Project 11

Name/title of the PhD course	**FOOD SCIENCE**
Name of the PhD coordinator	Prof. Amalia Barone
Name/Title of the PhD project	***Microbiome mapping in meat food chain from farm-to-fork***
Department of reference	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	The relationship between foods and their microbiome is fundamental to ensure food quality and safety and an early detection of food pathogens and spoilage microorganisms is an important step that can help to control a foodborne outbreak or limit food losses.Current methods for monitoring the microbial contamination in the food chains rely on culture-dependent analyses. However, innovative approaches have been tested as an alternative to culture-dependent procedures to track foodborne pathogens or spoilers in foods and food-handling environments with high precision and sensitivity, as well as in short times. The advent of high-throughput sequencing (HTS) technologies, also known as next-generation sequencing (NGS), is revolutionizing food microbiology: they present higher sensitivity compared with culture-dependent and other culture-independent approaches, allowing the detection of subdominant communities that may play an important role in the studied ecosystem. 'Omics may be successfully implemented within the food industry, for microbiome mapping in the processing plant environment, microbial source tracking investigation or for monitoring the product shelf-life, identifying the presence of microbial spoilers and how processing/storage conditions may affect microbial dynamics. In addition, thanks to novel algorithms and bioinformatics tools, it is possible to reconstruct microbial genomes from metagenomics reads, allowing strain typing and monitoring without prior cultivation.
Project Research plan	The aim of the PhD project is to map the microbiome across the raw meat processing chain, from farm to retail. Two different chains will be followed: beef and lamb meat. Environmental samples (surface swabs) will be taken along the whole chains: at the farms (e.g., from animal skin and teats, animal barns, racks, feeding), slaughterhouses (e.g., carcass surface, tools, operator's hands, walls, cold rooms), trucks used for the transport, processing, and packaging facilities. In addition, meat samples will be collected at each step. Samples will be processed by shotgun metagenomics, to obtain a map of the microbiome across the chains and individuate possible contamination routes. Metagenomes will be also screened for the presence of relevant genes possibly involved in spoilage-related (e.g., production of off-odors, slime, biofilm production) or harmful activities (e.g., production of toxins, virulence factors, antimicrobial resistance). In addition, using advanced comparative genomics analyses, genomes of relevant microbial species will be reconstructed directly from metagenomics reads. This will allow *in-situ* monitoring of different strains from the same species, to track their origin along the different steps of the food chain. Metagenomics data will be integrated with metadata regarding the process (e.g., cleaning and disinfection procedures, temperature, flows of people and materials) to understand how these factors may affect microbiome dynamics, with the final aim to provide the meat industry with useful information that may help in the design of novel quality and safety management plans.Finally, ad-hoc experiments will be also designed to evaluate the impact of storage conditions (e.g., temperature, packaging type, gaseous atmosphere) on microbial dynamics. Samples will be analyzed using the same metagenomics approach described above. In addition, microbial metabolites will be also monitored by gas-chromatography coupled to mass-spectrometry (GC-MS). Integration of metagenomics with metabolomics will allow to identify specific microbial markers able to predict the product shelf-life and spoilage dynamics.
Research and Training Innovative aspects	Metagenomics revolutionized our way to approach microbial ecology studies. However, its use in food microbiome studies is still limited. In particular, the use of shotgun metagenomics will be able to provide information on the genomic potential of the microbiome, in the production of spoilage-related, as well as potentially dangerous activities (e.g., virulence factors, production of toxins). These data will be integrated with metadata about product

	composition, technological process and storage conditions to understand how these factors may modulate microbiome composition and potential activities. Data collected will allow the development of an innovative approach to ensure meat safety and quality, that will be implemented in the quality management plan of the industry.
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	During the 1st and 2nd year of the PhD, the student will spend a **total of 6 months at Dawn Meat Group** (https://dunbia.com) and will be involved in their business activity. The Group comprise Dawn Meats and Dunbia and is a major beef and lamb processor with 22 sites across Ireland and United Kingdom. The PhD student will also have the opportunity **to spend 6 months during the 3rd year of PhD at the Department of Food Hygiene and Technology of the University of Leon** in Spain (https://www.unileon.es/internacional; http://ictal.unileon.es/?page_id=376), working within the group of Prof. Avelino Alvarez-Ordóñez (https://www.researchgate.net/profile/Avelino-Alvarez-Ordonez).
