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Deciphering the Salivary Microbiome in Crohn's Disease Individuals with Different Factors Predisposing to Dysbiosis

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Introduction

- ✓ **Crohn's disease (CD), common in the UAE, is a chronic inflammatory disorder of the gastrointestinal tract.**
- ✓ **Dysbiosis can predispose to many diseases including CD (figure 1).**
- ✓ **This study aims to investigate the alterations in the salivary microbiome in patients with CD compared to health controls (HC).**

Methodology

- **Saliva samples were collected from CD and HC; 40 samples for each group.**
- **Information related to the participants' oral and general health was recorded (figure 2).**
- **DNA was extracted from saliva.**
- **Oxford nanopore sequencing technology was performed for salivary microbiome profiling (figure 3).**

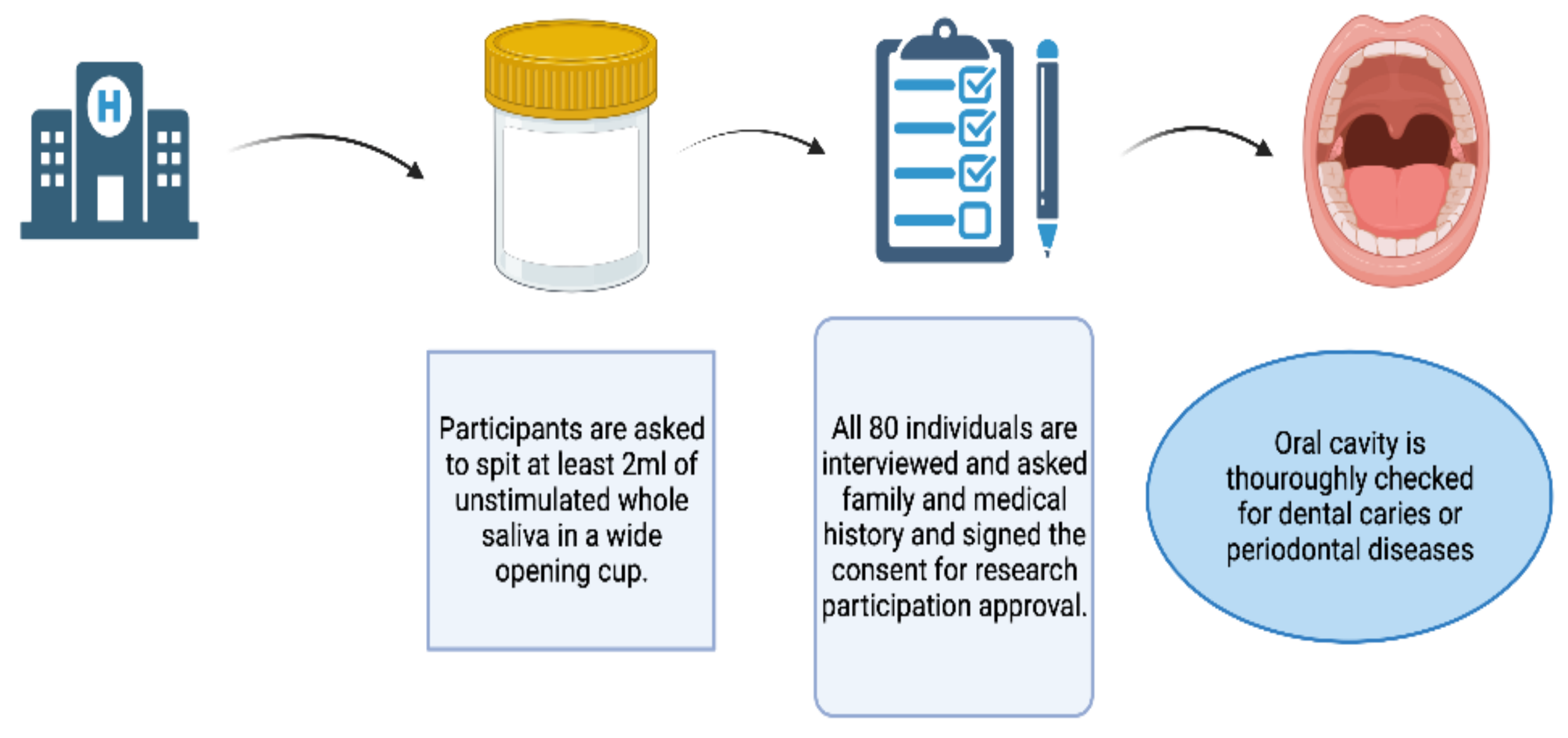

Figure 2. Schematic diagram of data collection steps

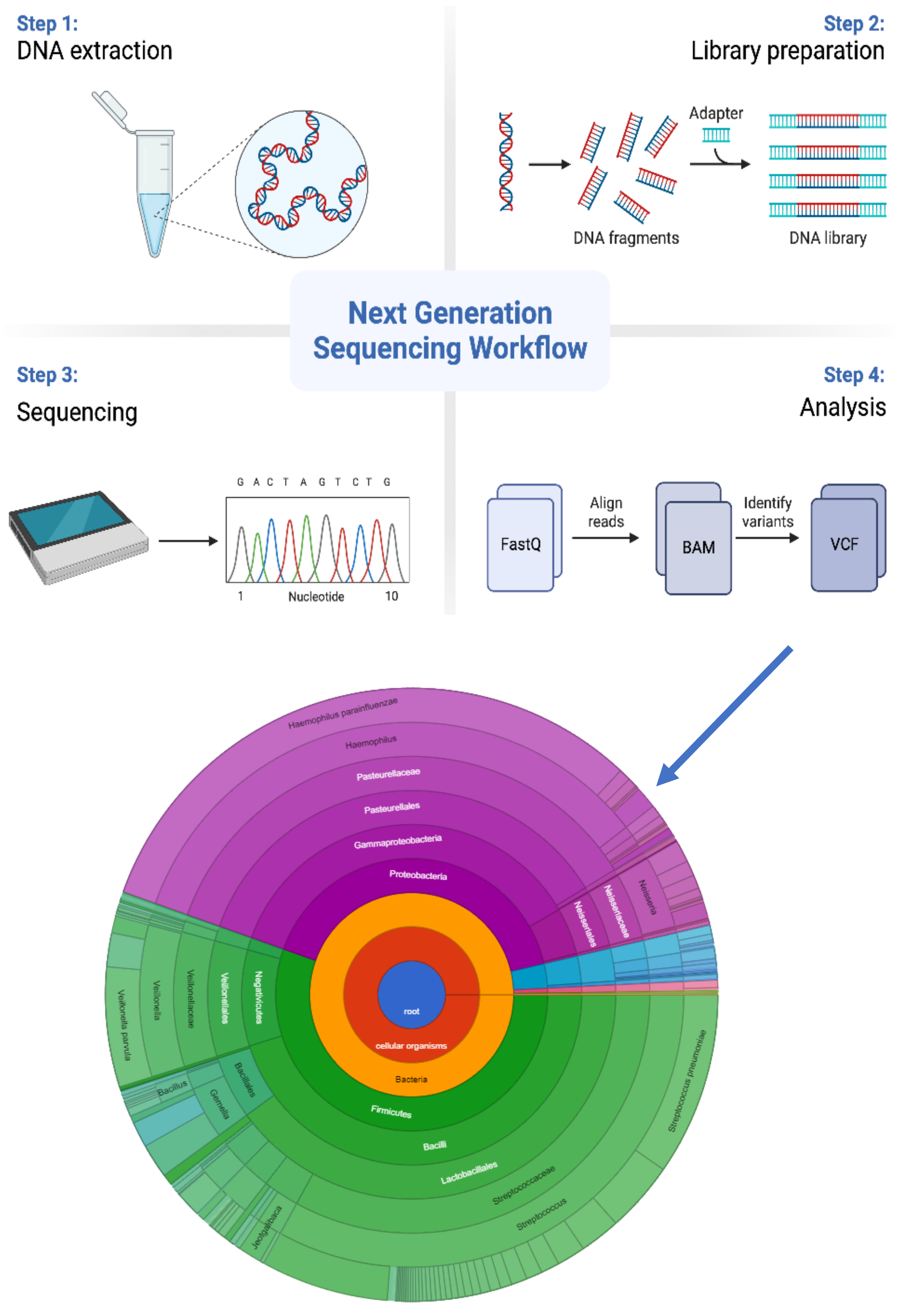

Figure 3. Next generation sequencing workflow & microbiome profiling

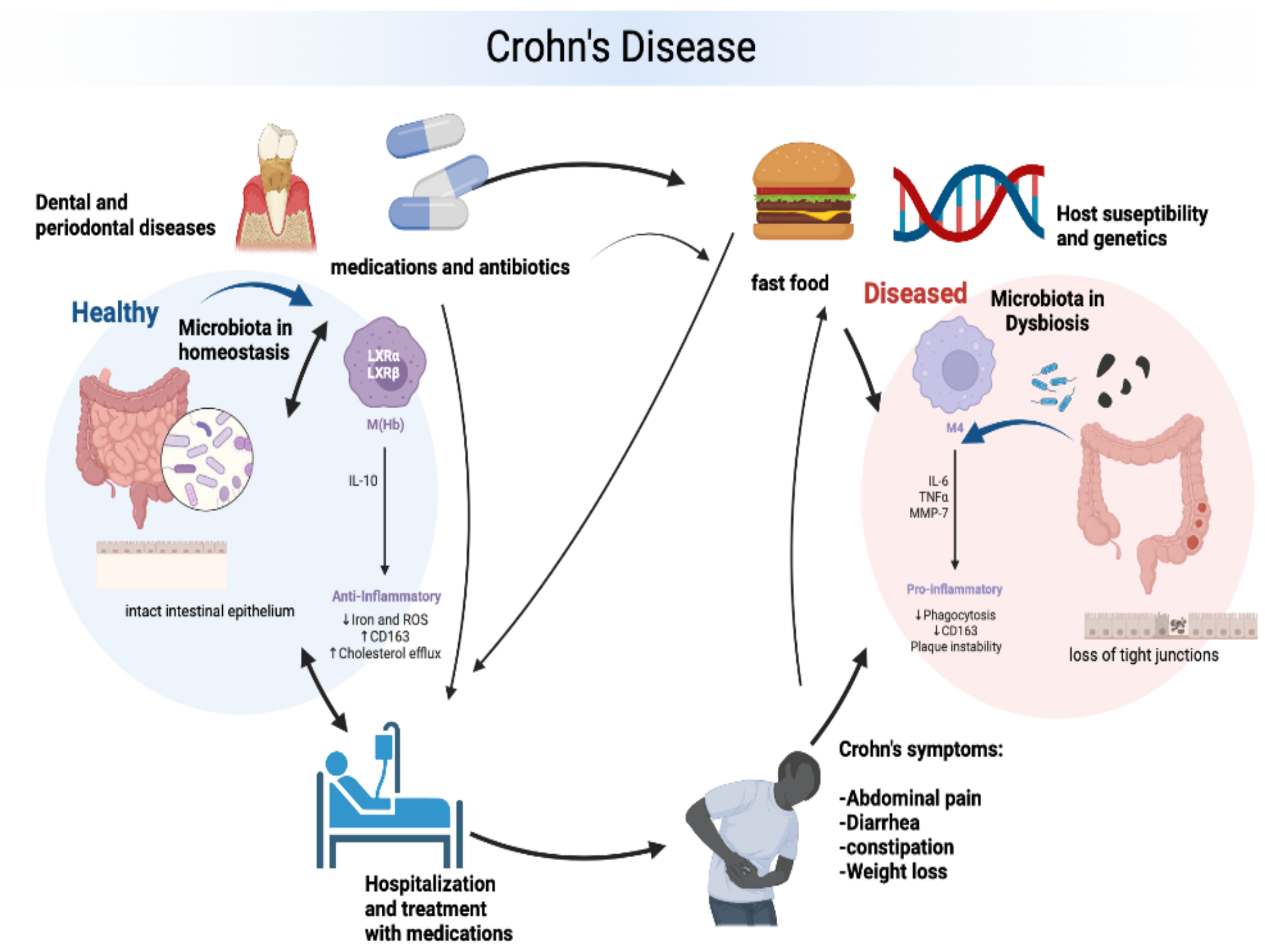

Figure 1. Possible causes of dysbiosis as a consequence of disruptions in microbiome

Results

- ✓ **Obvious difference in the salivary microbiome of CD was found when compared to HC.**
- ✓ **Five dominant species were enriched in CD and depleted in HC, shown in figure 4.**
- ✓ **Oral health has paramount significance in the dysbiosis of the oral microbiota since most significant features are cariogenic (*Streptococcus mutans*) or periopathogenic (*Fusobacterium periodonticum*).**
- ✓ **Biologicals produces a novel species called *Simonseilla muelleri.***
- ✓ **When immunomodulatory agents were used in conjunction with biologicals, pathogenic species such as *Salmonella enterica, Escherichia coli, Klebsiella pneumoniae* and *Pseudomonas aeruginosa* were detected.**
- ✓ **Loss of bacterial diversity in CD was shown by alpha diversity indices (figure 5), as well as dissimilarity between CD samples through beta diversity.**
- ✓ **The activity of the disease, duration and the relapse of symptoms also led to dysbiosis, as all factors interact with each others (figure 6).**

