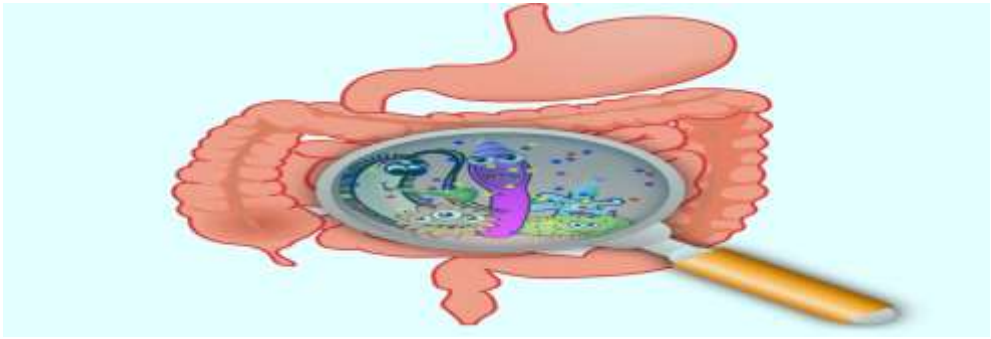
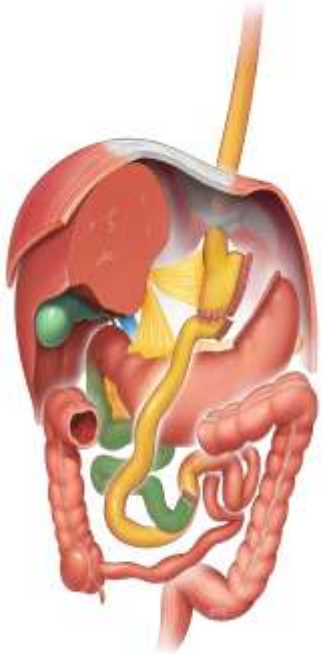
XXVI IFSO WORLD CONGRESS OF BARIATRIC & METABOLIC SURGERY

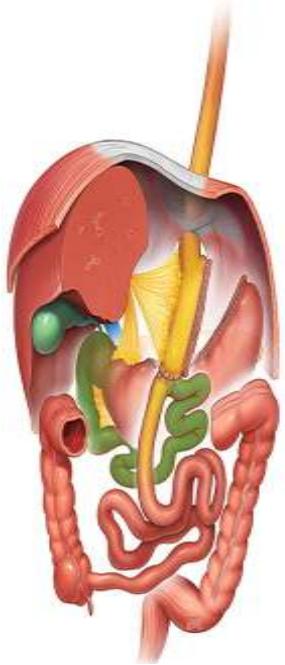
IFSO NAPOLI 2023

NAPLES, ITALY
AUGUST 30-SEPTEMBER 1, 2023
Congress President: Prof. Luigi Angrisani





Gut microbiota's shift 1 year after laparoscopic Roux-en-Y vs One Anastomosis Gastric Bypass



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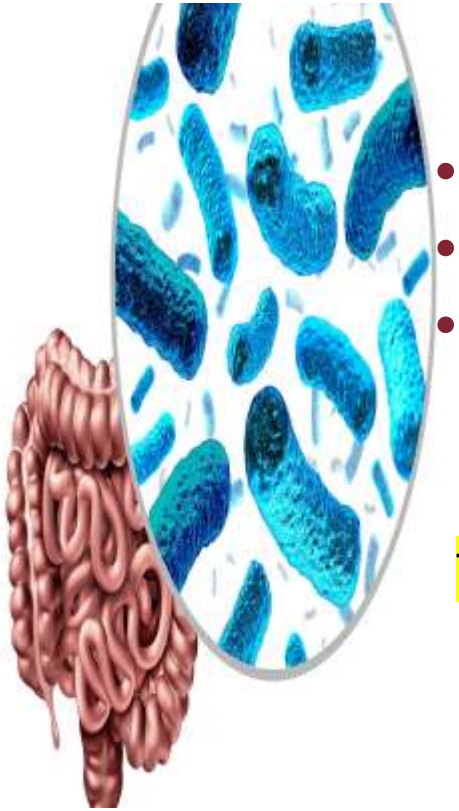
No potential conflict of interest to report

The study was partially funded, unconditionally by
- research grant from the University La Sapienza of Rome Ateneo's Funds 2017
- research grant from the European Association of Endoscopic Surgery (EAES) Research Program 2018
- Italian Society of Diabetology (SID) 2021 Research Reward "Premio SID Diabete e Ricerca"



BACKGROUND

- GM may contribute to obesity by altering the proportions in bacterial phyla
- GM may mediate some of the metabolic effects of BMS
- changes in its composition and diversity have been observed after RYGB

There are no prospective investigations of GM's SHIFT after OAGB vs RYGB in homogenous cohort of patients with severe obesity.

