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**EDITORIAL**

- 4419 Portal vein thrombosis in cirrhotic patients - it is always the small pieces that make the big picture
Gîrleanu I, Trifan A, Stanciu C, Sfarti C
- 4428 Novel targeting approaches and signaling pathways of colorectal cancer: An insight
Tiwari A, Saraf S, Verma A, Panda PK, Jain SK

MINIREVIEWS

- 4436 Carcinogenesis on the background of liver fibrosis: Implications for the management of hepatocellular cancer
O'Rourke JM, Sagar VM, Shah T, Shetty S

ORIGINAL ARTICLE**Basic Study**

- 4448 Sheng-jiang powder ameliorates obesity-induced pancreatic inflammatory injury *via* stimulating activation of the AMPK signalling pathway in rats
Miao YF, Li J, Zhang YM, Zhu L, Chen H, Yuan L, Hu J, Yi XL, Wu QT, Wan MH, Tang WF

Case Control Study

- 4462 Molecular evaluation of glutathione S transferase family genes in patients with sporadic colorectal cancer
Rodrigues-Fleming GH, Fernandes GMM, Russo A, Biselli-Chicote PM, Netinho JG, Pavarino ÉC, Goloni-Bertollo EM

Retrospective Cohort Study

- 4472 Barrett's esophagus with high grade dysplasia is associated with non-esophageal cancer
Bar N, Schwartz N, Nissim M, Fliss-Isacov N, Zelber-Sagi S, Kariv R

Retrospective Study

- 4482 Agitation thrombolysis combined with catheter-directed thrombolysis for the treatment of non-cirrhotic acute portal vein thrombosis
Wang CY, Wei LQ, Niu HZ, Gao WQ, Wang T, Chen SJ
- 4489 Ursodeoxycholic acid combined with percutaneous transhepatic balloon dilation for management of gallstones after elimination of common bile duct stones
Chang HY, Wang CJ, Liu B, Wang YZ, Wang WJ, Wang W, Li D, Li YL
- 4499 Postoperative survival analysis and prognostic nomogram model for patients with portal hypertension
Zhang YF, Ji H, Lu HW, Lu L, Wang L, Wang JL, Li YM

Observational Study

- 4510 Fungal dysbiosis predicts the diagnosis of pediatric Crohn's disease
El Mouzan MI, Korolev KS, Al Mofarreh MA, Menon R, Winter HS, Al Sarkhy AA, Dowd SE, Al Barrag AM, Assiri AA

CORRECTION

- 4517 Correction to "Maturity of associating liver partition and portal vein ligation for staged hepatectomy-derived liver regeneration in a rat model [*World J Gastroenterol* 2018 March 14; 24(10): 1107-1119]"
Tong YF, Cai XJ

Contents

World Journal of Gastroenterology
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Observational Study

Fungal dysbiosis predicts the diagnosis of pediatric Crohn's disease

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Abstract

AIM

To investigate the accuracy of fungal dysbiosis in

mucosa and stool for predicting the diagnosis of Crohn's disease (CD).

METHODS

Children were prospectively enrolled in two medical centers: one university hospital and one private gastroenterology clinic in the city of Riyadh, Kingdom of Saudi Arabia. The children with confirmed diagnosis of CD by standard guidelines were considered cases, and the others were considered non-inflammatory bowel disease controls. Mucosal and stool samples were sequenced utilizing Illumina MiSeq chemistry following the manufacturer's protocols, and abundance and diversity of fungal taxa in mucosa and stool were analyzed. Sparse logistic regression was used to predict the diagnosis of CD. The accuracy of the classifier was tested by computing the receiver operating characteristic curves with 5-fold stratified cross-validation under 100 permutations of the training data partition and the mean area under the curve (AUC) was calculated.

