Nematode homeobox cluster

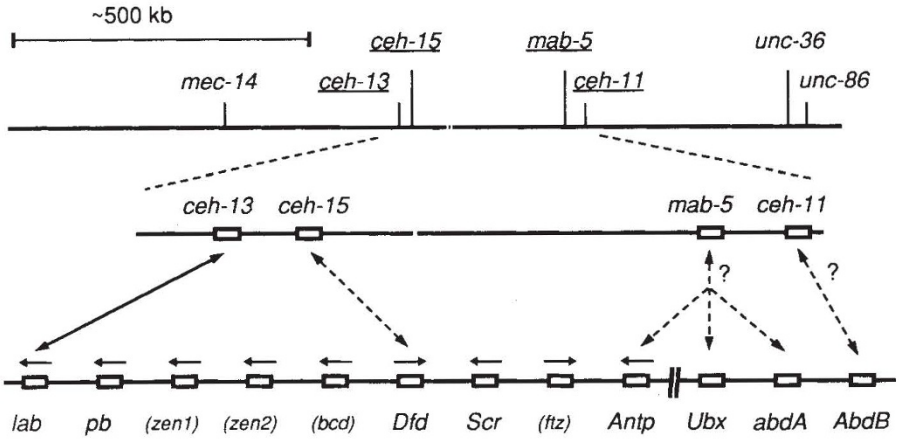
SIR – Clusters of *Antennapedia*-like homeobox genes have been found in *Drosophila* and in vertebrates (see ref. 1 for review) that show a remarkable similarity of organization and expression. Intriguingly, the order of the homeobox genes along the chromosome corresponds to the order of expression domains along the anterior–posterior axis of the animal.

A large-scale screening for homeobox-containing genes[2] in the nematode *Caenorhabditis elegans* did not initially reveal such clusters. But, as the *C. elegans* map has been further refined[3], a previously unmapped small contiguous set of cosmid clones (locus No. 38 in ref. 2) containing two homeobox genes, *ceh-13* (ref. 4) and *ceh-15* (hom-2/3 in ref. 5; C. Kenyon, personal communication) has now been located on chromosome III, to the left of the homeobox genes *mab-5* (ref. 6) and *ceh-11* (refs 4, 7; see figure). These four genes form a cluster of *Antennapedia*-like homeobox genes that appear to maintain the same anterior–posterior ordering found in flies and vertebrates.

The leftmost gene in the *C. elegans* cluster, *ceh-13*, has a homeobox of the *labial*-type (68% identical to *labial*), while that of *ceh-15* appears most similar to *Deformed*-type homeoboxes (77% identical). The homeobox of *mab-5* is 70–73% identical to a group of closely related (77–93% identity) *Antp*-like genes, that is, *Scr*, *ftz*, *Antp* (the best match), *Ubx* and *abd-A*. Flanking sequences like the hexapetide upstream of the *mab-5* homeobox (VFPWMK) do not aid in assigning *mab-5* to a particular type. It is thus conceivable that *mab-5* is the homologue of some ancestor of several fly homeobox genes. Like members of homeobox clusters in other species, *mab-5* has been shown to control cell identities in particular spatial domains[6]. The *mab-5* mutants affect cell identities in posterior regions of *C. elegans*, causing transformations to adjacent anterior cell identities.

If the order of homeobox genes along the chromosome were conserved between nematodes, flies and vertebrates, one might expect an *Abd-B*-type homeobox at the location of *ceh-11*. The homeobox of *ceh-11* is highly divergent from all the other *Antp*-like genes (maximum identity of only 57% to *Antp* and 53% to *Abd-B*). Nonetheless, it shares amino acids at certain positions with fly and/or vertebrate *Abd-B*-type homeoboxes which are not found at those positions in any of the other cluster homeoboxes. In fact, human homeobox clusters each contain five *Abd*-like homeobox genes[8], two of which are quite divergent. Thus either *ceh-11* is a divergent homologue of *Abd-B*-type homeoboxes, or perhaps a true *Abd-B* homologue remains to be detected. Genetic map position suggests that *ceh-11* could correspond to the gene *egl-5* (refs 4, 7), which functions posteriorly to *mab-5*.

Because *ceh-13* is clearly most similar to the *labial*-type genes that are expressed in anterior regions of fly and vertebrate embryos, and genetic analysis of the more distal *mab-5* show its involvement in posterior pattern formation[6], we conclude that these genes represent the evolutionary equivalent of the *Antennapedia*-type homeobox gene cluster in higher organisms. Further experiments should reveal whether there are other homeobox genes in this region, and what the most likely evolutionary relationship is between the *C. elegans* homeobox gene cluster and clusters in other organisms. Complete elucidation of the cluster structure will emerge from the *C. elegans* genome sequencing project, since these genes are part of the initial 3-megabase region to be sequenced.



Physical map of the central region of chromosome III of *C. elegans*. Genes are indicated and the homeobox genes of the cluster are underlined: *ceh-13* and *ceh-15* are about 50 kb from each other, as are *mab-5* and *ceh-11*. *ceh-15* is about 250 kb to the left of *mab-5*; the precise distance cannot yet be determined, as the physical link between these two genes is still tentative in one position where only YAC clones containing repetitive sequences at their ends provide an overlap. The cluster is schematically expanded underneath and compared to the *Drosophila* cluster[1,9] which is split into two complexes. Direction of transcription for the *Drosophila* homeobox genes is indicated. Genes in parentheses are not involved in anterior-posterior pattern formation. Non-homeobox containing genes in the *Drosophila* cluster have been omitted.

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Cannabis and night vision

SIR — *Cannabis sativa* is a controlled substance in Jamaica and its unauthorized use is of course illegal. But most fishermen in Kingston and its environs in Jamaica do smoke cannabis or drink an alcoholic extraction of mainly the green stems and leaves of the plant. The alcohol in this case is Jamaica's white rum. The fishermen travel long distances at night in open canoe-type fibre-glass boats. These boats often carry no lighting or compass, and for many years the men have claimed that their vision at night is much better after taking the rum–cannabis extract.

I decided to test this belief, and went with a crew on a dark night to a fishing cay approximately 40 miles south of Kingston. The approaches to the cay are shallow with an abundance of coral reefs, only a narrow entrance of deep water allowing boats to get close for mooring. I sat in the boat and listened for the sound of us running aground among the breakers on the reef but heard nothing, only to be told a short while later that the boat was being docked. At daybreak it was impossible to believe that anyone could navigate a boat without compass and without light in such treacherous surroundings. I was then convinced that the man who had taken the rum-extract of cannabis had far better night vision than I had, and that a subjective effect was not responsible. Note that the fishermen allowed about half-an-hour to an hour to elapse before setting out to sea after taking the extract. And I was told that the effect on