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## **Genetics of Chronic Pancreatitis**

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Chronic pancreatitis (CP) is characterized by irreversible morphological and functional alterations of the pancreas, clinically presenting with upper abdominal pain as well as exocrine and endocrine insufficiencies. CP morphologically characterized is bv pancreatic head enlargement, calcifications of the parenchyma, cystis and pancreatic stones. Unlike hereditary pancreatitis which is an autosomal dominant disease with 80% penetrance and variable expression, several etiologic risk factors and mechanisms underlying chronic pancreatitis have been proposed: calcification and obstruction within pancreatic ductules due to protein plugs, alcohol consumption which induces an intrapancreatic lipid deposition in the cytoplasm of acinar cells and generation of free radicals by oxidative stress, tobacco smoking through inhibition of pancreatic bicarbonate secretion, hypercalcemia through trypsinogen activation and trypsin stabilization, and hyperlipidemia [1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11].

In approximately one-third of chronic pancreatitis patients, no etiologic factor can be found and these patients are classified as having idiopathic disease; there are several reasons why it is believed that molecular and genetic factors are important in the predisposition to chronic pancreatitis [12, 13, 14, 15].

Since 1952, numerous studies have described cases of familial chronic pancreatitis. The attacks were characterized bv severe abdominal pain, fever, and marked elevation of serum amylase. Except for the last symptom. differentiation from familial Mediterranean fever, also called "familial paroxysmal peritonitis", might be difficult. The aminoaciduria was almost certainly an incidental finding since family members without pancreatitis showed it and also because other families with pancreatitis have not had this feature [16]. In 1967, Robechek described a family with five affected people [17]. He suggested that hypertrophy of the sphincter of Oddi together with a common ampulla of the biliary and pancreatic ducts may be the inherited factor. A number of important manuscripts pointed out the different features of the familial form of chronic pancreatitis; Mann and Rubin [18] described the occurrence of hyperparathyroidism in the multiple endocrine adenomatosis syndrome; McElroy and Christiansen [19] pointed out that thrombosis in the portal or splenic vein occurs with significant frequency, and Sibert [20] identified penetrance of the disease at about 80%; the mean age of onset was 13.6 years with two peaks, one at five years and one at 17 years. In 1982, Sarles et al. showed that "stone protein" could inhibit in vitro calcium carbonate nucleation and decrease the rate of crystal growth acting as a physiologic inhibitor of spontaneous calcium carbonate formation in supersaturated pancreatic juice [21].

In 1996, Le Bodiac [22] analyzed the genomic segregation of highly informative microsatellite markers in a French family of 147 individuals, 47 of whom had hereditary pancreatitis. Linkage was found between the disease and 6 chromosome 7q markers. That locus was found to encode carboxypeptidase A1 which is a pancreatic exopeptidase. In 1996 Whitcomb et al. carried out a genome wide linkage analysis on a family extensively affected by hereditary pancreatitis. Using genetic linkage studies, the hereditary pancreatitis locus was narrowed to the long arm of chromosome 7 [22, 23, 24]. Two main mutations in the cationic trypsinogen gene (PRSS1) have been identified in patients with hereditary pancreatitis: Arg->117His (R122H, originally called R117H) and Asn->21Ile (N29I, originally called N21I).

Trypsinogen is an inactive proenzyme for trypsin, which becomes active when an 8amino acid N-terminal peptide is removed.

It has been proposed that the Arg->117His mutation eliminates а trypsin-sensitive cleavage site on trypsin and leads to pancreatitis by rendering prematurely activated trypsin resistant to inactivation through autolysis or proteolysis by trypsinlike enzymes [25, 26, 27, 28, 29, 30, 31, 32]. The Asn->21Ile mutation, instead, could decrease autoactivation and autocatalytic zvmogen degradation without affecting trypsin stability or activity [33]. Other less common mutations of the same gene were observed: K23R, -28delTCC in the promotor region of the try4 gene, A16V and D22G. The effect of K23R could be to cause an alteration of the tertiary structure of the protein and of the trypsin inhibitor binding site while the effect of -28delTCC is only speculative at present; moreover, they do not result in the high-penetrance, autosomal dominant pancreatitis as seen with codon 29 and 122 mutations [34]. These findings suggest that prematurely activated trypsinogen is a critical

molecular step in the initiation of acute pancreatitis and links multiple episodes of acute pancreatitis developing into chronic pancreatitis. However, PRSS1 mutations cannot account for all mutations causing idiopathic hereditary pancreatitis or pancreatitis (60% of hereditary and less than 20% of idiopathic pancreatitis); mutations in cystic fibrosis transmembrane the conductance regulator (CFTR) were also found to be associated with chronic pancreatitis [35, 36, 37, 38, 39, 40].