RESULTS

All the children were Saudi nationals. There were 15 children with CD and 20 controls. The mean age was 13.9 (range: 6.7-17.8) years for CD children and 13.9 (3.25-18.6) years for controls, and 10/15 (67%) of the CD and 13/20 (65%) of the control subjects were boys. CD locations at diagnosis were ileal (L1) in 4 and colonic (L3) in 11 children, while CD behavior was non-stricturing and non-penetrating (B1) in 12 and stricturing (B2) in 3 children. The mean AUC for the fungal dysbiosis classifier was significantly higher in stools (AUC = 0.85 ± 0.057) than in mucosa (AUC = 0.71 ± 0.067) ($P < 0.001$). Most fungal species were significantly more depleted in stools than mucosal samples, except for *Saccharomyces cerevisiae* and *S. bayanus*, which were significantly more abundant. Diversity was significantly more reduced in stools than in mucosa.

CONCLUSION

We found high AUC of fungal dysbiosis in fecal samples of children with CD, suggesting high accuracy in predicting diagnosis of CD.

Key words: Fungiome; Mycobiome; Crohn's disease; Inflammation; Saudi children

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Core tip: We found high accuracy of fungal dysbiosis in predicting diagnosis of Crohn's disease (CD), a finding similar to bacterial dysbiosis. However, the higher area under the curve for the fungal dysbiosis classifier in stool (0.85 ± 0.057) than in mucosa (0.71 ± 0.067) ($P < 0.001$), contrasts with bacterial studies, suggesting higher accuracy of stool samples. Although the clinical application of this finding is limited at present by the high cost of fungal analysis, such information is

important from a scientific viewpoint, to increase the understanding of the role of fungal flora in CD and to stimulate further studies.

El Mouzan MI, Korolev KS, Al Mofarreh MA, Menon R, Winter HS, Al Sarkhy AA, Dowd SE, Al Barrag AM, Assiri AA. Fungal dysbiosis predicts the diagnosis of pediatric Crohn's disease. *World J Gastroenterol* 2018; 24(39): 4510-4516 Available from: URL: <http://www.wjgnet.com/1007-9327/full/v24/i39/4510.htm> DOI: <http://dx.doi.org/10.3748/wjg.v24.i39.4510>

INTRODUCTION

Inflammatory bowel diseases (IBDs), including Crohn's disease (CD) and ulcerative colitis, are chronic conditions. Their incidence is highest, with an increasing trend, in Western populations^[1,2]. However, their incidence is increasing in non-Western populations as well^[3,4]. The cause of CD remains unknown despite extensive research, and a multifactorial etiology has been suggested. In genetically-susceptible individuals, environmental triggering factors play a major role and diet and microbiota are the most relevant causative factors for children^[5]. Dietary components may act directly or through alteration of gut microbiota to initiate and maintain inflammation in susceptible subjects^[6,7]. Significant fungal dysbiosis has been demonstrated in adults and children with CD^[8-10]. Recent reports found high accuracy of bacterial dysbiosis in predicting the diagnosis of IBD in general and CD in particular^[11-13].

Despite the demonstration of fungal dysbiosis in adults and children with CD, there are no similar reports on the potential role of fungal dysbiosis in the diagnosis of CD. The objective of this report was, therefore, to evaluate the accuracy of fungal dysbiosis in stool and mucosal samples, for the diagnosis of CD in a cohort of non-Western children with new onset disease.

MATERIALS AND METHODS

Ethical considerations

This report is a portion of the main study project titled "Characteristics of inflammatory bowel disease in Saudi children". The study was reviewed and approved by the Institutional Review Board of the College of Medicine, King Saud University, Riyadh, Kingdom of Saudi Arabia (Approval number: 10/2647/IRB).

Study population, sample collection, storage, and processing

Children were prospectively enrolled in two medical centers: One university hospital and one private gastroenterology clinic in the same city of Riyadh, Kingdom of Saudi Arabia. The children were referred to these clinics for investigation of suspected IBD. The

children with confirmed diagnosis of CD by standard guidelines^[14] were considered cases and those in whom the diagnosis of CD was excluded were considered non-IBD controls. The most common final diagnoses in non-IBD controls were functional abdominal pain and polyps. Mucosal and fecal samples were collected from 15 children with confirmed CD and 20 controls without inflammation or infection. A total of 78 samples (58 from CD children and 20 from non-IBD controls) were obtained. Stool samples were collected before bowel preparation, and none afterward. Mucosal forceps biopsies were taken from various parts of the colon and ileum. All samples were put into cryovials without preservatives and transported immediately in ice to the laboratory and stored at -80 °C. At the end of the study, all samples were shipped by express mail in dry ice to MRDNA Laboratories (Shallowater, TX, United States) for microbiome analysis.

