2. Each metaphase chromatid showed two separate filaments (half-chromatids) usually connected at the centromere and telomere regions. Depending on the degree of the separation at the centromere level, the metaphase chromosome may exhibit ring-shaped or eight-like chromatids. At the EM, a gap between both annular 'half-chromatids' could be observed (Figure 3, A, B, C, D). Although the half chromatids showed longitudinal striae, the number of the component filaments could not be determined. There remains the question whether the striae end as free subfilaments at the telomere, or constitute a part of a single, longitudinally bent filament at the telomere region.

The morphology of the chromosomes after chloroform treatment suggests some similarity with the model proposed by STUBBLEFIELD and WRAY[4] for the mammal chromosome. According to this model, each anaphase chromatid consists of 2 half-chromatids, each of which has 2 deoxyribonucleoprotein ribbons linked to a single core and presenting epichromatin loops, laterally attached.

The chloroform effect has been followed up in several experiments. Figure 1 and 2 show aspects usually seen, Figure 3 shows a most uncommon aspect. In preparations treated over long periods of time, as well as in preparations treated with chloroform prior to fixation, the chromosomes were found to lose their integrity making any analysis difficult.

Our observations on the morphology of chromosomes after chloroform treatment suggest a multistranded or at least a binemic model. How could an uninemic model fit the observations of well defined half-chromatids with evidently split telomeres? We suggest that the interphase chromosome consists at least of two DNA strands. During DNA synthesis they uncoil and the DNA helices replicate. The distribution of sister helices to the same or to different chromatids of the metaphase chromosome can only be elucidated by an investigation of TH_3 incorporation patterns.

The hypothesis of an unineme model was favoured by the finding of TH_3 heterolabelling in the second generation of DNA replication of mitotic chromosomes[15], while an isolabelling pattern has recently been described by PEACOCK[16]. Accepting the binemic model, TH_3 isolabelling or heterolabelling would depend on the distribution of the sister helices of each of the M_1 DNA molecule to the very same or different chromatids. More recently it was shown that mammal sex chromosomes become isolabeled at M_2[4].

Our autoradiographic findings, discussing the binemic hypothesis, will be reported elsewhere.

The existence of 'half-chromatids' should not be interpreted as an indication that drastic variations in DNA content among species with similar karyotypes are a consequence of differential polynemy. As a matter of fact, all species examined by us presented 'half-chromatids'. Yet, this also does not necessarily exclude polynemy, since elucidation with respect to the number of filaments within the 'half-chromatids' still needs better resolution.

The considerable difference in DNA content in the 2 anuran species of *Odontophrynus* used in this investigation is demonstrably the result of polyploidy. The high DNA content in *Eleutherodactylus binotatus* is assumed to be a consequence of remote polyploidization and/or interstitial duplications[13].

Zusammenfassung. Metaphasechromosome lassen nach Chloroform-Behandlung eine Aufteilung in Halbchromatide erkennen. Zytologische Befunde der Untersuchungen (Licht- und Elektronen-Mikroskop) weisen auf eine binemische Struktur des eukaryotischen Chromosoms hin.

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Chromosomal Identity of Black Rats (*Rattus rattus*) from the Galápagos Islands, Ecuador

Considerable interest has been given in recent years to the documentation of chromosomal variability in the cosmopolitan human commensal rodent, the black rat *Rattus rattus* (Linneaus). Two karyotypic morphs have been described: a $2n = 42$ morph from eastern[1] and southeastern[2] Asia and the Indian subcontinent[3]; and a $2n = 38$ morph from south India[4], western Asia[5], Europe[6], Africa[7], North America[8], South America[9], and Australasia[10]. The exact cytological relationships between these variants are now known from Giemsa-banding patterns, and consist of two Robertsonian fusions and 1 to 2 pericentric inversions[11]. In addition to the general polytypic nature of variability in diploid number summarized above, intrapopulation polymorphic systems have also

