showed less cytotoxic effect at the higher concentrations. It is uncertain whether the slightly lower mitotic rate in burro serum indicated a change in the cell cycle or simply a lengthened response time to the mitogen; however, we do not have any evidence that it influenced the SCE dose-response curves.

Discussion. Although serum of fetal calf origin is most commonly used in cell culture media, intuitively we would expect serum from adult animals to show a greater variability of composition and of SCE-inducing factors if they exist. The intent of testing sera from different burros was thus to use adult animals in order to maximize the likelihood of detecting differences. The similarity of SCE numbers in cells grown in sera from the different animals indicated that the inducing factor either occurs quite uniformly among individuals or is not prevalent at all in burro serum. Any contribution by factors carried into the cultures by the lymphocyte donor's serum would have been minor because of the relatively low volumes of inoculum used and would have been neutralized by the fact that the same volume of a donor's serum was added to each of the test cultures.

If serum contains factors that induce sister chromatid exchanges, then the number produced should be related to the concentration of serum to which the cells are exposed. Such a relationship is quite obvious for both lots of the Gibco serum used in this study, whereas the Hy-Clone and burro sera produced only slight increases at high concentrations. This situation suggests that while some commercially available sera do in fact contain a factor that causes SCE, this factor is not only absent from burro serum but probably occurs in these fetal calf sera as a contaminant rather than a normal constituent. Varying levels of contamination could have accounted for the difference in SCE induction by the sera tested by Kato and Sandberg[5], even after their heat inactivation and dialysis treatment had reduced the overall activity level. While our data provide no measure of a possible reduction in activity of the factor by heat treatment, it is obvious that the heat inactivation to which all our sera were treated did not eliminate the agent.

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Genes regulating the appearance of two kinds of fruit in *Microseris* strain B 87 (Asteraceae: Compositae)[1]

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Summary. The annual hybrid strain *Microseris* B87 *(M. pygmaea* × *M. bigelovii)* produces 2 kinds of fruit (achenes) on its flowering heads, outer hairy and inner smooth ones. 2 unlinked genes are identified that determine the relative number of hairy achenes, on a logarithmic scale.

The composite flowering heads of the Asteraceae offer unique possibilities for the genetical analysis of developmental control processes. Both the bractlike phyllaries surrounding the capitula, and the florets, arise from a continuous spirally arranged series of primordia. The production of these primordia can be regarded as a linear sequence in time. Genetic regulating mechanisms determine the kind of organ that arises at each homologous site. These regulating mechanisms appear to be irreversible switches. The spiral arrangement of the primordia on a dome-shaped head causes the typical appearance of a concentric arrangement of the various organs with the earlier ones (e.g. phyllaries) on the outside and the later ones (e.g. disk florets) on the inside. Any delay in the timing of the developmental switch will result in a broader ring of outer structures at the expense of inner structures. Variation of this kind is very common both in horticultural varieties of cultivated Asteraceae and in natural populations. We have begun using this effect in order to detect genes regulating development in the lactucean genus *Microseris.*

In the small annual species of the section *Microseris,* there is usually a rather clear distinction between outer florets giving rise to outer achenes and inner florets giving rise to inner achenes[3-5]. This distinction involves a series of characters. One of these, the hairy or furry appearance of the outer achenes as opposed to smooth inner achenes, is very easy to score in all achenes on a head, including sterile ones[4,5]. There are plants with no hairy achenes ever, plants with nothing but hairy achenes, and a whole series of intermediate types. Our preliminary estimate of at least 10 genotypes contributing to this variability[5] could mean that there are about 3 genes involved in the determination of the timing of the transition from hairy to smooth achenes in addition to genes that are responsible for the expression of the hairy character. Thus a complete analysis of the 'hairy achenes' polygenic system appeares to be feasible. Here we report the first results of the genetic analysis of the hybird strain B87. The exact strain designation is important because each of our annual strains is obtained by spontaneous selfings from one single ancestral plant. Each strain therefore represents a minute selection from the vast pool of genetic variation present in the genus, and the genetics of conspecific strains or of repeated hybridizations of the same taxa may be very different. Strain B87 consists of segregants from a single hybrid specimen between *M. pygmaea* (Chambers accession 246: few, weakly hairy, outer achenes, the inner achenes bearing a tuft of hairs on top) and *M. bigelovii* (Chambers accession 207: about 30% strongly furry outer achenes, the inner achenes without hairs either on the sides or on top)[6]. The F1 and a preliminary small F2 family of 10 plants, 8 of which gave rise to

