Plexiform neurofibroma mimicking a pancreatic cystic tumour

Pancreatic neurogenic tumours are extremely rare. Among benign neurogenic tumours, schwannoma is more frequently encountered. We report here the case of a plexiform neurofibroma, a type of neurogenic tumour in the pancreas, to our knowledge previously unreported.

History
A 44 year old Caucasian female patient was hospitalised for epigastric and right abdominal pain lasting for seven months. Abdominal ultrasound and computed tomography showed a cystic lesion located in the superior and anterior part of the pancreatic isthmus, with a maximal diameter of 3.5 cm (fig 1A, B). T2 magnetic resonance imaging demonstrated a trilobar cystic lesion with strong hyperintensity (fig 1B); no communication with the main pancreatic duct was noted at magnetic resonance cholangiopancreatography (fig 1C). Endoscopic ultrasound (EUS) showed a cystic lesion containing heterogeneous fluid (fig 1D). EUS guided fine needle aspiration provided mucoid fluid with no epithelial cells. Fluid pancreatic enzyme concentrations were 423 and 1204 U/l for amylase and lipase, respectively, while CEA, CA 19.9, and CA 72.4 were 17 ng/ml, 9 U/ml, and 140 U/ml, respectively. Despite the low CA 19.9 concentration and lack of mucinous cells in cystic fluid, other findings were consistent with a diagnosis of mucinous cystadenoma. Surgical exploration confirmed a cystic lesion of the superior part of the pancreatic isthmus, distant from the main pancreatic duct (fig 1A, B). Tumour enucleation was performed. On macroscopy there was a well delineated, trilobated, translucent mass, measuring 3.5 cm (fig 1E). The tumour consisted of aggregates of benign spindle cells embedded in a fibrillar matrix (fig 1F). These aggregates formed a thin rim around a large central low cellular zone of oedema and myxoid degeneration. The tumour cells expressed neurofilaments and S100 protein on immunohistochemistry. P53 immunostaining was negative and sparse nuclei were Ki67 positive. These features were consistent with a benign plexiform neurofibroma (PNF). No neurofibromatosis related lesions were found and no mutation of the NF1 (neurofibromatosis 1) gene was identified on analysis of DNA both from blood lymphocytes and tumour tissue. At follow up, two years after surgical resection, the patient did not present with any complaints and there was no evidence of pancreatic lesions.

Discussion
The presence of PNF in the pancreas has several clinical implications, as indicated by the present case. Firstly, PNF may mimic a pancreatic cyst, as was hypothesised in this case before surgery. The cystic appearance of neurogenic tumours is frequently encountered, with intratumoral oedematous and myxoid changes probably being the underlying lesions. A bright appearance on T2 weighted magnetic resonance images is a characteristic of PNF. Secondly, surgical
resection was necessary to exclude malignancy, which is more frequently encountered in PNF compared with classical neurofibromas. In addition to classical benign features, similar to published data on benign PNF, a high cell proliferation and p53 protein expression were absent in our case. Thirdly, PNF is a morphological variant of neurofibroma, generally considered pathognomonic for an NF1 syndrome. When diagnosed in adult patients, it is frequently a solitary tumour and is considered a mosaic located form of NF1 syndrome. The absence of detectable genetic abnormalities and other clinical NF1 syndrome-associated lesions in the present case could be explained by such a mechanism. For these patients, there is a low risk of developing other diseases associated with NF1 syndrome.

In conclusion, we have reported an uncommon case of PNF, unique in its pancreatic location. Intratumoral myxoid and oedematous changes that develop in this type of neurofibroma give a cystic appearance which may lead to a misdiagnosis of a pancreatic cyst. Such lesions should be added to the list of benign pancreatic tumours with a cystic appearance.

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References


No genetic association between EPHX1 and Crohn’s disease

In a case control study on the associations between functional genetic polymorphisms in biotransformation enzymes and Crohn’s disease, we found a strong association between the Tyr113His (348T>C) polymorphism in exon 3 of the microsomal epoxide hydrolase (EPHX1) gene and Crohn’s disease. The three referees all agreed that the study was interesting and should be published so that other groups can attempt to replicate the results in independent study cohorts. This was done recently by Cuthbert and colleagues (Gut 2004;53:1386) who investigated 333 controls and 307 patients with Crohn’s disease, and who were unable to reproduce our results. In addition, they reported that our data for the EPHX1 exon 3 polymorphism in the control group were not in Hardy-Weinberg equilibrium (HWE), as also noticed previously by Gyröffy and colleagues. Our data on EPHX1 exon 3 genotyping were obtained by restricted fragment length polymorphism (RFLP) analyses by applying the method described by Lancaster and colleagues.

