

15ª Reunião Anual da SPGH

QUINTA-FEIRA, 10 DE NOVEMBRO

- 14:00 Sessão de Abertura
Conferência de Abertura: Genómica 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
- 11:00 *Coffee Break*/Sessão de Posters
- 11:30 Comunicações Orais II
- 13:00 Almoço
- 14:00 Genética Forense
- 14:45 Genómica das Doenças Neurológicas e Neuropsiquiátricas
- 16:15 *Coffee Break*/Sessão de Posters
- 16:45 Comunicações Orais III
- 17:45 Boas Práticas em Genética Humana
- 20:00 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 Bioética
- 12:45 Conferência Prémio SPGH
- 13:15 Entrega dos Prémios de Investigação Clínica e Básica
Encerramento

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Novembro de 2011 > Lisboa, Portugal

15ª Reunião Anual da SPGH > Livro de Resumos



Sociedade Portuguesa de Genética Humana

15ª Reunião Anual
Livro de Resumos

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10 a 12 de Novembro de 2011 Lisboa, Portugal

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.