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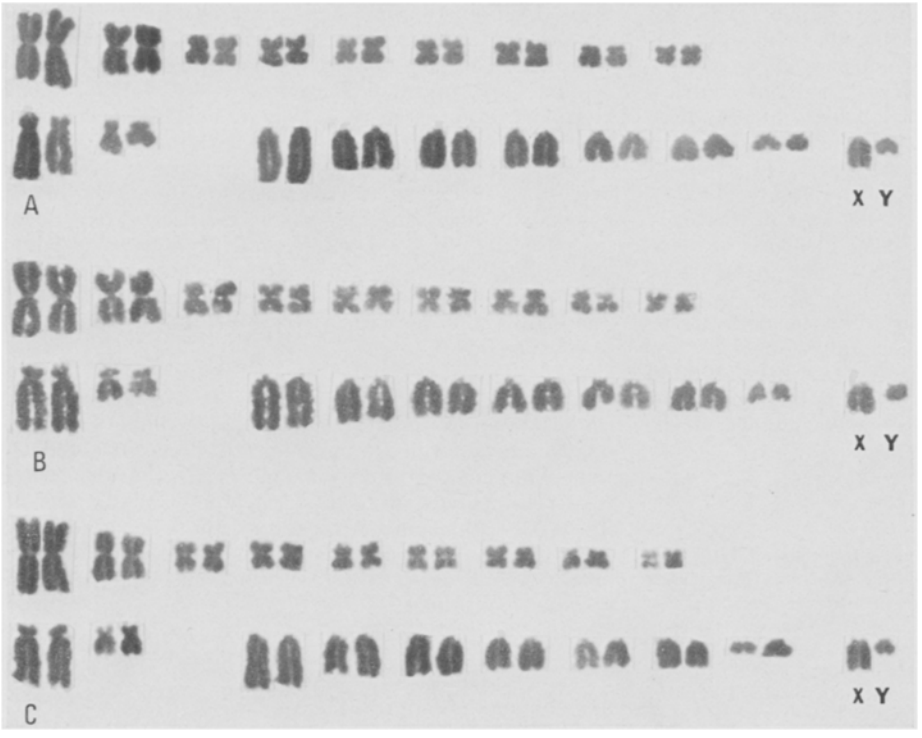

Karyotypes of *Rattus rattus* (Linneaus) from the Galápagos Islands: a) male, MVZ 145516, James Bay, Isla Santiago ('frugivorous' phenotype); b) male, MVZ 145468, east side Isla Pinzón ('rattus' phenotype); and c) male, MVZ 145490, Isla Baltra ('rattus' phenotype).

been described for one or both variants involving a diverse group of mechanisms: a) B-chromosome accumulation[12], b) pericentric inversions[13], or c) centric fusions[14]. Thus, a more thorough knowledge of the geographic extent of each numerical morph as well as the extent and nature of variability within given populations is of importance in understanding the evolutionary history of the species itself. In addition, since *R. rattus* is a 'weed' species in the classical definition[15], details as to the genetic foundations associated with its exceptional colonizing ability have great theoretical interest.

The present study concerns the karyological characterization of *Rattus rattus* from the Galápagos Archipelago, Ecuador. Black rats were introduced to the islands sometime before 1835, as Darwin collected the species on Isla Santiago (= James Island) in that year[16]. To date, the species has spread, presumably by the aid of multiple introductions, to inhabit 7 of the 16 major islands of the group, and has displaced the native rodents (genus *Oryzomys*) from 4 of these islands in the process[17]. In the typological sense, the 3 European subspecies (the nominal *rattus, alexandrinus*, and *frugivorous*) are known from the islands. However, the present authors follow more recent taxonomic opinions and apply the trinomial *R. r. rattus* to all morphs distinguished by pelage color alone since this presumptive subspecific character is determined merely by alternative alleles segregating at 2 non-linked autosomal loci[18].

Chromosomal preparations were made by the standard in vivo colchicine-hypotonic citrate-aceto-methanol fixative sequence described elsewhere[19]. 31 individuals of a total sample of 138 collected were karyotyped, including a representative sample from each island from which black rats are presently known as well as of each of the three pelage color variants. Voucher specimens in the form of study skin with skull or skeleton only from all individuals examined are deposited in the mammal collection of the Museum of Vertebrate Zoology (MVZ), University of California, Berkeley. Sample sizes, localities, and museum catalogue numbers are as follows: 3♂, Academy Bay, Isla Santa Cruz (MVZ 145394–145396); 2♂–2♀, Conway Bay, Isla Santa Cruz (MVZ 145473–145476); 2♂–2♀, Wreck Bay, Isla San Cristóbal (MVZ 145426–145429); 1♂–3♀, Black Beach, Isla Floreana (MVZ 145430–145433); 2♂–2♀, Caleta Tagus, Isla Isabela (MVZ 145438–145441); 2♂–2♀, east side Isla Pinzón (MVZ 145465–145468); 3♂–1♀, Isla Baltra (MVZ 145490–145493); 2♂–2♀, Bahia James, Isla Santiago (MVZ 145515–145518).