However, recently it was reported that a silent substitution polymorphism (G to A) at codon 119 of the EPHX1 gene may exist, which may flaw the polymerase chain reaction (PCR) RFLP method applied by us, as the presence of this polymorphism may disturb proper binding of the reverse primer, covering the 119 G>A area, resulting in over-classification of His113 alleles. Therefore, we developed a dual colour allele specific discrimination assay for genotyping the polymorphism at codon 113 of the EPHX1 gene. EPHX1 genotypes were detected with the iCycler iQ Multicolour Real Time Detection System (Bio-Rad Laboratories, Venneendaal, the Netherlands) using molecular beacons. PCR was performed with the forward primer 5’-CAA CTC CAA CTA CCT GAA G-3’ and the reverse primer 5’-TGA CAT ACA TCC CTC TCT GCT-3’ in the presence of the FAM labelled wild-type beacon (5’-GCC GAT GAT TCA CAG ATG CTC CTG CG-3’) and the HEX labelled mutant beacon (5’-GCC GAT ATT CAC AGA CAC CCT CAC TAT GGC G-3’). The 25 µl reaction mixture contained 200 ng of genomic DNA, 10 mM Tris/HCl (pH 9.0), 50 mM KCl 0.1% Triton X-100, 4 mM MgCl2, 0.25 mM dNTPs, 50 ng of each primer, 200 nM of each beacon, and 2.5 U Taq-DNA-polymerase. The PCR conditions were three minutes at 95°C, then 40 cycles of 30 seconds at 95°C, 30 seconds at 59°C, and 30 seconds at 72°C. Fluorescent signals were measured at 0.5°C/s, and samples were assigned using the iCycler iQ Optical System, software version 3.1. At each PCR run (in 96 well plates) sterile H2O instead of genomic DNA was added in several wells as a negative control. If the controls were not amplified, the PCR-RFLP analyses were performed in the first half of 1999, only some of the samples were still available (125 of 149 controls and 149 of 151 cases) and these were re-evaluated by the Cycler method.

Genotype distribution of the EPHX1 Tyr113His polymorphism in patients with Crohn’s disease and controls was now in HWE (x^2 = 4.74, p = 0.12 and x^2 = 0.82, p = 0.37, respectively) and genotype distribution was not significantly different between cases and controls (x^2 = 3.5, p = 0.17). The Tyr allele frequencies of 0.70 and 0.68 obtained for cases and controls, respectively, were similar to the corresponding values of 0.71 and 0.70, as reported by Cuthbert et al.

Thus in answer to the question as posed by Cuthbert et al: “Genetic association between EPHX1 and Crohn’s disease: population stratification, genotype error, and random chance?”, we can conclude that a genotyping error was responsible for our earlier published association between the EPHX1 Tyr113His polymorphism and Crohn’s disease. Similar genotyping errors may also be present in several other studies on the EPHX1 exon 3 polymorphism in association with a variety of diseases, as many studies were based on methods using a reverse primer covering the “119 silent mutation area” of the EPHX1 gene. This may also have consequences for interpretation of results in the cited papers. However, a rapid literature search by Pubmed revealed more than 100 papers on EPHX1 polymorphisms over the past 10 years, suggesting that many more papers may deal with genotyping problems, as outlined above.

In addition, Cuthbert et al also reported that another polymorphism tested in our study, the CPY1A1 exon 7 Ile/Val polymorphism was not in HWE in the control group. This is correct but this deviation from HWE may be attributed to random chance, due to the rarity of the Val allele in our population, which makes the x^2 test inappropriate under such conditions. For instance, genotype distribution is in accordance with HWE when only two individuals less would have been classified as Val/Val homozygotes.

We thank Cuthbert et al and Gyröffy and colleagues for their interest in our work. In addition, we conclude that (interpretation of) data in many other published studies on the EPHX1 Tyr113His (exon 3) polymorphism should be critically re-evaluated.

