Table 1. Effect of poly I • poly C on isoproterenol-stimulated DNA synthesis. Poly I • poly C, poly U, or DEAE dextran (250 μg doses) was injected intraperitoneally 10 minutes before isoproterenol (IPR), 4 mg intraperitoneally; tritiated thymidine was given subcutaneously (10 μc to each mouse) 26 hours after IPR; the animals were killed 30 minutes later (number of mice is shown in parentheses). The specific activity of salivary gland DNA is expressed in counts per minute per milligram of DNA (± standard deviation).

Treatment	Specific activity of salivary gland DNA
None (9)	2,457 ± 1021
IPR only (8)	21,080 ± 4028
Poly I • poly C + IPR (6)	3,081 ± 1600
Poly U + IPR (6)	11,695 ± 1046
DEAE-dextran + IPR (6)	12,058 ± 6400

Table 2. Effect of poly I • poly C on the synthesis of α-amylase in mouse salivary gland. All animals, except controls, received 4 mg of isoproterenol (IPR) intraperitoneally. Poly I • poly C (250 μg per mouse) was given 2 hours after IPR. α-Amylase activity (units of amylase per milligram of protein) was determined by the method of Bernfeld (*12*). Three to six animals per group (mean ± standard deviation).

Time after IPR (hr)	Treatment	Amylase
	None	12.6 ± 1.8
2	IPR only	1.7 ± 0.1
18	IPR only	8.2 ± 0.3
24	IPR only	9.4 ± 1.1
18	IPR + poly I • poly C	7.3 ± 0.7
24	IPR + poly I • poly C	7.5 ± 0.2

and mice (*9*). The enzyme is then resynthesized and, within 24 hours after IPR, its activity has returned to values just below those of control animals (*9*). Table 2 indicates that poly I · poly C, injected 2 hours after IPR (at the time of minimum α-amylase activity), has little effect on the reappearance of α-amylase activity at later times.

Gresser *et al.* (*3*) have demonstrated that survival of mice inoculated with tumor cells of viral etiology increases when the mice are treated with interferon preparations. They also showed that interferon preparations delayed the evolution of Friend and Rauscher leukemias in mice (*10, 11*) and stated that, although a direct action of interferon on the proliferation of viral-infected transformed cells could not be excluded, the antitumor effect of interferon was probably due to its antiviral property. Levy *et al.* (*11*) have shown that poly I • poly C inhibited the growth of a reticulum cell sarcoma, a lymphatic lymphoma, and a fibrosarcoma which apparently do not contain infectious oncogenic viruses. They postulated that the action of poly I · poly C could be due to (i) enhanced immunological rejection of foreign antigens; or (ii) a direct action on tumor such as an induction of modified ribosomes able to make even finer distinctions than those made by interferon-type ribosomes; or (iii) the possibility that poly I · poly C produces changes in the blood supply to the tumor with resulting ischemic necrosis. The results of our experiments cannot be explained in terms of a generalized toxic effect, and it is difficult to invoke an immunological mechanism in the inhibition of IPR-stimulated DNA synthesis. As to the antiviral action of poly I · poly C, one should consider the possibility that IPR induces the replication of a latent DNA-containing virus and that the development of this virus is blocked by poly I · poly C. However, the effect of IPR is a bona fide stimulation of cellular proliferation (*4, 6*), characterized by duplication of the amount of cellular DNA and by mitosis. That mitosis in mammalian cells may be regulated by a latent virus is a still unsupported possibility. Finally, the inhibitory effect of poly I · poly C on IPR-stimulated DNA synthesis resembles closely that of low doses of actinomycin D (*6*), and it is possible that it may exert an effect on the transcription of the cell genome.

FREDERIC T. SEROTA
RENATO BASERGA
Department of Pathology and *Fels Research Institute, Temple University School of Medicine, Philadelphia, Pennsylvania 19140*

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Chromosome Number Variation in a Stick Insect Didymuria violescens (Leach)

Abstract. *Seven major races, with diploid numbers ranging from 26 to 40, and three types of sex-chromosome mechanism were found in the Australian phasmatid* Didymuria violescens *(Leach). The differences between chromosome complements are mainly due to translocations between autosomes, and to translocations between autosomes and sex chromosomes. The geographic pattern of chromosome variation and the characteristics of hybrids implicate chromosomal rearrangements in mechanisms of speciation.*

