of sperm cells. Details of both methods have been published elsewhere[5,6]. Feulgen determinations on polychaete nuclei were standardized by including *Cirriformia filigera*, *Diopatra cuprea*, and *Arenicola cristata* in every series of measurements. Two species were assayed by both methods and allow a calibration of the Feulgen data in absolute terms. This calibration was refined further using data on crustaceans and Feulgen values of vertebrate species with known amounts of DNA. All calibrations agree closely and the *pico*-gram scale is probably accurate to within 10% or better.

The genome sizes expressed as DNA per haploid nucleus are listed in the Table in taxonomic sequence[7]. The 10-fold range from 0.7 *pg* for *Cirratulus grandis* to 7.2 *pg* for *Nephtys incisa* is comparable to the ranges found for the more variable vertebrate groups, i.e. teleosts and anurans. The frequency distribution of DNA contents is illustrated in the figure. Here again, as in some vertebrate groups[3] a logarithmic normal curve describes the observed distribution rather well. This may be taken to indicate an evolutionary history based on many cumulative smaller events. Occasional 1:2 relationships within a single family of polychaetes (Lumbrinereidae, Sabellidae) may reflect recent polyploid speciation. Speciation by polyploidization need not affect the smoothness of the distribution, if the doubled state is transitory and soon reduced by deletions.

Like many vertebrate groups the polychaetes show a smooth wide distribution of nuclear DNA amounts corresponding to a continuous wide variation of morphological types. Species in individual families usually have similar DNA amounts correlating with closer morphological similarity. This relationship between genome size and morphological diversities is not based on a one-to-one correlation of DNA amount with any morphological parameter. The limited size of the sample precludes the more detailed correlations which are already possible in vertebrates, where a striking correlation between small genome size and specialized morphology has been noted repeatedly[1,3]. Among the polychaetes, the more generalized errant species (following DAY's separation[8]) have an average genome size of 2.5 *pg*, while the more specialized sedentary species[8] average 1.8 *pg* DNA haploid. Among the latter, the very specialized filter and tentacular feeders alone average 1.6 *pg* DNA per haploid nucleus. These figures suggest a correlation between small genomes and specialization but they are at the lower limit of statistical significance and only a larger sample could verify this correlation for polychaetes.

The range in DNA content found in the polychaetes encompasses that of the mammals even though the mammalian modal value of 4 *pg* is twice as high as the polychaete mode of 2 *pg* (Figure). It is understandable that reduction of genome size can lead to considerably smaller DNA amounts in annelids when compared to the more complex mammals. It is more difficult to understand why even a generalized polychaete with a large amount of evolutionary potential should have as much DNA as we find in some species. Apparently one of the features of the genome of more complex animal groups is a more stringent control on genome variability[6]. Certainly the amount of DNA is under selective control and the similarities in the patterns encountered in the polychaetes and the vertebrates are striking.

Zusammenfassung. Bestimmung des DNS-Gehalts pro Zellkern in 36 Polychätenarten ergeben eine Häufigkeitsverteilung der Genomgrössen, die durch eine logarithmische Normalverteilung beschrieben werden kann. Eine Korrelation zwischen adaptiver Spezialisierung und reduzierten Genomen, wie sie bei Wirbeltieren gefunden wird, ist auch bei Polychäten angedeutet.

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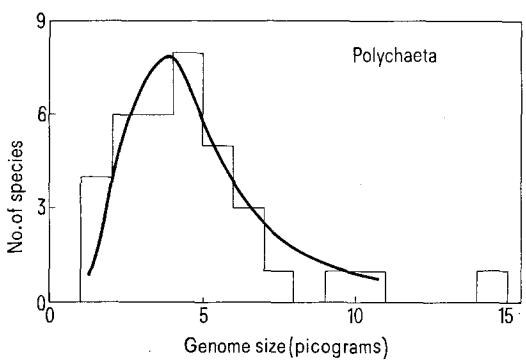

Diploid nuclear DNA amount of 36 species of polychaetes. The curve is a best fit logarithmic normal distribution for these data.