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Conflict of interest: None declared.
Transcriptional downregulation of the lactase (LCT) gene during childhood

Adult-type hypolactasia, characterised by bloating, gas formation, and diarrhoea after ingestion of lactose containing food, affects half of the world’s population. The molecular background of lactase non-persistence/persistence trait has been shown to associate with a single nucleotide polymorphism (SNP) C/T-13910 residing 13910 base pairs upstream from the 5’ end of the lactase (LCT) gene in an intron of the minichromosome maintenance (MCM6) gene. We have demonstrated a tridimensional distribution of lactase activity in the intestinal mucosa in adults, with low lactase activity (4–9 U/g protein) in those with the C/C-13910 genotype. The C-13910 and T-13910 allele show differential regulation of lactase promoter activity and binding capacity for the nuclear proteins in electrophoresis shift assay. Our recent analysis in a paediatric population demonstrated that the main time period for lactase downregulation in Finns and in Somalis is from five to 10 years of age. To further assess the role of the C-13910 allele in downregulation of lactase activity during development, we isolated lactase RNA from intestinal biopsy samples with verified C-13910 genotype and three with the C/C-13910 genotype. All subjects were heterozygous for the G/A-593 polymorphism residing in exon 1 of the LCT gene. Relative expression of lactase mRNA transcribed from the C-13910 and T-13910 allele was assessed by quantitative minisequencing using the G/A-593 polymorphism on the LCT gene as a marker. The methods used are described in detail by Kuokkanen and colleagues. The study was approved by the ethics committee at the Helsinki University Central Hospital. All families gave their informed consent.

Subjects with the C/T-13910 genotype (age range 10 months to 17 years) had high lactase activity, ranging from 21 to 113 U/g protein (mean activity 47 U/g protein; sample not available n = 2) except for one child presenting with low lactase activity (6 U/g protein). In this case the indication for endoscopy was exclusion of gastro-oesophageal reflux. Due to the very low lactase activity and the C/T-13910 genotype, mutations underlying congenital lactase deficiency (CLD) were screened for this patient and he was shown to be a carrier of a CLD mutation (unpublished data). Of the three subjects with the C/C-13910 genotype, the oldest subject aged 23 years had low lactase activity (6 U/g protein) as expected; the five year old subject aged 23 years had low lactase activity (4–9 U/g protein) in those with the C/C-13910 genotype. Expression transcribed from the C-13910 and the T-13910 allele in children younger than five years of age. In children over six years of age, relative lactase mRNA expression from the C-13910 allele was reduced to 18% and 16% compared with that from the T-13910 allele (fig 1, table 1).

Our results show an increasing imbalance in relative mRNA expression from the C-13910 and T-13910 alleles in children aged >5 years. These results support the earlier findings on transcriptional regulation of the lactase gene and the finding in our own laboratory that the persistent T-13910 allele was shown to represent a mean of 92% of expressed lactase mRNA in C/T-13910 heterozygous adults. The decline in lactase mRNA expression transcribed from the C-13910 allele in the intestinal mucosa occurs in parallel with the time period of the decline in lactase enzyme activity, indicating a causative role for the intronic region containing the C-13910 allele. Characterisation of the transcriptional regulators at the C-13910 enhancer element, and the exact mechanism underlying C-13910 allele specific downregulation of lactase activity awaits elucidation.

Acknowledgements

We are grateful to the children and their families for their participation. Ms Sari Nisam and Mervi Manninen at the Day Surgery Unit, Hospital for Children and Adolescents, are acknowledged for coordinating and managing the sample collection. Funding was provided by the Sigrid Juselius Foundation, Helsinki, Finland, the Helsinki University Hospital Research Funding, Helsinki, Finland, the Finnish Cultural Foundation, the Maud Kuusitalo Foundation, and The Research Foundation of Orion Pharma, Espoo, Finland.

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Table 1 Lactase activity, L/S ratio, and allelic ratio of the study subjects

