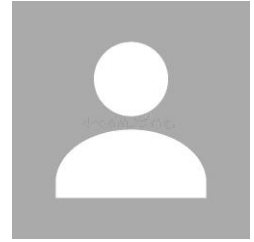


Nutritional psychiatry: Towards improving mental health by what you eat

Roger A H Adan¹, Eline M van der Beek²

¹TLI Foundation, USA

²Reina Sofia University Hospital, Spain



Abstract (600 Word Limit):

Does it matter what we eat for our mental health? Accumulating data suggests that this may indeed be the case and that diet and nutrition are not only critical for human physiology and body composition, but also have significant effects on mood and mental wellbeing. While the determining factors of mental health are complex, increasing evidence indicates a strong association between a poor diet and the exacerbation of mood disorders, including anxiety and depression, as well as other neuropsychiatric conditions. There are common beliefs about the health effects of certain foods that are not supported by solid evidence and the scientific evidence demonstrating the unequivocal link between nutrition and mental health is only beginning to emerge. Current epidemiological data on nutrition and mental health do not provide information about causality or underlying mechanisms. Future studies should focus on elucidating mechanism. Randomized controlled trials should be of high quality, adequately powered and geared towards the advancement of knowledge from population-based observations towards personalized nutrition. Here, we provide an overview of the emerging field of nutritional psychiatry, exploring the scientific evidence exemplifying the importance of a well-balanced diet for mental health. We conclude that an experimental medicine approach and a mechanistic understanding is required to provide solid evidence on which future policies on diet and nutrition for mental health can be based.

Importance of Research (200 Word Limit):

Keratins were the first group of into fills to have their X-ray diffraction pattern discovered. However, from a structural perspective, their molecular functions have been difficult to elucidate; this is in part due to the ability of keratins to form both stable heterodimers and homodynes in vitro—which led to the assumption that this can occur in the living cell (although this has been difficult to confirm)]. A phylogenetic tree of the human IntFil group reveals that all 18 IntFil genes of types III, IV, V and VI appear to be evolutionarily older than the keratin gene subsets (i.e., IntFil types I & II). It should be noted that the two synemin protein isoforms in the tree originate from one gene, and the three lamin isoforms are derived from one gene. Note that the IntFil genes of subgroups III, IV, V and VI are scattered among twelve chromosomes (Chr 1, 2, 3, 5, 8, 10, 12, 15, 17, 19, 20, 22); this is further evidence that these four IntFil subgroups are evolutionarily very ancient.

Biography (150-200 Word Limit):

Brian Thompson is a second-year doctoral student in Environmental Health Sciences at Yale University where he has gained experience from his teaching fellowship roles in both the Introductory Biostatistics and Introductory Toxicology courses. His research interests include understanding how cells of the central nervous system respond to both endogenous and exogenous stressors. His interest in climate change grew from a belief that climate change is the most consequential problem facing the world in the 21st century. Prior to his doctoral studies, Brian obtained a BS in Biochemistry from the University of Massachusetts Amherst. Ocular development is composed of a carefully orchestrated set of events that are easily perturbed, which results in a syndrome of diseases termed MAC (microphthalmia, exophthalmia and coloboma). For decades, previous research has largely been focused on elucidating the role of transcription factors in directing eye development. However, it is increasingly realized that oxidative stress also plays an important role in the eye development process. Despite these realizations, much remains to be known about the mechanisms by which oxidative stress influences eye development.

Information of Institute/ University/ Laboratory :(200 Word Limit)

Our founders worked together in public and private sector roles research, transformation and collaboration in a safe space. For more than 25 years, TLI's leadership team have developed strong working relationships with U.S. universities and aided in their varied pursuits of international, commercial and federal programs. Our strategic clinical and educational partners range from Mayo Clinic and Harvard University to top DC metro universities. TLI supports the Mayo Clinic, Johns Hopkins University, and the Uniformed Services University of the Health Sciences (USUHS), and the Bridging Advanced Developments for Exceptional Rehabilitation (BADER) Consortium which supports the University of Delaware, Harvard, and the Mayo Clinic. Other clients have included UPMC, University of Washington, Yale University, Columbia University, Duke University, Oklahoma University, University of Nebraska, Henry M. Jackson Foundation, Robert Wood Johnson Foundation, and RAND Corporation.



References (15-20):

1. Benfey PN, Ren L, Chua NH. Tissue-specific expression from CaMV 35S enhancer subdomains in early stages of plant development. The EMBO journal. 1990 Jun;9(6):1677-84.
2. Horvath AJ, Forsyth SL, Coughlin PB.

Expression patterns of murine antichymotrypsin-like genes reflect evolutionary divergence at the Serpina3 locus. Journal of molecular evolution. 2004 Oct 1;59(4):488-97.

3. Ludwig Y, Zhang Y, Hochholdinger F. The maize (*Zea mays* L.) AUXIN/INDOLE-3-ACETIC ACID gene family: phylogeny, synteny, and unique root-type and tissue-specific expression patterns during

- development PloS one. 2013 Nov 1;8(11):e78859.
4. Segerman B, Jansson S, Karlsson J. Characterization of genes with tissue-specific differential expression patterns in Populus. *Tree Genetics & Genomes*. 2007 Oct 1;3(4):351-62.
 5. Campbell PD, Marlow FL. Temporal and tissue specific gene expression patterns of the zebrafish kinesin-1 heavy chain family, kif5s, during development. *Gene expression patterns*. 2013 Oct 1;13(7):271-9.
 6. Li IM, Liu K, Neal A, Clegg PD, De Val S, Bou-Gharios G. Differential tissue specific, temporal and spatial expression patterns of the Aggrecan gene is modulated by independent enhancer elements. *Scientific reports*. 2018 Jan 17;8(1):1-2.
 7. Ong CT, Corces VG. Enhancer function: new insights into the regulation of tissue-specific gene expression. *Nature Reviews Genetics*. 2011 Apr;12(4):283-93.
 8. Reed NA, Castellini MA, Ma H, Shearer TR, Duncan MK. Protein expression patterns for ubiquitous and tissue specific calpains in the developing mouse lens. *Experimental eye research*. 2003 Apr 1;76(4):433-43.
 9. Qian J, Jiang Z, Li M, Heaphy P, Liu YH, Shackleford GM. Mouse Wnt9b transforming activity, tissue-specific expression, and evolution. *Genomics*. 2003 Jan 1;81(1):34-46.
 10. Buggs RJ, Elliott NM, Zhang L, Koh J, Viccini LF, Soltis DE, Soltis PS. Tissue-specific silencing of homoeologs in natural populations of the recent allopolyploid *Tragopogon mirus*. *New Phytologist*. 2010 Apr;186(1):175-83.
 11. [Wong QW, Li J, Ng SR, Lim SG, Yang H, Vardy LA. RPL39L is an example of a recently evolved ribosomal protein paralog that shows highly specific tissue expression patterns and is upregulated in ESCs and HCC tumors. *RNA biology*. 2014 Jan 1;11\(1\):33-41.](#)
 12. Guo Y, Liu J, Zhang J, Liu S, Du J. Selective modes determine evolutionary rates, gene compactness and expression patterns in Brassica. *The Plant Journal*. 2017 Jul;91(1):34-44.
 13. Yang R, Wang X. Organ evolution in angiosperms driven by correlated divergences of gene sequences and expression patterns. *The Plant Cell*. 2013 Jan;25(1):71-82.
 14. [Bayer E, Thomas C, Maule A. Symplastic domains in the Arabidopsis shoot apical meristem correlate with PDL1 expression patterns. *Plant signaling & behavior*.](#)

