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Pancreatic Cancer Genetics

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Abstarc :

Although relatively rare, pancreatic tumors are highly lethal [1]. In the United States, an estimated 48,960 individuals will be diagnosed with pancreatic cancer and 40,560 will die from this disease in 2015 [1]. Globally, 337,872 new pancreatic cancer cases and 330,391 deaths were estimated in 2012 [2]. In contrast to most other cancers, mortality rates for pancreatic cancer are not improving; in the US, it is predicted to become the second leading cause of cancer related deaths by 2030 [3, 4]. The vast majority of tumors arise in the exocrine pancreas, with pancreatic ductal adenocarcinoma (PDAC) accounting for approximately 95% of tumors. Tumors arising in the endocrine pancreas (pancreatic neuroendocrine tumors) represent less than 5% of all pancreatic tumors [5]. Smoking, type 2 diabetes mellitus (T2D), obesity and pancreatitis are the most consistent epidemiological risk factors for pancreatic cancer [5]. Family history is also a risk factor for developing pancreatic cancer with odds ratios (OR) ranging from 1.7-2.3 for first-degree relatives in most studies, indicating that shared genetic factors may play a role in the etiology of this disease [6-9]. This review summarizes the current knowledge of germline pancreatic cancer risk variants with a special emphasis on common susceptibility alleles identified through Genome Wide Association Studies (GWAS)

Key Word :
pancreatic tumors

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