

Genotype phenotype relationship in Gaucher's disease in Egypt

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Background: Gaucher's disease is the most prevalent of the genetic lysosomal storage disorders. It is an autosomal recessive disease which was described by French physician Philippe Gaucher in 1858. It is caused by severe deficiency of glucocerebrosidase enzymatic activity with resultant accumulation of large quantities of glycolipid, glucocerebrosidase within the lysosomes of the phagocytic cells of the monocytes-macrophage system. Gaucher's disease is classified into three conventional types; type I: Chronic non-neuropathic form which usually found in adult especially in Jewish population, type II: infantile neuropathic form which always appears by 1 month of age as a rapidly progressive neurological affection, and type III: Juvenile sub-acute neuropathic with slowly progressive neurological disease that begins during childhood or adolescence. The aim of this study is to investigate the genotypes of Gaucher's disease, the most prevalent mutation in Egypt and to assess if a genotype-phenotype relationship could be elicited.

Patients and Methods: The present study included 20 Gaucher's disease documented patients; they were 10 males and 10 females. Their ages ranged from 3 to 23 years with of a mean of 10.10 and median of 6 years. All patients were subjected to clinical evaluation, revision of their filed clinical progress, radiological and laboratory data including full blood count, b-Glucocerebrosidase enzyme assay, liver enzymes, bone marrow and splenic aspirate. In addition, we studied the most common GBA mutations using strip assay which based on the reversed-hybridization principle. The assay covered 8 of the most frequent GBA mutations: 45GG (G>A), IVS11 (G>A), N370S (A>G), V394L (G>T), L444P (T>C), R463G (G>A) and 2 recombinant alleles (RecNcil, Rec TL).

Results: Neither the age of patients, age of onset of the disease nor the sex showed significant relation with homozygosity Vs double heterozygosity or the different genotype groups. The most common mutations found in this study were L444p/ L444p (homozygous) and L444p/IVS11 (double heterozygous); 8 patients each (40%) followed by L444p/D409H (double heterozygous) in 3 patients (15%) whereas N370S/N370S (homozygous) was the least common mutation found in only 1 patient (5%). Allele frequency showed that L444p was found in 75.0% of studied chromosomes, IVS11 in 20%, D409H in 5%, whereas N370s was in only 5%. As for family history, 40% of cases had positive consanguinity; with 20% of patient parents being first cousins. All homozygous cases showed positive consanguinity (4 cases), where as only 5 cases of 11 of the double heterozygosity showed positive consanguinity. Also all patients with the genotypes L444p/ L444p and N370S/N370S were from consanguineous parents; 8 of 8 and 1 of 1 respectively. On the other hand, the 3 patients with genotype L444p/D409H had negative consanguinity, while the genotype L444p/IVS11 showed 5 of 8 cases with positive consanguinity and only 1 case with negative consanguinity.

Conclusion: The most common mutations found in our study were L444p/ L444p homozygous and L444p/IVS11 double heterozygous. L444p was the most common allele. Analysis for the most common mutation was the method of choice for identification of Gaucher's disease carriers. Both age of the patients and onset of the disease had no significant relation with either homozygosity Vs. double heterozygosity or the different genotype groups. Gaucher's disease occurred with equal frequency in males and females. Patients with homozygous gene mutations tend to have consanguineous parents. Neurological manifestations, growth retardation and chest symptoms were the most common clinical conditions reported in studied cases. None of the previous conditions were significantly associated with certain genotype. No correlation was detected between genotype or homozygosity Vs heterozygosity on one side and either age of patients, age of onset or clinical manifestations on other side.

Keyword: GD (Gaucher's disease) – GBA mutations – Reversed hybridization – Homozygous – Double heterozygous.