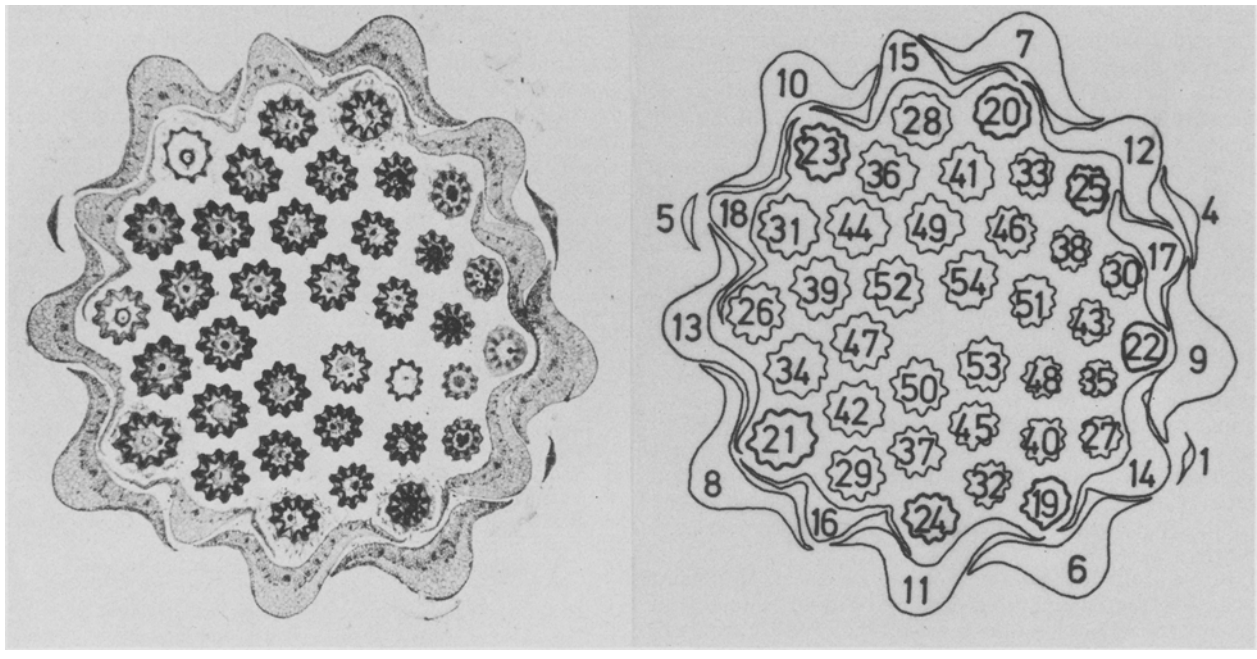

Fig. 1. Cross-section through a maturing capitulum of strain B87. The organs are numbered in phyllotactic sequence. 3 of 5 outer phyllaries are sectioned. There are 13 inner phyllaries, 7 hairy achenes marked by a thicker outline, and 29 smooth achenes; lf = 3.40.

