[TITLE]

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# Introduction

Irritable bowel syndrome (IBS) is a common chronic gastrointestinal disorder that is associated with changes in bowel habits. IBS is estimated to occur in 10-15 percent of the populations in Western Countries with higher prevalence in women (Hungin et al., 2005). Although IBS does not increase mortality risk (Staller et al., 2020), it dramatically affects patients’ quality of life and work productivity (Paré et al., 2006). The indirect effect of lower work productivity and the direct effect of utilisation of healthcare resources cost the United States of America 1.6 billion US dollars in 2000 (Sandler et al., 2002). To date, IBS is diagnosed based on symptoms and rule-out approach (Spiller et al., 2017; Khan and Chang, 2010). This has led to delay in the diagnostic of IBS (International Foundation for Functional Gastrointestinal Disorders, 2002) and misdiagnosis of other diseases as IBS (Burgmann et al., 2006; Card et al., 2013). Therefore, an advanced diagnostic method is needed for IBS.

It is apparent that IBS is associated with changes in the central nervous system and the digestive system (Horwitz and Fisher, 2001). Although studies are still being conducted to investigate the pathophysiology of IBS, there were evidences that showed the gut microbiota are associated with alteration in gastrointestinal in motility (Kabouridis et al., 2015), visceral hypersensitivity (Crouzet et al., 2013), abnormal brain-gut communications (Nobuyuki et al., 2004), autonomic dysfunction (Patel et al., 2012), and activation of immune system (Dlugosz et al., 2015), which contributed to the development of IBS (Cowell et al., 2005). This provides an insight that the gut microbiome could be a centre of focus for IBS management.

Microbiome analysis is an emerging technology that has shown promising advancement in diagnosis of gastrointestinal diseases, including IBS (Claesson et al., 2017). This review describes gut microbiome analysis and how it can be used to diagnose IBS. Microbiome analysis is compared with the traditional method of IBS diagnosis based on symptoms. Microbiome analysis is shown to be a more accurate and quicker diagnostic procedure than symptom-based diagnosis.

# Gut microbiome analysis

Microbiota refers to the collection of microorganisms that are present in a sample while microbiome is the collective coding capacity of the microorganisms in the sample. On average, humans host around 0.2 Kg of bacteria, with the bacteria concentration of 1011/mLand 108/mL in the colon and ileum, respectively (Sender et al., 2016). The gut microbiota influences the brain and can cause reactions in the immune system and signalling functions (Galland, 2014). This is very important in IBS as it is associated with the gut brain axis dysregulation (Bhattarai et al., 2017), which could be influenced by the microbiota. Faecal samples showed significant difference gut microbiota between IBS patients and healthy control (Codling et al., 2010). As such, gut microbiome analysis is a potential diagnostic tool for IBS (Claesson et al., 2017, Chong et al., 2019).

The gut microbiome analysis involves sample collection, extraction of nucleic acids, and bioinformatics analysis. Faecal samples are common for gut microbiome analysis but luminal brush, rectal swab, colonic lavage, pinch biopsy, and submucosal biopsy could also be used. Faecal collection is non-invasive and does not provide discomfort to the patients but there could be potential contaminations, whereas rectal swab may provide discomfort. The rest of sampling collection methods require endoscopy but provide better information about host-microbe interactions (Claesson et al., 2017). Storage of sample is very important for the further steps of the analysis. Previous studies have shown not freezing the samples for four days provide stability but if frozen, swab, fecal occult blood test, and stored in 70% ethanol, highest accuracy will be obtained (Sinha et al., 2016; Vogtmann et al., 2017; Wu et al., 2018). Choosing and storing sample types would be the first crucial step in the gut microbiome analysis.

Extraction methods of nucleic acids, DNA and/or RNA, may vary due to different circumstances. Using commercial DNA extraction kits could be cost-effective and less time-consuming. The results may vary between different extraction kits but optimisation and use of sensitive and specific detective method such as TaqMan Polymerase Chain Reaction (PCR) may combat this problem (Persson et al., 2011).

# Symptom-based diagnosis

# Compare and contrast

# Conclusions

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