AIMS

- to compare GM's composition in subjects with severe obesity eligible for BMS and with / without metabolic syndrome.
- to compare OAGB vs RYGB microbiota profile shift at 1 year and its impact on the metabolic and nutritional status.

MATERIAL & METHODS 1

Centers
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Department of Clinical Medicine and Surgery, University of Naples "Federico II", Naples, Italy Prof. B. Capaldo

- prospective, randomized study, multicenter: 3 high volume Italian bariatric centers
- Registered on clinicaltrials.gov 2018 (Unique Protocol ID: NCT03412149)
- approved by the local committees
- conducted in accordance with the principles of Good Clinical Practice and STROBE checklist

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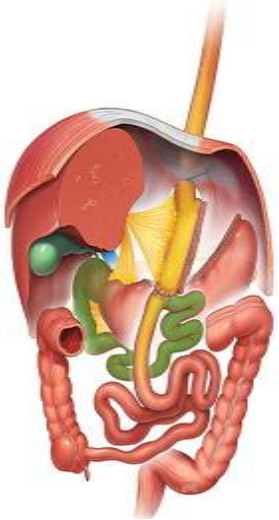
MATERIAL & METHODS 2



84 patients with severe obesity randomized in 2 groups
between 2018 - 2020
Fecal (for GM) and blood samples were collected
preop (T0) and at 12 mo (T1)

Inclusion criteria

Aged 18–65 years old
BMI 40–55 kg/m²
non-smokers
Informed consensus agreed

Exclusion criteria

corticosteroids, vitamin E, fish oil treatment;
antibiotics or probiotics treatment 2 months prior to surgery
chronic gastrointestinal diseases or syndromes;
previous bariatric and/or HPB surgery; and gallstones
severe esophagitis (LA classification > B)
severe GERD and large hiatal hernia

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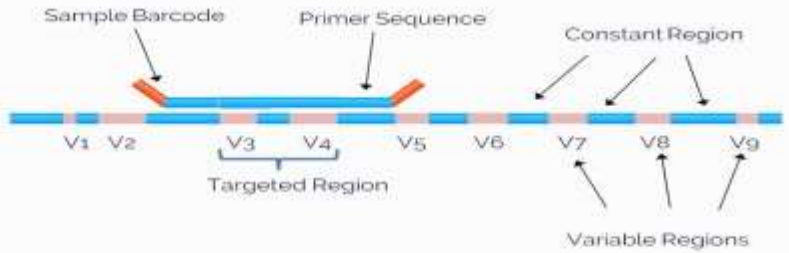


MATERIAL & METHODS 3

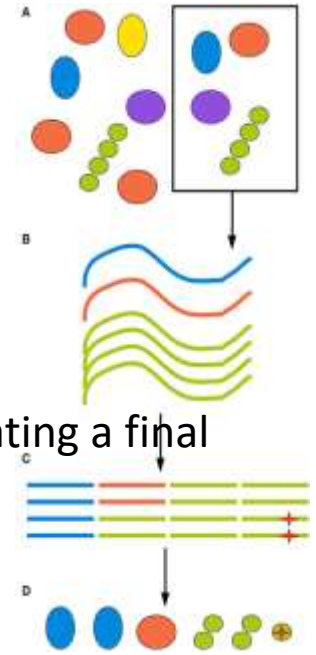
Sample processing and 16S rRNA gene sequencing, Bioinformatics and statistics analyses

1. Fresh stool samples were collected before and 1 y after surgical intervention and stored at -80°C until processing.
2. DNA isolation was performed within a biological safety and sterile cabinet
The extracted DNA was stored at -20˚C until further analysis.

3. Before library preparation, the isolated DNA was quantitatively evaluated
4. V3–V4 hypervariable regions from the **16S rRNA gene** were amplified by using the primers and conditions
Extracted DNA (2.0ng) was used as the template in a 50-µL PCR volume

5. Purified amplicons were used to generate DNA libraries, which were submitted to sequencing on the Illumina MiSeq instrument (Illumina). The raw sequencing reads were processed.

MATERIAL & METHODS 3



6. Bacterial community analysis was performed in R studio version 4.0.2 using the phyloseq software package.

7. This resulted in 8,160,105 reads (median value = 78,519 reads) accounting for a total of **907 bacterial taxa.**

An additional taxonomic filter was applied to remove low-prevalence taxa (Patescibacteria and Tenericutes), generating a final dataset that accounted **8,159,323 reads (median value = 78,519reads) accounting for 904 taxa.**

8. Alpha diversity was measured using the observed species index, Shannon index, Pielou's Evenness and Faith's diversity.