All animals examined, regardless of locality or pelage coloration, possessed a diploid number of 38. Moreover, no variation, either numerical or morphological in nature, was observed within any one population sample. The karyotype for those rats examined was internally consistent and appears identical to described and figured $2n = 38$ complements from other parts of the world. The

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autosomal complement consists of one pair of large, one pair of medium, and 7 pairs of small meta-submetacentrics; one pair of large and one pair of small subtelocentrics; and 7 pairs of medium to small acrocentrics. The *X*-chromosome is a medium-small acrocentric and the *Y*-chromosome is a small acrocentric equivalent in size to the smallest autosome. Karyotypes representative of three island populations are given in the Figure.

The discovery of the 38-chromosome form of the black rat in the Galápagos is not particularly surprising since these rats have the European appearance in all other respects.

It is of some interest, however, that the populations examined appear to epitomize a generality of a very low to non-existent level of chromosomal variability exhibited by all 'introduced' populations of black rats the world over. Despite a rather wide range in variability of expressed types of chromosomal rearrangements within the species as a whole, no population as yet from Africa, Australasia, or the Americas (all with $2n = 38$) has exhibited any form of chromosomal variability. This lack of variation at the chromosomal level is also paralleled by a similar consistent low level of genic-based variability as judged by allozyme studies[20]. Therefore, at least in the case of the black rat, exceptional colonizing ability is not associated with any increased genetic variance (as measured by chromosomal or genic characters) as might be expected. Quite to the contrary, the success of the species may be due instead to an extremely well-integrated and rigid genotype with extreme flexibility only at the phenotypic level[21].

Resumen. Muestras de ratas negras (*Rattus rattus*) de siete islas del Archipiélago de Galápagos fueron examinadas para estudios de chromosomas. El número diploide de todos los animales es 38 y los cariotipos son idénticos a los de las poblaciones europeas, americanas, y australianas. La conclusión general es que la falta de variabilidad cariotípica de las poblaciones introducidas se explica por la capacidad de ratas de establecerse por medio de cambios fenotípicos.

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Museum of Vertebrate Zoology, 2593 Life Sciences Building, University of California, Berkeley (California 94720, USA), 22 April 1974.

[20] J. L. PATTON, S. Y. YANG and P. MYERS, unpublished data.

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Sex Attractant Inhibitors of the Codling Moth *Laspeyresia pomonella* L.

Sex attraction in lepidoptera is often inhibited by compounds closely related to the attractant chemical, but differing by the position or geometry of a double bond or the presence or absence of an ester function[1,2]. Due to their effectiveness in counteracting response to pheromones, inhibitors may have a potential use in insect control.

In a search for strong inhibitors of the codling moth, *Laspeyresia pomonella*, sex pheromone, we have employed the routine procedure[1] of adding various chemicals[3] to cylindrical traps baited with *trans*-8, *trans*-10-dodecadien-1-ol[4] (Codlemone[5] caps) or with 3 virgin females. The tests with different chemicals were conducted over various time intervals in apple orchards at Opfershofen and Tägerwilen during the codling moth flights of 1972 and 1973.

The Table lists the catches with each chemical as compared with those of the control group over the same time period. Of all compounds tested, *cis*-8-dodecenyl acetate was the strongest codling moth inhibitor. Catch was reduced by ca. 90% with 1 mg of this chemical (No. 16), and almost totally with 5 mg (No. 17). Instead of codling moths, these traps attracted males of the plum fruit moth, *Grapholitha funebrana*, probably from stands of plum trees outside the apple orchard. *Cis*-8-dodecenyl acetate has been known as a sex attractant of this insect[6]. Compared with catches with this chemical alone, Codlemone seemed to have no effect on plum fruit moth males.

A number of other chemicals also significantly inhibited codling moth attraction. 3 compounds were tested against virgin females, *cis*-8-dodecenyl acetate (16 and 17) which was a strong inhibitor, and *cis*-10 and *trans*-10-dodecenyl acetate (Nos. 21 and 22) which were moderate inhibitors of Codlemone. All 3 chemicals were strong inhibitors of male attraction to females. As strong evidence has been obtained for the identity of *trans*-8, *trans*-10-dodecadien-1-ol with the natural codling moth pheromone[7], our results seem to suggest that the females emit this compound at a lower rate than Codlemone caps since their attractancy was reduced more drastically by inhibitors.

Structures of codling moth inhibitors found in this study are listed in the Figure in order of decreasing inhibition. Although prolonged tests might have altered the

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