

Investigation of the interaction between human gut microbiota and disease state: from dysbiosis to symbiosis

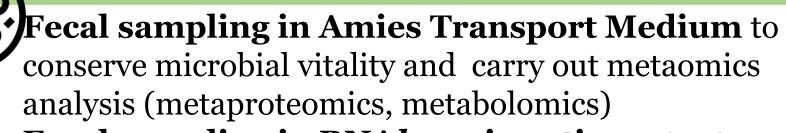
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To date, few international projects studied the intra- and inter-individual variability to underline the **possible role of microbiota in pathologies onset**. In this scenario, the **definition of recruiting protocols** and the **collection of biological samples** - from healthy subjects and patients – is necessary to provide significant data to highlight the microbiota-pathology correlations.

1. Defination of sampling method

Sampling kit constitution



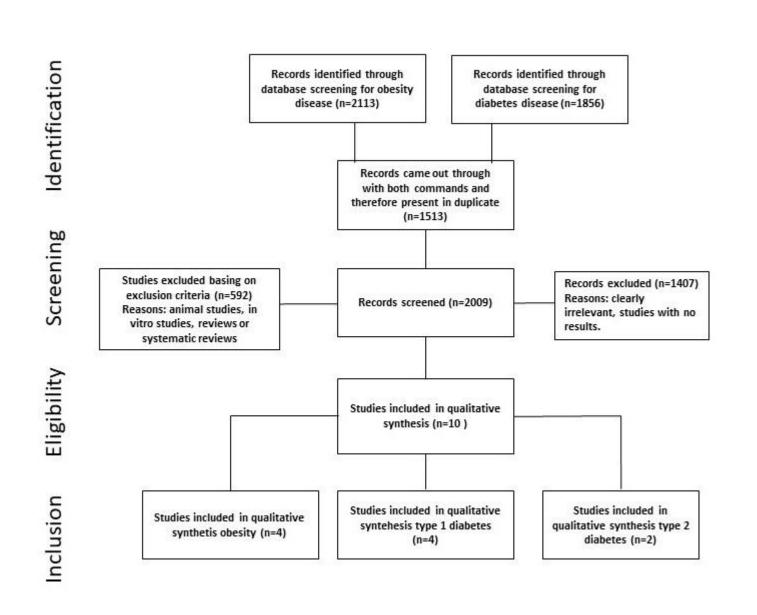


- **Fecal sampling in RNA***later* **in ratio 1:1** to store and stabilize the integrity of genetic material and carry out analyzes of 16S rDNA metagenetics
- One sterile and empty devices for **urinary samples** to store in the biobank
- One sterile and empty devices for **salivary samples** to store in the biobank

Pathologies and subjects selection

| Subject condition | Pathology Type | N° of subjects | RNAlater (stool) | AMIES TM (stool) | Urine |
|--------------------------------|------------------|----------------|------------------|------------------|-------|
| Healthy | | 105 | 105 | 105 | 105 |
| IgAN | Nephropathic | 30 | 30 | 30 | 30 |
| ADPKD | Nephropathic | 30 | 30 | 30 | 30 |
| CKD advanced | Nephropathic | 25 | 25 | 25 | 25 |
| DKD | Nephropathic | 30 | 30 | 30 | 25 |
| Biting obesity | Metabolic | 25 | 25 | 25 | 25 |
| Obesity | Metabolic | 25 | 25 | 25 | 25 |
| Metabolic syndrome | Metabolic | 25 | 25 | 25 | 25 |
| DMT1 | Metabolic | 25 | 25 | 25 | 25 |
| DMT2 | Metabolic | 25 | 25 | 25 | 25 |
| Recurrent cervico- | Gynecological | 25 | 25 | 25 | 25 |
| vaginitis | Gynecological | 25 | 25 | 25 | 25 |
| Endometriosis | Gynecological | 25 | 25 | 25 | 25 |
| Repeated implantation failures | Gynecological | 25 | 25 | 25 | 25 |
| Lung cancer NSCLC | Oncological | 25 | 25 | 25 | 25 |
| CDI | Antibiotic | 30 | 30 | 30 | 30 |
| MDRO | resistance | 25 | 25 | 25 | 25 |
| IBD | Antibiotic | 80 | 80 | 80 | 80 |
| IBS | resistance | 40 | 40 | 40 | 40 |
| Hepatic | Gastrointestinal | 25 | 25 | 25 | 25 |
| encephalopathy | Gastrointestinal | | | | |
| 1 1 2 | Liver | | | | |
| Total | | 670 | 670 | 670 | 670 |

2. Review drafting



Food diary filling

| <u>Giorno</u> | DATA | <u>:</u> | | | | | |
|---|----------------------------------|---------------------------------------|--|-------------------------------|---|------------------------------|----------|
| COLAZION | E | | | | | | |
| Latte: | intero | | scremato [| 3 | parzialmente | scremato | |
| Quantità: | n bicchiei | ri oppure | ntazze | oppure | altra qu | antità | |
| Aggiunta di | zucchero o miele: | n. | cucchiaini | oppure | n | cucchiai | |
| Succo di fr | utta: | n | bicchieri | oppure | n | tetrapak | |
| | da (specificare tipo | | o miele: ncu | | | | |
| | | | | | | | |
| quantità): | | Zucchero | | cchiaini | | intero C | 5 |
| quantità): Yogurt : | | Zucchero bianco 🗖 | o miele: ncu alla frutta | cchiaini | nagro 🗖 | | J |
| quantità): Yogurt : | nvasetti ottate o gallette di | Zucchero bianco riso: n.2. | o miele: ncu alla frutta | cchiaini n le o marm | nagro □ nellata: n 2 cu | cchiaini | |
| quantità): Yogurt: Fette bisco | nvasetti ottate o gallette di | Zucchero bianco riso: n.2. | o miele: ncu alla frutta Mie | cchiaini n le o marm | nagro □ nellata: n 2 cu (spec | cchiaini | |
| quantità): Yogurt: Fette bisco Biscotti: | nvasetti ottate o gallette di | Zucchero bianco riso: n.2. nbiscotti | o miele: ncu alla frutta Mie | cchiaini n le o marm oppure n | nagro □ nellata: n 2 cu (spec grammi | cchiaini cificare il tipo | |
| quantità): Yogurt: Fette bisco Biscotti: Cereali: | nvasetti ottate o gallette di | Zucchero bianco riso: n.2. nbiscotti | o miele: ncue alla frutta Mie ncucchiai onfezionata | cchiaini n le o marm oppure n | nagro □ nellata: n 2 cu (spec grammi .artigianale ⊠ | cchiaini cificare il tipo | |

To patients and healthy volunteers is asked to fill a **food diary relating to the three days** prior to the collection of biological samples in order to evaluate the influence of food intake and specific dietary habits on the **composition of the microbiota** and on the **progression of considered pathologies**



Due to association between microbial alterations and various pathologies, 21 diseases with different origin (gastrointestinal, metabolic, renal, oncological, gynecological,



16S rRNA marker gene sequencing does not provide sufficient information about the microbioma plasticity. In this light, among omics technologies, **metabolomics and metaproteomics can allow a better understanding of microbiome adaptation to specific conditions as a disease progression.**

A review focused on highlighting the current shortage of studies which applied metaproteomics, alone or in combination with other omics, in a way to have a more complete framework of microbiotapathology crosstalk, was near to be finalized.

