WITH GASTROINTESTINAL DISORDERS

## Natálie Mlčůchová, Petra Bořilová Linhartová

RECETOX, Faculty of Science, Masaryk University, Kotlarska 2, Brno

## **BACKGROUND**

Gastrointestinal diseases (GDs), including gastrointestinal malignities, represent a heterogeneous range of disorders with different etiologies, and overlapping, nonspecific symptomology. A complex network comprising the host microbiome, metagenome, metatranscriptome, human transcriptome, human epigenome and exome considerably impacts the etiopathogenesis of GDs.

**OUTCOMES** 

## **AIMS**



description of the microbiome in the oral cavity, esophagus, stomach, duodenum and stool



determination of diagnostic markers at the level of: the host <u>microbiome</u>

MUNI RECETOX

authority can be held responsible for them.

This study was supported by the Ministry of Health of the Czech Republic, grant Nr. NU20-03-00126,

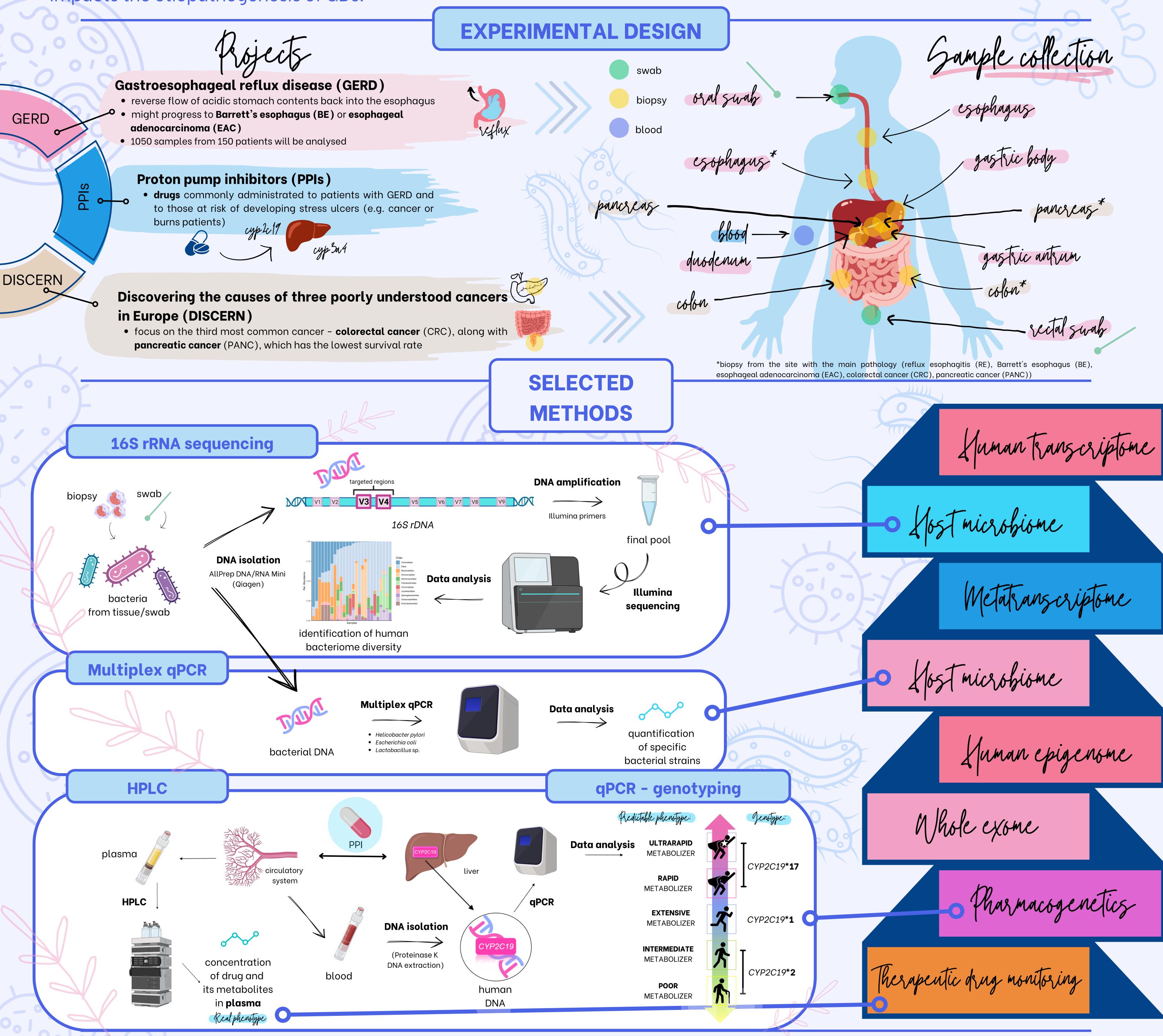
and by the Ministry of Health of the Czech Republic - conceptual development of research

organization. The authors also thank Research Infrastructure RECETOX RI (No LM2023069, MEYS CR, 2023–2026). Funded by the European Union, DISCERN (101096888). Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or European Health and Digital Executive Agency. Neither the European Union nor the granting



host genes

individualisation of pharmacotherapy



• composition and relative abundance of microbiota in the gastrointestinal tract in patients with RE/BE/EAC

• potential prognostic and predictive tools to distinguish between healthy and pathological conditions and

between pathological conditions themselves (BE/EAC)