Ontologies Classes Object Properties Data Properties Annotation Properties Individuals Datatypes Clouds

Class: Family_History_LC

Annotations (4)

- rdfs:comment "Environmental factors and somatic events are the major factors contributing to the development of sporadic lung cancer. Genetic factors are also a significant contributor, but only a few specific genes and other genetic factors affecting lung cancer have been identified to date (6,18). Twin studies are a valuable source of information to unravel the epidemiology of cancer. Comparison of the concordance of cancer between monozygotic (genetically identical) and dizygotic (sharing half of the segregating genes) twins may reveal the influence of hereditary or environmental factors on the familial pattern of cancer (19). A twin study revealed that shared environments and lifestyles, but not genetic factors, affect the onset of lung cancer, and that smoking habits are likely the reason for the familial pattern of lung cancer in twins (20). Another study suggested that genetic factors do not exhibit strong prognostic value for lung cancer risk in twins (18). In addition, a low probability of lung cancer development was observed in a person whose identical twin was suffering from lung cancer (21). Conversely, a previous study (6) assessed the risk of lung cancer in 45,000 twins (monozygotic and dizygotic) and demonstrated that monozygotic and dizygotic twins had a 7.7- and 6.7-fold increased risk, respectively (6). These results reflected the combined effect of genetic and environmental factors. Previous studies have demonstrated that factors such as having an affected first-degree relative, early-onset lung cancer and multiple affected family members significantly increase the risk of lung cancer (22,23). The relatively strong influence of genetic factors among first-degree relatives suggests that major gaps exist in our knowledge of the genetics of lung cancer."(xsd:string)
- rdfs:comment "Familial cancer is characterised by gene mutations in two or more first-degree relatives diagnosed with the same type of cancer; this condition is influenced by a hereditary predisposition, variable gene penetrance and environmental factors (1). Familial cancer is attributable to shared genetic and environmental factors. Hereditary predisposition, which is passed through successive generations of a family, has been implicated in 10–15% of cancer cases. Breast, colon, bladder and ovarian cancers are commonly associated with an hereditary predisposition (69,70). The majority of patients with cancer have no family history of cancer, and genetic alterations are somatic (only in the cancer cells) rather than germline (heritable variation in the lineage of germ cells). Approximately 1–5% of human cancers develop because of known germline defects (69,71). In general, all major hereditary cancer types differ from their sporadic counterparts with respect to the underlying physiological and pathological mechanisms (1,71). Genome-wide association and susceptibility studies are useful for the evaluation of inherited genetic risks in populations with unique characteristics or environmental exposure. Currently, research on hereditary cancer is regarded as being of primary importance with an immediate health impact. The discovery of tumour-predisposing mutations and the development of appropriate genetic tests are crucial for the identification of healthy individuals who are at risk of certain cancer types, and thus may benefit from timely medical intervention (71). Identifying driver mutations and screening high-risk populations for germline mutations can reduce the mortality rate among cancer patients. For example, intensive surveillance programmes ensure an early diagnosis, and preventive surgery may reduce cancer-associated mortality (1,72). A comprehensive review identified 54 hereditary cancer syndromes. The majority of these cancer-susceptibility syndromes are autosomal dominant, including retinoblastoma (Rb), Li-Fraumeni syndrome, neurofibromatosis, von Hippel-Lindau (VHL) disease, familial adenomatous polyposis and hereditary breast and ovarian cancer (73). Certain genetic mutations have been associated with specific types of hereditary cancer; associations have been reported for Rb and the Rb tumour suppressor gene, Li-Fraumeni syndrome and the P53 tumour suppressor gene, VHL disease and the VHL tumour suppressor gene, and familial adenomatous polyposis and the adenomatous polyposis coli tumour suppressor gene. Hereditary cancer syndromes have also been associated with oncogenic mutations. Hereditary forms of medullary thyroid cancer develop because of inherited mutations in the RET oncogene; thus, these forms of cancer are sensitive to the RET tyrosine kinase inhibitor Vandetanib (74). Some hereditary cancers have been associated with mutations in multiple genes. A list of genes causing hereditary breast cancer is rapidly expanding, of which breast cancer 1 (BRCA1) and BRCA2 are the most studied. BRCA1 and 2 genes have a central role in the DNA repair system via homologous recombination, and their absence increases cell sensitivity to particular DNA damaging agents (75,76). Approximately 15% of ovarian cancers are also caused by the inherited BRCA1 and BRCA2 mutations. BRCA1- and BRCA2-related cancers show various genetic abnormalities, although both exhibit increased numbers of gross chromosomal aberrations and a high tumour grade (77). Familial colorectal cancer (CRC) usually develops early, and almost all tumours result from hereditary non-polyposis CRC (78). CRC is triggered by defects in the DNA repair system, usually germline mutations in the Mut L homolog 1, Mut S homolog 2, postmeiotic segregation increased 2 and Mut S homolog 6 genes (78,79). In addition, high-level microsatellite instability has been observed in CRC patients (80). Hereditary tumours are increasingly recognised as exhibiting distinct bio-clinical characteristics, and thus require tailored treatment strategies. With the increasing risk of familial cancers, identification of culprit genes in families is imperative. Such investigations will permit the identification of individuals and families who are at a high risk of a

