phenotypic effects of this long tandem duplication are not certain since it has been detected only once in a larva.