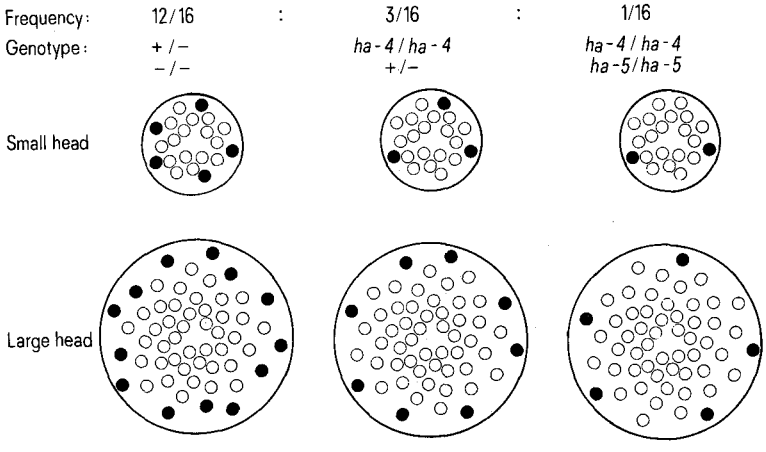

Fig. 2. Idealized diagrams of the achene arrangements found in the F2 of strain B87. Full circles symbolize hairy achenes.

small F3 families, showed partial dominance for the *bigelovii*-like phenotype with an F1 average and F2 total mean of about 27% hairy achenes and a segregation of phenotypes with increasingly fewer hairy achenes from about 30% down to virtually none. Offspring/parent regression resulted in a heritability estimate of 77%. During the 1978/79 growing season we have analyzed another 132 F2 plants and additional plants in the 8 F3 families from the earlier F2. These have led to the identification of genes in 2 linkage groups and their interactions in the determination of the 'hairy achenes' phenotypes.

The analysis of the genetic determination of the proportion of hairy achenes has shown that the gene interaction is multiplicative and that the various phenotypes form a logarithmic series of values. This result corresponds to the very old observation that the numbers of similar organs on composite capitula bear a close relationship to the Fibonacci series (1, 1, 2, 3, 5, 8, 13, 21 etc.)[7] in which each term is the sum of the two preceding ones and in which the ratio between each term and the next converges on a constant, 0.618 ... . These numerical relations have been found, for instance, for ray florets, for the number of phyllaries and the total number of florets in several species, and for the numbers of various kinds of fruits on mature heads of *Calendula*[8]. In all of these cases, a genetic (or an environmentally induced) change in the number of parts is more likely to approach the next Fibonacci number in one jump than to lead to a continuous change. The situation is similar for hairy achenes in *Microseris* (figure 1) even though there are a few complications. Firstly, the relative proportion of hairies rather than their absolute number is determined. The same genotype that produces 13 hairies among a total of 55 achenes will produce 5 among a total of 21 in a depauperate head (figure 2). Secondly, these ideal proportions are rarely reached, mainly because there is likely to be a deficit of inner, non-hairy, achenes. It is easy to imagine some determinative process in early development that sets up a pattern of organ primordia. This pattern may then be fully elaborated, or differentiation may cease before the innermost primordia have given rise to organs.

Due to the logarithmic nature of the determinative process we have not used the ratio of hairies to total achenes directly but its logarithm to the bases 0.618 (see above). Thus a head bearing all hairies has an lf of zero, one showing a simple Fibonacci ratio, say 34 hairies in 55, has an lf value of unity, and so on to very small ratios of hairies. The determination becomes difficult below about 3.4% hairies, i.e. an lf value of 7.

The pair of genes that we have identified as operating on this ratio has been designated 'hairy achenes-4' and 'hairy achenes-5', because only the homozygous recessive genotype *ha-4/ha-4* permits the lf value to go beyond 4 (14.6% hairies or fewer) while *ha-5* has to be homozygous in addition to *ha-4* in order to achieve lf values above 5 (9.0% hairies or fewer, figure 2). As a 1st approximation both genes have dominant alleles in the *M. bigelovii* genome, and *ha-4*$^+$ is epistatic over *ha-5*.

