Fourier analysis of vertebral shape change due to growth and selection for large and small body size

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Summary. Fourier analysis of videodigitised outlines of mouse vertebrae from two stocks, a pseudo-longitudinal series of mice aged 25–60 days and one selected for large or small body size over many generations shows that the shape changes due to normal growth are not similar to those produced by selection for body size.
Key words. Fourier analysis; growth; selection; size; shape.

Those biological variables which are under genetic control are amenable to selection. Classical theory suggests that if we choose size as a criterion for selection we also modify shape. This size-related shape change is usually thought of as the result of differential multiplicative growth and mechanical influences.

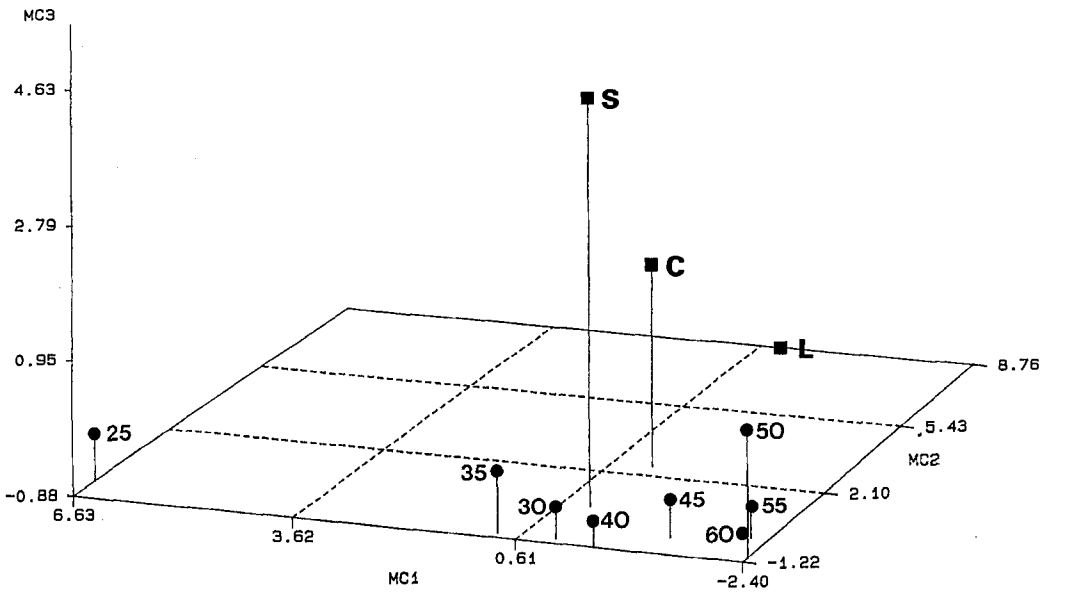

Figure 1. Canonical analysis of the first 40 Fourier components for T1 vertebrae. F_1 of CBA × BALB/c are marked 25 d–60 d according to age. QA series mice are marked large (L), control (C), small (S), respectively. The first three axes accounted for 82% of the total variance.

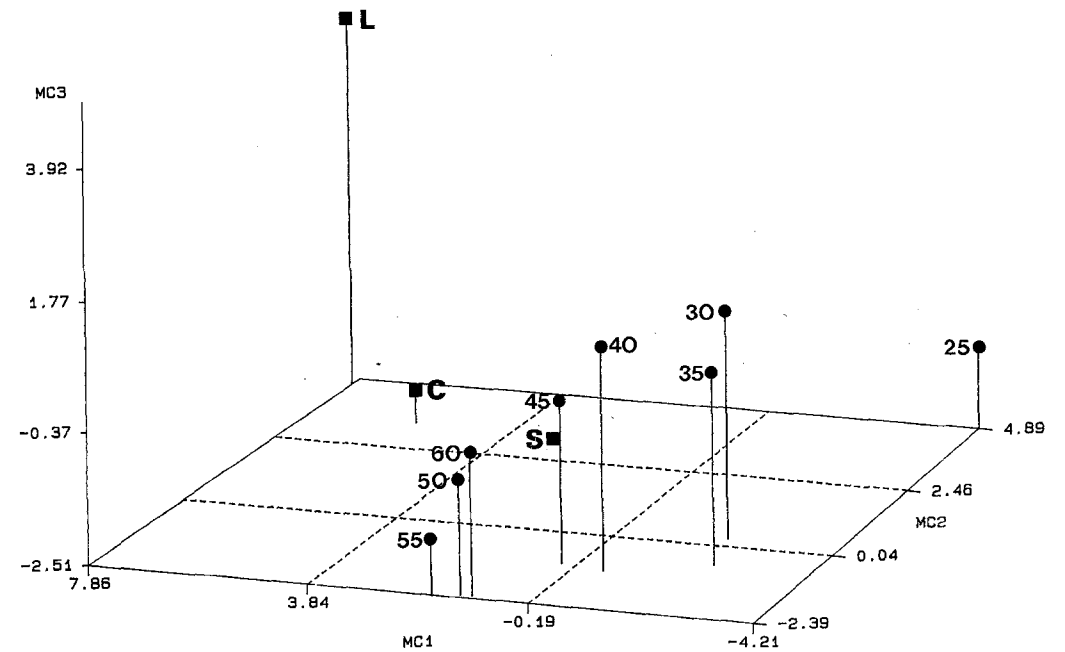

Figure 2. As figure 1, but for T2 vertebrae. The first three axes accounted for 77% of the total variance.

