

Fine-scale analysis of the human brain yields insight into its distinctive composition

April 12 2012

Scientists at the Allen Institute for Brain Science have identified similarities and differences among regions of the human brain, among the brains of human individuals, and between humans and mice by analyzing the expression of approximately 1,000 genes in the brain. The study, published online today in the journal *Cell*, sheds light on the human brain in general and also serves as an introduction to what the associated publicly available dataset can offer the scientific community.

This study reveals a high degree of similarity among [human](#) individuals. Only 5% of the nearly 1,000 genes surveyed in three particular regions show differences in expression between humans. In addition, comparison of this dataset to data in the Allen Mouse [Brain](#) Atlas indicates great consistency between humans and mice, as the human visual cortex appears to share 79% of its [gene expression](#) with that of the mouse.

The dataset, which is publicly available online via the Allen Brain Atlas data portal as part of the Allen [Human Brain Atlas](#), holds promise for spurring further discoveries across the research community. Specifically, it contains detailed, cellular-level in situ hybridization [gene expression data](#) for about 1,000 genes, selected for their involvement in disease or [neural function](#), in two distinct cortical areas of several disease-free adult human brains, both male and female.

Genes analyzed in this study fall into three categories: genes that serve as indicators of cell types found in the cortex, genes that are related to

particular neural functions or diseases of the [central nervous system](#), and genes that hold value for understanding the neural evolution of different species.

Human brain

The analysis published today reveals high consistency of gene expression among different regions of the human cortex—the outer rind of the mammalian brain responsible for sophisticated information processing—specifically the temporal and visual cortices. The vast majority of genes expressed in these areas, 84%, demonstrate consistent expression patterns between cortical areas. This finding supports the hypothesis that there are common principles of organization and function that apply throughout the cortex, and therefore studying one area in great detail—the visual cortex, for example—may hold promise for uncovering fundamentals about how the whole brain works. The study also illustrates widespread conservation of gene expression among human individuals. The study reports that of the genes analyzed, only 46 (5%) showed variation in expression among individual, disease-free human brains in the [cortical areas](#) examined.

Distinctions among species

Several findings in the study point to differences and similarities between humans and mice. As the mouse is the most common model for the study of human brain function and diseases, it is crucial to understand how well it represents the human system and where its accuracy may be limited. Overall, the results of this study indicate good conservation of gene expression between the two species. While the majority of gene expression is similar, the authors of the study report some striking differences.

The findings reveal distinct molecular markers specific to each species. Tracing those genes attributable to particular cell types—the building blocks of brain circuits—the study authors point to a unique molecular signature for each cortical cell type. These molecular signatures may reflect and contribute to species-specific functions.

According to the study, only 21% of gene expression in the visual cortex exhibited differences between human and mouse, but the nature of those differences may reveal more about what makes us uniquely human. While very little variation among genes in the disease and evolution categories was observed, substantial variation was reported among genes in the cell types category, with a marked number of those genes known to be involved in cell-to-cell communication. These data suggest that intercellular communication may be a key link to unique brain function in humans.

Advancing the field

To date, other studies examining human gene expression have employed either a segmented region of the brain or a select set of genes without specific anatomic information. This human brain dataset as well as the Allen Mouse Brain Atlas and the hundreds of studies published using its data demonstrate that adding high-resolution, cellular-level spatial information to gene expression profiling studies allows scientists to learn a great deal more about how [genes](#) contribute to cell types, neural circuits, and ultimately brain function.

The study published today offers a deep introduction to the kinds of information that can be mined from this [dataset](#) and the types of hypotheses that it can be used to test. The entire body of data is incorporated into the Allen [Human Brain](#) Atlas and is freely available via the Allen [Brain Atlas](#) data portal at www.brain-map.org.

More information: Zeng et al., Large-Scale Cellular-Resolution Gene Profiling in Human Neocortex Reveals Species-Specific Molecular Signatures. *Cell* (2012) [doi: 10.1016/j.cell.2012.02.052](https://doi.org/10.1016/j.cell.2012.02.052)

Provided by Allen Institute for Brain Science

Citation: Fine-scale analysis of the human brain yields insight into its distinctive composition (2012, April 12) retrieved 14 May 2024 from <https://medicalxpress.com/news/2012-04-fine-scale-analysis-human-brain-yields.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.