This interpretation is based on the observation that only 11 of 142 F2 plants had fewer than 9% hairies. 1 F3 family raised from such a plant bred true for lf values above 5 (15 specimens). The ratio of 11/142 (0.077) is near 1/16 (0.063) expected in a 2-gene system with dominance and epistasis.

The epistatic gene can be followed by 2 linked markers that affect achene morphology. One of these, hairy, with the alleles weak and dense (D) affects the degree of hairiness of the hairy achenes. Since the dominant allele, hy^D, is linked with *ha-4*$^+$, plants with a higher proportion of hairy achenes also have more densely furry ones. The other marker, absence of tuft, *at*, is recessive to an allele causing an apical tuft of hairs on the inner, non-hairy, achenes. Since the recessive allele of *at* is linked with *ha-4*$^+$, plants homozygous for *ha-4*$^+$ can be distinguished by the absence of a tuft on the inner achenes from heterozygous ones in which there is a tuft. On this basis the 3 genotypes +/+, +/*ha-4* and *ha-4/ha-4* occur in the ratio of 35:69:38 in the F2. The 11 plants with lf values above 5 belong to the latter 38.

This analysis of the genetics of capitulum differentiation is only a beginning. There are obviously more factors involved, and the interactions are more complex than they appear here. The table shows that an analysis of the F3 families reveals a more complex interaction between *ha-4* and *ha-5* than simple dominance. As mentioned above, there are also strain differences. Chambers has shown that the tuft in another cross between *M. pygmaea* and *M. bigelovii* is determined by 2 genes[4]. One of these 2 genes may be our *at*, but an unequivocal identification awaits further work.

Range of values for the lf (logarithm to base 0.618) of the ratio of hairy to total achenes for the 6 genotypes homozygous for *ha-4* alleles. The values are based on segregation in F3 families. Genotypes heterozygous for *ha-4*$^+$/*ha-4* should correspond exactly to the homozygous dominant ones

	ha-4$^+$/*ha-4*$^+$	*ha-4/ha-4*
ha-5$^+$/*ha-5*$^+$	2.1–2.9	3.0–3.9
ha-5$^+$/*ha-5*	2.9–3.0	3.9–4.9
ha-5/ha-5	3.3–3.9	5.1–∞

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Chromosome variability in Brazilian specimens of *Rattus rattus* (2n = 38)[1]

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Summary. In 8 specimens of *Rattus rattus* collected in the state of São Paulo, Brazil, a diploid number of 2n = 38 was found. Contrary to the supposed lack of karyotypic variability in South American populations, 5 specimens were found to be heterozygotes for a pericentric inversion in the autosome no. 8.

The black rat *(Rattus rattus)* which is widely distributed all over the world shows geographical chromosome variability as well as several types of intrapopulation polymorphism, due to Robertsonian fusions, pericentric inversions and supernumerary chromosomes[3–5]. Polymorphic variations of C-band patterns are also found[6]. 3 geographical variants, the Asian (2n = 42), the Ceylon (2n = 40), and the Oceanian (2n = 38) types have been described. It is suggested that the Asian karyotype is the ancestral form and that the 2 others developed sequentially by centric fusions[3,5,6].

It is supposed that *R. rattus* from European populations with an Oceanian karyotype was introduced in South America[3]. In fact, all specimens heretofore collected in Argentina, Brazil, Chile, Ecuador and Venezuela have disclosed the same karyotype (2n = 38)[7–10]. The lack of chromosomal variability is, according to Patton and Myers[10] characteristic of all introduced populations of black rats in Europe, Australia, Africa and America. However, in a sample of *R. rattus* from Europe, a polymorphism due to supernumerary chromosomes has been found[11].

Reig et al.[9] suggested that the 2n = 42 form might have migrated to South America also, but the descendants of such stocks either have not yet been discovered or they were unsuccessful as colonizers. The present paper reports the cytogenetic studies on *R. rattus* collected from different areas of the state of São Paulo (Brazil), which reveal a structural rearrangement in the autosome No. 8 in some of the specimens.

3 males were collected from Americana, 2 males and 2