9. Beta diversity was measured by Bray-Curtis and Weighted Unifrac distance and visualized by principal coordinate analysis.

10. Statistical differences were assessed by Kruskal-Wallis test for alpha-diversity or the PERMANOVA test for beta diversity.

Relative abundances were calculated at phylum and genus levels statistical significance was assessed by the Kruskal-Wallis test.

RESULTS TO

- *No differences regarding anthropometric, nutritional parameters, except for vitamin D.*
- ***The alpha and beta diversity** examinations showed no statistical differences in GM profile.*
- ***There were no significant differences in the top ten genera.***
- *Data on **BACTEROIDES** (inversely related to triglycerides and LDL and directly related to HDL levels) and on **FIRMICUTES** (opposite trend) relative abundances suggest no differences among the three conditions: MS, pre-MS and obesity*
- *No correlation between the relative abundance of the main phyla and plasmatic glucose levels was observed.*

- ***Conclusions:** In a selected cohort of patients with obesity, MS did not affect the preoperative GM's profile.*

Severe obesity, per se, seems to be an independent condition affecting GM.

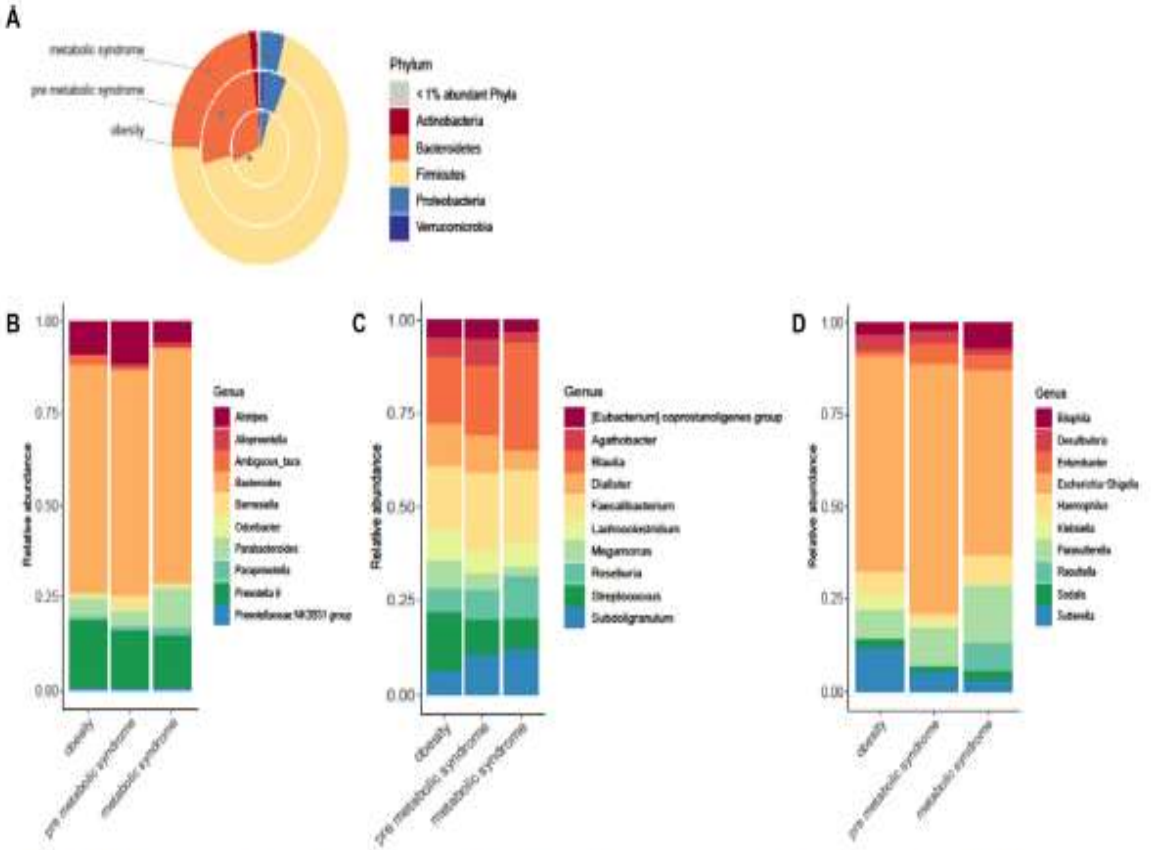


Fig. 2 – Microbiota composition differences between patients with obesity, pre-metabolic and patients with metabolic syndrome. (A) Pie chart showing the relative abundances of the main phyla identified in the three groups. Stacked bar plot showing the average relative abundance of the 10 most represented genera within the major phyla that compose the gut bacterial community of the three groups, *Bacteroidetes* (B), *Firmicutes* (C) and *Proteobacteria* (D).