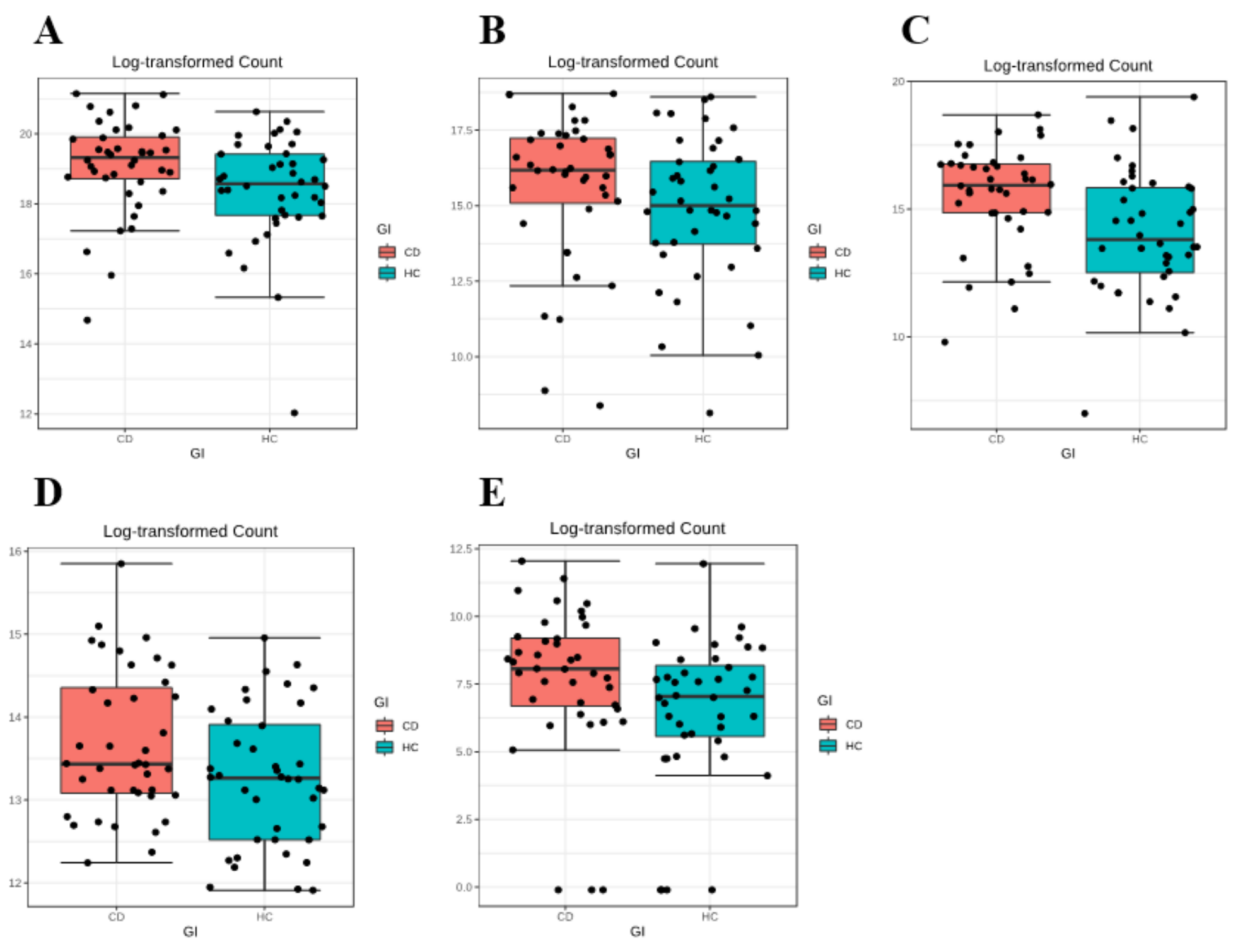

Figure 4. Significant bacterial species detected in the saliva of CD patients. A. *Veillonella dispar,* B. *Megasphaera stantonii,* C. *Prevotella jejuni* D. *Dolosigranulum pigrum,* and E. *Lactobacillus backii*

