

Plants see hormone as toxic pollutant

Ethylene gas, a by-product of incomplete combustion, is a pollutant associated not only with industrial manufacturing but also with urban automotive exhaust. Ironically, the simple hydrocarbon is also a natural plant hormone. Because ethylene can encourage premature ripening, it is used agriculturally to make an entire crop ripen at once for a single harvesting or to put the color in early-picked fruit.

What George E. Taylor and his colleagues at Oak Ridge (Tenn.) National Laboratory were curious to find out was whether plants respond to chronic low-dose exposures of this chemical as though it were a toxic pollutant — regardless of any subtle, slow-acting hormonal action that might also be occurring. Their experiments with several important crops now suggest that some plants indeed respond immediately and adversely to ethylene gas.

The researchers worked with corn, soybeans, peanuts, tobacco and seedlings of the green ash tree. Except for corn, which for unknown reasons showed no adverse reaction to any concentration of ethylene, the plants responded in a dose-dependent fashion by reducing both their photosynthesis and respiration.

These changes, says Taylor, suggest that the site of ethylene action is the stomata—the little openings on the underside of leaves through which gas exchange occurs. However, since stomata changes were not noticed in all of their adversely affected plants, Taylor says a closing down of stomata apertures may be secondary to changes in a more fundamental mechanism regulating photosynthesis, involving an unhealthy buildup of carbon dioxide concentrations in leaves.

Writing in the May ENVIRONMENTAL SCIENCE AND TECHNOLOGY, Taylor and co-workers report that after three- to six-hour exposures to ethylene at concentrations of 3.7 parts per million (ppm) in air, the photosynthetic rate fell in some of the more sensitive species, including soybeans and peanuts, by more than 60 percent. A mere 0.9-ppm exposure cut their photosynthesis by almost a third. And such effects occur very rapidly, Taylor says, sometimes “in less than half an hour.”

Although only a handful of published studies have quantified ethylene concentrations in air, Taylor says, some of the reported values do approach levels that affected plants in his study. Moreover, ethylene levels tend to peak when photosynthetic activity is at its highest. If decreases in photosynthesis occurred for prolonged periods, plant growth and crop yields would be stunted, he says.

— J. Raloff

Modular evolution: Mix-and-match genes

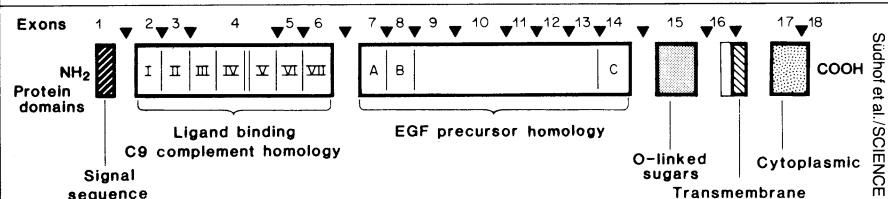
The evolutionary process may assemble new genes from copies of pieces of various older genes, rapidly building new functions from a novel collection of already reliable parts. This modular view of evolution, under discussion for almost a decade, has just received its first strong evidence. Researchers have discovered that a gene important in the accumulation of cholesterol in human cells is made up of segments shared with several quite distinct genes. Walter Gilbert, who proposed the idea of modular genes in the 1970s while at Harvard University, now calls this finding “a dramatic example” supporting his conjecture.

The newly analyzed gene encodes the membrane molecule that binds and

share much of their sequences as “supergene families,” implying a common ancestry.

Detailed analysis of the LDL receptor gene reveals a series of 18 exons, which correspond closely to the functional domains of the protein. Four of the five boundaries between domains are marked by introns. In addition, seven of the introns fall between repeats of a sequence.

The first exon encodes an amino acid sequence, called the signal sequence, that is clipped from the LDL receptor before it appears on the cell surface. The next five exons encode the binding site for the cholesterol molecule. The binding site is made up of a 40-amino-acid



A mosaic gene: The gene for the LDL receptor is divided by introns (arrowheads) into 18 exons. Some of these divisions correspond to the six functional domains (heavy outlines) of the protein and some to the boundaries of repeated sequences (I-VII and A-C). The DNA sequence encoding the second domain is related to the gene for an immune system protein, C9 complement. The sequence of the third domain is related to three blood-clotting proteins and to the precursor to the peptide hormone epidermal growth factor (EGF).

transports one type of cholesterol, low-density lipoprotein (LDL), into a cell. This membrane molecule is made up of several parts, each performing a different function. The gene behind the membrane molecule also contains distinct parts, called exons, separated by much longer stretches of DNA, called introns or intervening sequences, that do not code for any portion of the protein molecule. Some of these exons are strikingly similar, though not identical, to gene segments of proteins having very different roles, report Thomas Südhof, Joseph L. Goldstein, Michael S. Brown and David W. Russell of the University of Texas Health Science Center at Dallas and colleagues at Chiron Corp. in Emeryville, Calif.

The analysis of the LDL receptor gene “provides strong evidence in support of Gilbert’s original hypothesis that introns facilitate the evolution of apparently diverse genes by allowing recruitment of exons encoding functional domains,” the scientists say in the May 17 SCIENCE. “Our findings also lend support to the concept that the LDL receptor is a mosaic protein whose gene is built up of exons that have been borrowed from or loaned to other genes and is thus a member of several supergene families.” Scientists have defined sets of genes that

sequence, repeated seven times (I-VII). This repeated unit closely resembles an amino acid sequence, which appears only once, in the human blood plasma molecule called the C9 component of complement.

The next domain of the LDL receptor resembles a portion of the protein that is the precursor to the peptide hormone epidermal growth factor (EGF). The scientists suggest that the EGF precursor may be a membrane-bound protein like the LDL receptor. The location of introns in the two gene regions is also similar. In addition, both the LDL receptor domain and the corresponding region of EGF precursor contain a sequence repeated three times (A,B,C). This sequence also appears in three blood-clotting proteins.

The remaining domains of the LDL receptor provide the sites for sugar attachment; a segment that goes across the cell membrane; and a stretch of amino acids that falls on the cytoplasmic side of the membrane and anchors the receptors to their characteristic surface sites, structures called coated pits.

The researchers expect the analysis of the LDL receptor gene to be useful in the study of the inherited disease called familial hypercholesterolemia, a common cause of atherosclerosis and heart attacks.

— J. A. Miller