I have found extensive chromosomal variation in *Didymuria violescens* (Leach). This phasmatid is endemic to Australia and is distributed in the southeastern region of the continent. It occurs in the sclerophyllous Eucalypt forests of the coast and adjacent highlands, extending from southern Queensland south to Victoria, then westward to the Mount Lofty Ranges in South Australia. Within this area, seven races differing in chromosome number have been discovered (Fig. 1). The distributions of these are often contiguous and exhibit a mosaic pattern which was constant in successive seasons. The seven races possess distinct karyotypes, but they appear morphologically indistinguishable. On the available evidence (*1*), all would be referred to one species. These insects are generally sedentary. The adult males are capable of limited flight, but the females have very small wings and cannot fly. Dispersal is slow and is restricted to movement between trees either through the canopy or on the ground.

Diploid chromosome number varies from 40 to 26 in females. Four races have the XO(male):XX(female) sex-chromosome mechanism that is characteristic of phasmatids (*2*). These are the 39 male:40 female race of predominantly coastal distribution, the 37:38 race of the central eastern highlands of New South Wales, the 35:36 race of the southern highlands (New

South Wales and Victoria) and the 31:32 race found in the northern tableland region of New South Wales. The other three races have derived sex-chromosome mechanisms of the neo-XY(male):XX(female) type, in which autosomal material has been incorporated into the sex-chromosome system. Simple derivations of the system found in the 32(XY) and 30(XY) races are possible, merely by the translocation of the long arm of one acrocentric autosome onto the primitive metacentric X chromosome, converting it to a neo-X chromosome (*3*). At meiosis in the male, the homologous autosome pairs with one arm of the neo-X chromosome and thus functions as a neo-Y chromosome. Similar evolutionary transformations of the sex-chromosome mechanism have been observed in a number of orthopteroid insects including phasmatids (*2*, *3*). The 26(XY) race possesses a more complex neo-XY system, in which the terminal portions of both arms of neo-X and neo-Y chromosomes pair to form a very unequal ring bivalent at meiosis. This implies multiple changes—autosomal material must have been translocated onto both arms of the original X-chromosome. So far as I am aware, this novel sex-chromosome constitution has not previously been found in any orthopteroid insect.

Comparison of the chromosome complements of the XO races reveals a sequence in the number of pairs of long metacentric chromosomes. The 40, 38, 36, and 32 female karyotypes possess one, two, three, and five pairs of long metacentric chromosomes, respectively. There is a general relationship between these four karyotypes in that an increase in the number of long metacentric chromosomes is accompanied by a decrease in the number of medium-sized acrocentric chromosomes. However, the correspondence is not exact over the whole series. Some whole-arm transfers between autosomes have occurred, but more complicated changes have also been involved, both here and in the derivation of the XY races. Thus the total number of major chromosome arms in the complement of each race does not remain constant, but shows a reduction with decrease in chromosome number (Fig. 2).

The 39:40 race is apparently the most primitive. First, it has the most extensive distribution (Fig. 1) and is found in the greatest diversity of coastal and mountain habitats. Second, it has the primitive XO(male):XX(female)

