Genes that determine immunology and inflammation modify the basic defect of impaired ion conductance in cystic fibrosis epithelia


INTRODUCTION

Cystic fibrosis (CF) is the most common severe, monogenic, autosomal recessively inherited disease, affecting 1 out of 3200 newborns in the Caucasian population. The manifestation of the multiorgan disease varies among individuals and even among siblings homozygous for the most frequent disease-causing lesion F508del-CFTR. Improvement of medical care throughout the last decades has increased the patient’s life expectancy from less than 5 years in the 1940s to 37 years estimated for the current CF population, demonstrating convincingly that mainly non-genetic factors determine the disease outcome.

ABSTRACT

Background The cystic fibrosis (CF) basic defect, caused by dysfunction of the apical chloride channel CFTR in the gastrointestinal and respiratory tract epithelia, has not been employed so far to support the role of CF modifier genes.

Methods Patients were selected from 101 families with a total of 171 F508del-CFTR homozygous CF patients to identify CF modifying genes. A candidate gene based association study of 52 genes on 16 different chromosomes with a total of 182 genetic markers was performed. Differences in haplotype and/or diplotype distribution between case and reference CF subpopulations were analysed.

Results Variants at immunologically relevant genes were associated with the manifestation of the CF basic defect (Praw < 0.0001 at IL1B, TLR9, TNFα, CD95, STAT3 and TNFR). The intragenic background of F508del-CFTR chromosomes determined disease severity and manifestation of the basic defect (Praw = 0.0009). Allele distributions comparing transmitted and non-transmitted alleles were distorted at several loci unlinked to CFTR.

Conclusions The inherited capabilities of the innate and adaptive immune system determine the manifestation of the CF basic defect. Variants on F508del-CFTR chromosomes contribute to the observed patient-to-patient variability among F508del-CFTR homozygotes. A survivor effect, manifesting as a depletion of risk alleles at modifier genes. Awareness of non-genetic factors such as improvement of patient care over time is crucial for the interpretation of CF modifier studies.

This paper is freely available online under the BMJ Journals unlocked scheme, see http://jmg.bmj.com/site/about/unlocked.xhtml

Copyright Article author (or their employer) 2010. Produced by BMJ Publishing Group Ltd under licence.
their genome, can be compared to deduce the influence of inherited factors on the phenotype. They proposed to enrich for informative patient pairs with extreme phenotypes that can be selected from a cohort for candidate gene analysis and described CF modifier genes on six chromosomes. In this study, the objectives are: (1) to qualify the relative impact of the CFTR gene, environmental and other inherited factors on CF disease severity; (2) to identify genetic modifiers for the CF basic defect; and (5) to observe whether or not these are the same genes that modify CF disease severity. We have tested a total of 182 genetic markers targeting 52 candidate gene loci on 16 different chromosomes for their association with CF disease severity and the manifestation of the CFTR mediated basic defect, by genotyping a cohort composed of 101 families with a total of 171 F508del-CFTR homozygous patients. Among these are 12 genes studied as CF modifiers by others, to identify additional genes which represent plausible modifier candidates such as direct interaction partners of CFTR, alternative ion channels and components of the innate immune system, and 14 candidate genes which were selected by transcriptome analysis comparing intestinal epithelial biopsies of controls and CF patients. To our knowledge, this is the only study on CF modifiers that combines the powerful approach to analyse affected sib pairs while at the same time exploiting the polygenic contrast between informative extreme clinical phenotypes.

**METHODS**

**Patients and phenotypes**

This study reports on clinical data from 466 twin and sibling pairs and genetic data from 101 CF families, 85 of which are a subgroup of the twin and sibling study cohort. Enrolment of patient pairs into the association study was based on one of the following criteria: the twin or sibling pair exhibits an extreme clinical phenotype and/or the patient was characterised for the CF basic defect. Sixteen unrelated F508del-CFTR homozygotes from the CF clinic in Hannover were included who participated in an analysis of the basic defect and transcriptome in the intestine to define 14 candidate genes (van Barneveld et al., 2010, unpublished data).

We selected the 12% most informative pairs from the entire sample of 318 CF twin and sibling pairs by a ranking algorithm that relies on two clinical parameters most sensitive for course and prognosis of CF. These 37 dizygous F508del-CFTR homozygous patient pairs, enrolled due to their contrasting extreme clinical phenotype (Figure 1), were comparable with respect to their birth cohort.