As the skeleton matures it also changes shape: this is concomitant with an increase in size. Previous studies on size-selected mice [1-4] suggest that changes in muscle development, fat deposition and cell size and number in lung, liver, spleen and kidney are produced by an accelerated passage through the growth process. Is this also true for shape changes in the skeleton? If so mice selected for large size should resemble full grown unselected mice and those selected for small size should resemble more juvenile stages of growth.

We tested this hypothesis by performing Fourier analysis on videodigitised images of the first and second thoracic vertebrae of mice selected for body size and of a pseudo-longitudinal series of unselected mice. We [5] have previously described a method for converting videodigitised images of mouse vertebrae to polar coordinates, adjusting them to a standard area, finding a mean shape and converting this to Fourier components. Multivariate analysis of the first n Fourier components (where n is chosen to give good discrimination between mean shapes) gives a generalised distance between shapes, i.e. a measure of their overall difference. The vector of the line joining the centroids of the shapes may be used to discriminate between similar and dissimilar changes. The mice used were a) the QA series of Falconer [6] which were made up of 29 unselected control animals, 30 selected for large size and 28 selected for small size over 13 generations [7] and b) 142 F_1 individuals from a cross of Balb/c and CBA inbred strains aged 25–60 days and sacrificed at 5-day intervals [8].

The first 40 Fourier sine and cosine components from the mean shapes of each series were entered into a canonical analysis. For T1 vertebrae (fig. 1) it is quite clear that the major part of the shape difference is along axis 1, with the bones arranged in rough order of age, and the 25-day-old vertebrae well separated from the rest [8]. The large–control–small axis is also linear but almost orthogonal to that of the age series. For T2 (fig. 2) a similar picture is obtained, with size variation due to selection for size and that due to normal growth again being almost orthogonal.

It is thus clear that our measure of vertebral shape behaves differently from the other parameters which have been studied in mice selected for size. Whilst muscle development, fat distribution, and cell number and size in a number of organs respond to selection by an accelerated passage through the growth process vertebral shape responds quite differently: presumably those features of shape which differ between 25- and 60-day-old mice are not those which differ between large and small mice. Exactly where these differences lie cannot be examined by Fourier analysis. We are presently developing techniques which will allow us to accurately localise such differences in shape.

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Crystal cell pattern modification in a melanotic tumor strain of *Drosophila melanogaster*

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Summary. 3rd instar larvae of the melanotic tumor *tu-pb* strain of *Drosophila melanogaster* hold a lower number of free-circulating crystal cells in their hemolymph than the wild type ones. This pattern could result from an abnormal retention of mature crystal cells in the hematopoietic organs, as the strong hemocyte melanization inside the lymph glands of heat-treated *tu-pb* larvae seems to demonstrate. Melanotic tumor formation and modification of the crystal cell pattern may be related.
Key words. Crystal cells; hemolymph; lymph gland; melanotic tumor.

Crystal cells (fig. 1) comprise 5–10% of larval hemocyte population in *Drosophila melanogaster* [1]. They are the source of hemolymph phenoloxidase activity owing to the prophenoloxidases carried in their paracrystalline inclusions [2]. Like other blood cell types, crystal cells are produced in the hematopoietic organs (the lymph glands) and periodically released into the hemolymph [3].

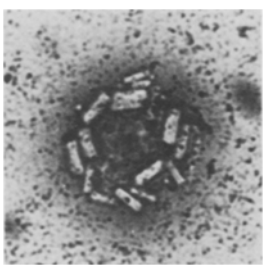

Figure 1. Crystal cell from larval hemolymph. ×4650

At present, *Black cells (Bc,2-80.6)* and two alleles of the lozenge locus, *lz(rfg)* and *lz(s)*, are the only reported mutants which specifically affect the crystal cells. Prophenoloxidases are activated in situ in *Bc* mutant larvae and, as a consequence, the crystal cells are blackened and lack paracrystalline inclusions; the pigmented hemocytes can be seen beneath the integument as individual cells and in the first pair of lymph glands [4].

Phenoloxidase activity is not detectable in cell free extract of *Bc/Bc* larvae (lethal condition) whereas *Bc/+* extract has less than half the activity of +/+ [5].

Crystal cells do not differentiate in *lz(rfg)* or *lz(s)* larvae and the enzyme activity is absent in the hemolymph. It is likely that the *lz* locus influences the differentiation of mesodermal cell clones that give rise to the larval crystal cells [6].