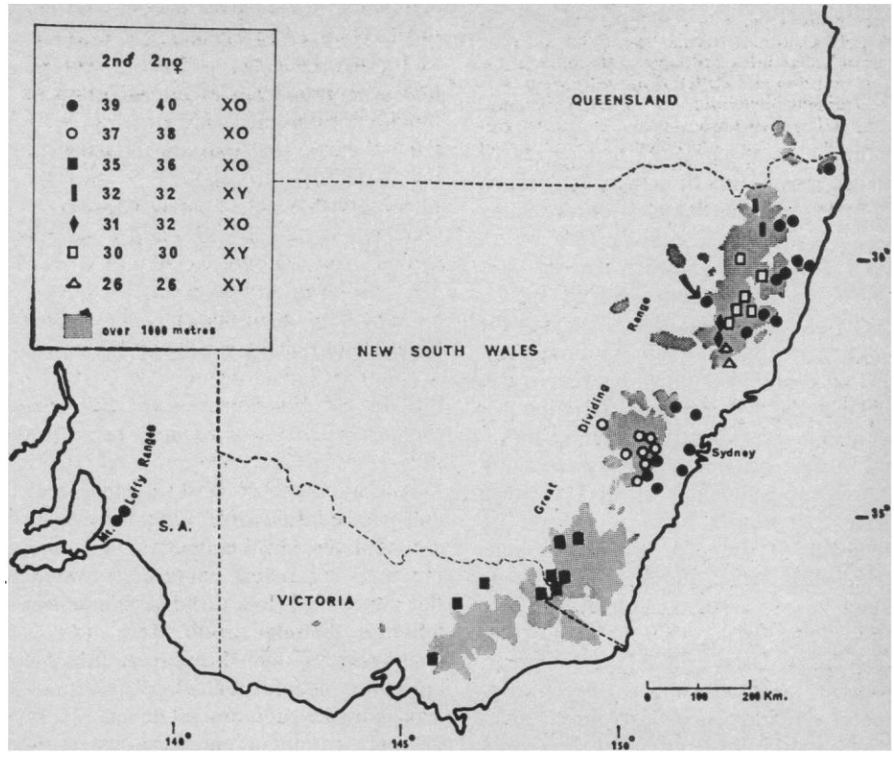

Fig. 1. Distribution of the seven chromosome races of *Didymuria violescens* (Leach) in southeastern Australia. The arrow indicates an isolate of the 39 : 40 race on the western side of the Great Dividing Range. The map is based on examination of approximately 500 individuals, collected in the summers of 1966–67, 1967–68, and 1968–69.

sex-chromosome constitution. Third, its distribution is disjunct, with two significant isolates. It is suggested that the conditions of greater moisture that existed during the Pleistocene may have permitted a broader distribution of *Didymuria* than conditions permit now, with extensions to the western slopes region and a connection to the Mount Lofty Ranges near Adelaide. These hills now provide a moist enclave or refuge area for an isolate of the 39:40 race, which is separated from the main distribution to the east by semiarid and arid country. The second isolate, west of the Great Dividing Range in New South Wales (Fig. 1, arrow), has no present connection with the 39:40 race on the coast and eastern side of the mountains. It could thus be a relic occurrence of the former wide distribution of the primitive race. It seems probable that evolution has tended toward a decrease in chromosome number. Change in number has been partially due to fusions between acro-

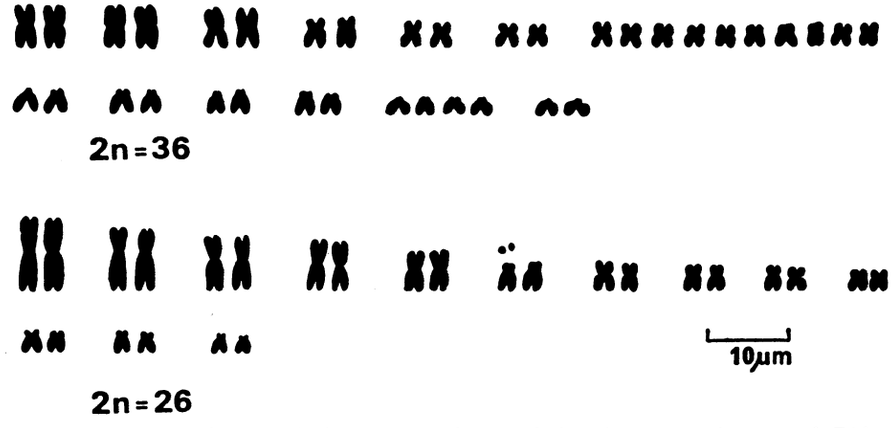

Fig. 2. Representative female karyotypes of two of the chromosomal races of *Didymuria violescens*, obtained from mitoses of ovarian follicle cell treated with Colcemid.

centric autosomes, rather than dissociation of metacentrics.

Interpretation of this cytogenetic situation in terms of the role of chromosomal rearrangements in evolution demands a knowledge of the degrees of reproductive isolation between races. Chromosomal differences of the magnitude found here must create reproductive barriers between races. This partial isolation could lead to speciation. The expected reduction in the fertility of hybrids should impose restrictions on gene flow between races and should also promote selection for secondary reproductive isolating mechanisms. At present, there are few indications of significant barriers between races. Laboratory crosses between individuals of different karyotypes have produced viable F_1 hybrid progeny which are reasonably fertile. In the field, zones of overlap between races have been discovered in certain areas. Within these zones, mating is apparently random, and involves chromosome hybrids as well as the parental races.