<table>
<thead>
<tr>
<th>Age (y)</th>
<th>C/T-13910 genotype</th>
<th>Lactase activity (U/g protein)</th>
<th>L/S ratio</th>
<th>Allele ratio (%)</th>
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</thead>
<tbody>
<tr>
<td>0.8</td>
<td>CT</td>
<td>85</td>
<td>1.11</td>
<td>48/52</td>
</tr>
<tr>
<td>1.1</td>
<td>CT</td>
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<td>52/48</td>
</tr>
<tr>
<td>4.0</td>
<td>CT</td>
<td>31</td>
<td>0.49</td>
<td>49/52</td>
</tr>
<tr>
<td>4.3</td>
<td>CT</td>
<td>53</td>
<td>0.48</td>
<td>42/58</td>
</tr>
<tr>
<td>4.7</td>
<td>CT</td>
<td>40</td>
<td>0.62</td>
<td>40/60</td>
</tr>
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<td>4.9</td>
<td>CT</td>
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<td>0.08</td>
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</tr>
<tr>
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<td>48/52</td>
</tr>
<tr>
<td>6.7</td>
<td>CT</td>
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</tr>
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<td>7.6</td>
<td>CT</td>
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<td>11.1</td>
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</tr>
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<td>14.9</td>
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<td>40/60</td>
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<td>17.0</td>
<td>CT</td>
<td>29</td>
<td>0.62</td>
<td>40/60</td>
</tr>
<tr>
<td>13.8</td>
<td>CT</td>
<td>29</td>
<td>0.62</td>
<td>40/60</td>
</tr>
<tr>
<td>11.1</td>
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<td>40/60</td>
</tr>
<tr>
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<td>24</td>
<td>0.28</td>
<td>51/49</td>
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<tr>
<td>22.8</td>
<td>CT</td>
<td>6</td>
<td>0.08</td>
<td>49/51</td>
</tr>
</tbody>
</table>

*Defined by assessing cSNP G/A-593 in exon 1 of the lactase LCT gene.
†Carrier of a CLD mutation (unpublished data.)
Cystic fibrosis transmembrane regulator gene carrier status is a risk factor for young onset pancreatic adenocarcinoma

Pancreatic adenocarcinoma is the fourth leading cause of cancer death in the USA. Although predominantly a cancer of the elderly, approximately 20% of patients are diagnosed under the age of 60 years. Younger patients are likely the best candidates for early surgical intervention, and patients at risk for young onset cancer comprise a logical focus for screening or prevention.

Carriers of mutations in the gene that encodes the cystic fibrosis transmembrane conductance regulator (CFTR) are associated with chronic idiopathic pancreatitis. Chronic pancreatitis, in turn, increases the risk for pancreatic cancer by 26-fold. Therefore, we hypothesised that mutations in CFTR may confer a higher risk of pancreatic cancer. From October 2000 to April 2004, pancreatic cancer patients seen at the Mayo Clinic were ultra-rapidly recruited to our study, with more than 75% of all such patients seen at the Mayo Clinic enrolled in the registry. This represents a substantial improvement over population based pancreatic cancer epidemiological studies, with participation rates ranging from 34.6% to 45.6%. Informed consent and institutional review board approval were obtained. As a pilot study, 33 patients were selected in whom a pathological diagnosis of pancreatic cancer was also noted at the time of pancreatic cancer surgery. The patients ranged in age from 41 to 81 years (median 65), and seven of the 33 had a diagnosis of pancreatic cancer made at least one year prior to cancer diagnosis. These patients were screened for variants in CFTR using the Taq-It Mutation Detection Kit, a clinically available kit testing for 40 mutations.

Comparison of CFTR mutation frequencies detected in the young onset pancreatic cancer cohort versus the clinical database

<table>
<thead>
<tr>
<th>Young onset pancreatic cancer cases ((&lt;)60 y old at diagnosis, n = 166)</th>
<th>Mayo Clinic clinical database reference group (n = 5349)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CFTR mutation non-carriers</td>
<td>152</td>
</tr>
<tr>
<td>CFTR mutation carriers</td>
<td>14</td>
</tr>
<tr>
<td>Mutation distribution</td>
<td></td>
</tr>
<tr>
<td>AF508</td>
<td>12</td>
</tr>
<tr>
<td>R175H</td>
<td>1</td>
</tr>
<tr>
<td>G551D</td>
<td>6</td>
</tr>
<tr>
<td>G542X</td>
<td>4</td>
</tr>
<tr>
<td>N1303K</td>
<td>1</td>
</tr>
<tr>
<td>1717+1G-T</td>
<td>2</td>
</tr>
<tr>
<td>3849+10kbC-T</td>
<td>2</td>
</tr>
<tr>
<td>R560T</td>
<td>2</td>
</tr>
</tbody>
</table>

Young onset pancreatic cancer cases were more frequent carriers of the CFTR mutations compared with patients in the control database (odds ratio 2.18 (95% confidence interval 1.24–3.29); p = 0.006).

