cell (designated Z1.ppp) becomes the anchor cell and another, cell (Z1.aaa) becomes a ventral uterine precursor cell.

The Horvitz group has shown that the level of *lin*-12 activity is the important factor in specifying the fates of these cells. Mutations resulting in increased activity of the gene cause both cells to develop into ventral uterine precursor cells. In contrast, if the mutations result in absence or inactivation of the *lin*-12 product, both develop into anchor cells. In other words, the gene acts as a binary switch to determine which of two possible fates will be that of the cells. During normal development, the Horvitz group postulates, *lin*-12 activity is high in the ventral uterine precursor cell and low in the anchor cell.

The gene has analogous effects on additional pairs of homologous cells that would ordinarily follow different developmental paths. The genetic locus appears to be active at just the times the cell fates are being determined.

The development of some of the cells whose fates are determined by *lin*-12 is influenced by neighboring cells. In those cases, the MIT workers suggest, the cell-cell interaction acts by setting the level of *lin*-12 activity. In others, the level of the gene activity appears to be internally programmed. Additional genes that affect cell fates are being analyzed in Horvitz's laboratory and elsewhere.

Another contribution that will facilitate studies of gene activity during *C. elegans* development has been made by Robert Herman of the University of Minnesota, who has devised a new method for making genetic mosaic roundworms. Such animals consist of cells of differing genetic compositions.

Mosaics have long been used to study developmental genetics in the mouse and fruit fly, but the availability of the lineage map for *C. elegans* adds a new dimension to the information that can be gained from mosaic analysis. "Given the technique and the lineage it is possible to determine the cell division at which the mosaic arises," Horvitz says. "You can ask about gene action in single cells." For example, Herman has determined that certain mutant genes that affect movement probably act in particular neurons in one case and in muscle cells in another. All in all, the foundation has now been laid for rapid progress in the genetic analysis of development in *C. elegans*.—**JEAN L. MARX**

This is the second of a series of articles on the development of Caenorhabditis elegans. *The first, "Why is development so illogical?", appeared on 22 June.*

New Tool for Amino Acid Analysis

A new technique for the analysis of amino acids was reported at the recent meeting of the Federation of American Societies of Experimental Biology and will be the subject of an article in a forthcoming issue of the *Journal of Chromatography* by Waters Associates of Milford, Massachusetts. The new method allows the quantitative derivatization of both primary and secondary amino acids in one simple step and promises analysis times of less than 15 minutes. One investigator who has used the new method, David Klapper of the University of North Carolina, calls it "spectacular for routine analyses."

Amino acid analysis is, of course, already a reliable and widely used technique. Each of the systems in use has certain deficits, however. Precolumn derivatization with *ortho*-phthalaldehyde (OPA) or dansyl chloride is the most common technique, but OPA does not react directly with secondary amines and dansyl chloride and its byproducts can interfere with analyses. Postcolumn derivatization is typically less sensitive and more complex. Certain pairs of amino acids are also difficult to separate on the conventional ion-exchange columns, furthermore, and all the methods require 30 minutes to 2 hours per analysis. The new technique, originally developed by George Tarr of the University of Michigan, appears to solve most of these problems.

The method, called "Pico-Tag," is based on the well-known derivatizing agent phenyl isothiocyanate (PITC), which has been used for more than 30 years in the Edman degradation method for sequencing peptides. PITC reacts with free amino acids to yield phenylthiocarbamyl (PTC) amino acids, which can then be separated on a special reversed-phase high-performance liquid chromatography (HPLC) column. The PTC-amino acids have a strong ultraviolet absorbance, so that quantities as small as 1 picomole can be detected. Because PITC forms the same chromophore with primary and secondary amines, no special procedures are necessary for analyzing secondary amino acids.

The method is not suitable for automation, but most of the manual work can be done in a short time with the use of a special Pico-Tag Work Station, says Steven Cohen of Waters. Preparation of the PITC reagent takes only 2 minutes; addition of reagent to 12 samples takes another 2 minutes. The samples are allowed to react for 20 minutes before excess reagent and byproducts (which are all volatile) are removed at reduced pressure, a process that typically takes about 30 minutes. The samples can then be fed into an HPLC column automatically. Approximately 60 samples can be analyzed per 24-hour workday, says Cohen.

The Pico-Tag method, Cohen says, is probably best for analysis of amino acids produced by carboxypeptidase digestion. It should also be "an ideal tool" for screening HPLC fractions: if the peak is divided into several fractions, the composition across the peak is an indication of the purity. Potential problem areas include proteins mixed with high concentrations of salts, lipids, or detergents, and protein hydrolysates produced with sodium hydroxide or methanesulfonic acid. Procedures have not yet been developed for removing the reagents or contaminants, and high quantities may interfere with the analysis.

Investigators who have already used the new system are quite happy with it. James Riordan of Harvard Medical School, for example, says that "it is really much better than what we had before. It has lowered our routine sensitivity by a factor of 50 and has reduced analysis time from 2 hours to 20 minutes." Christian Anfinsen of Johns Hopkins University says his system is "working very well. It gives us fast, good, and highly reproducible results, even with high amounts of salt present." Klapper says that his results with the new system are "about as good" as with his previous system but that the new technique is much faster; this speed allows him, for example, to "look at every single peak off a preparative HPLC run." Tarr has analyzed about 5000 samples with the system, he says, "and it works well with just about everything we've tried."—**THOMAS H. MAUGH II**