Uncovering resilience in pigs:

A real-time farmers' feedback approach to gain fundamental insights in pigs' resilience

Research plan

1. Excellence

1.1 Quality and pertinence of the project's research and innovation objectives

Resilience is a multifaceted concept overlapping with related concepts such as robustness, tolerance, and resistance (Putz et al., 2019). **Animals that are minimally affected by challenges, and rapidly return to the state pertained before a challenge, are considered resilient** (Berghof et al., 2019). This implies that disturbances may affect animals to varying extents. As a result, deviations in longitudinal data can serve as a metric for overall resilience. Animals demonstrating greater resilience typically experience fewer or smaller deviations from their performance and demonstrate prompt recovery following a challenge (Scheffer et al., 2018; Figure 1).

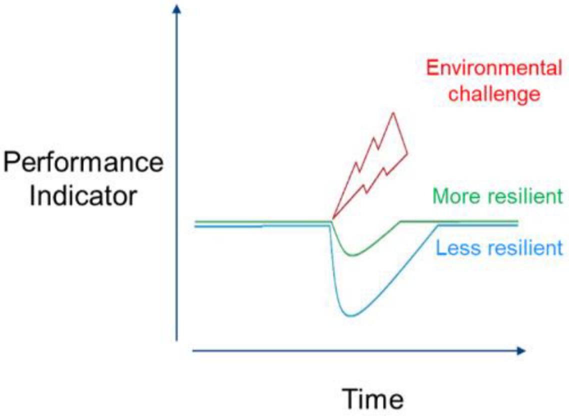


Figure 1. Graphical representation of resilience hypothesis.

Automated feeding stations (AFS) are the state-of-the art method for high-throughput phenotyping in pigs. My previous research using post-hoc analyses showed that weight and feed intake collected from AFS serve as well-suited proxies to identify resilient pigs (Gorssen et al., 2023). Furthermore, these resilience traits were heritable (10-30%) and favorably genetically correlated with health and welfare related traits, such as tail biting and mortality (Gorssen et al., 2024). AFS offer great possibilities to monitor these traits in large animal groups, and hence provide convenient access to data that allow the phenotyping of resilience indicators in high throughput. With the current proposal, I will develop **new, real-time (ad-hoc) approaches to gain fundamental insights into the complex genetic architecture underlying resilience and address the following scientific gaps**:

Firstly, sensor data in AFS are susceptible to technical errors and noise, necessitating data filtering to avoid biased estimates of resilience (Garrido-Izard et al., 2022). **The establishment of standardized guidelines and a universally applicable quality control (QC) method will facilitate transferability and replicability across studies**. Secondly, resilience quantification currently occurs post-hoc, limiting our understanding of the exact challenges contributing to perturbations. **Real-time monitoring of resilience will provide invaluable insights into causality between deviation patterns and specific challenges, potentially leading to the development of a monitoring and decision support tool based on on-farm sensor data**. Thirdly, little is currently known about the underlying biology of resilience. **Access to large cohorts of phenotyped and genotyped pigs will facilitate elucidating complex biological mechanisms underlying resilience. These findings will be valuable to improve pig breeding programs. The fundamental genetic insights gained** will possibly aid the development of new drugs and/or biological assays to phenotype (young) pigs for resilience.

The main novelty of this project is the integration of farmers' feedback in a real-time prediction algorithm using cutting-edge data analytic methods to detect perturbations in pigs' body weight, feed intake and feeding behavior. This methodology will generate a uniquely large dataset which will allow us to understand and classify the causality of perturbations and resilience in-depth. Moreover, combining these refined resilience phenotypes with genome sequence information will enable us to investigate the largely unknown underlying genetic architecture of resilience. While this project will focus on pigs, the outcomes will be applicable to diverse animal species, promising substantial and far-reaching impacts.

1.2 Soundness of the proposed methodology

This project has three main goals which will be achieved by combining high-throughput phenotyping and genotyping technologies. The first goal is to develop a real-time prediction model based on preprocessed AFS data to generate alerts for perturbed pigs. The second goal is to establish a web application to collect farmer's feedback on the perturbed pigs and presumed challenges. These efforts will enhance predictive modeling and resilience phenotype optimization. The third goal is to leverage these new resilience phenotypes in genome wide association studies (GWAS) using whole genome sequence data, aimed at uncovering new genetic variants underlying resilience in pigs.

Three specific research objectives related to three work packages (WP) are formulated. The precise work plan for these work packages is explained in detail in section 3.1.

Objective 1: Establish a real-time prediction model to detect perturbed pigs (WP1)

Objective 2: Establish a web application to collect farmers' feedback, categorize individuals based on challenge categories, predict causality and refine resilience phenotypes (WP2)

Objective 3: Identify candidate genes associated with pig resilience through novel resilience phenotypes using an (imputed) whole-genome sequence information GWAS approach (WP3)

Risks and mitigation for Objective 1: Developing a universal quality control pipeline and real-time prediction algorithm might not be transferable to a completely different setting. For example, the developed methodology could work on AFS data from intensive pig farms but might be suboptimal for other systems. This risk is mitigated by validating our methodologies between two different breeding organizations collaborating in this project and between different pig populations within an organization. Although this is a potential risk, this would not compromise the further work packages, as the developed methodology would still work for our specific settings.

