Table 1. Variance and coefficient of variation for the three genotypes in the two experiments performed. σ^2 = variance; n = sample size; c.b.= coefficient of variation.

genotype	F/S	F/F	S/S	Pool of homozygous (F/F + S/S)	
σ^2	1.9185	2.1582	2.2415	2.2063	Experiment A
c.v.	0.0853	0.0914	0.0917	0.0918	
n	817	432	344	776	
σ^2	2.3840	3.0184	3.2675	3.1365	Experiment B
c.v.	0.0928	0.1033	0.1064	0.1048	
n	582	285	255	540	

Table 2. F values in the analysis of variance.

Comparisons	F/S vs F/F	F/S vs S/S	F/S vs Pool homo. (F/F+S/S)	F/F vs S/S
Experiment A	1.1249 n.s.	1.1683 *	1.15 *	1.0385 n.s.
Experiment B	1.2761 * *	1.3705 * *	1.3156 * *	1.0825 n.s.

n.s.=not significant; * = P < 5%; * * = P < 1%.

The differences in level of variation between heterozygous and both types of homozygous and between heterozygous and homozygous combined (F/F+S/S) (Tables 1 and 2), are consistent with observations compiled by Lerner and the other authors previously cited, and reject the null hypothesis tested here.

No significant difference in variance between F/F and S/S homozygous type were found, thus indicating that the level of variation of the homozygous individuals is independent of the particular allele for which these individuals are homozygote.

References: Eanes,W.F. 1978, Nature 276:263-264; Kat,P.W. 1982, Am.Nat. 119:824-832; Lerner,I.M. 1954, In: Genetic Homeostasis (Oliver & Boyel, Edinburgh); Mitton,J.B. 1978, Nature 273:661-662; Soule,M. 1979, Evolution 33:396-401.

Sato, T. Kansas State University, Manhattan, Kansas USNA. A new homoeotic mutation affecting antennae and legs.

We have isolated a new homeotic mutation which arose spontaneously in the stock of $T(1;3)bxd^{111}/TM1$ (Lewis 1981); for reasons described below, the variant is denoted Bristle on arista of Manhattan (symbolized Ba^m). Preliminary experiments showed it to be a second chromosomal, recessive variant. Male and female homozygotes are viable and fertile, and they show partial transformation of antennae to legs, as well as deletion of some leg structures. Tarsal tissue sometimes including claws develops in place of arista and part of the third segment of antenna (Fig. 1). The third antennal segment usually resembles a patchwork of incompletely differentiated leg cuticle, whereas the first and second segments of antenna are unaffected.

For legs, the region affected is restricted to the distal part and seems to be common in all legs (Fig. 2). Abnormal bristle patterns including reversed polarity appear around segmental boundary between tibia and basitarsus in less extreme cases. This segmental boundary is often very incomplete and accompanied by extrusion of supernumerary cuticles (Fig. 2G and H). In more extreme cases, deletion of distal tibia and whole basitarsus is revealed by missing or reduction of numbers of bristles typical to these parts, e.g., transverse rows on prothoracic leg, apical bristle on mesothoracic leg and preapical bristles on all legs for tibia as well as transverse rows on pro- and metathoracic legs for basitarsus (Fig. 2D, E, F). Frequently in these cases, the number of tarsal segments is also reduced to two or three and

