bees. For the period in between, KUHN[6] found a correlation between the composition of RNA and behaviour. Our results can not be compared to these findings, because the technique of gel-electrophoresis used by KUHN did not give quantitative data concerning the total RNA value of the brain.

Autoradiographical investigations have suggested, that newly emerged bees have a higher rate of synthesis than foraging bees. Therefore the decrease of RNA must be due to a higher rate of degradation of long-life or precursor RNA rather than to a decrease of the rate of recently synthesized RNA. 40–51 day-old summer bees show a second decrease in the amount of RNA of about 20%, whereas the DNA remains constant (Table).

These findings lead to three main questions: 1. Why is the biggest amount of RNA found on day −2? No more cell divisions take place at this time[5]. 2. Immediately after emergence (day 0 to 1) the decrease of RNA appears to slow down. Autoradiographical investigations might show whether the destruction of RNA is delayed, or whether the rate of synthesis of the RNA is slightly increased. 3. Why does the RNA decrease again in old summer bees? In July 1972, 2% of 350 marked bees reached an age of 50 days. The amount of RNA found in winter bees never showed a level as low as the one of 40–50-day-old summer bees (Table). Is the near end of life a reason for this second decrease of the RNA? Or is the second decrease a reason for the death of the bees? We have no control experiments on winter bees, because we do not know their exact lifespan. We suggest that the course is about the same with a much longer period of more or less constant amounts of RNA[7].

Summer bees compared to winter bees

	Summer bees Age (days) 15–20	21–30	40–51	Winter bees (Nov.-March)
RNA $\bar{x}$	680 ± 36	697 ± 41	547 ± 65	711 ± 56
n	7	7	6	44

Classes of age (days after emergence). Mean amount ($\bar{x}$) of RNA per brain, measured as absorbance at 260 nm in 200 µl NaOH/HCl solution per brain.

Zusammenfassung. Aus Gehirnen von Bienen verschiedener Altersstufen wurden DNS und RNS extrahiert und deren Mengen spektrophotometrisch bestimmt.

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[6] O. KUHN, E. KUBLI and E. HAUSCHTECK-JUNGEN, Experientia *28*, 982 (1973).

[7] The authors thank Miss T. EGLOFF for technical assistance.

[8] Zoologisches Museum der Universität Zürich.

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Chromosomes and Giemsa-Bands of the Idaho Spotted Ground Squirrel, *Spermophilus brunneus* (Howell)

The ground squirrel subgenus *Spermophilus* in North America consists of 8 species: *S. townsendii*, *S. washingtoni*, *S. brunneus*, *S. richardsonii*, *S. armatus*, *S. undulatus* (= *parryii*), *S. columbianus*, and *S. beldingi*[1]. Earlier investigators arrived at different views concerning the subspecific or specific status of taxa now ranked within *S. townsendii* and *S. richardsonii*, and the composition of various supraspecific groups[2,3]. Relevant to this report, DAVIS[3] recognized 2 species-groups within the subgenus *Spermophilus* occurring in Idaho: 1. big-eared ground squirrels; *S. beldingi*, *S. richardsonii aureus*, *S. columbianus*, *S. armatus*, and *S. brunneus*; 2. short-eared squirrels; *S. mollis* (= *townsendii*). DAVIS[3] differentiated *S. brunneus* from *S. townsendii* on the basis of its shorter and coarser pelage, absence of a white ventrolateral stripe, certain cranial characters, the conspicuously larger ears, and spotted brown dorsal coloration. However, HOWELL[2] previously concluded that *S. brunneus*, despite its much larger ears, exhibited external and cranial characters similar to the *S. washingtoni* group, which he in turn regarded as comparing most closely with *S. idahoensis* (= *townsendii*). Recently NADLER[4] analyzed chromosomes from all species of the subgenus except *S. brunneus* and found that diploid numbers conformed to the big-eared ($2n$ = 30–36) and short-eared ($2n$ = 36–46) groups; the possibility that *S. brunneus* might belong to the short-eared group or occupy an intermediate position within the subgenus was postulated.