CF basic defect phenotypes derived from intestinal current measurement (ICM) and nasal potential difference measurement (NPD) were obtained for 71 patient pairs. Briefly, secretagogues that activate or block ion channels, ion exchangers or components of the cellular signal transduction pathways were applied by superfusion of the surface of the lower nasal turbinate or to excised rectal suction biopsies mounted in a micro-Using chamber using a fixed sequence of defined pharmacologically active substances.

Based on the sib pairs’ clinical phenotype and the individual’s manifestation of the CF basic defect, subgroups were defined as cases and references for an association study (figure 1). These subgroups are by definition partially (clinical phenotype vs ICM) or nearly completely (ICM and NPD phenotypes) overlapping sets of patient pairs (see supplementary material for details).

This study was approved by the ethics committee of the Medizinische Hochschule Hannover. Written informed consent was obtained from all participants or their parental guides.

**Candidate genes and genetic markers**

Genotypes of two indels, 101 single nucleotide polymorphisms (SNPs) and 79 microsatellites were analysed for this study. Seventy-three markers were developed de novo for this study, building on raw genomic sequences containing microsatellite repeats within or near the targeted candidate gene to develop polyallelic markers (40 microsatellites) or on the public SNP database (55 diallelic markers). To compensate for the loss of power inflicted upon the study by the limited sample size of subgroups stratified for extreme clinical phenotypes (being infrequent by definition) or for basic defect phenotypes such as F508del-CFTR homozygotes who display CFTR mediated residual function (being infrequent due to the aetiology of the disease), care was taken to include only informative markers in the study: between one and 15 microsatellite motifs (median: four motifs) were tested per candidate gene locus to obtain one marker with a suitable polymorphism information content of 0.61–0.91 (mean 0.76) per targeted candidate gene. SNP markers were preselected based on HAPMAP data. Technical details on all markers and genotyping methods are provided in the supplementary material.

**Genetic modelling**

Genetic modelling was done with the LISREL8 software package. Briefly, covariance matrices from standard normal distributions derived from weight for height and forced expiratory volume in 1 s as percentage of predicted value (FEV₁%,pred) data were used to fit a model taking genetic effects as well as random and shared environmental effects into account. Applicability of the model was judged by the Aikaike information criterion.

**Association study**

Genetic data for the association study was evaluated using the FAMHAP software package which allows family based analysis and accepts data evaluation in association studies on unrelated individuals as well as on affected sib pairs. All case-reference comparisons were carried out using 10,000 Monte-Carlo simulated datasets. Nuclear families were analysed by the transmission–disequilibrium test (TDT) extended to both nuclear families with more than one affected child and to multi-marker haplotypes. To allow a comparable assignment of weighted haplotype explanations, the entire genotyping data were provided as training set to FAMHAP for all case-reference comparisons.

All candidate genes were analysed for an underrepresentation of alleles among transmitted chromosomes (TDT) as well as by case-reference comparisons for their association with disease severity (two case-reference comparisons), ICM (two case-reference comparisons) or NPD (three case-reference comparisons). Assignment of case and reference status is outlined in figure 1 and detailed in the supplementary material. To confirm observed associations, we have employed within-dataset validation strategies using partial replicates as detailed in the supplementary material. Significance within the entire dataset of 182 markers was conservatively judged by Bonferroni correction for 200 independent markers (threshold \( P_{\text{raw}} = 3 \times 10^{-4} \) for \( \alpha = 0.05 \)) or 52 independent loci (threshold \( P_{\text{raw}} = 9 \times 10^{-4} \) for \( \alpha = 0.05 \)).
Subsamples of F508del homozygotes were selected for the association study based on the clinical phenotype or the basic defect phenotype which was measured by nasal potential difference measurement (NPD) and intestinal current measurement (ICM). In total, 171 patients from 101 families were genotyped. Two patients with CFTR mutation genotypes other than F508del/F508del were only included for the phenotype ‘DIDS-sensitive chloride conductance’ determined by ICM. The association study compared subsets of affected patient pairs in their manifestation of the clinical phenotype, and correspondingly only dizygous pairs were included. In case of case—control comparisons of the basic defect in subsamples of unrelated index cases, one twin per monozygous twin pair was added to the cohort. For the association study on ICM phenotypes, 16 families with F508del homozygous offspring recruited from the CF clinic in Hannover, Germany were included. Integers within this figure correspond to the number of independent families while all numbers in brackets refer to the number of individual patients. Relative proportions of samples and subsamples stratified for extreme phenotypes are displayed on the basis of the number of independent nuclear families—that is, of sib pairs instead of individual patients—in order to represent sample sizes based on their number of independent genetic contributions which define the effective number of chromosomes considered for the genetic association study. Integers on top of diagrams report the sample size as the sum of all subgroups. Integers adjacent to diagrams report sizes of subgroups which are visualised as slices. For subgroups consisting of 540, 466 and 318 pairs, the entire circle diameter corresponds to the sample size. For subgroups consisting of 46 and 55 families, the sample size is represented in proportion to the larger datasets by the circle diameter carrying the sample size label (white central circle with red rim on top of the diagram). Composition of subgroups stratified for manifestation of the basic defect is displayed on the basis of individual patients. The numbers displayed for the contrasting phenotypes analysed in the case—control scenarios show the effective sample size, taking into account that sib pairs who show a discordant basic defect phenotype can contribute to one out of two (NPD phenotypes) or one out of three (ICM phenotypes) subgroups only in the association study.