particular cancer, as well as the active implementation of preventive measures. Researchers are interested in using familial cancer models to identify individual and groups of genes responsible for cancer development, to identify novel cancer-associated genes and biomarkers, and to estimate the risk of cancer in members of the general population. Studies on familial cancers have revealed various important oncogenes and tumour suppressor genes, including BRCA1, BRCA2, Rb and VHL (77,78). These findings provide opportunities for the prevention of cancer and the early detection of cancer through evidence-based screening. Familial risk of lung cancer Lung cancer is predominantly associated with environmental factors, including smoking and air pollution; however, familial causes of lung cancer cannot be ignored. Familial aggregation of lung cancer is frequently observed in clinical studies (81–84). Familial lung cancer is more complex than other familial cancers, and can be caused by shared environmental factors or shared genetic factors among family members (85). The role of genetic factors in tumour development in lung cancer is poorly understood, as genetic factors are masked by the influence of environmental factors, including smoking, air pollution and coal burning (86). The development of lung cancer in never-smokers is a complex clinical problem, and a large number of studies have indicated that individuals with a family history of lung cancer are two- to three-fold more susceptible to lung cancer development than those without such a history; this association is strongest for those whose siblings have been affected by lung cancer (22). The risk of lung cancer in individuals with a family history of cancer among first-degree relatives is increased by ~50% compared with those without a family history, and this association is not affected by gender, ethnicity, histological types and other known lung cancer risk factors (23). Studies on familial cases of lung cancer have provided evidence for hereditary transmission of lung cancer from one generation to the next generation. Approximately 8% of lung cancers are inherited or occur as a result of a genetic predisposition (82,87). In a previous study, first-degree relatives of a lung cancer proband had a greater than normal likelihood of developing cancer compared with other non-smokers because of genetic recombination (83). Lung cancer rates in Xuanwei (Yunnan, China) are 4–5 times higher than the average in China, and air pollution is the main reason for lung cancer in Xuanwei. Often, multiple members of families in this region are diagnosed with lung cancer (4). Aside from the environmental factors, genetic factors have also been associated with the risk of lung cancer, particularly among women in Xuanwei (88). A study in China determined the risk of lung cancer among the relatives of a patient with lung cancer and found that female relatives, particularly the mothers, had a higher risk of developing lung cancer than male relatives. However, the exact genetic mechanisms influencing lung cancer susceptibility in female relatives in China are unknown (89). Indoor cooking is still practiced in some rural areas of China and in numerous other countries; this practice can be considered an important risk factor for lung cancer among women (11). The abovementioned studies suggest that lung cancer is likely to develop in genetically predisposed individuals."(xsd:string)

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parental probands is authentic, whereas risk analysis between siblings without affected parents provides clues about possible recessive effects (90). The database is used to search for evidence of a genetic predisposition to lung cancer; several studies found that a familial risk for lung cancer among offspring was increased to 1.77% when the parents were affected, and that the risk was higher among siblings (2.15%) than between offspring and parents (72). An Icelandic population was investigated to assess the contribution of genetic factors to the risk of lung cancer development; the investigation involved 2,756 patients and revealed the importance of genetic susceptibility in the progression of lung cancer (87). Notably, their results demonstrated that a familial predisposition positively influenced lung cancer development due to the significantly increased risk ratio (RR) for the first-, second- and third-degree relatives of lung cancer patients (87). However, shared environmental factors could not be ignored, as a considerably increased RR was also observed in the spouses of lung cancer patients (87). Another study investigated the association between lung cancer and genetic factors in 102,255 patients; it was demonstrated that the risk of lung cancer development was significantly elevated among the first-degree relatives of a lung cancer patient (91). When a family history of tobacco exposure was accounted for, the results suggested that females were more likely to develop lung cancer than males (91). A previous study estimated the risk of lung cancer among the white and black relatives of a proband, and demonstrated that the first-degree relatives of a black individual with early-onset lung cancer had a greater risk for lung cancer than their white relatives, and the risk was significantly increased by a history of tobacco smoking (92). In addition, an elevated risk was observed among individuals whose father or siblings were affected by lung cancer; both males and females were similarly affected. These findings support the aggregation of lung cancer in families (84). A previous study investigated the importance of smoking and a family history of various respiratory diseases in women with lung cancer; there was a significant association between lung cancer and both smoking and a family history of respiratory disease (93). In addition, women with a history of bronchitis, pneumonia and emphysema were shown to have a higher risk of developing lung cancer than those with a family history of asthma or hay fever (93). Population-based studies on familial lung cancer have indicated that genetic factors increase the risk for lung cancer, although environmental factors remain the most important causes. Furthermore, the genetic susceptibility for lung cancer is higher in females than in males."(xsd:string)

- rdfs:comment "Lung cancer, which has a low survival rate, is a leading cause of cancer-associated mortality worldwide. Smoking and air pollution are the major causes of lung cancer; however, numerous studies have demonstrated that genetic factors also contribute to the development of lung cancer. A family history of lung cancer increases the risk for the disease in both smokers and never-smokers. This review focuses on familial lung cancer, in particular on the familial aggregation of lung cancer. The development of familial lung cancer involves shared environmental and genetic factors among family members. Familial lung cancer represents a good model for investigating the association between environmental and genetic factors, as well as for identifying susceptibility genes for lung cancer. In addition, studies on familial lung cancer may help to elucidate the etiology and mechanism of lung cancer, and may identify novel biomarkers for early detection and diagnosis, targeted therapy and improved prevention strategies. This review presents the aetiology and molecular biology of lung cancer and then systematically introduces and discusses several aspects of familial lung cancer, including the characteristics of familial lung cancer, population-based studies on familial lung cancer and the genetics of familial lung cancer."(xsd:string)

Superclasses (1)

- Causes_and_Risks_LC

OWL HTML inside