
JOHN HARDY

CV

PARTICIPANT AT:

BRAIN HEALTH. FROM GENES TO BEHAVIOUR, IMPROVING OUR LIVES



October, 6th-7th, 2015, Barcelona

John Hardy, Professor of Molecular Neuroscience, Reta Lilla Weston Laboratories, UCL Institute of Neurology, London, UK

Prof John Hardy is a geneticist and molecular biologist whose research interests focus on neurological disease. Dr. Hardy received his B.Sc. (Hons) degree from the University of Leeds, UK (1976) and his Ph.D. from Imperial College, London, UK where he studied dopamine and amino acid neuropharmacology. Dr. Hardy received his postdoctoral training at the MRC Neuropathogenesis Unit in Newcastle upon Tyne, UK and then further postdoctoral work at the Swedish Brain Bank in Umeå, Sweden where he started to work on Alzheimer's disease. He became Assistant Professor of Biochemistry at St. Mary's Hospital, Imperial College, London in 1985 and initiated genetic studies of Alzheimer's disease whilst there. He was appointed Associate Professor in 1989 and then took the Pfeiffer Endowed Chair of Alzheimer's Research at the University of South Florida, in Tampa in 1992. In 1996 he moved to the Mayo Clinic in Jacksonville, Florida, as Consultant and Professor of Neuroscience. He became Chair of Neuroscience in 2000 and moved to NIA as Chief of the Laboratory of Neurogenetics in 2001. He won the MetLife, the Allied Signal and the Potamkin Prize for his work in describing the first genetic mutations, in the amyloid gene in Alzheimer's disease, in 1991. He was Head of the Neurogenetics Section, National Institute of Ageing, Bethesda, USA and in 2007 took up the Chair of Molecular Biology of Neurological Disease at the UCL Institute of Neurology. With over 23,000 citations, He was elected a Fellow of the Royal Society in 2009, and a Fellow of the European Molecular Biology Organisation in 2013.

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ABSTRACT

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Genomic Analysis of Neurodegenerative Disease

Because of the advances in DNA/RNA chip and sequencing technologies it is now possible to systematically find any type of genetic risk. Mutations which cause disease can be found by positional cloning and exome or genome sequencing, high risk loci can be identified through exome sequencing and burden analysis and low risk, common variants can be found by genome wide association studies. These technological advances have resulted in the identification of a very large number of pathogenic loci for many neurological syndromes including dementias and parkinsonisms. Coupled with these genetic advances, the same technologies also allow us to assess gene expression in a genome wide and systematic way. In his lecture he will summarise the genetic advances for all the major neurodegenerative diseases and discuss how bioinformatic analysis is now allowing us to make sense of these findings and helping us to move from seeing pathogenesis one gene at a time, to seeing pathogenesis as a process involving connected networks of genes and proteins.

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