Contents available at ScienceDirect
Diabetes Research and Clinical Practice
ELSEVIER
International Diabetes Federation

Characterization of gut microbiota in patients with metabolic syndrome candidates for bariatric/ metabolic surgery: Preliminary findings of a multi-center prospective study

RESULTS T1: 54 pts randomized in 2 groups

SURGICAL

Mortality, conversion rate and hospital readmission for reoperation were nil in both groups.

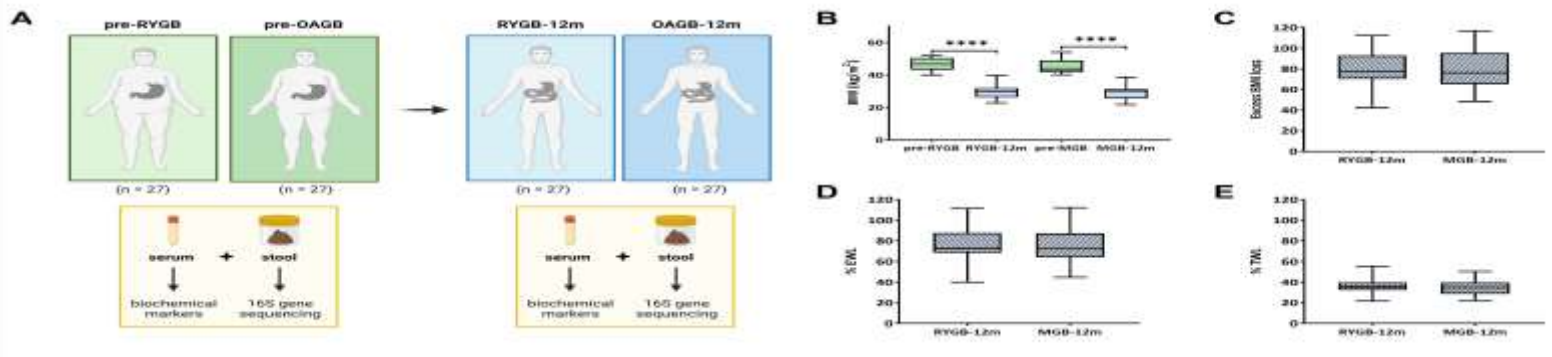
all patients were free of PPI treatment, followed a standard vitamins supplementation, and did not receive antibiotics.

a significant decrease in weight, BMI, neck circumference, waist and hip was observed ($p < 0.001$)

