



Dysbiosis of gut microbiome is associated with rupture of cerebral aneurysm

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Abstract

The relationship between the gut microbiome and aneurysm rupture is unclear. We compared the gut microbiome in patients with unruptured intracranial aneurysms (UIAs) and ruptured aneurysms (RAs) to identify the specific bacteria causing the rupture of CAs. Their gut microbiomes were analyzed using 16S rRNA sequencing. Subsequently, PCR was performed to identify the specific species. The gut microbiome in the RA and UIA groups exhibited significantly different taxonomies. The abundance of the genus *Campylobacter* and *Campylobacter ureolyticus* was significantly higher in the RA group. The gut microbiome profile of patients with stable UIAs and RAs were significantly different. The genus *Campylobacter* and *Campylobacter ureolyticus* may be associated with the rupture of CAs.

Significance of the research and Future perspective

The gut microbiome profile of patients with stable UIAs and RAs were significantly different. The genus *Campylobacter* and *Campylobacter ureolyticus* may be associated with the rupture of CAs. With the results of this study, we expect that adding gut microbiota as a new factor will allow us to predict the rupture of unruptured cerebral aneurysms with higher accuracy. In addition, we believe that this will lead to a new treatment for unruptured cerebral aneurysms by manipulating the gut microbiota.

Life science

Background & Results

Background

Environmental factors are important with respect to the rupture of cerebral aneurysms (CAs). However, the relationship between the gut microbiome, an environmental factor, and aneurysm rupture is unclear. Therefore, we compared the gut microbiome in patients with unruptured intracranial aneurysms (UIAs) and ruptured aneurysms (RAs) to identify the specific bacteria causing the rupture of CAs.

Methods

A multicenter, prospective case-control study was conducted over one year from 2019 to 2020. The fecal samples of patients with stable UIAs and RAs immediately after onset were collected. Their gut microbiomes were analyzed using 16S rRNA sequencing. Subsequently, a phylogenetic tree was constructed and PCR was performed to identify the specific species.

Results

A total of 28 RAs and 33 UIAs were included in this study. There was no difference in patient characteristics between RAs and UIAs: age, sex, hypertension, dyslipidemia, diabetes status, BMI, and smoking. No difference was observed in alpha diversity; however, beta diversity was significantly different in the unweighted UniFrac distances. At the phylum level, the relative abundance of *Campylobacter* in the RA group was larger than that in the UIA group. Furthermore, the gut microbiome in the RA and UIA groups exhibited significantly different taxonomies. However, *Campylobacter* was focused on because it is widely known as pathogenic among these bacteria. Then, a phylogenetic tree of operational taxonomic units related to *Campylobacter* was constructed and four species were identified. PCR for these species identified that the abundance of the genus *Campylobacter* and *Campylobacter ureolyticus* was significantly higher in the RA group.

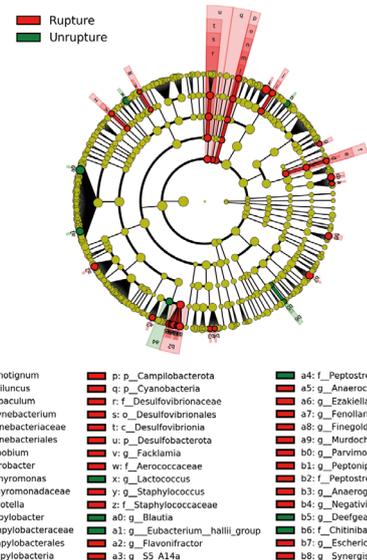


Fig. 1: LEfSe analysis
Bacteria common in patients with subarachnoid hemorrhage are shown in red.

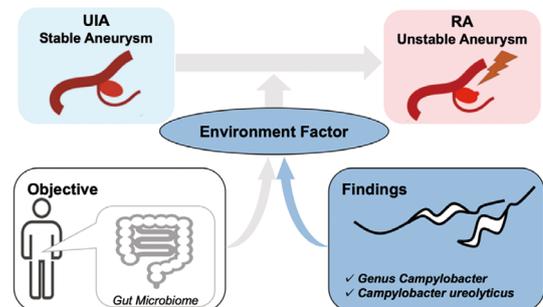


Fig. 2: Graphical abstract
The genus *Campylobacter* and *C. ureolyticus* may be associated with the rupture of cerebral aneurysms.

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