Risks and mitigation for Objective 2: WP2's success hinges on the establishment of a reliable real-time prediction algorithm for perturbations. However, given the availability of large datasets for model training and previous expertise in the proposed methodologies, we are confident this will be achieved. The primary risk associated with engaging farmers in data collection is their limited time, resulting in inaccurate or delayed responses to alerts. To mitigate the risk, a close collaboration with two large, well-structured pig breeding organizations is made, ensuring that farm employees will provide feedback. Additionally, the application will undergo thorough testing and follow-up to minimize technical errors.

Risks and mitigation for Objective 3: Although imputation and GWAS pose complexities, the expertise of the host group minimizes associated risks. The absence of overlapping QTL regions across different pig populations is a potential challenge. In this case, no strong candidate genes will be detected, but the trait heritability will be partitioned onto different functional genomic features.

The proposed methodology is underpinned by a robust interdisciplinary approach using state-of-the art technology and methodologies, integrating concepts from phenomics, precision livestock farming and genomics. AFS will generate high-quality longitudinal phenotype data on an individual pig level. Current advances in dynamic modelling will be used to do quality control on these data, develop a real-time model to detect perturbed pigs and refine resilience phenotypes via predictive modelling. These refined resilience phenotypes will be combined with (imputed) genomic sequence data to detect genomic variants associated to resilience in pigs. This integration ensures a holistic analysis of the resilience in pigs and the development of innovative solutions.

The project actively incorporates gender analysis and diversity considerations at multiple levels. Both males, castrates and female pigs will be included in the analyses, although most pigs in these purebred facilities are male pigs. Regarding diversity, we will analyze and compare data from four different breeds and seven different genetic lines from two different breeding organizations.

In alignment with the principles of open science, the project commits to transparency by documenting the developed methods and processes and making them available to other researchers. Moreover, open-access publications and outreach activities will disseminate findings to both academic and non-academic audiences. The host group has a policy of publishing findings early and open access via pre-prints, and publicly sharing methodologies via their GitHub page (https://github.com/AnimalGenomicsETH).

The project aligns with the FAIR principles for managing data and research outputs by implementing a structured approach to data collection, analysis, and sharing. Data generated through AFS will undergo quality control and will be integrated into real-time predictive models and a web application for farmer feedback. Interoperability is achieved by developing universally applicable algorithms and using standardized formats like R-packages, while the use of open platforms, such as GitHub, ensures reusability. Collaboration with breeding organizations ensures real-world application. The data management plan will address these practices in detail.

1.3 Quality of the supervision, training and of the two-way transfer of knowledge between the researcher and the host

The main research activity of the Animal Genomics group of supervisor Professor Hubert Pausch lies in the analysis of phenotypic, genetic and genomic data in large farm animal mapping cohorts to identify trait-associated loci. As such, **the Animal Genomics group is an ideally suited host for a project involving phenomics and genomics in pigs**. Doctoral students and postdoctoral scientists from diverse backgrounds investigate various aspects of genotype and phenotype integration. Through collaborations with pig breeding associations, the group has collected a **large collection of genotyping and sequencing data from pigs to enable sequence variant imputation and association testing which is foreseen for WP3**. Prof. Hubert Pausch is member of the COST action «EuLiPhe» demonstrating the Animal Genomics group is well-connected with colleagues working in phenomics and phenotype to genotype mapping, facilitating networking activities for me. Moreover, professor Pausch has ample experience in guiding doctoral and postdoctoral researchers, as he has been the supervisor of 11 postdocs and senior scientists and 13 doctoral students since 2017.

The expertise of several scientists in the Animal Genomics group is an asset to the project. For example, Dr. Naveen Kadri is a renowned expert in genome wide association studies, and Dr. Alexander Leonard is an expert in processing whole genome sequences. Moreover, the Animal Genomics group has a long-standing collaboration with SUISAG, one of the main data providers. **Collectively, the proposed research is well-embedded in the research environment of the Animal Genomics group and ideally complements ongoing activities.**

I have extensive experience in investigating sensor data and exploiting these data to derive and characterize heritable resilience indicators. These skills are complementary to the methods repertoire of the Animal Genomics group and will allow differentiating between resilient and less resilient genotypes also in other species than pigs.

1.4 Quality and appropriateness of the researcher's professional experience, competences, and skills

My expertise and professional experience uniquely position me to successfully deliver the objectives of this project. My academic and professional track record demonstrate a robust foundation in the genetics of resilience in pigs, directly aligning with the proposal's objectives and scope. This project builds upon substantial groundwork laid during my recently completed PhD, further leveraging my expertise to advance the field. Moreover, as a son of pig farmers with previous experience in pig experiments, I am ideally placed to conduct this project which combines data collection at the farm level, interaction with farmers and breed associations, data analysis, and bioinformatics.