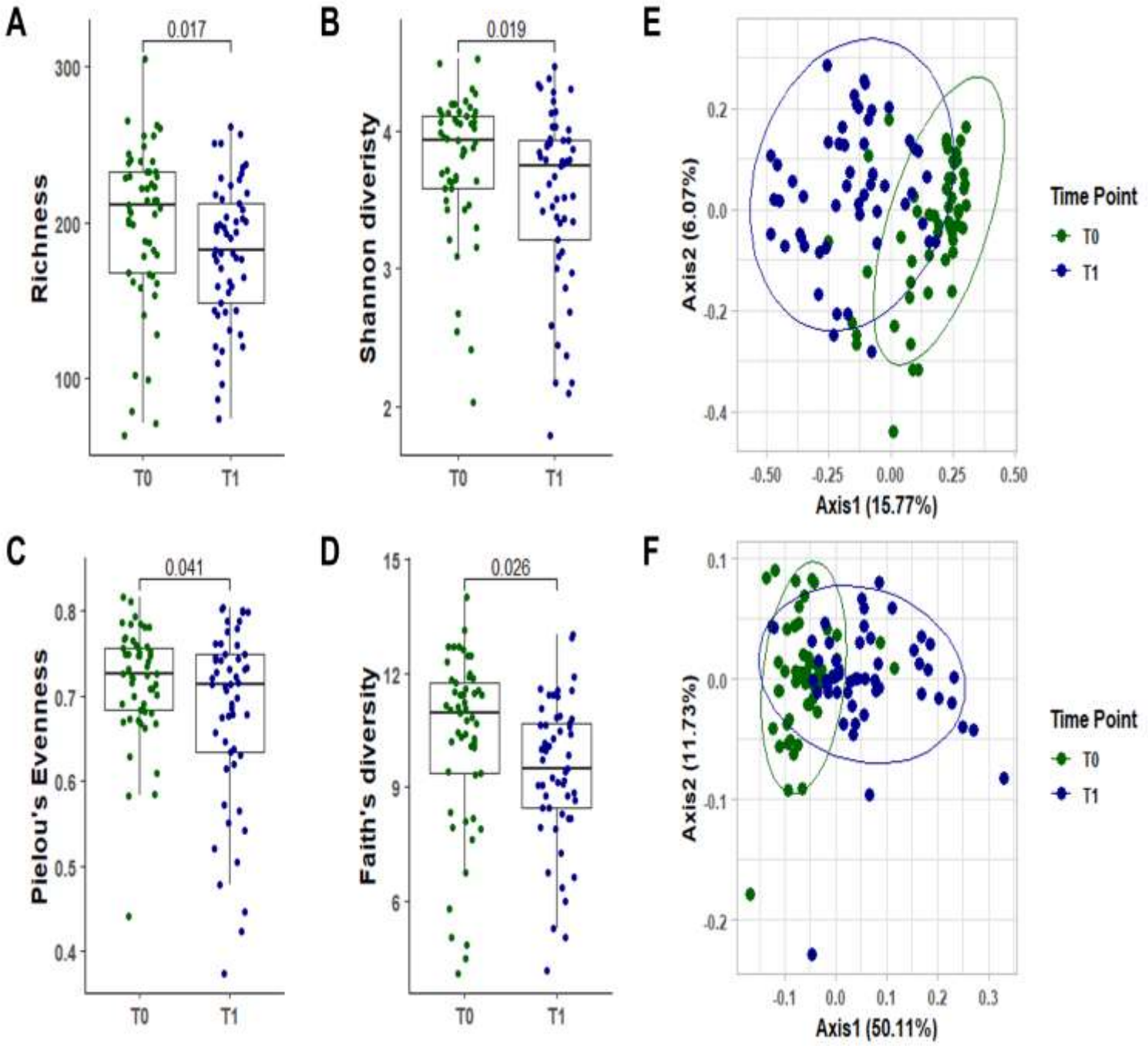
METABOLIC

hemoglobin, HbA1c, glucose, triglycerides, cholesterol, LDL, ferritin and cortisol were significantly reduced, while vitamin D was significantly increased.

An overall significant variation was detected in anthropometric and serum nutritional parameters at T1.



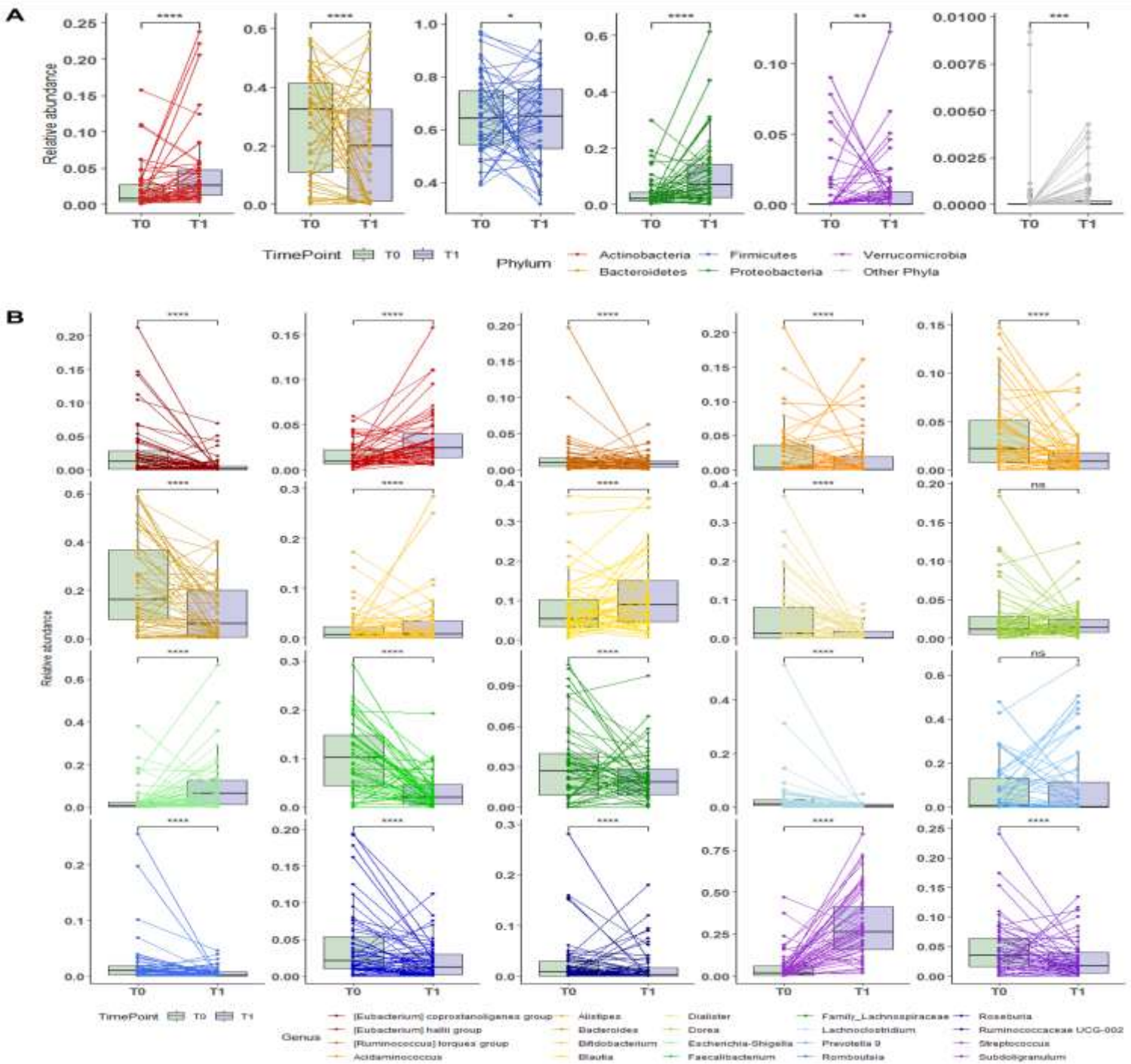
No differences at T1 were observed between RYGB and OAGB



