APPLICATION OF GENOMIC TOOLS IN CANCER RESEARCH

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Carcinogenesis is a multi-step process, which is the outcome of the accumulation of genetic and epigenetic events. The orders in which these molecular events occur form the genetic pathways. The precise pattern of genetic altérations differs between cancers of different types, and of the same type, but is not random. Complete description of these genetic pathways will be achieved by high-throughput analysis of both inherited and somatic genetic alterations in hundreds of tumours from familial and sporadic origin. The role of common genetic variation in determining the range of individual susceptibility within the population is increasingly recognized, and will be addressed using information from the Human Genome Project. DNA microarray and SNP have become the most widely used functional genomic tools. Microarray technology has provided the ability to analyse the expression profiles for thousands of genes, and a wealth of new information that should aid in cancer diagnosis and ultimately in therapy. The SNP project has generated important resources for the assessment of common genetic variants in cancer predisposition. The medicine in the 21st century will be so called 'personalized medicine' based on the new information of patients and diseases.