Effects of Chlorella supplement on intestinal environment, such as improvement of constipation

Presented at the 13th Annual Meeting of the Japanese Society for Complementary and Alternative Medicine (2010)

[Study Objectives]

Constipation is a common problem in women and elderly individuals. It compromises the intestinal environment and increases the products of intestinal putrefaction, which may significantly damage the patient's health by decreasing immunity, increasing the risk of cancer, and aging. Chlorella is rich in dietary fibers, amino acids, vitamins, and minerals. We studied the effects of Chlorella on constipation and intestinal microflora in the intestinal environment.

[Method of experiments]

The subjects of the study were 11 women with constipation tendency (defecation frequency of 3–5 times/week). The total study period was 5 weeks. The subjects took 40 Chlorella tablets (8 g) for 3 weeks, followed by a 2-week withdrawal period. To investigate the effects of Chlorella supplementation, the subjects recorded the fecal amount and defecation frequency every day. Feces were sampled 3 times in total, namely, before treatment (D0), at the end of treatment (D21), and after withdrawal (D35), to analyze the intestinal microflora by Nagashima's method of terminal restriction fragment length polymorphism (T-RFLP) ¹⁾. The subjects also documented the contents of meals every day.

[Results]

Chlorella increased both fecal amount and defecation frequency compared with those before treatment (Table 1).

Table 1 Effects of Chlorella on fecal amount and defecation frequency in constipated women

	Baseline	W1	W2	W3	W1 of withdrawal	W2 of withdrawal
Fecal amount (number/week)	9.2 (4.9)	12.8 (5.8)	13.2 (6.8)*	11.8 (7.8)	13.4 (7.0)	10.7 (4.9)
Defecation frequency (number/week)	4.36 (0.81)	5.82 (1.47)*	6.00 (1.61)*	5.55 (2.25)	5.82 (2.18)*	5.09 (1.58)

Value is mean (standard deviation). The fecal amount is expressed as the number of feces of large chicken egg size. *Dunnett's test, p < 0.05

The overall composition of intestinal microflora showed a \geq 20% change between before and after treatment (D0 and D21) in 4 of the 11 subjects. The intestinal microflora needs to be evaluated based on its overall composition. Currently, however, we do not have sufficient data to clarify the correlation between intestinal microflora composition and health condition. In our study, we used a change in the composition of each bacterial group as a measure of the

effectiveness of Chlorella. The one or more compositions among Bifidobacterium, Lactobacillus, or Bacteroides increased by $\geq 30\%$ in 7 of the 11 subjects (Table 2). Bacteroides have been reported to exert a more potent intestinal immunostimulatory action than Lactobacillus.

Table 2 Changes in the composition of each bacterial group

Subject	į										
Assumed bacterial group	1	2	3	4	5	6	7	8	9	10	11
Bifidobacterium	0.300	0.128	-0.285	-0.858	0.033	0	0.635	- ∞	-0.220	0.267	0.395
Lactobacillus	-0.779	-0.200	- ∞	-0.214	0.319	0	0.625	-0.333	- ∞	$+\infty$	3.600
Bacteroides	0.347	0.043	-0.170	0.326	0.079	-0.108	0.104	1.153	0.112	-0.083	-0.083

Calculation formula: D21/(D0 + D35)/2-1

There was a tendency of inverse correlation between the % increase in the fecal amount and the % change in intestinal microflora (Fig. 1). This finding indicates that subjects with a large change in intestinal flora tend to defecate more.

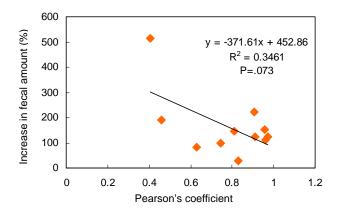


Fig. 1 Changes in intestinal microflora and % increase in fecal amount

The study showed that Chlorella supplement significantly increased fecal amount and defecation frequency, which appear to be attributable to the nutrients contained in Chlorella, including dietary fibers and minerals. The study also suggested that Chlorella changes the intestinal microflora and thereby contributes to improvement of the intestinal environment. To confirm this assumption, however, further studies need to be accumulated.

<<Description of terms>>

¹⁾ Nagashima's T-RFLP method: While the conventional culture method identifies only approximately 20–30% of the overall intestinal bacterial population, this technique allows comprehensive analysis of the intestinal flora to some extent by utilizing bacterium-specific DNA.

<< Presentation at a scientific meeting>>

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Presenters: Hideo Takekoshi, Masako Saito, and Hirofumi Chubachi

Affiliation: Sun Chlorella Corporation

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