The evolution of tissue-specific expression patterns, as well as their clinical importance

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Abstract (600 Word Limit):

Emerged to provide mechanical support for plasma membranes contacting/interacting with neighboring cells and the extracellular matrix. Keratin genes make up the majority of IntFil genes. Whereas the first keratin gene arose in a sponge and three genes in arthropods, lungfish and amphibian genomes experienced more rapid increases in keratin genes, coinciding with the land-sea animal divergence (440 to 410 million years ago). There are 18, 17, and 24 non-keratin IntFil genes in the human, mouse, and zebrafish genomes, respectively. 27 of the 28 type I "acidic" keratin genes are found on chromosome 1.2, while all 26 type II "basic" keratin genes are found on chromosome. On Chr 11 in mice, 27 of the 28 type I keratin genes are grouped, and at Chr 12q13.13, all 26 type II "basic" keratin genes clustered. On Chr 11, 27 of the 28 type I keratin genes are grouped, whereas all 26 type II keratin genes are concentrated on Chr 15. There are 18 type I keratin genes on five chromosomes and three type II keratin genes on two chromosomes in zebrafish. Types I and II keratin clusters, which reflect evolutionary blooms of keratin genes along a single chromosomal segment, are found in all land animal genomes examined, but not in fish genomes; such rapid gene expansions are likely due to sudden requirements for many novel paralogous proteins with divergent functions to enhance species survival following the sea-to-land transition. Tissue-specific keratin expression across the human body was recreated using data from the Genotype-Tissue Expression (GTEx) project. Similarities in gene expression patterns were discovered using clustering. By end of the Cambrian explosion (~ 500 million years ago), intermediate filament (IntFil) genes had become well established in the Animalia Kingdom and began expanding rapidly, encoding novel proteins that were necessary for species survival among metazoans. These IntFil genes played dynamic roles in cell integrity and structural scaffolding—more specifically, to provide mechanical support for plasma membranes where they come into contact with other cells and with the extracellular matrix. The development of high-throughput genomic-sequencing technology has substantially aided the discovery of new members of the IntFil group. Unfortunately, the identification of these novel IntFil group members, particularly the keratin genes, has severely confounded and muddled the nomenclature of these genes.

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.

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