Behavior

Teenagers' drug use drops

Self-reported use of illicit drugs by high school seniors continued a decade-long decline in 1989, while alcohol and cigarettes remained the most widely used drugs among the students, according to a national survey released last week.

The annual survey of 17,000 seniors is conducted by researchers at the University of Michigan in Ann Arbor.

Overall, 19.7 percent said they had used an illicit drug in the previous month, compared with 21.3 percent in 1988 and nearly 40 percent in 1979. Seventeen percent of the seniors reported using marijuana in the prior month – down from a peak of 37 percent in 1979. Cocaine consumption was reported by 2.8 percent of the students, sustaining a steady slide from 6.7 percent in 1985. Amphetamine use in the previous month was about 4 percent last year, having dropped from 12 percent in 1980. The reported use of tranquilizers, barbiturates and methaqualone remained at extremely low levels.

However, disturbing signs also appeared. Reported use of PCP, a hallucinogen with dangerous effects, rose in the month before the survey from 0.3 percent in 1988 to 1.4 percent in 1989. Heroin use was infrequent, but rose from 0.2 percent to 0.3 percent over the same time period. Crack cocaine use in the prior month fell from 1.6 percent in 1988 to 1.4 percent in 1989, but the percentage of seniors reporting crack use in the past year was 3.1 percent in 1989, the same as in 1988.

Overall, the survey probably underestimates illicit drug use, acknowledges study director Lloyd D. Johnston, because it does not account for high school dropouts. Federal data indicate about 27 percent of U.S. teenagers are dropouts.

Alcohol has long been reported as the most commonly consumed drug in the senior survey, and 1989 was no different in that respect. Sixty percent of the seniors said they had used alcohol in the past month, down from a peak of 72 percent in 1980. One-third of the students reported consuming five or more alcoholic drinks in a row sometime during the previous two weeks.

Rates of cigarette smoking have not changed substantially over the past decade, with 29 percent of the seniors in 1989 reporting cigarette use in the past month and 19 percent reporting daily cigarette use. This finding is "by far the most disappointing part of the story," Johnston says.

Triple Tourette's

A set of triplets, born in Sweden 57 years ago, was separated shortly after birth and each child was reared by an adoptive family. Although the two girls and one boy did not reunite until they were 47 years old, each developed Tourette's disorder by age 5, thus providing "unique evidence that genetic factors are important in the development of this disorder," according to a report in the February AMERICAN JOURNAL OF PSYCHIATRY.

Tourette's disorder involves repeated, multiple tics of the face, body and voice. Eye blinking is a common symptom, as are sticking out the tongue, clearing the throat, stuttering and uttering senseless sounds or obscenities.

The triplets do not share carbon-copy symptoms of Tourette's disorder, note Nancy L. Segal of the Minnesota Center for Twin and Adoption Research in Minneapolis and her coworkers. The man suffers predominantly from frequent eye blinking. One of his sisters is troubled mainly by head jerks, shoulder jerks and kicking leg movements, as well as by periodic facial tics and grunts. The other experiences infrequent eye blinking and facial tics accompanied by right-leg kicking when she is outdoors.

Environmental events may have helped to create the variation in symptoms, the researchers say. However, scientists do not know how family and social factors might influence the expression of Tourette's disorder.

Biochemistry

Gene jumbling yields improved enzymes

Guided by chemical and physical rules, strings of linked amino acids twist, bend and fold into functional three-dimensional proteins. For about a decade, researchers have used a technique called site-specific mutagenesis to interchange amino acids at individual locations in a protein and study the functional consequences. But since scientists have only partial knowledge of the rules involved and so cannot reliably predict outcomes of particular mutations, some have likened the technique to shooting in the dark.

Harvard University biochemist Jeremy R. Knowles and his co-workers have now developed a technique that produces almost all possible single-site mutations in a protein and thus can help provide the basic data for such predictions.

The researchers begin by inserting a gene into a strain of bacteria. This specific gene codes for a "sluggish" version of an enzyme called triose phosphate isomerase (TIM), crucial to cellular digestion of glucose. After generating random mutations throughout the gene, the scientists extract the mutant genes from the bacteria and insert them into a bacterial strain that lacks its own copy of an isomerase gene. Without either their own or an inserted TIM gene, these microbes die off in a growth medium that lacks the chemical lactate.

The medium thus serves as a laboratory version of natural selection, "choosing" only improved enzymes from among nearly 2 million mutations, Knowles says. In the January PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES (Vol.87, No.2), the scientists report identifying six mutants that showed up to 20 times as much catalytic activity as the starting TIM. Knowles says he expects that running the most active mutants through more mutation-and-selection cycles should lead to enzymes that show even more activity.

"It's a classic piece of work," says biochemist Charles Craik of the University of California, San Francisco, adding that the technique might even empower researchers to change an enzyme's function. "Then you would be taking evolution in your own hands," he says.

More ways to build the same protein

Imagine a hat filled with 20 kinds of beads. How many tries would it take to randomly extract 100 beads, one by one, that string into a specific sequence of bead types? The sun would probably burn out first.

Does the same hold for linking 20 kinds of amino acids into huge protein molecules that have specific bioactive shapes?

The answer would be yes if a particular protein function could emerge from only one specific sequence of amino acids. But a new computer model suggests that the odds for a random sequence of monomers to take on a particular shape are far higher than previously thought.

The model simulates how water-dissolved polymers such as proteins fold into three-dimensional shapes. The computer creates random sequences of either water-loving or water-avoiding monomers and then calculates which of each sequence's possible shapes harbor the least energy and therefore are the most stable forms. "We found that lots of different sequences give you the same structure," says Ken Dill of the University of California, San Francisco.

In the January PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES (Vol.87, No.2), Dill and coauthor Kit Fun Lau say the result suggests that even complex catalytic proteins were relatively frequent, random inventions in a prebiotic soup of amino acids. Proteins populate all cells, and many theorists have argued that functional proteins may not have been so difficult to assemble from scratch. The new model adds punch to that argument, Dill says, by providing a means for quantifying the likelihood of such chance constructions.