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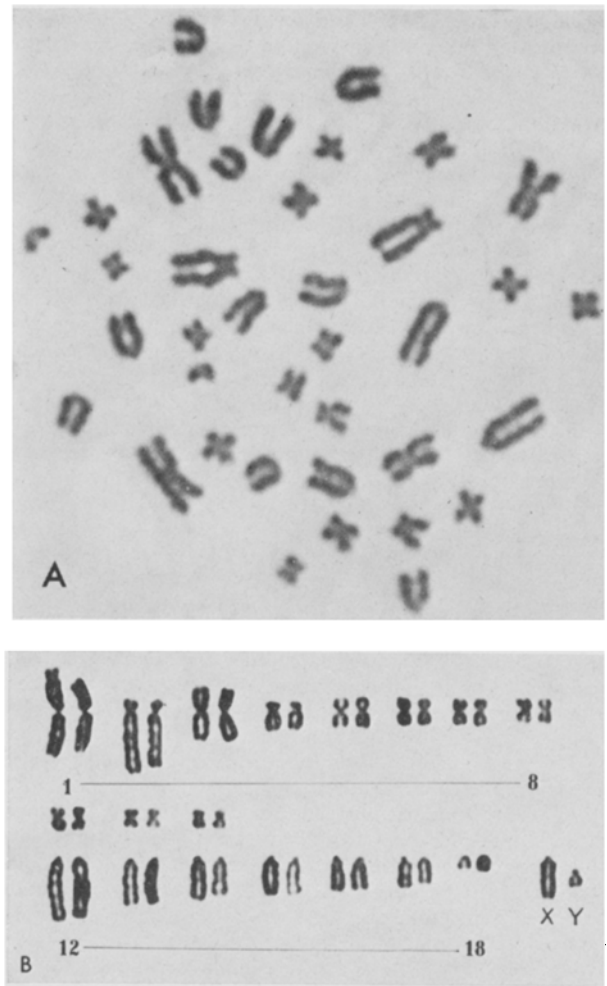
Endophenotype of Mysore (South India) Population of the Black Rat (*Rattus rattus* L.)

Karyological studies of *Rattus rattus* are interesting, contradictory and intriguing[1-3]. BADR and BADR[1] reported 3 coexistent chromosome numbers namely 38, 42 and ± 54. Occurrence of 38 chromosomes was reported by BIANCHI et al.[4] in 2 South American populations. CAPANNA et al[5-7] claimed similar number in Italian, West European and African populations. Reports on the Asian populations[1] always showed 42 chromosomes. Karyological studies of 3 separate populations of *Rattus rattus* of Mysore area (South India) showed that the diploid number is 38 (11 pairs of biarmed chromosomes, 7 pairs of acrocentrics + X and Y both being acrocentric). Further 25–30% of the first pair of chromosomes are heteromorphic. Comparison of the karyotype of Mysore population with those of Italian (CAPANNA et al., MCN. *10*, 4 (1969), personal commun.) and South American and



A) Chromosomes of *Rattus rattus* (female) $2n = 38$. B) Karyogram of *Rattus rattus* (male) $2n = 38$.

Italian[4,5] shows that the karyotype under study constitutes an intermediate condition and there is an inverse relationship of the number of biarmed chromosomes to the number of acrocentrics. Further the chromosomes of Mysore population differs from the standard type (Dr. T. C. Hsu, personal commun., July 1971) with $2n = 42$ in a) absence of 4 pairs of acrocentric chromosomes, b) absence of 1 pair of submetacentric chromosomes and c) presence of 2 pairs of metacentric and 1 pair of large subtelocentric chromosomes. While structural polymorphism exists in different populations, it is the authors' considered opinion that Robertsonian centric fusion and centric dissociation might have played their role in reducing the number from 42 to 38 in Mysore populations.

Résumé. Contribution à l'étude du polymorphism chromosomique chez le rat noir *Rattus rattus* L.

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Evidence for a Transmissible Substance Affecting Pigment Synthesis in *Pisum*[1]

Among the numerous chlorophyll mutants of *Pisum*, *alt* is especially distinctive[2–5]. Homozygous recessive plants (*alt/alt*) exhibit normal pigment development until they reach the 5 or 6 node stage; then above a rather sharply defined zone of transition the tissue is bleached white (Figure 1), further growth is checked, and the mutant plants die without producing seeds.

In order to investigate the nature of the mutant we first performed grafting experiments using *alt/alt* and normal (*Alt/Alt*) plants as partners. The graft partners were placed in contact after removing a thin tangential slice of nodal tissue from the normal (*Alt/-*) donor plant as well as from the recipient *alt/alt* plant. The site of the graft for the recipient plant was in the region of normal green tissue, usually the 3rd or 4th vegetative node.

The basal or axillary buds in the first 3–4 nodes of the main stem of the mutants are activated by decapitation or by loss of apical dominance following the death of the apical meristem, but such branches – which are chlorotic even though they arise from the region of the plant which is green – soon die. Successful graft transmission of an active substance resulted in the formation of chlorophyll in the basal or axillary branches of the mutant. These branches ultimately produced flowers, fruits, and seeds. Seeds produced in this manner on *alt/alt* tissue, when planted, all gave rise to plants with the mutant phenotype.

The mutant expression was attenuated by low light intensity ($<$ 500 ft-c) in a growth chamber. The leaves above node 6 or 7 were only partially chlorotic and sufficient pigment was present to sustain weak growth, the plants eventually reaching the fruiting stage of development but dying before mature, viable seeds were formed.

We next attempted to extract, isolate, and chemically identify the graft-transmissible substance present in normal plants but deficient in the mutant. For this a bioassay was devised (Figure 2). Mutant plants were decap-

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