Didymuria offers one more example of a species with a geographic pattern of differentiation of chromosomal types. This kind of pattern has been described in a variety of organisms (*4*). A common picture is emerging of species or species complexes which consist of several chromosomal forms, occupying contiguous areas with zones of overlap. In the zones of overlap hybridization is possible, but because of the karyotypic differences involved hybrids will be of somewhat reduced fecundity. Mainly on the basis of his detailed studies in the *viatica* group of wingless grasshoppers (*4*), White has proposed a model of "stasipatric" speciation, in which chromosomal rearrangements are of prime importance as initiators of speciation (*5*). He has compared this to the "saltational" model of speciation (*6*), in which structural reorganization of the karyotype is also the main factor. It is clear that many of the instances of chromosome variation in both plants and animals are highly significant in relation to a general mode of speciation in which chromosomal differentiation is the basic and primary process. This is one of the strategies of speciation probably employed much more widely than is usually supposed.

ELYSSE CRADDOCK
School of Biological Sciences,
University of Sydney,
Sydney, Australia

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Mites and Commercial Extracts of House Dust

Abstract. *North American and European house dust mites have been found in the dusts used in the manufacture of commercial extracts of house dust.*

Allergy to house dust is widespread and has been managed for years by the use of house-dust extracts, which are prepared from dust collected by vacuum sweepers. Thus the dust is not just material floating in air, but most is dust from vacuumed surfaces. In some cases dusts from beds, overstuffed furniture, and daybeds are preferred (*1*). In the preparation of extracts, dust samples are washed in ether and then extracted with water or buffered aqueous saline. These extracts can then be used for skin testing or the management of house-dust allergy in sensitized patients.

The allergenic component of house dust is associated with mites of the genus *Dermatophagoides* (*2*). The original report indicated that *Dermatophagoides pteronyssinus* (Trouessart, 1897) was responsible. In Columbus, Ohio, the most common mite associated with house dust was *D. farinae* Hughes, 1961 (*3*). It is suggested that both species be called "house-dust mites" and that they be differentiated from each other by referring to them as "European" and "North American," respectively.

Dusts used in the manufacture of commercial extracts were passed through 1.000-, 0.500-, 0.250-, and 0.125-mm sieves. The dust retained by all sieves was examined for mites. Two 0.5-g samples were examined upon receipt of the samples. The remainder of the sample was then incubated for from 2 to 3 months at room temperature with relative humidity of 75 percent maintained by an aqueous solution

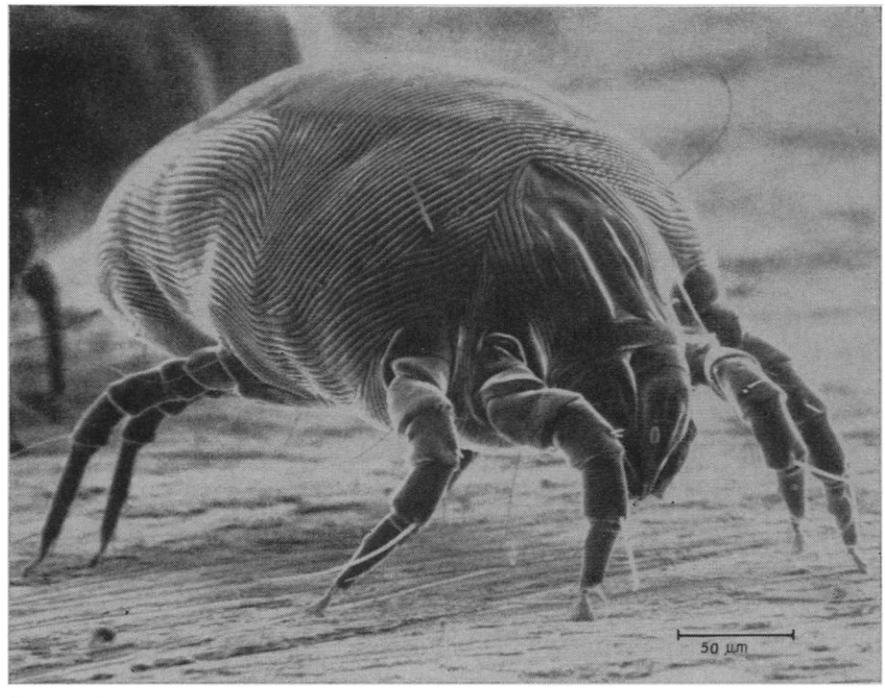

Fig. 1. The protonymph of the North American house-dust mite *Dermatophagoides farinae* Hughes, 1961 (× 300).