CFTR functions as a chloride channel. CFTR, expressed in pancreatic tissue and mutations or particular polymorphisms of this gene, together with other genetic and environmental factors, could be risk factors for chronic pancreatitis, by altering the pancreatic flow and composition. In 1998, Sharer studied 134 consecutive patients with chronic pancreatitis [35]. DNA was examined for 22 mutations and the noncoding sequence of thymidines in intron 8 of the CFTR gene. None of the patients had a mutation on both copies of the CFTR gene. Thirteen percent had a CFTR mutation on 1 chromosome, as compared with a frequency of 5.3% among 600 local unrelated partners of people with a family history of cystic fibrosis (P<0.001). A total of 10.4% of the patients had the 5T allele in intron 8, which is twice the expected frequency (P=0.008). Patients with a CFTR mutation were younger than those with no (P=0.03). mutations None had the combination of sinopulmonary disease, high sweat electrolyte concentrations, and low nasal potential-difference values which is diagnostic of cystic fibrosis.

Similarly, Cohn *et al.* studied 27 patients (mean age at diagnosis, 36 years), who had been referred for an evaluation of idiopathic pancreatitis [36]. Their DNA was tested for 17 CFTR mutations and for the 5T allele in intron 8. They found that 10 patients with idiopathic chronic pancreatitis (37%) had at least one abnormal CFTR allele. In 3 patients both alleles were affected.

The cystic fibrosis gene can cause idiopathic pancreatitis when present in the heterozygous state in association with the variable number of thymidines in intron 8 of the CFTR gene, specifically the 5T allele.

In 2000, a correlation between serine protease inhibitor (SPINK1) mutations and the disease was found [39, 40, 41, 42]. SPINK1 is a peptide which specifically inhibits trypsin (about 20% of potential trypsin) by physically blocking the active site. Because gain of function trypsin mutations cause acute and chronic pancreatitis, it was hypothesized that loss of the trypsin inhibitor function would have similar effects and indeed, the role of SPINK1 N34S and P55S mutations in chronic pancreatitis emerged. Witt et al. [39] studied 96 children and adolescents with chronic pancreatitis and found a nonsense mutation in the SPINK1 gene in 18; in 6 of these patients, the mutation was homozygous. Only 1 out of 279 healthy controls was heterozygous and no homozygous individuals were found. The same group found a heterozygous mutation destroying the translation initiation codon of SPINK1 in a patient with hereditary pancreatitis; the mutation was also found in the affected grandfather and in the unaffected father. However, because N34S and P55S mutations are common in the general population (2%) while idiopathic chronic pancreatitis is rare, SPINK1 mutations appear to act as disease modifiers and the disease mechanism is more complex than an autosomal recessive one. However, mutations in SPINK1 or in PRSS1 could lead to an imbalance of proteases and their inhibitors within the pancreatic parenchyma, resulting in an inappropriate conversion of pancreatic zvmogens to active enzymes with autodigestion and inflammation [41, 42].

A growing body of data supported the association of SPINK1 and CFTR mutations with chronic pancreatitis and in 2002, Audrezet *et al.* systematically analyzed the entire coding sequence and exon/intron junctions of the PRSS1, SPINK1, and CFTR genes in 39 white French patients with idiopathic chronic pancreatitis [40]. One patient had a nonsense mutation (R122H) in the PRSS1 gene; four patients had the same nonsense mutation in the SPINK1 gene, three in heterozygosity and one in homozygosity

(N34S) and eight patients carried one of the most common mutations of the CFTR gene. A trans-heterozygous with state sequence variations in the SPINK1/CFTR genes was found in three patients. The results demonstrated that about one-third of the patients labeled as having idiopathic chronic pancreatitis had, in fact, a genetic defect.

Immunologic events are also believed to be involved in the pathogenesis of chronic pancreatitis [43]; T-lymphocytic infiltration of the exocrine pancreas in patients with chronic pancreatitis has suggested that cellmediated immune mechanisms may play a part in the pathogenesis of this disease [44, 45]. Normal pancreatic epithelial cells did not express HLA-DR antigens but abnormal expression, by exocrine epithelial cells, of class or class either Π major Ι histocompatibility complex (MHC) determinants or both has been found in chronic pancreatitis. In general, MHC class I present antigens derived from intracellular proteins (self and nonself) to CD8+ T cells. Class II molecules present antigens derived from endocytosed extracellular proteins to CD4+ T cells, which may stimulate both Band T-cell-mediated immune responses [46, 47, 48, 49].

Among HLA-DRB1 genes, DRB\*04 was shown to be significantly higher in chronic pancreatitis patients than in controls.

HLA DRB1\*0401 contains the QKRAA amino acid sequence in its third hypervariable region and the QKRAA sequence is also expressed by several human pathogens. T cells may be triggered in the pancreatic tissue upon exposure to foreign peptides similar enough to cross-react and to break immunological tolerance [50].

