Mutational spectrum of APC and genotype-phenotype correlations in Greek FAP patients.

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Source

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Abstract

BACKGROUND:

Familial adenomatous polyposis, an autosomal dominant inherited disease caused by germline mutations within the APC gene, is characterized by early onset colorectal cancer as a consequence of the intrinsic phenotypic feature of multiple colorectal adenomatic polyps. The genetic investigation of Greek adenomatous polyposis families was performed in respects to APC and MUTYH germline mutations. Additionally, all available published mutations were considered in order to define the APC mutation spectrum in Greece.

METHODS:

A cohort of 25 unrelated adenomatous polyposis families of Greek origin has been selected. Genetic testing included direct sequencing of APC and MUTYH genes. APC gene was also checked for large genomic rearrangements by MLPA.

RESULTS:

Analysis of the APC gene performed in a Greek cohort of twenty five FAP families revealed eighteen different germline mutations in twenty families (80%), four of which novel. Mutations were scattered between exon 3 and codon 1503 of exon 15, while no large genomic rearrangements were identified.

CONCLUSION:

This concise report describes the spectrum of all APC mutations identified in Greek FAP families, including four novel mutations. It is concluded that the Greek population is characterized by genetic heterogeneity, low incidence of genomic rearrangements in APC gene and lack of founder mutation in FAP syndrome.