Scientists question rise in autism

In response to an apparent rise in the incidence of autism, the American Academy of Pediatrics has issued new guidelines to assist pediatricians in diagnosing the condition (*Pediatrics*, **107**, 1221; 2001). Reportedly, autism has increased as much as 10-fold in the last few decades, from 1 in 2,500 in the 1970s to 1 in 250 in the 1990s. However, epidemiologists see nothing unusual or alarming in these statistics and propose that the increase stems from a broadening of the conceptualization of autism to include milder and more prevalent forms of the disorder.

Broadening the diagnostic spectrum for a disease is common as that disease becomes better understood, according to Robert Davis, associate professor of

Epidemiology at the University of Washington. "We see the tip of the iceberg first—not only with autism, but with a lot of other diseases. It's remarkable and the increase is striking, but it's not surprising," says Davis.

Catherine Lord, professor of Psychiatry at the University of Chicago, explains that the move to broaden the definition stems directly from research. For example, Michael Rutter and Susan Folstein, from the Institute of Psychiatry in London, found that while only 60% of monozygotic twins were concordant for autism, almost all the rest had difficulties in language or social skills, something that looked like a milder version (*Nature*, **265**, 726; 1997). And Lorna Wing of the United Kingdom Medical Research

Council's Social Psychiatry Unit found the same triad of impairments—poor language comprehension, limited social reciprocity, and limited play—in autistic and in idiopathic mentally retarded children (*Journal of Autism and Developmental Disorders*, **9**, 11; 1997).

Also folded into the mix is a better social awareness and understanding of the disease, which has made physicians more willing to make the diagnosis. Fifteen years ago there was no benefit to giving a child a diagnosis of autism. "It was merely a label, it led to children being ostracized, and there was no treatment for it. It was all loss with no gain," says Davis. Now the situation is reversed. Early intervention with autistic children works so well now that there is no drawback, and in fact much to be gained by making the diagnosis.

The development of reliable diagnostic techniques will help determine whether the increase in incidence can be accounted for solely by changes in the definition and reporting practices. In a recent retrospective study of several hundred children, Karin Nelson and coworkers from the United States National Institute of Neurological Diseases and Stroke and California Birth Defects Monitoring Program found elevated levels of several neuropeptides and trophins in neonates who later were diagnosed as autistic or mentally retarded (*Annals of Neurology*, **49**, 597; 2001). But coauthor Judith Grether cautions that although these data suggest that markers in the peripheral blood correlate with outcome, a test for autism is still a long way off. For one thing, they did not find a marker that could distinguish autism from mental retardation.

Meanwhile, the reports of increased incidence have not gone unnoticed by US Congressman Dan Burton, the grandfather of an autistic child and a proponent of the theory that regressive or acquired autism is caused by the measles-mumps-rubella vaccine. Although the US Institute of Medicine rejects claims of a causal relation between the two in a new review (see <http://books.nap.edu/html/mmr/>), Burton is to request additional funds of \$20 million for research on autism, and has introduced a bill to expand provisions of the childhood vaccine injury act.

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Europe to standardize bacteria research

In an effort to better compare strains of bacteria from country to country, the European Union has established a genetic epidemiology network, funded through its Fifth Framework Program, which will standardize the identification of epidemic and virulent bacterial clones (www.ewi.med.uu.nl/gene).

So far, European laboratories have lacked a uniformed process for characterizing different strains of bacteria and a common language with which to describe them. Without such standardized data, opportunities to counter outbreaks of bacterial infections have been lost. Project director Sylvain Brisse, a specialist in bacterial diversity from the University Medical Center in Utrecht, the Netherlands, found that with no common inventory, scientists have been duplicating work on strains of bacteria in different countries.

The GENE Project will comprise a network of 18 laboratories in 13 different countries that will carry out automated bacterial strain DNA fingerprinting of fifteen of the most common bacterial pathogens starting with *Staphylococcus* and including *Listeria*, *Campylobacter* and *Legionella*. Once properly characterized, different bacterial strains' epidemiological dynamics could be monitored, controlling their spread among hospitals and between countries and pinpointing

strains with increased virulence or epidemic potential.

"It's an evolutionary genetics approach to understand how bacterial populations evolve," says Brisse, adding that the task is a substantial one because the diversity within an individual species such as *Escherichia coli* is greater than that within primates. "It means a strain of *E. coli* identified in one Dutch patient is as different as a case in an Italian hospital as a lemur is to an orangutan; and it is important to identify these different strains reliably as not all are equally dangerous or epidemic."

Achieving a common language requires a common technology. The project will rely on ribotyping using an automated riboprinter to generate the standardized genetic fingerprints. This technique analyzes a fundamental portion of the bacteria's DNA ribosomal RNA genes, which along with their variable flanking regions, can be used to identify the mutations between different strains. Other forms of typing—such as pulse-field gel electrophoresis used by the United States Center for Disease Control's PulseNet to identify food borne infections—take longer but scan the whole genome therefore discriminating more precisely between genetically similar strains.

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