

Genetics of body plan: From fly to human

Some fruit flies have legs growing out of their heads, where antennae should be. Others have different body segments that have taken an abnormal developmental turn. Genetic analysis of these bizarre insects led scientists to identify insect genes that control the basic body organization laid down early in embryonic development. But for animals other than insects, investigators have had few clues to the genetic control of growth and differentiation. Now scientists, following a promising lead from the insect development-controlling genes, report they have evidence of genes likely to play a role in directing embryonic development in a wide variety of animals, ranging from earthworm to human.

These findings may be "a major breakthrough in understanding vertebrate development," comments Gary Struhl of Harvard University. He explains, "... it means that many of the principles which govern the development of insect segments might have direct counterparts in vertebrate systems."

In the fruit fly, there are two major groups of development-controlling genes, called homeotic genes. A stretch of 180 nucleotides now has been identified that is extremely similar in three genes of each group of homeotic genes. The geneticists have dubbed this shared region "the homeo box."

Animals of many species have genes containing a stretch of DNA closely resembling the fruit fly *Drosophila melanogaster* homeo box, report William McGinnis, Walter J. Gehring and colleagues at the University of Basel in Switzerland. In experiments described in the June CELL, they used radioactively labeled DNA segments containing the homeo box to detect related genes in different organisms.

The scientists have discovered sequences resembling the homeo box in three invertebrates with segmented bodies: an earthworm, a beetle and another species of fruit fly. A similar sequence has also been detected in all vertebrates so far examined: frog, chicken, mouse and human. The scientists point out that vertebrates can be considered segmented animals because the basic organization of their skeleton, nervous system and muscle arises from a repeated embryonic structure.

The homeotic sequence has not been detected in animals that do not have a segmented body plan. Those examined so far include the bacterium *Escherichia coli*, a yeast, the parasitic worm nematode and a sea urchin.

Although homeo boxes have not been identified in bacteria and yeast, the proteins of these organisms have been a source of insight into the possible importance of the homeotic gene segments.

Because many nucleotide changes do not result in amino acid changes, proteins may have similarities that are not apparent in their DNA sequences. In the July 5 NATURE, Allen Laughon and Matthew P. Scott of the University of Colorado in Boulder report that the 60-amino acid sequence represented by the fruit fly homeo box includes a region similar to regions of some bacterial proteins that bind to specific DNA sequences. The rest of the sequence is likely to bind nonspecifically to DNA. Therefore Laughon and Scott suggest the homeo box encodes a portion of a DNA-binding protein, and thus may participate in gene regulation.

In a similar approach, the Basel scientists compared known amino acid sequences with the sequence represented by the homeo box. Of more than 2,000 known sequences in a computer bank, the homeo box sequence most closely resembles parts of two yeast proteins. These

proteins control expression of many genes important in yeast mating, and they may also control genes involved in a form of cell differentiation. John C.W. Shepherd and colleagues at Basel say in the same issue of NATURE, "... it is remarkable that the yeast mating type genes should have been found to have homologies with these *Drosophila* homeotic genes, because both are among the very few genes known to control the stable determination of cell types."

Work on a frog gene containing a segment "extremely homologous" to the fly homeo box provides further suggestion of the developmental importance of these vertebrate genes. Andrés E. Carrasco, also at Basel, and colleagues report in the July CELL that this gene of the frog *Xenopus laevis*, like the fly homeotic genes, is active at defined times early in embryonic development. The scientists speculate, "If the frog gene cloned here eventually turns out to have functions similar to those of the fruit fly genes, it would represent the first development-controlling gene identified in vertebrates." —J.A. Miller

Glimpsing the top of the particle pile

After burrowing through data representing the debris scattered by massive collisions between speeding protons and antiprotons, researchers now suspect that they have finally caught a glimpse of the elusive "top" or "t" quark. The t quark, the object of ardent searches at several laboratories (SN: 3/19/83, p. 182), is the sixth and final member of the quark family of fundamental particles to be discovered. The most widely accepted theory of particle physics postulates that nearly all subatomic particles are built up of various combinations of these six types, or "flavors," of quarks.

"It's very exciting and has a lot of physics implications," says particle physicist Anne Kernan of the University of California at Riverside. Kernan leads one of three U.S. groups collaborating with about 150 scientists from eight nations at the CERN laboratory in Geneva, Switzerland, where the announcement of the discovery was made last week. Carlo Rubbia of Harvard University heads the overall effort, known as the UA1 collaboration.

Evidence for the t quark was found in the decay of W particles, which were discovered last year and which embody the weak interaction, one of the four classes of natural forces (SN: 2/5/83, p. 84). The W, with a rest mass of about 80 billion electron-volts (80 GeV), decays almost immediately to form either a pair of quarks, or a lepton (electron, muon or tau particle) and a neutrino. Using data from experiments run last year, the researchers found five events that fit one of the predicted decay patterns that are supposed to generate a t quark. In these events, W particles decay to form a t quark and an an-

tibottom quark. The t quark then decays into a b (bottom) quark, an electron or a muon, and a neutrino.

"There should be a note of caution," Kernan told SCIENCE NEWS. "There's a lot of work to be done to make the result really solid." Another large international group of scientists (designated UA2) working at CERN has also looked for the t quark but because of limitations in their apparatus has not found it yet.

One important task is to pin down the t quark's exact mass. The mass appears to be between 30 and 50 GeV, says Kernan. This makes the t quark the heaviest of the six flavors of quarks. "We should also be able to find the t quark decaying into three quarks," she adds.

The UA1 scientists hope to gather 10 times as much data from an experimental run due to start in September. "There'll be fairly quick progress, I think, even with the kind of limited statistics that we have at the moment," says Kernan.

Moreover, "whenever there's a quark, you always have the corresponding quark-antiquark bound state," says Kernan. This so-called "toponium" bound state, made up of a top quark bound to an antitop quark, looks like it will have roughly the same mass as a W particle. "That could give rise to all kinds of interesting effects," says Kernan.

Meanwhile, Japanese scientists, who are now building an electron accelerator limited to about 30 GeV and who were hoping to study toponium, are waiting nervously for the t quark mass to be determined exactly. Kernan says, "There's a big chance that toponium will be beyond their reach."

—I. Peterson