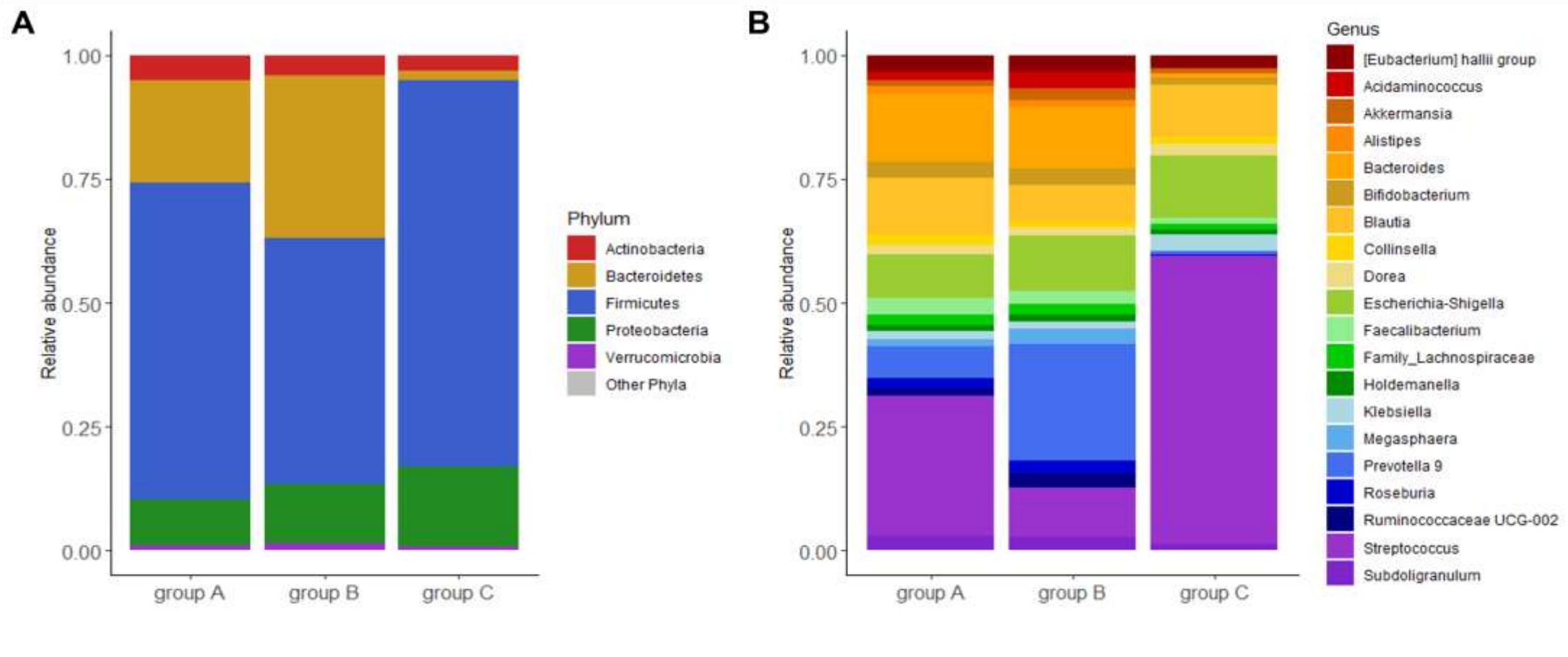
GM composition at 1 year showed
a significant decrease in overall microbial diversity
An increase of the Firmicutes/Bacteroidetes (F/B) ratio

- **BMS significantly impacts on gut microbiota alpha diversity (lower values post intervention) and beta diversity**

BMS determines significant changes in the bacterial community phylum (**A**) and genus level (**B**).