The present paper describes the chromosomes of *S. brunneus*, compares the giemsa-band pattern of that species with *S. townsendii mollis* which shares a similar $2n$ of 38 with *S. brunneus*, and discusses the evolutionary implications of the data.

Materials and methods. The following specimens were examined: 1. *Spermophilus brunneus* (Howell), Idaho, Adams Co., 3 miles south and 1.5 miles east of Bear Post Office, 3 females and 5 males; *Spermophilus townsendii mollis* (Kennicott), Idaho, Cassia Co., Burley, 3 females and 3 males.

Chromosomes were analyzed from femoral bone marrow and giemsa-band preparations were made from marrow cell suspensions according to SEABRIGHT[5]. Giemsa-band patterns, based on 5 mitotic figures from a male *S. brunneus*, one cell from a female *S. t. mollis*, and 5 from a male *S. t. mollis*, were diagramed to represent the composite results for each species. The bands were consistent from cell to cell within a species, although bands of certain chromosomes sometimes stained lightly or were indistinct in individual cells.

Results. All *S. brunneus* had a $2n$ = 38 and karyotype containing 14 metacentric, 16 submetacentric, and 6 sub-

[1] E. R. HALL and K. R. KELSON, *The Mammals of North America* (Ronald Press, New York 1959), vol. 1.

[2] A. H. HOWELL, N. Am. Fauna *56*, 1 (1938).

[3] W. B. DAVIS, *The Recent Mammals of Idaho* (Caxton Printers, Caldwell, Idaho 1939).

[4] C. F. NADLER, J. Mammal. *47*, 579 (1966).

[5] M. SEABRIGHT, Chromosoma *36*, 204 (1972).

telocentric autosomes, a submetacentric X and a small acrocentric Y chromosome (Figure 1). Arranged in that manner (Figure 1) the karyotype closely resembled that of *S. townsendii mollis* and *S. townsendii idahoensis* with $2n = 38$[4,6] except for the presence of slightly longer short arms (subtelocentric) in 2 of the 3 pairs of chromosomes (16, 18) of *S. brunneus* that are comparable to the 3 pairs of acrocentrics reported in *S. townsendii*.

Comparison of giemsa-banding in *S. brunneus* and *S. t. mollis* (Figure 2) indicated similar patterns in pairs 1–5 and 8–13. Among the smaller chromosomes, which were more difficult to analyze due to an apparent greater chromosomal contraction, pairs 14, 15, and 18 exhibited differences in the number of bands in the long arms. The absence of bands in autosome pairs 6 and 7, and the Y chromosome of *S. brunneus* may reflect less intense staining of the cells in that species. Thus based on G-bands, chromosomal homology is demonstrable in 13 of 18 autosomal pairs and the X chromosome.

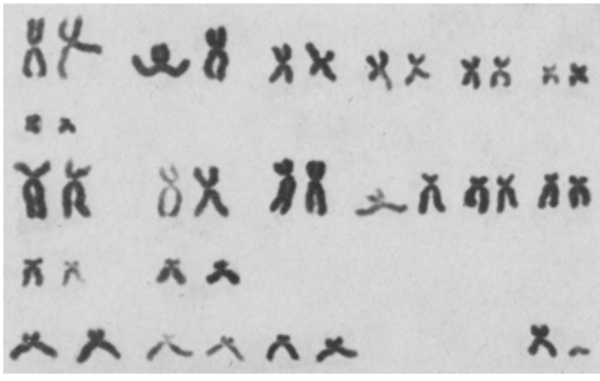

Fig. 1. Karyotype of a male *S. brunneus* ($2n = 38$), × 2800.

