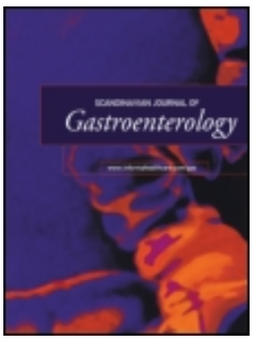

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Increased number of *Candida albicans* in the faecal microflora of chronic fatigue syndrome patients during the acute phase of illness

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Chronic fatigue syndrome (CFS) is an illness characterized by unexplained disabling long-term fatigue [1]. The patients often describe an infectious-like illness onset, which suggests micro-organisms as the triggering factors. Interestingly, treatment with an oral antifungal drug together with a special diet to reduce candidiasis [2], and immune stimulation with a staphylococcal vaccine have improved the health of CFS patients [3].

Humans depend on a well-functioning microflora for their well-being. Lower concentrations of *Escherichia coli* in the total intestinal microflora have been observed in CFS patients [4]. In the present study we have evaluated different aspects of the intestinal microflora in faeces of CFS patients and healthy controls.

Participants

Faecal samples were collected from CFS patients in the acute phase of the illness ($n = 20$; 14 F, 6 M, average age 41 years), from the same patients when in remission, and from healthy controls ($n = 19$; 15 F, 4 M, average age 46 years) (Biobank Biologicalmark CFS, Karolinska University Hospital, Huddinge, Sweden). None of the patients had a diagnosis of irritable bowel syndrome (IBS).

Methods

The participants were asked to grade their level of fatigue, muscle problems and function of short-term memory and concentration according to a visual analogue scale (VAS) questionnaire at the time of sampling.

We investigated the composition of the aerobic and anaerobic microflora, the number of staphylococcal spp, *Clostridium* spp, *E. coli* and *C. albicans* using culture techniques.

Enterobacteriacae were identified with the API-20E test kit (Bio Mérieux, Marcy I'Etoile, France), anaerobic microorganisms by gas liquid chromatography metabolites from glucose, and *C. albicans* by the germ-tube test [5]. A multivariate analysis test one-way analysis of variance (ANOVA) was used for statistical testing.

Results

A significantly higher number of *C. albicans* was found in CFS patients when in the acute phase of illness compared with when in remission (see Table). Significance was reached when all three symptoms from the VAS questionnaire were included separately (Table). *C. albicans* was found in 12 out of 20 patients in the acute phase (median $= 9.5 \times 10^2$, range $= (2.0 \times 10^2 – 2.0 \times 10^4)$), 6 of 20 patients in remission (1.5×10^2, ($1.0 \times 10^2 – 7.5 \times 10^3$)) and in 10 of 19 healthy controls (1.7×10^3, ($1.0 \times 10^2 – 5.5 \times 10^3$)).

We did not find any differences in the total number of aerobic and anaerobic bacteria or in the number of staphylococci, clostridia or *E. coli* in the faecal microflora of patients when in the acute

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Table I. Mean values of the symptoms rated in the VAS questionnaire and statistical results.

	All CFS patients ($n=20$)		CFS patients with *C. albicans* ($n=13$)		CFS patients without *C. albicans* ($n=7$)		
Symptom	Remission	Acute phase	Remission	Acute phase	Remission	Acute phase	One-way ANOVA
Fatigue	5.7	8.8	6.0	9.4	4.9	7.6	$F(1.38)=12.49$, $p=0.001$
Muscle	3.5	6.2	3.5	7.1	3.5	4.4	$F(1.38)=7.76$, $p=0.008$
Short term memory	5.8	7.9	6.0	7.9	5.3	7.8	$F(1.38)=6.68$, $p=0.014$)

Abbreviations: VAS = visual analogue scale; CFS = chronic fatigue syndrome; ANOVA = analysis of variance.

phase of illness versus when in remission, or between CFS patients and healthy controls.

Chronic intestinal candidiasis, mucous membrane overgrowth of *C. albicans*, has previously been suggested to be a causal factor in CFS [2]. It is also possible that increased levels of *C. albicans* function as an indicator of an ecological disturbance that plays an important role in the symptom profile of the illness.

We suggest that further studies should include a larger study cohort. The culture techniques could cause biased results since not all bacterial groups are cultivable. With molecular techniques a larger microbial diversity can be studied.

Comments

We have shown that CFS patients, without IBS, have an increased number of *C. albicans* in their intestinal microflora during the acute phase of illness. It remains unclear what effect an increased number of *C. albicans* has for the onset of CFS. It could be a marker of an ecological disturbance, or it could contribute to the symptoms observed in CFS or be a causal factor.

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