Acknowledgements

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Distal intestinal obstruction syndrome in the early postoperative period after lung transplantation in a patient with cystic fibrosis: morphological findings on computed tomography

Distal intestinal obstruction syndrome (DIOS) occurs in 19.9% of adults with cystic fibrosis (CF). Usually the diagnosis is based on history, physical examination, and plain abdominal roentgenogram. The increased risk of gastrointestinal complications such as DIOS is well known after lung transplantation. Due to the added risk of gastrointestinal surgery in the postoperative period and the generally good response to conservative treatment, it is necessary to distinguish DIOS from other gastrointestinal complications. Nevertheless, descriptions of computed tomographical patterns of DIOS in the international literature are rare.

We present the case of a 34 year old male suffering from end stage CF. Because of gastrointestinal manifestations of CF, the patient had exocrine pancreas insufficiency. As a consequence of deterioration in respiratory function, lung transplantation was performed. Despite enzymatic and propulsive medical treatment the patient developed an acute abdomen during the postoperative period. To determine the cause of his symptoms abdominal radiographs and computed tomography were performed. Abdominal plain films showed remarkably little abdominal gas and poor delineation of the abdominal organs (fig 1A). Contrast enhanced computed tomography showed massive dilatation of the small bowel and proximal colon with marked swelling of the intestinal wall (fig 1B, C). The lumen of the small intestine and proximal part of the ascending colon were filled with a homogeneous mass (fig 1B) with increasing roentgen opacity from the duodenum (approximately 19 Hounsfield units (HU)) to the right hemicolon (approximately 39 HU). Isolated air fluid levels were seen in the small bowel. The transverse, descending, and sigmoid colon were thin with only little faeces. There was no evidence of external compression. Based on these findings a diagnosis of DIOS was made. Laparotomy, performed due to failure of medical treatment, confirmed the diagnosis.

DIOS is unique to patients with cystic fibrosis. Intestinal obstruction developed due to accumulation of highly viscous muco-faculent material in the terminal ileum and right hemicolon. Pancreatic insufficiency is a prerequisite for DIOS but is not its only pathophysiological cause. Other factors such as reduced intestinal water content, lower luminal acidity of the foregut, accumulation of intraluminal macromolecules, dehydration of the mucus layer due to altered intestinal secretion, and slow intestinal transit contribute to the development of DIOS.

Plaint films are only of limited value in differentiating DIOS from other causes of acute abdomen. In the case of DIOS, they usually show typical signs of a small bowel ileus but other frequent reasons for ileus in patients with CF (for example, adhesions, intussusception, paralytic ileus due to perforated appendicitis, or Crohn's disease) cannot be excluded without further investigation. In our case, abdominal plain films showed no typical signs of small bowel ileus but little abdominal gas with poor delineation of the abdominal organs leading to the differential diagnoses of ascites, colitis, mesenteric infarction, and proximal bowel obstruction. In contrast with the plain abdominal radiograph, computed tomography showed the criteria of DIOS. The small bowel was completely filled with a homogenous mass with increasing roentgen opacity from the duodenum (approximately 19 HU) to the right hemicolon (approximately 39 HU), suggesting increasing viscosity of the intestinal content due to water absorption. In accordance with previous descriptions of DIOS, obstruction occurred in the right hemicolon.

Our case showed that abdominal plain films, as used in previous studies, are not adequate for the diagnosis of DIOS. Computed tomography can reveal the characteristic signs of DIOS and exclude inherent differential diagnoses. We have demonstrated for the first time that DIOS causes increasing opacity of intestinal contents during small intestinal passage, suggesting increasing viscosity.

References

Figure 1 (A–C) Abdominal plain film showing remarkably little abdominal gas and poor delineation of the abdominal organs. Markedly distended small bowel loops and right hemicolon (white arrow) completely filled with a homogenous mass. Swelling of the intestinal wall with increased contrast material enhancement. Thin transverse and descending colon with only few faeces (black arrows).
Association of a new cationic trypsinogen gene mutation (V39A) with chronic pancreatitis in an Italian family

Predisposition to hereditary pancreatitis has been associated with mutations in three genes: protease, serine, 1 (PRSS1), which codes for cationic trypsinogen,\(^7\) cystic fibrosis transmembrane conductance regulator (CFTR),\(^6\) and serine protease inhibitor Kazal type 1 (SPINK1).\(^6\)

We have identified a novel PRSS1 mutation in seven subjects with chronic pancreatitis (CP) from three generations of an Italian family. The index patient was a 57 year old man with CP referred to our hospital for ductal adenocarcinoma of the pancreatic head. Eleven relatives were examined, and an uncle, also with CP, had died in an accident.