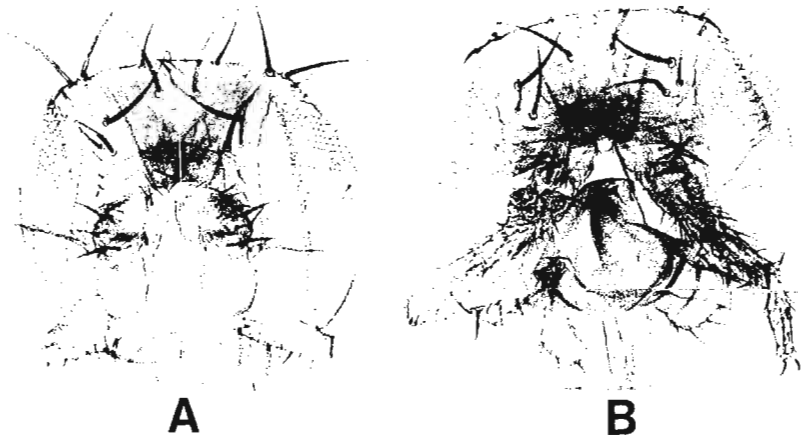

Fig. 1. Transformation of arista to tarsi. Female flies were fixed in three parts 70% ethanol and one part glycerol, and internal tissues were dissolved by heating in 10% KOH solution. After washing in water and then in n-propanol, cuticles of head were dissected and mounted in Euparal.

A, Wild-type (Canton S).
B, Ba^m homozygote.

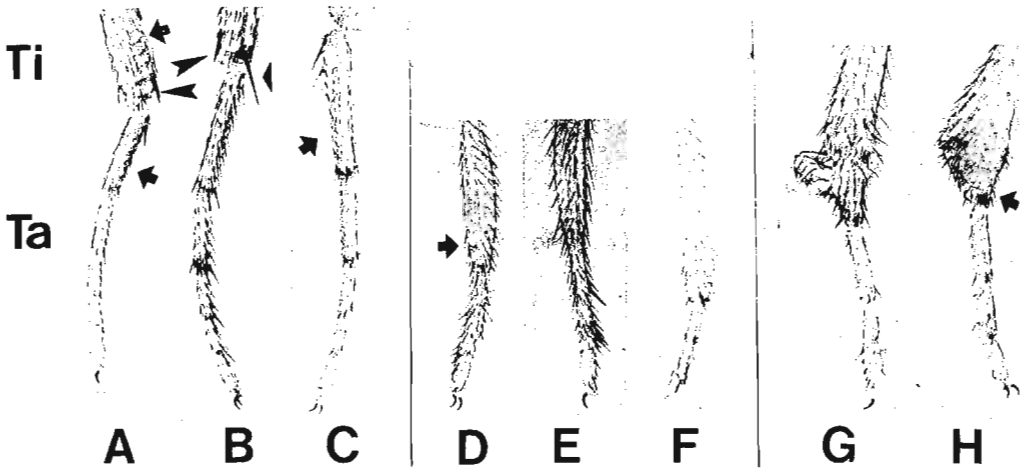

Fig. 2. Deletion in legs. Cuticles of pro-(A,D,G), meso- (B,E), and metathoracic (C,F,H) legs of female flies were prepared and mounted as described in Fig. 1. Distal portion of tibia (Ti) and tarsi (Ta) are shown in this figure. Note the characteristics of each leg; transverse rows (⬆), preapical (➤) and apical (◗) bristles. A-C, Wild-type (Canton S). D-H, Ba^m homozygote.

tarsal segmental boundaries are very obscure. In the most extreme cases, claws are missing. Thus, all tarsal segments can be affected by this mutation. However, proximal segments (trochanter, coxa and femur) and proximal tibia are unaffected. Although distal portion of legs are variably affected, a few transverse rows consistently remain on the distal tibia of the prothoracic leg in most cases, if not all, suggesting that there might be a defined limit of domain of action of this mutation near the distal tip of tibia. Expressivity is variable and significantly higher in females than in males. Penetrance is also dependent on the genetic background, but more than 90% under an optimum condition. The arista phenotype is more penetrant than leg phenotype, and the methathoracic legs show higher penetrance than other legs.