Fungal DNA extraction and sequencing

Fungal DNA was extracted using the Mobio PowerSoil kit as per the manufacturer's instructions (Mobio, Carlsbad, CA, United States). Amplicon sequencing service (bTEFAP®) was performed at MRDNA Laboratories and used for the fungal analysis^[15]. The internal transcribed spacer primers, ITS1F (CTTGGTCATTAGAGGAAGTAA) and ITS2R (GCTGCGTTCTTCATCGATGC), were used. A single-step 30-cycle polymerase chain reaction (PCR) with HotStart *Taq* Plus Master Mix kit (Qiagen, Valencia, CA, United States) was employed. Samples were sequenced utilizing Illumina MiSeq chemistry following the manufacturer's protocols.

The Q25 sequence data derived from the sequencing process was processed using the MRDNA ribosomal and functional gene analysis pipeline (www.mrdnab.com). Sequences were depleted of barcodes and primers, short sequences of < 150 bp were removed, and sequences with ambiguous base calls were removed. Operational taxonomic units were defined by clustering at 3% divergence (97% similarity), followed by removal of singleton sequences and chimeras. Final operational taxonomic units were taxonomically classified using BLASTn top hit analysis against a curated database derived from RDP II and NCBI (<http://rdp.cme.msu.edu> and www.ncbi.nlm.nih.gov, respectively) and compiled into each taxonomic level as both "counts" and "percentage" files.

Statistical analysis

All analyses were performed using Python and scikit-learn^[16]. Custom functions implementing the permutation test were written to detect the taxa with abundances significantly different between CD and control samples. When more than one sample was available from the same patient for analysis, the log relative abundances from these samples were averaged.

It has been shown that variations in species abundance are better captured by a log-transformed

than a linear scale, improving the statistical power^[13]. Therefore, we followed this approach. In addition, rare taxa (< 1% abundance or absent from > 50% of the samples) were removed to improve the statistical power. Statistical significance was assessed *via* a permutation test (Fisher's exact test), which yielded raw, uncorrected *P*-values. These were transformed into *q*-values (corrected *P*-value) that measure the probability of false discovery following the Benjamini Hochberg procedure^[17]. We considered associations statistically significant only when the corrected *P*-values were less than 0.05.

A linear logistic regression classifier (linearmodel. LogisticRegression) in scikit-learn, Machine Learning in Python^[16], was used to predict CD based on the subject's microbiota. The accuracy of the classifier was tested by computing the receiver operating characteristic (ROC) curve with 5-fold stratified cross-validation under 100 permutations of the training data partition. We partitioned the data into randomly assigned training and test sets 100 times; in each case, the classifier was trained on 4/5 of the data and tested on 1/5 of the data (*i.e.* 5-fold cross-validation).

Alpha diversity, a measure of genera richness (number of genera), was evaluated using the Shannon index. We used Fisher's *t*-test to determine *P*-values for alpha diversity.

The difference in community composition (Beta diversity) was quantified by the Bray-Curtis distance, which accounts for both patterns of presence-absence of taxa and changes in their relative abundances. Nonparametric multidimensional scaling (NMDS) was applied to visualize the distance between mucosa and stool samples taken from CD and control subjects. NMDS quantifies the dissimilarity in community composition between samples *via* a combination of presence-absence and absolute abundance of taxa. For the data shown, the separations were analyzed by the ANOSIM or analysis of (dis)similarity. The ANOSIM statistic compares the mean of ranked dissimilarities between groups to the mean of ranked dissimilarities within groups.

