Multi-omics and Alzheimer’s disease: a slower but surer path to an efficacious therapy?

Sanjay W. Pimplikar
Department of Pathology, Case Western Reserve University, Cleveland, Ohio

Submitted 15 May 2017; accepted in final form 15 May 2017

ALZHEIMER’S DISEASE (AD) is a slowly progressing neurodegenerative disorder of complex, and as yet uncertain, etiology. With a rapidly aging population in Western societies, AD poses a significant burden on resources. Because of the increasing threat it poses to healthcare systems, AD has been a focus of intense investigations for the past three decades. This has resulted in a fairly good understanding of the disease at the cellular, genetic, and pathological levels (1) and has yielded a number of experimental therapeutic drugs. Also, the availability of a large number of animal models has allowed for rapid testing of the potential therapeutic drugs. Unfortunately, despite spectacular success in preclinical disease models, all of the potential drugs have failed in human trials (2).

Although the exact reasons for the failure is not known, new information from genetic, cell, molecular, and neuroimaging studies has started to shed some light on why the drug trials failed in humans. Findings from multiple investigations show that AD is a complex, multifactorial disorder and the late-onset sporadic form of AD, which accounts for about 96–98% of AD cases, results from a complex interaction of genes and environment with biological aging (indeed, aging is the most significant risk factor for developing AD). It is becoming increasingly clear that the prevailing view of the pathogenic mechanism of AD is oversimplified and provides at best an incomplete picture of the disease’s pathogenic mechanisms (3). An emerging view of the disease (Fig. 1) suggests that memory impairment and dementia result not as a linear consequence of an initial pathogenic event but rather through nonlinear interactions that involve multiple brain cell populations (neurons, astrocytes, and microglia), pathogenic forms of proteins tau and amyloid-β, and altered signaling pathways as the brain ages. Healthy brain aging preserves these interactions, causing only age-associated general decline in memory and cognitive function. By contrast, unhealthy aging causes dysbalanced interactions that impair neuronal function and, thus, result in mild-cognitive impairment and eventually giving rise to AD (4).

Not only do different types of brain cells (especially the microglia) play an important role in AD pathogenesis, unhealthy aging affects each cell type at multiple levels. Thus, harmful changes at epigenomic, transcriptomic, proteomic, metabolomic, and lipidomic levels together result in neurodegeneration and give rise to AD. Therefore, a more complete understanding of the human disease can only be achieved through “big data” composed of the above-mentioned omics on blood, cerebrospinal fluid, and brain samples from autopsy materials. Luckily, development of large-scale omic platforms (6) and progress in various neuroimaging modalities (5) together with advances in bioinformatics and computational programming have already started to generate “big data” information from AD patients and age-matched healthy cohorts. The accompanying review article by H. Zetterberg (7), which is the first in a Themed set of Reviews on “Omic and Systems Biology Approaches in Neurodegenerative Diseases,” succinctly reviews the advances made in the field. The omic studies advance our knowledge of AD at multiple levels. These data help identify biomarkers that help in better disease diagnosis and help predict disease progression. More importantly, the omic data also help in understanding the potential pathogenic mechanisms and therefore yield new and efficacious therapies.

While these investigations at the systems levels utilizing human samples will certainly advance our understanding of the disease and bring us closer to an effective treatment of AD, many challenges still remain. Perhaps the most formidable challenge lies in elucidating the biological meaning of various omic data. By its very nature, the omic data tend to be heterogeneous and show wide variability. Thus, many assumptions are made by statisticians to make the underlying biological trends visible. However, such assumptions can also lead to false biological interpretation. Therefore, going forward, researchers who are comfortable with both biology and statistics will be required to identify and extract the correct biological meaning from the omic data. This will also require new statistical tools to analyze the data and identify the correct underlying biological information. However, ability to think in a nonlinear manner while analyzing the omic data for biological relevance will be important since simultaneous interactions between scores of proteins, lipids, and metabolites will rarely result in a simple deterministic outcome. Such fresh thinking will be the most crucial factor as new biological insights are applied to conceptualize AD disease mechanisms. Perhaps, lack of intellectual boldness and limited thinking may also have contributed to a string of failed clinical trials.

DISCLOSURES
No conflicts of interest, financial or otherwise, are declared by the author.

AUTHOR CONTRIBUTIONS
S.W.P. prepared figure; drafted manuscript; edited and revised manuscript; approved final version of manuscript.
Fig. 1. A schematic view of how brain aging regulates the nonlinear interactions between various brain cell populations and pathogenic forms of tau and amyloid-β proteins affecting synaptic activity and neurocognitive functions. Healthy brain aging preserves these physiological interactions and maintains normal cognition. However, these interactions become dysfunctional as a result of unhealthy brain aging, which impairs synaptic activity and neurocognitive function and ultimately leads to AD.