Bioinformatics Studies of Genes that Cause Lysosomal Storage Diseases. A Comparison of GLA, GBA and NPC1

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Lysosomal storage diseases fall under the umbrella of Inborn Errors of Metabolism, comprised of some 750 metabolic disorders and result from irregularities in metabolic pathways. Examples of lysosomal storage disease include Niemann-Pick (NP) types A, B, and C1/2, as well as Fabry and Gaucher disease. While the diseases are caused by a mutation in a single gene, typically multiple mutations are mapped to the same gene locus. For example, for Niemann-Pick Type C1 disease, more than 180 mutations have been mapped to the *NPC1* gene locus.

Niemann-pick type C1 and C2 result from mutations in the *sphingomyelin phosphodiesterase* 1 (SMPD1) gene, while mutations for Fabry and Gaucher disease affect the *galactosidase alpha* (GLA), and *glucosylceramidase beta* 1 (GBA1), respectively. As all three diseases fall under the category of Lysosomal Storage Diseases, it is plausible, and we hypothesize that the genes share some DNA identity. To compare the DNA sequence for potential similarities, the DNA sequences for the three genes were obtained from NCBI. We used the bioinformatics software Jalview for the comparisons. A sequence comparison among the three genes indicated sequence similarity between GBA and GLA at 61 %, GBA and NPC1 at 22% and GLA and NPC1 at 11%. Additionally, the % nucleotide content comparison of the three genes indicated that the % composition of each nucleotide was within a relatively narrow range. Given that the three genes code for three proteins that have different functional properties, the finding that there is low DNA similarity is not surprisingly, particularly in light of the fact that GBA and GLA which share the most functional similarities also exhibit the most DNA sequence similarity. By extension, GBA and GLA show the most dissimilarity to NPC1 and this coincides with functional differences as well. Future directions are discussed.