In other words, subsets of unrelated patients were defined by an index case strategy whereby extreme basic defect phenotypes were selected for in pairs for whom discordance ICM or NPD was observed. As NPD measurements were obtained for two siblings of a pair in most cases, two subsets for each case—control test were evaluated to provide an internal control depending on which sibling was assigned at random to be the index case. Candidate genes were interrogated for their association with disease severity using the phenotypic contrast between concordant/mildly affected patient pairs, concordant/severely affected patient pairs, and discordant patient pairs. For this purpose, 37 dizygous pairs—representing the 12% most informative patient pairs of the entire sample—were selected based on a non-parametric ranking algorithm as described previously. NPD data were used firstly to enquire for an association with discordant patient pairs. For this purpose, 37 dizygous pairs were obtained for two siblings of a pair in most cases, two subsets for each case—control combination were evaluated to provide an internal control depending on which sibling was assigned at random to be the index case. Candidate genes were interrogated for their association with disease severity using the phenotypic contrast between concordant/mildly affected patient pairs, concordant/severely affected patient pairs, and discordant patient pairs. For this purpose, 37 dizygous pairs—representing the 12% most informative patient pairs of the entire sample—were selected based on a non-parametric ranking algorithm as described previously. NPD data were used firstly to enquire for an association with discordant patient pairs. For this purpose, 37 dizygous pairs were obtained for two siblings of a pair in most cases, two subsets for each case—control combination were evaluated to provide an internal control depending on which sibling was assigned at random to be the index case. Candidate genes were interrogated for their association with disease severity using the phenotypic contrast between concordant/mildly affected patient pairs, concordant/severely affected patient pairs, and discordant patient pairs. For this purpose, 37 dizygous pairs—representing the 12% most informative patient pairs of the entire sample—were selected based on a non-parametric ranking algorithm as described previously. NPD data were used firstly to enquire for a...
RESULTS

Inherited, environmental and maternal factors influence CF disease manifestation

We have compared intrapair differences in weight expressed as percentage of predicted weight for height (wfh%) and CF population centiles for the lung function parameter FEV1% (FEVPerc) and conducted genetic modelling on 466 (wfh%) and 318 (FEV1%) patient pairs (figure 2). While monozygous twins were more concordant in their FEVPerc than either dizygous twins or sibs, all twins were more concordant than sibs in their wfh% irrespective of their zygosity status. This indicates that the shared pre- and early postnatal period which distinguishes twins from sibs is associated with lower intrapair differences in wfh% while concordance in lung function is dominated by genetic factors as only monozygous twins share their entire genetic information in contrast to dizygous twins or siblings who have half of their genetic information in common. The results of the genetic modelling analysis imply that inherited factors have a larger impact on the patient-to-patient variation in wfh% than for lung function (figure 2B). These data are in accordance with heritability estimates from other CF twin and sibling cohorts.4

