

Project 1

Name/title of the PhD course	FOOD SCIENCE
Name of the PhD coordinator	Prof. Amalia Barone
Name/Title of the PhD project	<i>Strain-level and genome-wide catalogue of bacteria from European PDO fermented foods</i>
Department of reference	Department of Agricultural Sciences (DAS; www.agraria.unina.it).
Working conditions, research team, infrastructures, equipment	The DAS is one of the largest Departments of the University of Naples Federico II and the coordinating Department of the Task Force on Microbiome Studies at UNINA. The staff working at DAS includes more than 140 scientists and 60 administrative staff members. The multidisciplinary research activities carried out are related to food science, agriculture and environment. The quality of the research carried out at DAS is recognized for its excellence at both national and international level: in the last five years members of the DAS have published an average of 100 articles per year ranked in the first quartile (Q1) of their respective subject categories of the Journal Citation Report (ISI Web of Science). DAS hosts a number of different research units whose activities are consistent with the scope of the PhD project, including the Division of Microbiology and Food Science and Technology. The PhD student will work in a team set at the Division of Microbiology, that hosts laboratories fully equipped for traditional and molecular microbiology, as well as metagenomics. In addition, the team has access to the University datacenter SCOPE (Cooperative System for multidisciplinary Scientific Computing), a set of computing and storage resources, is available at UNINA for computationally intensive data analysis. The team has extensive experience in microbial ecology, metagenomic, bioinformatics and data science and is/was involved in several National and European projects focused on the study of the microbiome in complex environments, particularly during food production and spoilage and on the influence of diet or specific dietary components on the human microbiome.
Scientific context	Food fermentations are ancient processes that date back to the introduction of agriculture and animal husbandry, approximately 10,000 years ago, when they were used for food preservation. Artisanal fermentation methodologies, based on serial inoculation in a process known as back-slopping, have been increasingly replaced by highly controlled, reproducible, and safe industrial processes using selected microbial strains. This practice, although ensuring food safety and quality standardization, strongly reduced the microbial diversity, also leading to a flattening of sensorial properties. Traditionally-fermented foods usually harbor a complex microbiota, characterized by a wide variety of microbial species and strains, that are responsible for the specific sensorial traits of the product. In particular, several PDO fermented foods are obtained using a traditional fermentation. The microbiome of these products can be considered as a fingerprint and is an excellent target to characterize the authenticity and identity of the product.
Project Research plan	The aim of the PhD project is to develop a map the microbiome of traditionally-produced European PDO fermented foods (e.g., cheeses, fermented meats) applying a shotgun metagenomic approach. Data analysis will allow to evaluate the taxonomic and functional composition of the microbiome, identifying key microbial genes/pathways possibly associated with the development of specific microbial metabolites/sensorial patterns. Moreover, the genomes of the most important species will be assembled and extracted from metagenomics reads. The patterns of distribution and prevalence of different strains will be assessed, identifying strains specific for each product and characterizing their functional potential. Data about microbiome composition and functions will be integrated with other metadata collected about the process technology (e.g. time, temperature and humidity during ripening, type of starter, ingredients and raw materials, etc.) and chemical composition (proteolysis and lipolysis indices, pH, water activity, volatile compounds), defining the microbiome features responsible for the product quality. In addition, Metagenome-Assembled Genomes (MAGs) will be reconstructed from metagenomics reads, to develop a genomic catalogue of microbial strains from EU fermented foods and verify if specific strains are selected in different products, according to the geographical origin or the process technology. All the information collected will be used to develop classification models allowing the discrimination of a specific food type based on its microbiome. On a subset of selected foods, microbial strains isolation will be also carried out, to create a collection of strains to be tested in the industry
Research and Training Innovative aspects	The use of shotgun metagenomics in food microbiome studies is still limited. However, it can be extremely useful to identify the specific microbiome assembly leading to the particular traits of a typical fermented food. In particular, the project aims to characterize the genomic potential of the microbiome of typical PDO fermented foods, to identify the microbial genes involved in the production of the specific organoleptic traits. A huge genomic collection of microbial strains involved in fermented foods production will be created. These data will be integrated with metadata about product composition and the technological process to understand how these factors may modulate microbiome composition and potential activities. The expected results will be of interest for PDO consortia, producers, legal authorities and consumers and may be of help for the identification of frauds and the authentication of PDO products