Main Supervisor: Dr Francesca De Filippis (https://www.docenti.unina.it/francesca.defilippis; personal website: https://sites.google.com/view/francescadefilippis)	
Brief CV	Assistant Professor of Microbiology at the Department of Agricultural Sciences of UNINA. Since 2021, she is member of the Professor Board of the PhD School in Food Science and of the Managing Board of the Task Force on Microbiome Studies. She is Associate Editor for the section "Microbiome" of the journals "Foods" and "Food Research International". She supervises/ed 2 Post-Doctoral fellows, 3 PhD students in Food Science and >40 MSc and BSc students during the preparation of their experimental theses. She carried out research activities in recognized international laboratories working in the microbial ecology field: Argonne National Laboratory (USA) in 2013; APC Microbiome Institute of the University College of Cork (Ireland) in 2014. Her research interests span from food microbiology to the inter-connections among diet-human microbiome-health. She is expert in the application of metagenomics, metatranscriptomics and comparative genomics to the study of microbial ecology in foods and human gut. Her leading international position in the field has been widely recognized: she was included in the list of the top 2% world scientists across all fields of 2019 and 2020 by Stanford University and she was also nominated among the top 0.1% world experts in Food Microbiology by Expertscape (https://expertscape.com/ex/food+microbiology).
Publications	Francesca de Filippis is co-author of 83 publications in international peer-reviewed journals and 4 book chapters (2012-21), attracting >3,900 citations and leading to a H-index of 36 (Scopus, Jan. 2022). Selected 5 recent publications on microbiome field: **-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. Nat Comm 12:5958. **-De Filippis, F.,** Pasolli, E., Ercolini, D. 2020. The food-gut axis: lactic acid bacteria and their link to food, the gut microbiome and human health. FEMS Microb. Reviews 44:454-489. **-De Filippis F,** Pasolli E, Tett A, Tarallo S, Naccarati A, De Angelis M, Neviani E, Cocolin L, Gobbetti M, Segata N, Ercolini D. 2019. Distinct genetic and functional traits of human intestinal *Prevotella copri* strains are associated with different habitual diets. Cell Host & Microbe 25:444-453. **-De Filippis, F.,** La Storia, A., Villani, F., Ercolini, D. 2019. Strain-level diversity analysis of *Pseudomonas fragi* after *in situ* pangenome reconstruction shows distinctive spoilage-associated metabolic traits clearly selected by different storage conditions. Appl. Environ. Microbiol. 85:e02212-18. **-De Filippis F,** Pellegrini N, Vannini L, Jeffery IB, La Storia A, Laghi L, Serrazanetti DI, Di Cagno R, Ferrocino I, Lazzi C, Turroni S, Cocolin L, Brigidi P, Neviani E, Gobbetti M, O'Toole PW, Ercolini D. 2016. High-level adherence to a Mediterranean diet beneficially impacts the gut microbiota and associated metabolome. Gut 65:1812–1821.
Projects participation	She leads/participates to several National and International projects on the study of microbial ecology in human and food ecosystems. A recent list includes: • 2021-23 FOODMICROHERITAGE: *Quality and authenticity protection of artisanal fermented foods through the characterization and conservation of their microbial and genetic heritage*, granted by the Italian Ministry of Foreign Affairs and International Cooperation. Role: Principal Investigator • 2020-23 DiTECT: *Digital TEChnologies as an enabler for a conTinuous transformation of food safety system*, funded by EU within the H2020 Programme. Role: co-leader of Research Unit • 2019-23 POLLGUT: *Linking environmental pollution and gut microbiota in individuals living in contaminated settlements*, funded by the Italian Ministry of Health. Role: Principal Investigator • 2019-23 SHEALTHY: *Non-thermal physical technologies to preServe HEALTHiness of fresh and minimallY processed fruit and vegetables,* funded by EU within the H2020 Programme. Role: team member and task leader • 2019-23 MASTER: *Microbiome Applications for Sustainable food systems through Technologies and EnteRprise* funded by EU within the H2020 Programme. Role: co-leader of Research Unit