Association study

Candidate genes were interrogated for their association with disease severity using the phenotypic contrast between concordant/mildly affected patient pairs, concordant/severely affected patient pairs, and discordant patient pairs. For this purpose, 57 dizygous pairs—representing the 12% most informative patient pairs of the entire sample—were selected based on a non-parametric ranking algorithm as described previously.1 NPD data were used: first, to enquire for an association with sodium transport via the amiloride sensitive proportion of the potential, using the upper and lower 30% of the entire sample to define extreme phenotypes; secondly, to evaluate an association with residual chloride secretion activated by chloride-free gluconate solution and isoproterenol; and thirdly to analyse a contribution by the selected candidate genes on adenosine triphosphate (ATP) stimulated chloride response. Basic defect assessed by ICM was evaluated using a set of patients devoid of residual chloride secretion as controls. The pleiotropic chloride channel inhibitor DIDS, to which CFTR is not sensitive, was used to discriminate significance mediated by alternative channels which are DIDS sensitive.10 11 After correction for multiple testing, significance at the following loci and for the following phenotypes was retained: 12q13/TNFR, P < 0.0004 (NPD_ATP); 12p13/CEACAM, P = 5 x 10^-6 (FEVPerc); and 16p13.3/NHERF2, P < 0.05 (wfh%: P = 0.0005 (disease severity cis); 11q13/GSTP1, P = 0.0006 (NPD_ATP); 12p13/TNFR, P = 0.0004 (NPD_GL/Iso) and P = 0.0005 (NPD_ATP); 12q13/KRT8, P = 0.0004 (ICM_Res); 16p13.3/NHERF2, P = 0.0001 (ICM_Res). We have previously reported an association with DIDS-sensitive residual chloride secretion in ICM at the CLCA4-gene cluster12 and an association with disease severity for LEP,16 CD95,17 TNFR,18 SCNN1B,18 SCNN1G,18 at the CEACAM1 gene cluster,19 20 and at a paternally imprinted gene on 7q34.21 Association of these genes with other phenotypes are reported here for the first time.

Informative microsatellite markers allow the assessment of candidate genes as CF modifiers

Most candidate gene association studies in CF rely on the typing of polymorphisms which are suspected or known to alter the performance of the gene or its protein product,12 23 a strategy that cannot be applied as long as functional variants are unknown to date. Building on our previous experience,18 22 we developed informative microsatellite markers to interrogate these genes (see supplementary material for details). Results of the association study are displayed in figure 3. To confirm initial findings by microsatellite markers, a low density SNP scan was done for PRSS8, KRT8/KRT18, TLR4 and IL1B, and previously obtained genotyping data10 was evaluated for basic defect phenotypes at SCNN1B/SCNN1G and TNFR/SCNN1A. Significance after correction for multiple testing was retained for the
association of the member of the CFTR network NHERF2 with DIDS insensitive residual chloride secretion detected by ICM ($P_{\text{raw}}=0.0001$, diplotype model; $P_{\text{raw}}=0.0007$, haplotype model; $P_{\text{raw}}<10^{-5}$, accumulation of rare alleles among patients with residual function; figure 3 and figure 4). NHERF2 was interrogated with two microsatellite motifs located at a distance of 30 kb and 70 kb. Seven further genes are encoded on the segment between marker and targeted candidate gene. Even though none of these can be reasonably associated with CF pathophysiology, neighbours of the targeted candidate gene have to be considered; we observed an association of the response to gluconate and isoproterenol in NPD at the TNFR/SCNN1A locus (figure 3). Haplotype analysis of the 12p13 locus with four intragenic markers for each of the two neighbouring genes TNFR and SCNN1A revealed that the effect is mediated by the cytokine receptor TNFR and not by the subunit of the amiloride sensitive epithelial sodium channel SCNN1A (figure 4).

Diversity of the F508del-CFTR genetic background determines the clinical variability of F508del-CFTR homozygotes

