15ª Reunião Anual da SPGH

QUinta-feira, 10 de Novembro

14:00 Sessão de Abertura
  Conferência de Abertura: Genética e Saúde Pública
15:00 Genética e Cancro
17:00 Coffee Break/Sessão de Posters
17:30 Comunicações Orais I
19:15 Assembleia Geral da SPGH

Sexta-feira, 11 de Novembro

9:00 Doenças Raras
10:00 Coffee Break/Sessão de Posters
11:30 Comunicações Orais II
13:00 Almoço
14:00 Genética Forense
14:45 Genética das Doenças Neurológicas e Neuropsiquiátricas
16:15 Coffee Break/Sessão de Posters
16:45 Comunicações Orais III
17:45 Raras Práticas em Genética Humana
19:00 Jantar do Congresso

Sábado, 12 de Novembro

9:00 Genética das Doenças Cardiovasculares
11:00 Coffee Break/Sessão de Posters
11:30 Comunicações Orais IV
12:15 Mesa Redonda de Teoria
12:45 Conferência Prêmio SPGH
13:45 Entrega dos Prêmios de Investigação Clínica e Básica
Encerramento
EVALUATING THE INFLUENCE OF FOUR VARIANTS DETECTED IN THE FRAXA AND FRAXE LOCI

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Of the seven folate-sensitive fragile sites cloned in the human genome, only two have a proven clinical expression, FRAXA and FRAXE, the former with a well-documented clinical impact. The expansion of over 200 [CGG] triplets in the Fragile Mental Retardation 1 gene (FMR1), FRAXA locus, is associated with the Fragile X Syndrome (FXS), the most common form of familial severe mental retardation/intellectual disability. The prevalence of FRAXE full mutations is much lower, and is frequently associated with non-syndromic X-linked mental retardation (FRAXE-MR). This phenotype is due to the silencing of the Fragile Mental Retardation 2 gene (AFF2), as a consequence of a [CCG] expansion to more than 200 hyper-methylated triplets located upstream of the gene. Molecular diagnosis of FXS and FRAXE-MR typically rely on techniques such as PCR (for pre-screening), Southern blotting and linkage analysis based on microsatellite markers. The latter is of particular interest in atypical or complex cases. Additional molecular tools are also currently available such as fluorescent methylation-specific PCR, Multiplex Methylation-Specific Real-Time PCR and Methylation-specific MLPA (Multiplex Ligation-dependent Probe Amplification). In the course of FXS and FRAXE-MR molecular diagnosis using standard molecular methodologies, four variants were identified. Three of them are in the FRAXA locus, two in the 5'UTR region of the FMR1 gene, NM_002024.5: c.-412G>C and NM_002024.5:c.-68T>G; and one is in the amplified fragment of the polymorphic marker FRAXAC1, located ~7kb upstream the [CGG] region, g.146986184_146986185insAAGCAGA. The remainder is in the FRAXE locus, positioned in the promoter region of AFF2 gene, NT_011681.16: c.-3101G>A. Herein, we describe the characterization of these four variants and illustrate how, besides increasing genetic diversity, they in fact influence the interpretation of results in the context of FXS or FRAXE-MR diagnosis.