Congenital malformations and alcoholic, biliary, obstructive, and autoimmune pancreatitis were ruled out. Eleven subjects gave their written consent to the study.

The cystic fibrosis assay (CF-OLA; Applied Biosystems, California, USA) was used to look for 31 frequent CFTR mutations in all subjects. The five exons of the PRSS1 gene were sequenced with the oligonucleotides described by Nishimori and colleagues.\(^6\) The four SPINK1 exons were investigated by denaturant gradient gel electrophoresis (DGGE). No CFTR or SPINK1 mutations were found although subject III-8 (with CP) carried the N130K mutation in heterozygosis in the cystic fibrosis gene.

The PRSS1 exon 2 sequence of the index patient revealed a T>G change at nucleotide 116 (c.116T>G) causing a valine to alanine substitution at codon 39 (V39A). This mutation was present in another six subjects with CP, diagnosed from exocrine insufficiency and computer tomography and magnetic resonance imaging demonstrations of typical ductal alterations and parenchymal calcifications. Two of these patients were also diabetic. In a further two patients, the genetic analysis was not performed, but CP was confirmed by clinical and morphological findings. The remaining four subjects had a normal pancreas and did not carry the V39A mutation (Fig 1).

The lod score calculated for the association between V39A and CP was z = 3.0 at θ = 0.0. This mutation was not found in a DGGE investigation of 130 patients with sporadic CP.

Mean age of the patients was 47.22 (±13.64) years (median 54 (range 25–60)). Mean age at onset was 30.0 (±7.35) years (median 32 (range 19–40)) whereas in patients displaying other PRSS1 mutations, onset was typically during childhood or adolescence.\(^7\)

An acute attack requiring hospitalisation formed the clinical overture in six of the nine CP patients. The other three (III-4, III-5 and IV-2) presented morphological and functional evidence of CP at the time of the study but were asymptomatic. It is clear therefore that damage to the pancreas may occur prior to the clinical onset of CP.

In hereditary CP, the mechanism of the R122H mutation has been elucidated.\(^1\) This mutation removes a hydrolysis start site and makes both trypsin and trypsinogen autolysis resistant. A similar mechanism has been proposed for the N29I mutation which alters protein conformation and masks the R122 site.\(^7\)

Valine 39 is evolutionarily conserved in the trypsinogen gene of all terrestrial vertebrates\(^7\) and would thus seem of importance in the protein’s structure and function. As V39 is only 10 amino acids distant from N29, its replacement by alanine may result in abnormal conformation of the peptide and mask arginine 122 against enzymatic degradation. Further work is needed to define the mechanism and confirm this interpretation.

In conclusion, the presence of the V39A mutation in seven of the CP patients, its absence in their healthy relatives, the 3.0 lod score, and the strong evolutionary conservation of V39, all indicate that the novel mutation is the cause of CP in this family.

Acknowledgements

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Figure 1  Pedigree showing the age of subjects, and for those with pancreatitis (black symbols) their age at onset (where known). WT, wild-type (that is, subjects without pancreatitis and without the V39A mutation); black triangle, index patient; ?, no clinical or genetic data available.
ITPA genotyping is not predictive for the development of side effects in AZA treated inflammatory bowel disease patients

We read with interest the letter by Colombel et al on the non-predictive value of ITPA genotyping for the development of myelosuppression after azathioprine (AZA) treatment (Gut 2005;54:565).

The level of thiopurine methyltransferase (TPMT) activity is determined by a common genetic polymorphism. It was shown that low TPMT activity is linked to a higher relative risk of development of myelosuppression after AZA treatment.1 Testing for TPMT genotype before the start of AZA treatment is of limited clinical value as myelosuppression resulting from TPMT mutations occurs in less than one third of patients with myelosuppression.3

Polymorphisms in genes encoding inosine triphosphate pyrophosphohydrolase deficiency (ITPA), another enzyme involved in metabolism of AZA, have also been suggested to be associated with the development of side effects in AZA treatment.4 Colombel et al show that there was no difference in the frequency of ITPA polymorphisms in 41 patients who were homozygous for the ITPA 94 C>A polymorphism as none was included either in our study or in Colombel’s. Instead, ITPA polymorphisms are associated with the development of side effects.5 Therefore, further research on the risk of developing side effects in homozygous ITPA patients is desirable.