Gut microbial community identifies three groups following bariatric surgery

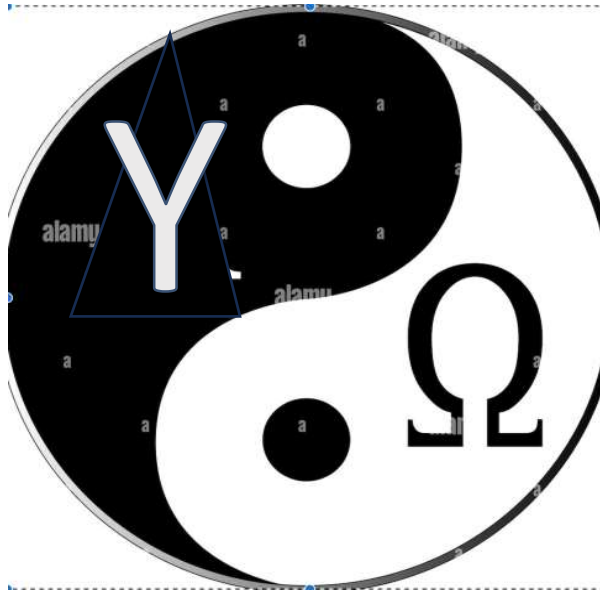


Conclusions

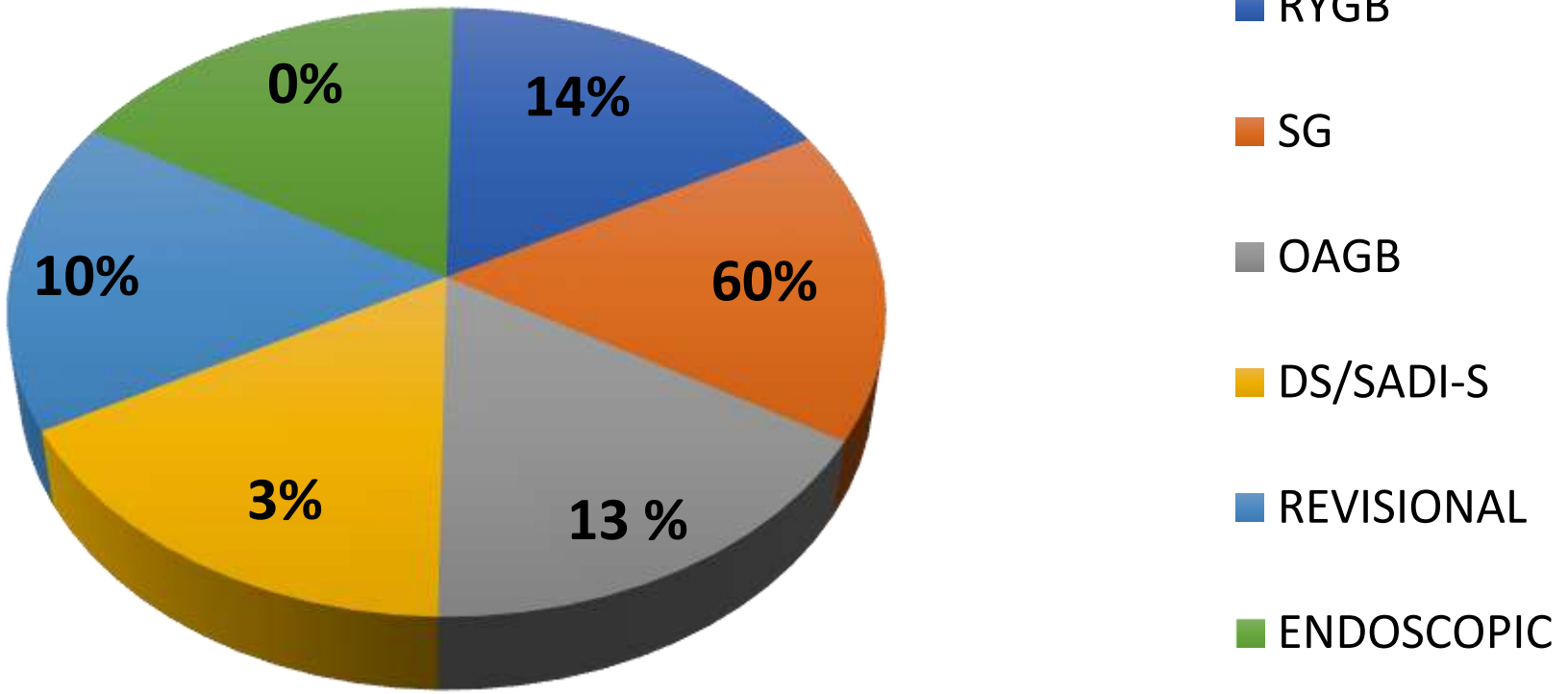
*Take home message

BMS promotes a dramatic change in GM composition one year postop.