The statistical analyses in this article were performed and reviewed by the coauthors Kirill S Korolev, PhD and Rajita Menon, PhD from the Bioinformatics Program, Boston University, Boston, MA, United States.

RESULTS

Demographic data

All children were Saudi nationals. There were 15 CD children and 20 controls; mean age was 13.9 (range: 6.7-17.8) years for CD children and 13.9 (3.25-18.6) years for controls, and 10/15 (67%) of the CD and 13/20 (65%) of the control subjects were boys. At diagnosis, CD locations were ileal (L1) in 4 and ileocolonic (L3) in 11 children, while CD behavior was non-stricturing and non-penetrating (B1) in 12 and stricturing (B2) in 3 children. Controls included all patients with no evidence of IBD

Table 1 Fungal species abundance in mucosa and stool of controls

Fungal species	Mucosa abundance, %	Stool abundance, %	Ratio	P value
<i>Volvariella dunensis</i>	0.027	0.0013	0.047	0.036
<i>Lepraria humida</i>	0.015	0.0010	0.063	0.042

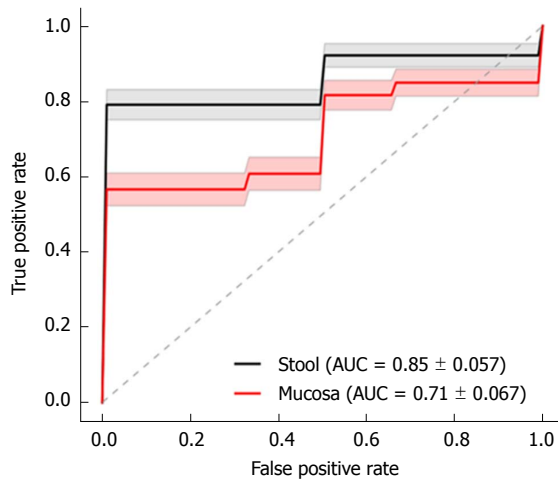


Figure 1 Dysbiosis score classification curve to distinguish between children with Crohn's disease and controls. The receiver operating characteristic (ROC) curve demonstrated the logistic regression dysbiosis classifier. The mean ROC curve for stool (solid black line) and mucosal (solid red line) dysbiosis scores in fungi cohorts is shown. The standard deviation from 100 permutations is shown in gray and light red shading. The area under the curve for stool dysbiosis is significantly higher than in mucosal dysbiosis, using a Fisher's *t*-test computed $P < 0.001$.

or other causes of inflammation. The final diagnoses in control subjects were juvenile polyps, recurrent abdominal pain, recurrent cyclic vomiting or other functional gastrointestinal disorders.

Fungal dysbiosis

In a previous report, description of fungal community structure in mucosa and stool in children with CD relative to controls indicated significantly-abundant CD-associated taxa included Psathyrellaceae ($P = 0.01$), Cortinariaceae ($P = 0.04$), Psathyrella ($P = 0.003$), and Gymnopilus ($P = 0.03$). Monilinia was significantly depleted ($P = 0.03$), whereas other depleted taxa, although not statistically significant, included Leotiomyces ($P = 0.06$), Helotiales ($P = 0.08$), and Sclerotiniaceae ($P = 0.07$)^[10].

Prediction analysis

The mean area under the ROC curve (AUC) for the fungal dysbiosis classifier is illustrated in Figure 1, indicating a significantly-higher AUC in stools (0.85 ± 0.057) than in mucosa (0.71 ± 0.067) ($P < 0.001$).

