HHS Public Access

Author manuscript

Nature. Author manuscript; available in PMC 2015 April 24.

Published in final edited form as:

Nature. 2013 August 1; 500(7460): 34–35. doi:10.1038/nature12457.

From big data to mechanism

Vivek Swarup and **Daniel H. Geschwind**

is in the Department of Neurology, and **Daniel H. Geschwind** is in the Department of Neurology and the Semel Institute, David Geffen School of Medicine at UCLA, University of California Los Angeles, Los Angeles, California 90095-1761, USA.

Daniel H. Geschwind: dhg@mednet.ucla.edu

Abstract

The gene variant *APOE4* is the most common genetic risk factor associated with late-onset Alzheimer's disease. A comprehensive, multilayer study reveals the molecular and cellular signatures of *APOE4* in humans.

Alzheimer's disease is a genetically complex neurodegenerative condition typically associated with ageing. Reporting on *Nature*'s website today, Rhinn *et al.*[1] use an integrative genomic approach based on analysis of transcriptional networks in human brain to uncover new relationships between this disorder, ageing, and the gene apolipoprotein E, or *APOE*, shedding light on molecular mechanisms that connect this gene to the processing and transport of amyloid precursor protein — considered to be a primary effector of the disease. To validate their hypotheses, the authors follow bioinformatic analyses with multiple levels of experimentation, impressively demonstrating the power of network biology.

Recent genome-wide association studies (GWAS) and transcriptomic studies have implicated[2,3] a wide set of pathophysiological mechanisms in Alzheimer's disease, including innate immunity, cellular uptake of molecules by the process of endocytosis and their intracellular trafficking. However, a variant of *APOE* called *APOE4* remains the most common genetic risk factor, with the largest effect in late-onset Alzheimer's disease (LOAD)[4]. Therefore, understanding how *APOE4* conveys disease risk and its relationship with ageing remains a research imperative.

Rhinn *et al.* start with a simple, but previously unexplored, set of comparisons using published data on gene expression in the cerebral cortex region of the human brain to address a question widely debated in the field: do the molecular mechanisms underlying LOAD differ between those who carry *APOE4* and those who do not?

To discern the independent effects of disease and *APOE* status, the authors compare *APOE4*-negative healthy individuals with both *APOE4*-negative LOAD patients and *APOE4*-positive healthy individuals. Remarkably, they find that the total cellular transcript (transcriptome) profile of healthy *APOE4* carriers overlaps to a large extent with that of

LOAD patients, and that the overlapping set of transcripts (designated A/E) most closely resembles the changes in transcript profile observed during the transition from normal to incipient LOAD — an early phase of Alzheimer's disease. These data indicate that the *APOE4* status of an individual reflects a prodromal, or 'primed', state for developing LOAD.

Notably, transcriptional changes observed during normal ageing (through comparison of those under 75 years of age with those over 85) overlapped significantly with LOAD, but not with changes specific to *APOE4* carriers. That certain transcriptional alterations in LOAD are seen either with ageing or with *APOE4* status suggests that the contributions of *APOE4* to LOAD are mechanistically distinct from those of ageing. A potential caveat of this analysis, however, is the use of a hard categorical cutoff of age 75, rather than, for example, 65 — the age below which Alzheimer's disease is considered early onset. In this regard, a non-categorical quantitative analysis of transcripts associated with ageing should provide maximum analytical power.

"This work is exemplary in demonstrating the extraordinary value of publicly available data resources."

Network-level co-expression analyses have been used successfully before to investigate disease-related molecular pathways in various neuropsychiatric[5,6] and neurodegenerative disorders, including Alzheimer's disease[3,7]; such analyses permit an unbiased, systems-level understanding of disease mechanism. Rhinn and colleagues' work differs from other network-based co-expression approaches in focusing on differential co-expression — that is, on changes in co-expression patterns observed between control and disease samples. The authors, who used a transcriptome-wide network-analysis tool called differential co-expression correlation analysis (DCA), provide extensive experimental support for the targets identified, which adds an unprecedented level of validation.