The bypass technique **Y vs Ω** **DID** NOT impact differently on GM, with similar effect on weight loss and comorbidities resolution/improvement.



However, we identified three clusters of patients at 1 year across the two study groups showing different microbial signatures that will be evaluated in the long-term to disclose eventual impact on clinical outcomes.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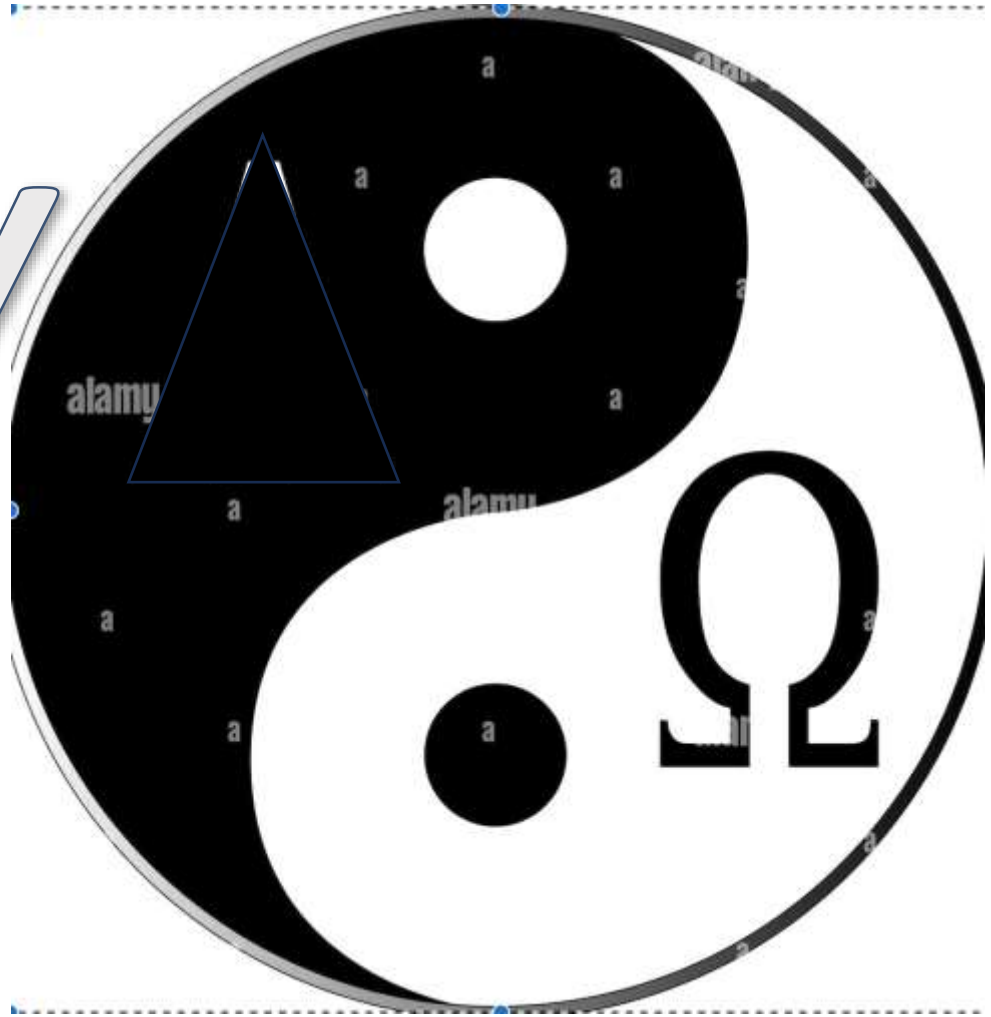

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Different clusters, showing characteristic alpha and beta diversity and microbial composition, are identified at 12 months post-surgery.

Dirichlet-Multinomial Mixture Model (DMM) was used to search for groups of samples that were like each other. The number of clusters was identified, sampled sorted following this identification in three groups. Group A (28 samples), group B 14 samples and group C 10 samples. Alpha diversity was assessed as richness (**a**), Shannon diversity index (**b**), Pielou's Evenness (**c**) and Faith's diversity (**d**) and represented as dot plot chart. Box plot chart reports median and 25th and 75th percentiles. Principal coordinates analysis (PCoA) was used to represent *Weighted Unifrac* and *Bray-Curtis* beta diversity (**e** and **f**, respectively). Statistical differences between the three were assessed by (PERMANOVA) test. Relative abundances of the main phyla (**g**) and top 20 genera (**h**) were analysed and represented as bar chart. Statistical differences were evaluated using Kruskal-Wallis test followed by Bonferroni's correction.