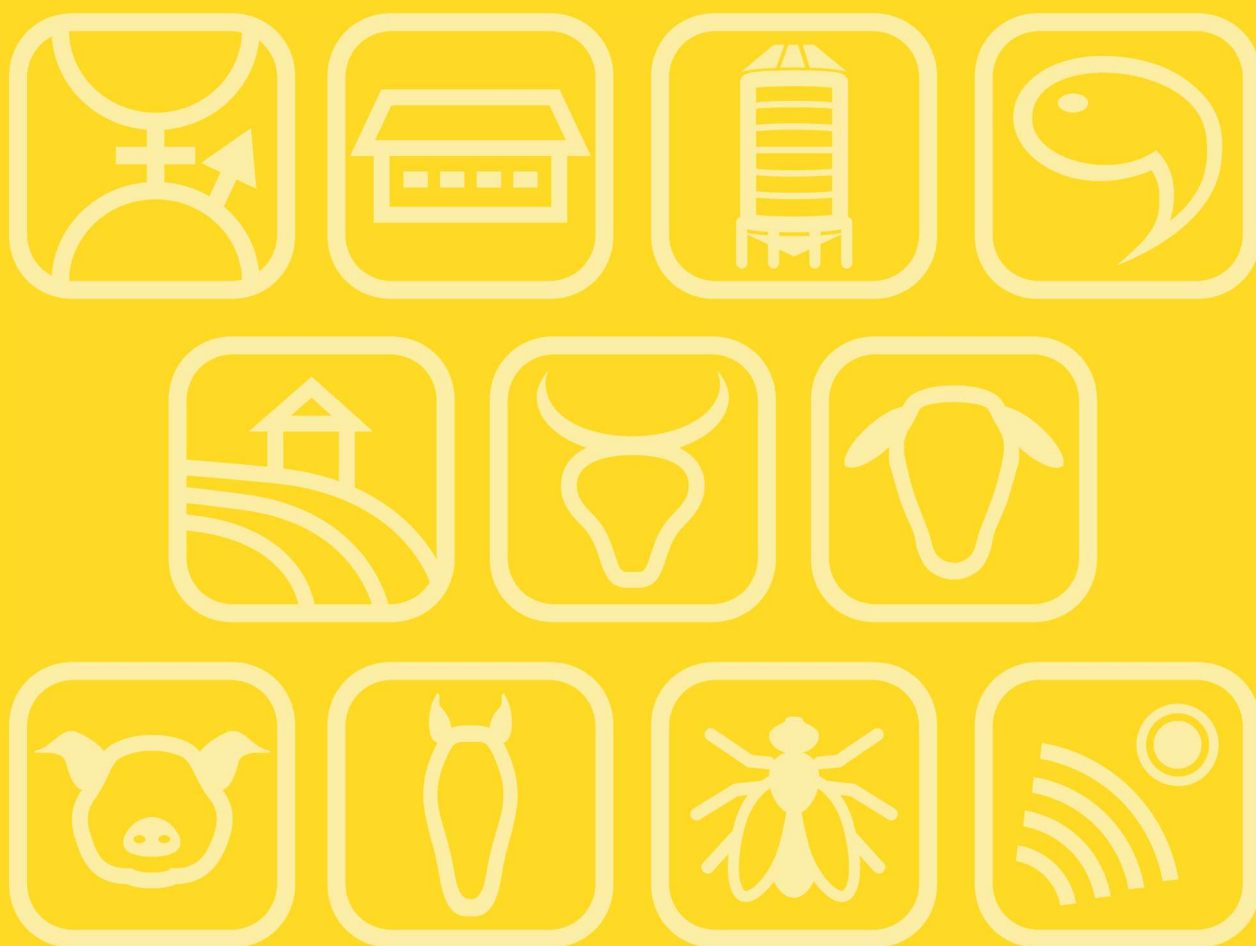


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Improving research quality and collaboration by developing standard operating procedures

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European Pig Research Infrastructures (PRI) are increasingly collaborating, reinforcing the need for robust and reproducible data collection to ensure high quality research. In addition to standardisation of analytical methods and reporting of appropriate validations, standardisation of Specific Experimental Procedures (SEP) is equally important as they can affect the quality of results. For instance, different sampling methods may involve different degrees of invasiveness and have differing impacts on behaviour and emotional states, which may ultimately affect the results. Standardisation of SEPs also makes it easier to compare results, especially in the era of meta-analysis. A Standard Operating Procedure (SOP) is a step-by-step guide to performing a SEP. A specific task of the PIGWEB project, which has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101004770, is to develop SOPs for methods to collect common biological samples (blood, faeces, urine, saliva) and measurements (carcass and body composition) that also take into account the 3R principles. A general template, including materials, equipment, prerequisites and a description of the SEP was created and filled in by the partners to collect the SEPs used in the different PRIs. Five working groups in different areas then exchanged and defined the best practices for a SEP, with consideration of the 3Rs and a focus on promoting animal welfare. The use of common SOPs within and across PRIs has many advantages and provides a solid basis for obtaining high quality data, promoting animal welfare standards and improving research collaborations.

Streamlining pig microbiome studies: Improving efficiency through reproducibility and comparability

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The microbiome plays a critical role in animal health and productivity, with the porcine microbiome being a key marker of pig health and farm productivity. Despite its importance, variations in technical and methodological approaches don't allow the comparability and reproducibility of microbiome studies in pigs. Addressing this challenge, our project introduces a pioneering effort to standardize microbiome research in farm animals, using pigs as a model. We aim to develop a standardized working protocol complemented by documentation guidelines. This is expected to enable the comparison of microbiome data across diverse laboratories, facilitating rapid conclusions on the practical relevance and application of findings to enhance livestock welfare, health, and performance and support sustainable agricultural practices. Around 2886 publications were screened to identify relevant protocols from sampling to bioinformatics analysis. Metadata of 461 publications met the eligibility criteria of being in vivo studies and possessing sequencing data that is publicly available. To create a template for metadata collection, information regarding sample collection, storage, DNA extraction, sequencing platforms and strategies, quality control and clustering tools, taxonomic annotation tools and databases, and functional annotation tools and databases were collected. Our findings highlight the need for standardized protocols to ensure comparability and reproducibility in pig microbiome research, leading to more efficient research outcomes.