Pain-Predicting Genes

Scientists in Australia and Austria have described a "network map" of genes involved in pain perception, with remarkable similarity from fruit flies to people. The work should help identify new analgesic drugs. Dr. Greg Neely from the Garvan institute of Medical Research in Sydney and Professor Josef Penninger from the Austrian Academy of Sciences in Vienna had previously screened the 14,000 genes in the fly genome and identified 580 genes identified with heat perception. In the current study, using a database from the U.S. National Center for Biotechnology Information, they noted roughly 400 equivalent genes in people, 35 percent of which are already suspected to be pain genes.

The map they constructed using fly and human data includes many known genes, as well as hundreds of new genes and pathways, and demonstrates exceptional evolutionary conservation of molecular mechanisms across species. This should not be surprising, as any creature must be able to identify a source of pain or danger in order to survive.

Comparing fly with human data, they could see that a particular kind of molecular signaling (phospholipid signaling), already implicated in pain processing, appeared in the pain network. Further, they demonstrated the importance of two enzymes that make phospholipids, by removing those enzymes from mice, making them hypersensitive to heat pain. These results are now published online in the international journal *PLOS Genetics*.

"Pain affects hundreds of millions of people and is a research field badly in need of new approaches and discoveries," said Dr Neely. "The fact that evolution has done such a remarkable job of conserving pain genes across species makes our fly data very useful, because much of it translates to rodents and people. We are able to test our hypotheses in mice, and if a gene or pathway or process functions as we predict, there is a good chance it will also apply to people."

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