Inter-Multidisciplinary aspects	The project will integrate competences from different areas: microbiology, food technology, bioinformatics and data science. The student will be trained to classical microbiology, as well as to the most advanced high-throughput sequencing and metagenomics techniques. In addition, he/she will be involved in metagenomics data analysis, acquiring competences in bioinformatics, data science and machine-learning applied to food microbiology.
Secondment opportunities	<p>The PhD student will spend a 6-months secondment period at Sacco Srl (Cadorago, Italy), which is part of Sacco System (https://www.saccosystem.com). Sacco is an international company specialized in the development and commercialization of microbial starter cultures and probiotics. During the secondment, the student will be co-supervised by Dr Fabio Dal Bello (https://www.linkedin.com/in/fabio-dal-bello-434bb03b/?originalSubdomain=it), Scientific Director at Sacco System and responsible of Research & Development projects. At Sacco, the student will be involved in the process leading to the development and industrial scale-up of a microbial starter culture for fermented food production, in the testing of the production of relevant metabolites (e.g., bacteriocins) and in the optimization of the best growth conditions for the industrial production.</p> <p>In addition, the student will spend 6 months at Teagasc (https://www.teagasc.ie), the Irish Agriculture and Food Development Authority (Carlow, Ireland). Teagasc is the Irish body providing integrated research, advisory and training services to the agriculture and food industry. Prof Paul D. Cotter will be the co-supervisor at Teagasc. Prof Cotter is Head of the Food Biosciences Department and Professor at the APC Microbiome Institute of the University College of Cork. He is a molecular microbiologist with a particular focus on the microbiome of foods and food chains. During the secondment, the student will specialize in advanced bioinformatics analysis of metagenomics data.</p>
Main Supervisor: Prof Danilo Ercolini (https://www.docenti.unina.it/danilo.ercolini)	
Brief CV	Full Professor of Microbiology at the Department of Agricultural Sciences of UNINA, where he previously was Associate Professor (2011-15) and Assistant Professor (2002-11). He is director of the Department of Agricultural Sciences (since 2021), coordinator of the Task Force on Microbiome Studies (since 2017) and Scientific Coordinator of the project CRESCENDO. From 2016-2021, he was coordinator of the PhD School in Food Science. He is Associate Editor of the journals “mSystems” and “Applied and Environmental Microbiology.” He supervises/ed 15 Post-Doctoral fellows, 6 PhD students in Food Science and >30 MSc and BSc students during the preparation of their experimental theses. His research interests span from food microbiology to the inter-connections among diet-human microbiome-health.
Publications	<p>He is co-author of 176 publications in international peer-reviewed journals, attracting >12,300 citations and leading to a H-index of 62 (Scopus, Jan. 2022). Selected 5 recent publications on microbiome field:</p> <ul style="list-style-type: none"> -De Filippis, F., Paparo, L., Nocerino, R., Della Gatta, G., Carucci, L., Russo, R., Pasolli, E., Ercolini, D., Berni Canani, R. 2021. Specific gut microbiome signatures and the associated pro-inflammatory functions are linked to pediatric allergy and acquisition of immune tolerance. <i>Nat Comm</i> 12:5958. -Pasolli, E., De Filippis, F., Mauriello, I.E., Cumbo, F., Walsh, A.M., Leech, J., Cotter, P.D., Segata, N., Ercolini, D. (2020) Large-scale genome-wide analysis links lactic acid bacteria from food with the gut microbiome. <i>Nat Comm</i> 11:2610. -De Filippis, F., Pasolli, E., Ercolini, D. (2020) Newly explored <i>Faecalibacterium</i> diversity is connected to age, lifestyle, geography, and disease. <i>Curr Biol</i> 30:1–12. -Meslier, V., Laiola, M., Roager, H.M., De Filippis, F., Roume, H., Quinquis, B., Giacco, R., Mennella, I., Ferracane, R., Pons, N., Pasolli, E., Rivellese, A.A., Dragsted, L.O., Vitaglione, P., Ehrlich, D.S., Ercolini, D. (2020). Mediterranean diet intervention in overweight and obese subjects lowers plasma cholesterol and causes changes in the gut microbiome and metabolome independently of energy intake. <i>Gut</i> 69:1258-1268. -De Filippis, F., Pasolli, E., Tett, A., Tarallo, S., Naccarati, A., De Angelis, M., Neviani, E., Cocolin, L., Gobbetti, M., Segata, N. and Ercolini, D. (2019) Distinct genetic and functional traits of human intestinal <i>Prevotella copri</i> strains are associated with different habitual diets. <i>Cell Host & Microbe</i> 25:444-453.
Projects participation	<p>He is/was Scientific Responsible of several National and International projects on the study of microbial ecology in human and food ecosystems. A list includes:</p> <ul style="list-style-type: none"> -2020-23 DITECT: <i>Digital TEChnologies as an enabler for a conTinuuous transformation of food safety system</i>, funded by EU H2020 Programme. -2019-23 MASTER: <i>Microbiome Applications for Sustainable food systems through Technologies and EnteRprise</i> funded by EU H2020 Programme. -2016-19 DINAMIC: <i>Diet-induced Arrangement of the gut Microbiome for Improvement of Cardiometabolic health</i>, funded by the Italian Ministry of Research within the JPI – Healthy diet for a healthy life. -2019-23 PRIN2017: <i>Microbiome-tailored food products based on typical Mediterranean diet components</i>, funded by the Italian Ministry of Research -2008-11 SYMBIOSIS-EU <i>Scientific sYnergisM of nano-Bio-Info-cOgni Science for an Integrated system to monitor meat quality and Safety during production, storage, and distribution in EU</i>, funded by EU within the FP7 Programme.