Of the 215 differentially expressed genes Rhinn *et al*. found by comparing *APOE4* carriers and non-carriers, 20 are top candidate 'network node' genes on the basis of their DCA ranking. Many of the node genes had been previously implicated in regulating amyloid precursor protein (APP) processing and intracellular sorting[8], supporting their relevance.

The authors performed various *in vitro* experiments to validate several of the node genes, in particular *SV2A* and *RNF219*. In cell lines and in human induced neurons, obtained by the process of cellular reprogramming, they show that *SV2A* affects APP processing through the regulation of endocytosis and intracellular trafficking. They also find that *RNF219*, which had not been previously associated with APP processing or Alzheimer's disease, acts as a nuclear regulatory mediator of APOE4-induced APP endocytosis and its processing by the β-secretase enzyme.

The researchers muster and analyse multiple independent data sets, including published GWAS, which provide further support for the key role of the DCA hits in *APOE4*-mediated susceptibility to Alzheimer's disease, and make a case for further testing and replication studies using this gene set. For example, they show that, together with the *APOE4* status, common genetic variants of *RNF219* and *FYN* — another node gene with a role in

endocytosis — are correlated with age of LOAD onset. Indeed, using publicly available human positron-emission tomography imaging data from the Alzheimer's Disease Neuroimaging Initiative, Rhinn *et al.* find that variations in *RNF219* significantly affect APP processing in *APOE4*-negative healthy individuals — consistent with a prodromal role of this, and possibly other, A/E genes.

Overall, the present paper significantly advances our knowledge of molecular and genetic mechanisms that modify LOAD risk, further implicating defects in endocytosis and intracellular trafficking in Alzheimer's disease development[9,10]. The identification of key regulatory molecules and pathways involved in *APOE*-based risk for LOAD sets the stage for investigating their link to other deficits in this disorder, including immune function and metabolism of hyperphosphorylated tau protein, which forms the disease's characteristic neurofibrillary tangles. Ultimately, such investigations should lead to molecularly targeted therapeutics.

By demonstrating distinct mechanisms that depend on *APOE* status in LOAD, another implication of this work is that different genetic forms or subtypes of Alzheimer's disease may have specific underlying mechanisms and respond differently to treatment. If so, as with cancer, therapies based on genetic and genomic diagnostics may be most effective.

This work is also exemplary in demonstrating the extraordinary value of publicly available data resources. Published data on human gene expression, Alzheimer's disease GWAS and neuroimaging provide the pillars of Rhinn and collaborators' paper. Integrative analyses of these data by the authors, and previously by others[3,7], weaken the view that substantive biological experimentation only takes place at the wet bench, and highlight the value of innovative re-analyses of existing data[6].

References

1. Rhinn H, et al. Nature. 2013 http://dx.doi.org/10.1038/nature12415.
2. Bettens K, Sleegers K, Van Broeckhoven C. Lancet Neurol. 2013; 12:92–104. [PubMed: 23237904]
3. Zhang B, et al. Cell. 2013; 153:707–720. [PubMed: 23622250]
4. Wijsman EM, et al. PLoS Genet. 2011; 7:e1001308. [PubMed: 21379329]
5. Voineagu I, et al. Nature. 2011; 474:380–384. [PubMed: 21614001]
6. Geschwind DH, Konopka G. Nature. 2009; 461:908–915. [PubMed: 19829370]
7. Miller JA, Oldham MC, Geschwind DH. J. Neurosci. 2008; 28:1410–1420. [PubMed: 18256261]
8. Minami SS, Clifford TG, Hoe HS, Matsuoka Y, Rebeck GW. Neurobiol. Aging. 2012; 33:825.e15–825.e24. [PubMed: 21741124]
9. Ihara Y, Morishima-Kawashima M, Nixon R. Cold Spring Harb. Persp. Med. 2012; 2:a006361.
10. Small SA, Gandy S. Neuron. 2006; 52:15–31. [PubMed: 17015224]