This new variant was mapped by balancing 818 2nd chromosomes transmitted by Ba^m/ix bw sp females. The genetic constitution of each chromosome was determined by subsequent outcrosses to flies bearing Sp L^{rm} Ba^m or ix bw sp chromosome. Ba^m was mapped to the distal right arm of the 2nd chromosome, 0.6 map unit (mu) to right of sp, based on four bw^+ sp^+ Ba^+ and one bw sp Ba^m recombinants. The observed map distances between ix and bw (37 mu) and bw and sp (4.4 mu) approximated standard values. We scored antennal and leg phenotypes independently, and there was no segregation between these phenotypes among 818 chromosomes examined. Therefore, Ba^m seems not to represent multiple mutations. In addition, Ba^m chromosome does not show any aberrancy in banding pattern of polytene chromosome. In trans heterozygotes, Ba^m is complemented by 3 distal deficiencies: Df(2R)Px (60B8-10;60D1-2), $Df(2R)Px^2$ (60C5-6;60D9-10), and $Df(2R)M\text{-}c^{33a}$ (60E2-3;60E11-12).

Sunkel (1983) has described dominant mutations at the Bristle on arista locus with phenotypes very similar to the variant described here. They are lethal when homozygous. He has mapped this locus 0.8 mu distally to sp, and within polytene chromosome region 60E1;2-4. Sunkel (1983) also reported that Ba^m/Ba^1 heterozygotes die as pharate adults with display of extreme malformations of antennae and legs. It appears, therefore, that Ba^m is a leaky mutation of that locus.

References: Lewis,E.B. 1981, v.23:189-208 in Developmental Biology Using Purified Genes (Brown & Fox eds), ICN-UCLA Symposia on Molecular and Cellular Biology, Academic Press, New York; Sunkel,C. 1983, Genetic and developmental analysis of the homeotic mutation Brista in Drosophila melanogaster, PhD thesis, University of Sussex.

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Drosophila of Black Hawk County, Iowa.

Drosophila have been collected from lowland forest, upland forest and sand prairie communities near Cedar Falls, Iowa. The lowland forest, dissected by a stream, consists primarily of box elder, black cherry, hackberry, black walnut, green ash and cork elm. The upland forest, situated on a river bluff dissected by numerous ravines which periodically contain water, consists of oak, hickory, basswood and maple. The rural sand prairie is a virgin mixed grass prairie traversed by a moist swale fringed by big bluestem and Indian grass with elevated xeric areas dominated by little bluestem.

The collection data are shown in Tables 1 (Lowland forest), 2 (Upland forest) and 3 (Sand prairie). All 1982 collections were made by netting flies attracted to buckets containing banana bait. In 1983 all collections were secured in traps baited with bananas (Heim 1978). For three of the species (D.affinis, D.algonquin and D. athabasca) the males can be readily distinguished but distinguishing the females is very difficult. If we only collected males of one of the three species, the females were assumed to be conspecifics; otherwise females were not separated as to species.

The species compositions in our collections from the three communities are compared in Table 4. D.affinis is the most abundant species in all three communities while D.falleni and D.putrida are common in all three. D.robusta is common in two and present in all three. D.tripunctata, although common in the lowland, is apparently absent from the other two communities. This species is most abundant in late summer and fall and may have been excluded from upland forest collections since that community was sampled much earlier in the year. We will sample the upland forest more extensively in the future and thus

Table 2. Upland forest community.

1982:	May		June		July	
Species	♂	♀	♂	♀	♂	♀
D.affinis	10*		103*		112	70
D.falleni	0	0	18*		76	68
D.robusta	0	0	0	0	43	65
D.putrida	0	0	28*		12*	
D.melanogaster	3*		0	0	0	0
Total collections	1		2		2	

* = not sexed.

Table 3. Sand prairie community. Note that a collection during April 1983 yielded no flies. (* = not sexed)

	1982		1983:									
	June		May		June		July		Aug.		Sep.	
Species	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀
D.affinis	56	21	0	2	3	7	2	12	2	14	0	0
D.algonquin	0	0	0		0	0	2		0	0	5	6
D.falleni	5*											
	21	0	0	0	0	0	0	1	0	0	0	0
D.putrida	16*		0	0	0	0	1	2	0	0	1	2
D.quinaria	0	0	0	3	0	0	0	0	0	0	0	0
D.buskii	0	0	1	0	0	0	0	0	0	0	0	0
D.robusta	0	0	0	0	0	0	0	0	0	0	2	0
Total collections	1		3		2		2		1		2	