This analysis was further expanded to demonstrate the difference in abundance and diversity between mucosa and stool in controls and children with CD separately. Table 1 shows a comparison of fungal abundance between mucosa and stools in controls,

indicating that only two species, *Volvariella dunensis* ($P = 0.03$) and *Lepraria humida* ($P = 0.04$), were significantly less abundant in stool than in mucosal samples. In contrast, about 50 species were significantly less abundant in stools of children with CD ($P < 0.05$) and only two species, *Saccharomyces cerevisiae* ($P = 0.02$) and *S. bayanus* ($P = 0.001$), were significantly more abundant in stools than in mucosal samples (Table 2). Alpha diversity, as measured by the Shannon Index and illustrated in Figure 2, was different in mucosa and stool. The stool community for children with CD was more than 5 times less diverse than that of mucosa ($P = 0.0001$), whereas in controls the reduction in stool diversity was statistically not significant ($P = 0.35$). Beta diversity, as measured by the Bray-Curtis distance and visualized by the NMDS in Figure 3, shows a significant difference in fungal community separation between mucosal and stool samples ($P = 0.005$).

DISCUSSION

Microbial dysbiosis in the form of depletion of beneficial organisms, expansion of harmful organisms, and reduced microbial diversity may occur independently or concurrently and result in significant effects on immune responses^[18]. Fungal dysbiosis demonstrated in Saudi children with CD is in line with previous studies^[19,20].

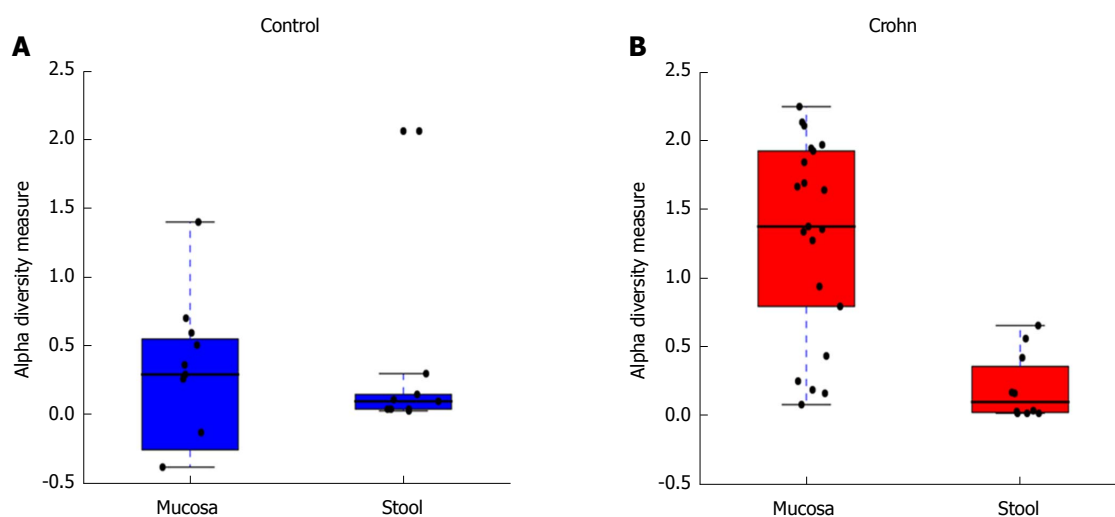
Key findings

This is the first report on the accuracy of fungal dysbiosis in mucosa and stools in predicting the diagnosis of CD in children. The main finding in this study is the high AUC for the fungal dysbiosis classifier, suggesting high accuracy in predicting the diagnosis of CD, which is in line with the high AUC for bacterial dysbiosis^[11-13]. However, the higher AUC for the fungal dysbiosis classifier is in stool (0.85 ± 0.057) rather than in mucosa (0.71 ± 0.067) ($P < 0.001$), in contrast with the higher AUC for bacterial dysbiosis in mucosal samples^[12-13]. Since this is the first report on fungal dysbiosis accuracy in predicting the diagnosis of CD, further studies are needed to clarify this result.