Cytokines and chemokines of the MHC play critical roles in the pathogenesis of autoimmune disease. Among these, tumor necrosis factor-alpha, derived from or lymphocytes, monocytes is а proinflammatory cytokine with pleiotropic biological effects. A growing body of data [51] has demonstrated a significant association of TNF-alpha polymorphism at position -308 with susceptibility to or severity of autoimmune and infectious disease [52, 53]. Moreover, recent studies on cultured epithelial cells deficient in keratin 8 (K8) and keratin 18 (K18), have demonstrated an increased sensitivity (nearly 100 times) to tumor necrosis factor-alpha (TNF-alpha) acting both as a grow factor and an apoptotic stimulus. This finding addressed the increased sensitivity of K8-cells to TNF, as fundamental in the resistance of epithelia to apoptosis during common inflammatory responses and in the persistence of K8 and K18 expression in carcinoma cells [54].

Important information regarding keratin obtained bv function was also the overexpression of mutant or ectopic keratins; the overexpression of human K8 in transgenic mice resulted in significant pancreatic acinar cell atrophy, dysplasia and progressive exocrine dysfunction [55]. Furthermore, a report from Omary et al. [56], demonstrated that G61C and Y53H mutations in keratin 8 gene may account for cryptogenetic liver disease by interfering with the normal organization of keratin filaments. The results from Casanova et al. and from Omary et al. uncovered a possible role as intermediate filaments for K8 in the pathogenesis of chronic inflammatory diseases of tissue containing K8,. Moreover, hepatocytes and pancreatic epithelial cells are unique in that express cytoplasmatic they K8/K18 exclusively.

Indeed, the G61C heterozygous mutation of the keratin 8 gene was found in six patients with chronic pancreatitis (P=0.006); none of the normal controls presented the mutation. No Y53H mutation was detected in any subject [57]. Mutations in the keratin 8 gene, together with other environmental factors (alcohol intake, smoking habits) and/or genetic factors, could predispose to chronic pancreatitis by interfering with the normal organization of keratin filaments.

Cytochrome P450IIEI (CYP2E1) is an ethanol-inducible enzyme; several novel polymorphisms in the CYP2E1 gene have been identified. CYP2E1 is one of the possible mechanisms for ethanol-induced oxidative stress in the pancreas, and the

associated oxidative stress may play a role in the pathogenesis of alcohol-induced pancreatitis. Analysis of the four CYP2E1 polymorphisms  $(-35{G(-35)T})$ , gene  $1019\{C(-1019)T\},\$ 4808{G(4808)A}, and 7668{T(7668)A), did not show any correlation with the susceptibility and pathogenesis of alcoholic pancreatitis [58]. Apart from alcohol abuse, chronic pancreatitis and pancreatic adenocarcinoma are associated with smoking and environmental aromatic hvdrocarbon Uridine 5'exposure. diphosphate glucuronosyltransferases are phase II detoxifying enzymes capable of tobacco-borne toxicant inactivation and cellular protection. Uridine 5'-diphosphate glucuronosyltransferases A7 (UGT1A7) gene polymorphisms in pancreatic diseases were analyzed [59] as candidate polymorphisms in association with pancreatic disease. Alterations of UGT1A7 functional properties may indeed potentially influence the risk of oxidative injury and therefore of chronic inflammation and cancer initiation. An association of chronic pancreatitis and pancreatic adenocarcinoma with low-activity polymorphisms of the xenobiotic-detoxifying enzyme gene UGT1A7 was seen.

Association studies between a disease and a marker locus are the best method for identifying susceptibility genes for complex diseases, such as chronic pancreatitis. Moreover, chronic pancreatitis has also a threshold character; therefore several genetic backgrounds could lead to the same clinical picture. Genetic analyses will become important in the diagnosis and classification of chronic pancreatic disorders in order to better define the etiology, the progression and the prognosis of the disease. Several attempts have been identify clinical, made to biochemical and histological parameters capable of predicting the prognosis of such diseases. However, all these prognostic scores rely on biochemical or clinical parameters which can be modified only in the very advanced phases of the disease. Therefore, at the time of diagnosis, they are unable to discriminate the patients who will undergo a rapidly progressive course from those who

will never have their quality and expectancy of life reduced by the disease.

New biological markers are therefore needed to identify genetic markers able to identify patients at risk of disease progression. Such new markers need to be identified on "pedigreed patients" carefully selected according to their pattern of disease progression. Moreover, molecular classification will help provide to identification of pancreatitis-associated genes and gene-environmental interactions in the pathogenesis of the disease.

Keywords Cystic Fibrosis Transmembrane Conductance Regulator; Cytochrome P-450 Enzyme System; Genetics; Glucuronosyltransferase; Keratin; Major Histocompatibility Complex; Mutation; Pancreatitis; Polymorphism, Genetic; Trypsinogen

Abbreviations CP: chronic pancreatitis; CYP2E1: cytochrome P450IIEI; K18: keratin 18; K8: keratin 8; MHC: major histocompatibility complex, UGT1A7: uridine 5'-diphosphate glucuronosyltransferases A7

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