References

Table 1 Side effects in 109 azathioprine treated inflammatory bowel disease patients related to their thiopurine methyltransferase (TPMT) and inosine triphosphate pyrophosphohydrolase (ITPA) genotypes

<table>
<thead>
<tr>
<th>Side effect</th>
<th>No polymorphisms (88 of 109)</th>
<th>TPMT polymorphisms (10/109)</th>
<th>ITPA polymorphisms (12 of 109)</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>*1/*3A</td>
<td>*1/*3C</td>
<td>*3A/*3A</td>
</tr>
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<td>0</td>
</tr>
<tr>
<td>Leucocytes</td>
<td>2&lt;4&lt;10^9/l</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Hepatotoxic</td>
<td>5</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Pancreatitis</td>
<td>5</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Gastrointestinal</td>
<td>7</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Other</td>
<td>8</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td>88</td>
<td>7</td>
<td>1</td>
</tr>
</tbody>
</table>

One patient was included in both the TPMT polymorphisms column and in the ITPA polymorphisms column as he was heterozygous for the TPMT*3A polymorphism and heterozygous for the ITPA 94 C>A polymorphism. Side effects categorised as “other” included rash, renal function disorders, vertigo, myalgia, and arthralgia.

Conflict of interest: None declared.

References
Lack of serum antibodies to membrane bound carbonic anhydrase IV in patients with primary biliary cirrhosis

Nishimori et al have recently reported the presence of autoantibodies against carbonic anhydrase IV (anti-CA IV) in patients with autoimmune pancreatitis (Gut 2005;54:274–81). Furthermore, serum antibodies to CA II (anti-CA II) were observed in several autoimmune conditions. We have now investigated the presence of anti-CA IV and anti-CA II in a large series of sera from patients with primary biliary cirrhosis (PBC) and controls. CA II is known to be expressed in the cytoplasm of various types of epithelial cells, including those lining bile ducts, renal tubules, and salivary ducts. For this reason, CA II was suggested as a common antigen in conditions characterised by an autoimmune aggression against epithelia. In autoimmune pancreatitis, serum anti-CA II are useful diagnostic tools while in PBC they were first detected by Gordon et al in 5/6 sera from patients with antimitochondrial antibody (AMA) positive PBC. Subsequent studies however demonstrated prevalence rates as high as 46% in PBC sera but failed to confirm their specificity for AMA negative sera.1 Interestingly, anti-CA II were also shown to inhibit enzyme activity.2

Apart from cytosolic CA II, the CA family also includes a highly active membrane bound enzyme that was coined CA IV.3 Both CA II and CA IV are abundantly expressed in human bile duct and epithelial cells. Interestingly, mainly due to the sequence homology between CA II and CA IV and CA IV localisation on cell membranes, Nishimori et al hypothesised that the exposed CA IV might be more immunogenic than cytosolic CA II. Seventy sera from patients with PBC (60 AMA positive; all anti-hepatitis C virus negative; 63 women; mean age 60 (SD 10) years) who attended our tertiary referral centre were consecutively enrolled in the study. Control sera were obtained from 50 healthy subjects matched with patients for sex and age class (≤50 v >50 years). All sera were tested by immunoblotting for anti-CA IV and anti-CA II as previously described.3,4 Briefly, proteins were denatured and separated (10 μg/lane) on a 1.5 mm sodium dodecyl sulphate-12% polyacrylamide gel. Proteins were then transferred onto nitrocellulose (pore size 0.45 mm) using a semi-dry transfer system. The nitrocellulose membrane (pore size 0.45 mm) using a semi-dry transfer system. The nitrocellulose membrane was cut into 4 mm strips and, after blocking with 5% non-fat milk, all strips were incubated with serum samples diluted 1:100 and 1:500 for anti-CA II and 1:100 for anti-CA IV. Rabbit horseradish peroxidase conjugated antibodies against human immunoglobulins G, A, and M (Dako, Glostrup, Denmark) was diluted 1:1000 and used as secondary antibody. Peroxidase development was obtained with 0.05% 4-chloro-1-naphthol in Tris buffered saline containing 20% methanol and 0.05% H2O2. A rabbit polyclonal antihuman CA IV antisera was used as a positive control throughout the study. CA IV antisera and anti-CA IV antisera were provided by Dr William S Sly (St. Louis, Missouri, USA).