The finding of significant differences in a large number of species between stool and mucosa in CD children compared to much smaller numbers of species in controls reflects the degree of disturbance of the fungal community in children with CD. In this study, except for *S. cerevisiae* and *S. bayanus*, which were significantly more abundant in stool samples ($P = 0.02$ and $P = 0.003$, respectively), the significantly lower abundance of most fungal species in stool than in mucosal samples indicates

Table 2 Fungal species abundance in mucosa and stool of children with Crohn's disease

Fungal species	Mucosa abundance, %	Stool abundance, %	Ratio	P value
<i>Volvariella dunensis</i>	0.06	0.0014	0.025	< 0.001
<i>Malassezia restricta</i>	0.09	0.0044	0.049	< 0.001
<i>Ceriporia lacerate</i>	0.03	0.0022	0.065	< 0.001
<i>Cl. Cladosporioides</i>	0.11	0.004	0.035	< 0.001
<i>Trametes hirsute</i>	0.048	0.0043	0.089	< 0.001
<i>Psathyrella artemisiae</i>	0.44	0.028	0.065	< 0.001
<i>Amyloporia</i> sp	0.027	0.0012	0.046	< 0.001
<i>Irpex</i> sp	0.095	0.0019	0.02	< 0.001
<i>Bjerkandera adusta</i>	0.022	0.0011	0.049	< 0.001
<i>Lepista sordida</i>	0.041	0.0015	0.037	< 0.001
<i>Cerrena</i> sp	0.022	0.0011	0.05	< 0.001
<i>Coprinellus radians</i>	0.034	0.0011	0.032	< 0.001
<i>Phlebia acanthocystis</i>	0.022	0.0011	0.048	< 0.001
<i>Leptosphaerulina</i> sp	0.037	0.0013	0.036	< 0.001
<i>Coprinus</i> sp	0.085	0.0019	0.022	< 0.001
<i>Malassezia globosa</i>	0.028	0.0026	0.095	< 0.001
<i>Alternaria alternate</i>	0.054	0.0037	0.069	< 0.001
<i>Ramalinopsis mannii</i>	0.066	0.0018	0.027	< 0.001
<i>Saccharomyces bayanus</i>	2.5	53	21	< 0.001
<i>Trichoderma hypocre</i>	0.022	0.0014	0.067	< 0.001
<i>Aspergillus penicillioides</i>	0.11	0.0066	0.062	< 0.001
<i>Psathyrella candolleana</i>	0.063	0.0059	0.093	< 0.001
<i>Cladosporium</i> sp	0.072	0.0053	0.074	< 0.001
<i>Aspergillus</i> sp	0.064	0.0049	0.076	< 0.001
<i>Galactomyces geotrichum</i>	0.079	0.0063	0.08	< 0.001
<i>Peniophora incarnate</i>	0.011	0.0027	0.25	< 0.001
<i>Eutypella</i> sp	0.038	0.0044	0.12	< 0.001
<i>Ophiocordyceps sinensis</i>	0.059	0.004	0.068	< 0.001
<i>Nakaseomyces candida</i>	0.12	0.0058	0.049	0.019
<i>Hypocrea ceramic</i>	0.02	0.0037	0.18	0.019
<i>Saccharomyces cerevisiae</i>	0.043	0.23	5.3	0.024

**Figure 2** Alpha diversity evaluated by the Shannon Index. Comparison between mucosa and stool in children with Crohn's disease (CD) and controls. Alpha diversity is significantly lower in stool than in mucosa in CD samples ($P = 0.0001$), while the difference is not significant in control samples ($P = 0.35$).

variation in dysbiosis between stools and mucosa and supports the variable accuracy in predicting the diagnosis of CD.

It has been suggested that the presence of some fungi in the gut may reflect environmental exposure, rather than colonization of the mucosa^[21]. However, reports indicate that many fungi, such as *Candida*, *Cryptococcus*, *Malassezia*, *Saccharomyces* and *Trichosporon* spp, have

been isolated from the stool of humans^[22,23]. Furthermore, the role of fungi in the pathogenesis of IBD has been suggested based on animal models of colitis. Pattern recognition receptors in the innate immune system cells include dectin-1, dectin-2, DC-SIGN, mannose receptor, and mannose receptor lectin^[24], and mice lacking dectin-1 had increased susceptibility to experimental colitis^[25]. In addition, treatment with antifungal drugs may