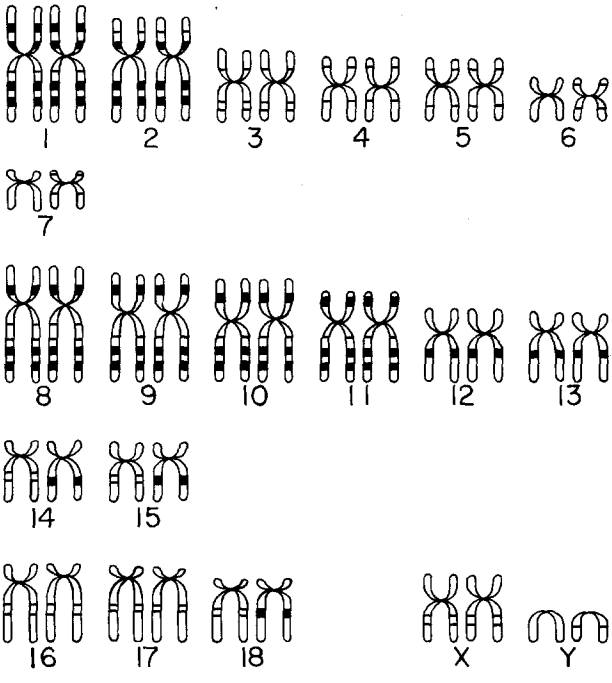

Fig. 2. Comparison of Giemsa-band patterns of *S. brunneus* and *S. townsendii mollis*. The left and right members of each diagramed pair represent *S. brunneus* and *S. t. mollis* respectively.

Discussion. The gross chromosomal similarity and degree of G-band homology now shown to exist between *S. brunneus* and those taxa of *S. townsendii* (*mollis, idahoensis*) contiguously distributed to the south provides new evidence for reappraising interspecific relationships in the subgenus *Spermophilus*. Despite some cranial and pelage similarities with *S. washingtoni*, chromosomes do not support the close relationship HOWELL[2] postulated between that species and *S. brunneus* because the former has a $2n = 36$ and a different karyotype[4]. Chromosomal characters also fail to support the view of DAVIS[3] that *S. brunneus* belongs to the big-eared group of ground squirrels because the latter exhibit *2n*s of 30–36[4].

Comparisons by starch-gel electrophoresis of proteins that exhibited variation between the big- and short-eared groups also bear on these relationships (in manuscript). *S. brunneus* had G6PD and hemoglobin fractions identical with squirrels of the big-eared group, and unlike all subspecies of *S. townsendii*. The transferrin (Tf) of *S. brunneus* was electrophoretically similar to Tf 5 of *S. parryii* (big-eared group) and not Tf 1 or 3 of *S. townsendii* and *S. washingtoni*. Leucine aminopeptidase of *S. brunneus* differed from the rapidly migrating fraction of all other Nearctic *Spermophilus* and instead resembled the slower fraction seen in some Asian species. Other enzymes (LDH, MDH, aldolase, α GPD) were monomorphic in all Nearctic taxa. Biochemical characters thus indicate a closer affinity to the big-eared species group.

The contradictory morphological, biochemical, and cytological evidence, coupled with the small, relict distribution of *S. brunneus* leads us to postulate that this species may be a link between the 2 rather diverse big- and short-eared groups of squirrels. If further biochemical and morphological analyses substantiate this hypothesis of intermediacy, the possibility that an *S. brunneus*-like ground squirrel with $2n = 38$ is ancestral within the subgenus must be entertained; earlier an ancestral $2n$ of 38 was also postulated for the subfamily Sciurinae as a whole[7]. In that case karyotype evolution in *Spermophilus* may have proceeded in 2 directions from 38 to 36–30 in the big-eared group and from 38 to 36 and to 46 in the short-eared group.

ВЫВОДЫ. Хромосомы и Г-полосы *Spermophilus brunneus* изучалы. Хотя кариотипы сходние, и гомология между 13 из 18 парами аутосомов, *S. brunneus* отличается от *S. townsendii mollis* ($2n = 38$) в других морфологических, меховых, и биохимических признаках; эти признаки соединяют *S. brunneus* с большеухей гууппой. Промежуточност признаков у *S. brunneus* предлагает что этот реликтовый вид, немного расходящийся из ранного прародителя у подрода *Spermophilus*.

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[6] C. F. NADLER, Cytogenetics *7*, 144 (1968).
[7] C. F. NADLER and R. S. HOFFMANN, Experientia *26*, 1383 (1970).
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