

Genetic Scanning for Nasopharyngeal Carcinoma

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PERSPECTIVE

What is Nasopharyngeal Carcinoma (NPC)?

NPC can be described as the development of cancer in the area of the head and neck which arises from epithelial cells and further covers the surface of the nasopharynx. This disease was firstly reported in the year 1901 and further, it was clinically characterized in the year 1922. It is an uncommon malignancy in the United States with an incidence of 0.5 to 2 in each of 1,00,000 squamous cell carcinomas in the head and neck. In many locations, however, including Southern China and Southeastern Asia, the incidence rates were found to vary between 15 and 50 per 1,00,000 people. In Alaska Eskimos and the Mediterranean Basin (North Africa, Southern Italy, Greece, and Turkey), there have been reports of intermediate incidence between 15 and 20 cases per 1,00,000 individuals. There is a male preponderance; with a ratio of roughly 2:1 between men and women. In general, NPC may occur in all ages but is distributed in a bimodal manner. The incidence peaks around 50-60 years, and in late childhood, a minor rise can be seen.

Genetic scanning of NPC

Nasopharyngeal carcinoma is one of the most frequent malignancies in South-East Asia, including Southern China, Hong Kong, Singapore, Malaysia, Taiwan, while it is rare in most regions of the globe for malignancy. In these nations, the incidence recorded is between 10 and 53 cases per 1,00,000 people. The incidence of Eskimos also ranges between 15 and 20 cases per 1,00,000 people, in Alaska, Greenland, and Tunisia. There is currently a lack of a clear and particular etiology for NPC. Generally speaking, both genetic and environmental factors are considered to result in NPC, including intake of certain salty foodstuffs and EBV infection. In both the Chinese and non-China patient cohorts, family clustered NPC was widespread.

Advancement in NPC genetic susceptibility searching

Additional evidence has emerged from a recent complicated segregation study of a China cohort to support a multifactorial NPC heritage mode. However, it remains uncertain about NPC's molecular genetic foundation. The majority of research that

investigates NPC sensitivity genes may be divided roughly into 2 methods and techniques: a directional replication approach and a functionality cloning. The primary objective of a positional cloning method is the genomic site (or locus) associated with the illness. The illness gene (or susceptibility genes) is then identified at this specific chromosomal region. Functional cloning, also known as the candidate gene-based method, calls for a sufficient previous understanding of the illness and the accompanying functional defects. Genes of candidates are identified based on this type of knowledge and then mutations are further identified and investigated in the genes of the candidate. These techniques are mutually complementary. The discovery of a candidate gene for functional cloning research can result from positional cloning techniques. On the other hand, the genomic locations of the susceptibility locus discovered by positions of clones are frequently confirmed using the functional cloning technique. Different types tell about the process for advancement of the NPC susceptibility genes identification based on these techniques.

- Search for genes with NPC sensitivity in positional cloning
- Functional cloning method for the discovery of NPC genes
- Progress to characterize somatic NPC genome anomalies
- Advancement on NPC genomic profiling and NPC copy number analysis
- NPC analysis of Loss of Heterozygosity (LOH)
- Cytogenetic analysis of NPC
- Expressional NPC genome-wide NPC analysis

Future perspectives

Southern Asian people are still puzzled by the great vulnerability to NPC. In recent developments in single nucleotide polymorphism and haplotype analysis, general genome screening and association studies, the genetic components underlying this mysterious malignancy can be deciphered. It is necessary to focus and further study the mobile genes involved in DNA damage and its relationship with Epstein-Barr Virus (EBV) entrance or latency. In the search for such susceptibility genes, newly deployed technologies like the high-density SNP array play a vital role. This same technology

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has also effectively been modified for the profiling of the LOH and Comparative Genomic Hybridization (CGH) in the cancer genome, placing it in a unique position in NPC research. Prior molecular research in NPC concentrated on the levels of DNA and chromosomes, but few focused on transcriptional and proteomic profiles. The transcriptome and proteomic investigations offer great problems with small biopsy materials and a high level of infiltration of non-malignant cells. Comprehensive expression profiling of NPC is now beginning to take center stage with signs of progress in micro-dissection and pre-amplification technology. This should

lead to significant translation results that promote the management of this condition. While considerably more information has been collected on genetic alterations to NPC, new developments in genomic technology (e.g., high-density SNP array) and the huge resources generated by the Human Genome Project will produce more discoveries. Strategic integration with several experimental applications (e.g. CGH, LOH, and micro-array expression) of data streams at diverse levels of biology (e.g. DNA, RNA, and protein levels). This would substantially strengthen our capacity to capture the NPC's accurate image.