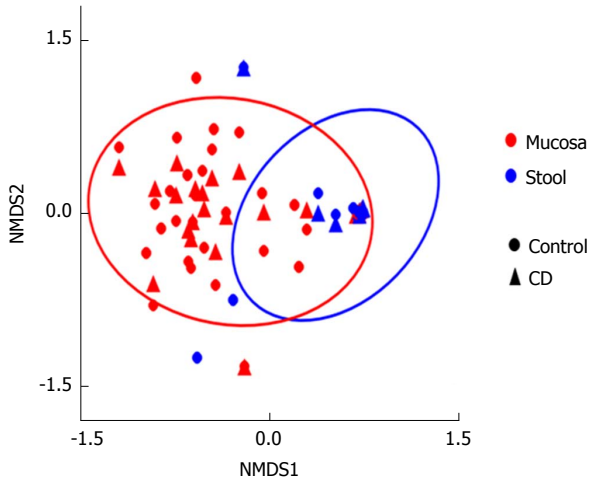


Figure 3 Beta diversity evaluated by Bray-Curtis distance and illustrated by the NMDS plot. This is a measure of beta diversity, and quantifies the similarity in abundance of taxa between samples. The ovals contain 95% of the probabilities for mucosa and stool. This plot shows a clear separation of mucosa and stool samples ($P = 0.005$). NMDS: Nonparametric multidimensional scaling; CD: Crohn's disease.

reduce the inflammation^[26].

Strengths and weaknesses of this study

The strengths of this study comprise the facts that it is the first to investigate the subject and provides inclusion of newly-diagnosed, treatment-naïve children with CD and controls from a well-defined population. Weaknesses include the relatively small number of cases which may be adequate for a first report. The controls were not completely healthy. Obviously, performing endoscopy and biopsies to exclude IBD in healthy children is unethical. Therefore, children who are free of IBD, infection and inflammation have been considered appropriate non-IBD controls.

In conclusion, the most important finding in this study is the high AUC in fecal samples of children with CD, suggesting high accuracy in predicting the diagnosis. Although, the clinical application of this finding is limited at present by the high cost of fungal analysis, such information is important from a scientific viewpoint, to increase the understanding of the role of fungal flora in CD and to stimulate further research, possibly leading to a "dysbiosis test" as a noninvasive screening tool for CD.

ARTICLE HIGHLIGHTS

Research background

Bacterial dysbiosis has been reported to predict the diagnosis of Crohn's disease (CD), but no similar reports for fungal dysbiosis exist. The study is of scientific significance to stimulate further research important for further clarification of the role of fungi in CD.

Research motivation

The role of microbiota in CD, bacterial or fungal, is of worldwide research interest. However, a key problem to be solved is whether dysbiosis is the cause or the result of inflammation. Solving this problem may facilitate discovery of

new microbiota-based treatment options. Regarding the accuracy of fungal dysbiosis in predicting the diagnosis, the main problem would be the current high cost of fungal analysis. Solving this problem could lead to development of a dysbiosis screening test for CD.

Research objectives

The objective of this study was to evaluate the accuracy of intestinal fungal dysbiosis as a predictor of CD. High accuracy was found. Future research is needed to confirm this finding and to develop low-cost fungal dysbiosis tests.

Research methods

Mucosal and stool samples were collected from children with CD at presentation and controls. Fungal DNA was extracted from these samples and sequencing was performed. Fungal abundance and diversities were determined. Fungal dysbiosis in children with CD was demonstrated. This is the first study of the accuracy of fungal dysbiosis in predicting the diagnosis of CD in children.

Research results

The main finding was the high accuracy of fungal dysbiosis in predicting diagnosis of CD. This should stimulate further research to confirm our findings and to develop a low-cost dysbiosis test.

Research conclusions

The high accuracy of fungal dysbiosis in predicting the diagnosis of CD is a new finding. The finding could lead to further research in the role of fungal dysbiosis in CD. A new theory suggests the possibility of design of a noninvasive fungal dysbiosis screening test for CD.

Research perspectives

The role of microbiota in CD may include development of a noninvasive screening test. Further research is needed to confirm the findings and to develop low-cost fungal analysis.

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