Results demonstrated no reactivity against CA IV in any of the PBC or healthy control sera. In similar to previous reports, anti-CA II antibodies were detected in 6/70 (9%) sera from patients with PBC but were absent in control sera.

In summary, we submit that the hypothesis that antibodies against the membrane bound CA IV may play a role in PBC should be rejected, based on our experimental data obtained on a large series of sera. Our finding may be secondary to a different cellular expression of CA IV in the target organ (that is, pancreatic and bile ducts) but only specific tissue studies can provide these answers. At present, therefore, anti-CA IV should be regarded as specific to autoimmune pancreatitis and research should focus on better defining their possible role in this condition.

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Conflict of interest: None declared.

References

Association of achalasia and dental erosion

Dental erosion is the dissolution of enamel and dentine caused by organic acids.1 The source of acid is normally either dietary or regurgitated lactic acid. Dental erosion is the dissolution of enamel and dentine. The aim of the study was to measure the prevalence of dental erosion in patients with achalasia strongly suggests that the source of the acid within the oesophagus is lactic acid unlike reflux disease where hydrochloric acid from the stomach is responsible.2 This study shows that in patients with achalasia, particular attention to the condition of their teeth needs to be addressed. In conclusion, achalasia is related to palatal dental erosion and the cause of the erosion is fermented foods and not regurgitated gastric juice.

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Conflict of interest: None declared.

References

BOOK REVIEW

New Techniques in Gastrointestinal Imaging

Many areas of radiology are rapidly developing new techniques to answer clinical problems or devising ways of refining current imaging techniques. Gastrointestinal imaging is no exception.

New Techniques in Gastrointestinal Imaging has been edited and written by experts in the field from the international community and encompasses the more recent developments in all aspects of gastrointestinal imaging. The book has been divided into chapters that either concentrate on a particular imaging technique (for example, computed tomography (CT) colonography) or those that cover recent developments in the investigation of a particular area (for example, the rectum). There are very comprehensive chapters covering the new CT and magnetic resonance (MR) techniques available for imaging the colon and small bowel. New CT and MR techniques for hepatic imaging are also included, with special reference to the development of CT angiography. There are excellent chapters on the use of microbubbles in ultrasound (US) and endoscopic US, both of which are good introductions to these techniques for those with limited previous knowledge or experience. Also included is a very useful chapter on positron emission tomography (PET) with a gentle introduction to the physics of the technique and current applications and limitations. New interventional imaging techniques are also covered, with chapters on radiofrequency ablation of liver lesions and on self expanding metallic stents in the colon.

I was however dismayed to find a section on defeating proctography, a technique I had rather hoped had been consigned to history. The current method seems to have changed little from my days as a junior registrar banished to the barium room although new MR techniques are described.

This book has been written to update the general radiologist in areas of gastrointestinal radiology that have changed significantly in recent times. This it does very well, with concise descriptions of the techniques, thorough discussions on clinical use, and handy tips on image interpretation. As such, there are chapters in the book that need some background knowledge of radiological techniques to appreciate the new developments (for example, CT and MR chapters on liver imaging). However, all chapters provide a good setting for each of the new techniques so that the interested gastroenterologist would find useful information on the current role of each investigation, its performance with relation to more established techniques, and future developments.

A Graham

CORRECTIONS

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In the Editor’s quiz: GI snapshot on p1272 of the September issue (D Joshi, J Dunga, A James and MM Yaqoob. An unusual case of hepatosplenomegaly. Gut 2005;54:1272; doi:10.1136/gut.2005.064824) the second author’s name should read Dungu not Dunga.

In the Gut Tutorial on p296 of the February issue the author’s name and affiliation was omitted. The details are as follows: Robin Spiller, Professor of Gastroenterology, Wolfson Digestive Diseases Centre, University Hospital, Nottingham NG7 2UH, UK.

In the Gut Tutorial on p555 of the May issue the author names and affiliations were omitted from the original publication. This has been updated on the Gut website. The authors and affiliations are as follows: S A Khan, A Miras, Liver Unit, Department of Medicine A, Faculty of Medicine, Imperial College London, St Mary’s Hospital Campus, South Wharf Road, London W2 INY, UK; M Pelling, Department of Radiology, Faculty of Medicine, Imperial College London; S D Taylor-Robinson, Liver Unit, Department of Medicine A, Faculty of Medicine, Imperial College London.