We have included intragenic and CFTR flanking markers in our association study. As the enrolled patients are F508del-CFTR homozygous, the major disease causing variant is identical for all study subjects. In contrast, these F508del-CFTR chromosomes differ at closely linked neighbouring SNPs.35–37 We tested in our association study whether these different F508del-CFTR alleles are asymmetrically distributed when comparing mildly and severely affected patients or subgroups stratified for the manifestation of the basic defect. We observed a significant association of the CFTR core haplotype to the response of the nasal epithelium to superfusion with amiloride ($P_{\text{raw}}=0.0009$; figure 3 and figure 4) and ATP ($P_{\text{raw}}=0.0008$; figure 3 and figure 4). Moderate association of CFTR was observed with CF disease severity and response to gluconate and isoproterenol in NPD ($0.001<P_{\text{raw}}<0.01$; figure 3 and figure 4). These findings demonstrate that the different F508del-CFTR alleles are
functionally non-equivalent. In other words, sequences adjacent to the F508del-CFTR mutation which are phylogenetically younger than the F508del variant and/or sequences in the vicinity of the CFTR gene allowing for allelic diversity among F508del chromosomes through recombination have a functional impact on the manifestation of the CF basic defect and disease severity. We would like to emphasise the point that variant F508del-CFTR genes ($P_{\text{best}} = 0.0009$) more than ENaC variants.
Host defence capabilities affect the manifestation of the CF basic defect

We selected cytokines as well as cytokine and pathogen receptors as candidate genes and tested these for an association with basic defect phenotypes. Minor (0.01<Praw<0.1; TLR5, CD44, IFNGRI, TLR4, TGFRI), moderate (0.001<Praw<0.01; IL1B, TLR9, TNFa, CD95, STAT3), and significant (0.0001<Praw<0.001; TNFR) associations of host defence genotype to basic defect phenotype were observed (figure 3). As none of these genes encode ion channels or their intermediate interaction partners, these genotype—phenotype relations were a priori unanticipated. However, crosstalk between the immune system and secretory properties of epithelial cells have been described before: for cytokines interleukin 10 (IL10), interferon γ (IFNγ), tumour necrosis factor α (TNFα), IL1B, transforming growth factor β (TGFβ), IL4 and IL13, alterations of CFTR and/or ENaC and/or CaCC expression and/or activity, resulting in altered ion and fluid transport, have been communicated.30–41 This has been interpreted as an unspecific host response to pathogens as the surface liquid is increased on the epithelium upon induction of a hypersecretory state by inflammatory stimuli,39 and consequently mucociliary clearance of the intruding pathogen will be alleviated. Our data show that the effect of the host defence system on ion conductance properties of CF epithelia outweighs the effect of major ion channels which we also analysed in our association study.

DISCUSSION

Modifier genes have been studied in CF since Zielenksi et al described CFM1 in 1999.25 Among those studies which analyse several candidate genes at once, one modifier only is reported.12 26 On the other hand, negative outcomes in these studies are often contradicted by other isolated reports (reviewed by Cutting24) and genetic modelling has led to the expectation that many more modifiers need to be uncovered in CF.25 26 This ambiguity is likely to be understood if non-inherited factors,6 which act differently between CF centres6 as well as between patients from different birth cohorts,5 are taken into account. Improvement of therapy, quality of life and life expectancy is at the heart of medical care for all diseases. However, the increase in lifespan among CF patients within the last decades is outstanding in comparison to other chronic diseases, signifying that better medication and improvement of therapeutic management dramatically alter the environment with which our patients have to cope. As a consequence, for the human geneticist studying a CF modifier in a cross-sectionally recruited patient sample, carriers of high risk alleles will be less frequent, especially among early born patient cohorts.20 Consequently, case–control comparisons might lack power to detect an allelic imbalance if the frequency of the risk alleles within the entire CF population is reduced owing to the survivor effect. If parental genotype information is available, the allelic bias introduced by a survivor effect can be visualised by comparing transmitted and non-transmitted alleles within CF families.18 In support of this, many loci reported in this article are positive in the transmission disequilibrium test (figure 3).