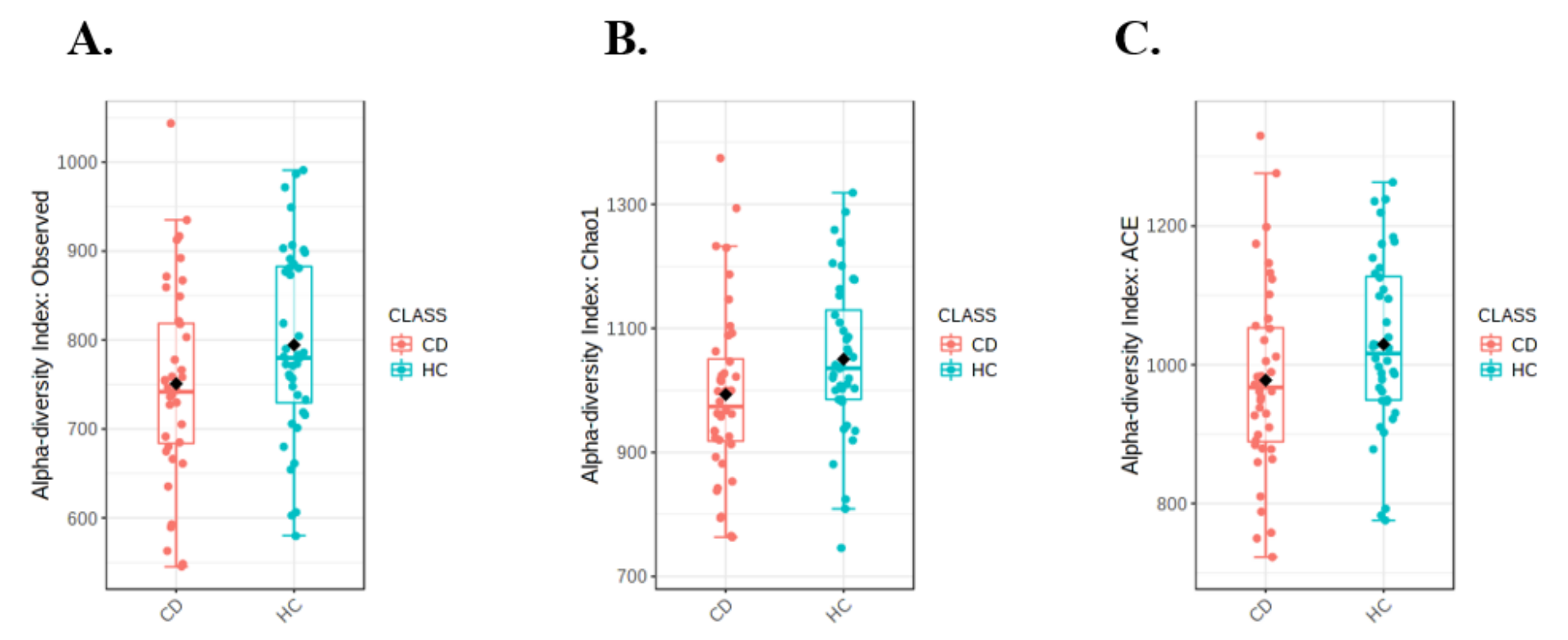

Figure 5. Alpha diversity indices A. Observed, B. Chao 1, C. ACE

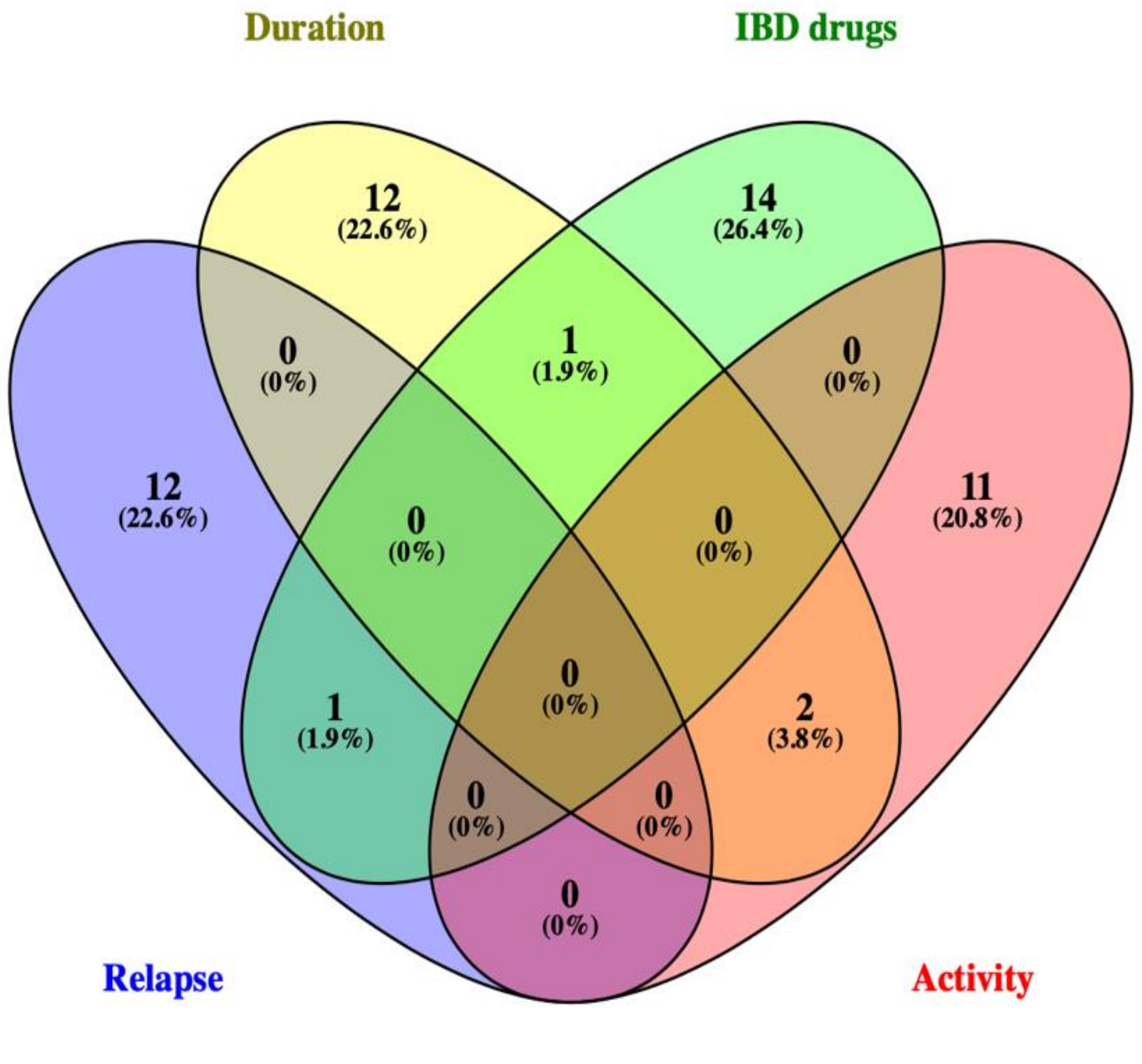

Figure 6. Venn diagram of exclusive and shared taxonomically unique microbiota at species level based on duration, IBD drugs, relapse, and activity

Discussion

- ✓ **Alterations of the composition of the salivary microbiome confirm dysbiosis in CD patients.**
- ✓ **The emergence of pathogenic species is an evidence of dysbiosis in CD, which can be induced by many factors including medications (1-2).**
- ✓ **Oral health is important according to the hypothesis that bacteria in the oral cavity is translocated into the intestine as each person can ingest 1-1.5 L of saliva per day (3).**
- ✓ **As a result, pathogenic oral microbes that are swallowed have the potential to disrupt the balance of the gut microbiota.**
- ✓ **Microbial metabolites might also be swallowed or absorbed; this can be another hypothesis explaining the effect of oral dysbiosis in the gut (3).**
- ✓ **It is found that the bacterial metabolites decrease the intestinal immunity and induce inflammation (4).**
- ✓ **In the Venn diagram, the overlapped species were marked as 0% indicating that each factor has its distinct and unique impact on the microbiome. This was altered by the combined effect of all the factors leading to dysbiosis.**

Conclusions

- ✓ **This study, established for the first time in the UAE, analyzed in-depth the salivary microbiome in CD and utilized a sequencing technique with high resolution to characterize microbiota down to the species level. In addition, the study involved multiple factors contributing to dysbiosis that added to its uniqueness.**
- ✓ **Dysbiosis in CD was attributed to the contributing factors that led to the disease pathogenesis. However, further studies are required to explore the effect of detected species on the disease activity.**
- ✓ **Microbiota homeostasis is the key to well-being; thus, restoring natural balance of microbiota can be a promising therapeutic approach.**

References

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