The impact of non-inherited factors on the course of CF disease, and moreover the change of these confounders over time, challenges classical strategies to validate findings of association studies. Ideally, replication studies with large sample sizes are used to verify findings. However, large CF patient samples are likely to be heterogeneous and thus will not share the major environmental determinants of CF disease progression. Taking this into account, we chose to replicate the findings of our association study using confirmatory CF endophenotypes and within-dataset validation strategies. No evidence for the role of the gene as a CF modifier was found for six loci. Isolated findings—defined as an association to only disease severity or only a basic defect phenotype—were observed for 20 genes. The remaining 26 loci analysed in this study are positive for both, an association with a clinical phenotype and a CF basic defect phenotype (see figure 3 and supplemental table S). As the basic defect in CF is correlated with disease severity,14 these consistent findings must be interpreted with caution with respect to the underlying causality. Either the gene analysed has a direct influence on the efficiency of F508del-CFTR processing and trafficking and thus causes a better phenotype; or alternatively, the patient subsamples analysed for CFTR mediated residual current in ICM or NPD can be considered as enriched with individuals who are mildly diseased due to the association of mild disease with residual function in respiratory and intestinal tissue.11 In the latter case, the findings of the association study do not necessarily imply a direct causal action of the analysed modifier on the CF basic defect, but can be interpreted as a supporting finding in two independent patient subsamples. As an example, the mild TNFR haplotype (allele 1-10-2-2 at markers rs767455, D12S889, rs1204474 and rs1204473) is significantly enriched on transmitted chromosomes in the entire European CF sibling population as indicated by TDT (Stanke et al,18 figure 3) and is associated with the discordant mildly affected phenotype (Stanke et al,18 figure 5) as well as with residual chloride secretion of the nasal epithelium (figure 4). As a causal interpretation, this might reflect the interaction of the cytokine pathway and ion secretory properties of the epithelium,25–41 promoting residual chloride secretion among carriers of the mild TNFR allele. Alternatively, as we observed residual chloride secretion more frequently among patients with mild disease phenotype,11 the TNFR association with the basic defect phenotype might reflect an overrepresentation of mild modifier alleles in this patient subgroup, which is equivalent to a replication study with confirmatory outcome.

In conclusion, describing modifiers in cystic fibrosis remains challenging even though the underlying disease is monogenic by definition. In contrast, the manifestation of endophenotypes such as diabetes, the CF basic defect and ultimately disease severity is most likely polygenic by nature, implying that when looking for CF modifiers, the same obstacles will be encountered as in complex diseases such as asthma or cardiovascular disorders. Based on our experience, we suggest that patient samples in which individuals share as many non-inherited characteristics as possible, and genetic markers which are selected for a high information content to overcome the loss of power in small sized study cohorts, will facilitate mapping of clinically meaningful CF modifiers in the future.

Acknowledgements We are indebted to all participating patients and their families, physicians, CF centres and staff for their time, cooperation and assistance. The authors also thank Professor T Epplen (University of Munster) for his contribution of the genomic sequence for two microsatellites used to interrogate the HLA class I and III gene loci.

Funding VK was a member of the International Research Training Group Pseudomomas: Pathogenicity and Biotechnology (IRTG653 of the Deutsche Forschungsgemeinschaft). The support of the Fritz-Thyssen-Stiftung (to FS and TB) for analysis of the SCNN1B/SCNN1G locus is gratefully acknowledged. MM Jr was...
The study was designed by BT, JJC and TFW. All authors have revised the manuscript. Analysis of clinical data was carried out by FS, MB and BT. JG and TFW are consultants to the European CF twin and sibling study for statistics. The concept of the study was designed by BT, JJC and TFW. All authors have revised the manuscript critically for content and have approved the final version.

Provenance and peer review Not commissioned; externally peer reviewed.

REFERENCES


Genes that determine immunology and inflammation modify the basic defect of impaired ion conductance in cystic fibrosis epithelia


J Med Genet published online September 12, 2010

Updated information and services can be found at:
http://jmg.bmj.com/content/early/2010/09/12/jmg.2010.080937

These include:

Supplementary Material
Supplementary material can be found at:
http://jmg.bmj.com/content/suppl/2010/09/21/jmg.2010.080937.DC1

References
This article cites 40 articles, 6 of which you can access for free at:
http://jmg.bmj.com/content/early/2010/09/12/jmg.2010.080937#BIBL

Open Access
This is an open-access article distributed under the terms of the Creative Commons Attribution Non-commercial License, which permits use, distribution, and reproduction in any medium, provided the original work is properly cited. The use is non-commercial and is otherwise in compliance with the license. See: http://creativecommons.org/licenses/by-nc/2.0/ and http://creativecommons.org/licenses/by-nc/2.0/legalcode.

Email alerting service
Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

Topic Collections
Articles on similar topics can be found in the following collections

Open access (184)
Molecular genetics (1254)
Cystic fibrosis (39)
Pancreas and biliary tract (110)
Genetic screening / counselling (886)
Immunology (including allergy) (604)

To request permissions go to:
http://group.bmj.com/group/rights-licensing/permissions

To order reprints go to:
http://journals.bmj.com/cgi/reprintform

To subscribe to BMJ go to:
http://group.bmj.com/subscribe/