I have consistently demonstrated academic excellence throughout my career, as evidenced by my summa cum laude master thesis results, a high quantity and quality of my scientific outputs and the awards earned for my research and conference presentations. These achievements underscore my ability to deliver high-impact research and contribute innovative solutions to complex problems.

2. Impact

2.1 Credibility of the measures to enhance the career perspectives and employability of the researcher and contribution to their skills development

This interdisciplinary project will contribute to my development as a highly skilled researcher specializing in livestock genomics and phenomics research. Expertise in bioinformatics and dynamic modeling of phenotypic data will be combined with genomic skills. This expertise is in high demand, both within and beyond academia. Moreover, I will intensively collaborate with two industry partners in this project, strengthening my network and skills. **This fellowship will offer a great opportunity to further develop an own line of independent research, boosting my academic career.**

I already developed a strong network of collaborators across academia and industry, evidenced in the collaborations for this project and my active membership of the COST action «EuLiPhe». However, this existing network provides a solid foundation for stakeholder engagement and collaboration, which I will further expand throughout this project, ensuring broad dissemination and application of the project's findings.

2.2 Suitability and quality of the measures to maximise expected outcomes and impacts, as set out in the dissemination and exploitation plan, including communication activities

To maximize the impact of this project, a comprehensive dissemination, exploitation, and communication strategy will be implemented, targeting a diverse range of stakeholders including the scientific community, the livestock industry and the general public.

Dissemination activities will focus on publishing findings in high-impact peer-reviewed journals and presenting at international conferences, such as the 2026 World Congress on Genetics Applied to Livestock Production (WCGALP) in Wisconsin and the 2026 European Federation of Animal Science (EAAP) conference in Hamburg. A public GitHub repository will host the developed quality control pipelines and predictive models, enabling reuse by researchers and industry professionals.

Exploitation measures aim to ensure that the project's outcomes, such as real-time prediction models and refined resilience phenotypes, are integrated into breeding programs and possibly into decision-support systems. Collaborations with SUISAG and Hendrix Genetics will facilitate the transfer of innovations into practical applications in pig breeding, while opportunities for commercializing the real-time monitoring application can be explored with industry stakeholders.

Communication and public engagement will emphasize raising awareness about animal resilience for sustainable farming. Interactive presentations at agricultural events, such as the yearly "Spring meeting" of the "Swiss Association for Animal Sciences", will foster direct dialogue with citizens. We will publish two laymans articles about the projects' results for publication in technical journals for farmers and breeders. I have ample experience with communcation to a broad audience, as is evidenced in the many presentations I gave and layman articles I published during my PhD.

The strategy for managing intellectual property (IP) in this project is designed to balance open access to research outputs with appropriate protection measures to support exploitation and ensure broad and impactful utilization of the results. IP arising from the development of real-time prediction models, web applications, and refined resilience phenotypes will be clearly identified and documented. Ownership will be determined based on the contributions of the partners (e.g., SUISAG, Hendrix Genetics, and ETH Zurich), in alignment with collaboration agreements established at the project's outset.

Software and tools, such as the quality control pipeline and predictive models, will be released under an open-source license (e.g., MIT) to encourage reuse by the scientific community while ensuring appropriate attribution. Key methodologies for real-time data processing and prediction algorithms that are central to commercialization will be safeguarded through controlled disclosure agreements with collaborating organizations at the start of the project. If significant technological innovations with commercial potential emerge (e.g., specific real-time monitoring tools or algorithms), patent applications will be pursued to secure exclusivity and incentivize investment in development. Non-commercial outputs, such as scientific publications, genetic insights, and basic research methodologies, will be shared openly to foster innovation and community engagement.

2.3. The magnitude and importance of the project's contribution to the expected scientific, societal, and economic impacts

The livestock sector is undergoing substantial transformations. Farmers need to improve animal health and welfare while decreasing environmental impact, thus ensuring efficient production (Rydhmer & Canario, 2014; Knap et al., 2023). In addition, projections show that global meat consumption will rise to 460-570 million tons per year by 2050, representing a 31% to 63% increase from current levels (Ritchie et al., 2023). For pigs in specific, the United Nations' Food and Agriculture Organization (FAO) projects a rise in consumption with 1.1% by 2030 (FAO, 2021). Moreover, the call to raise animals in more natural settings combined with climate change implies that animals will have to cope with greater environmental variation and must be adapted to their specific local environments. As a result, **there is a pressing demand for more resilient pigs genetically predisposed to have an improved welfare and better innate health in changing environmental conditions and societal context.** The project's results are expected to generate substantial impacts, delivering long-term benefits that extend beyond the project's immediate scope and duration.

Scientific impacts:

The project advances scientific understanding of resilience in pigs by uncovering the genetic architecture underlying this complex trait. The integration of high-resolution sensor data with genomic information will contribute new methodologies for phenotyping resilience, applicable across species. The real-time prediction models and quality control pipelines developed will provide reusable methodologies, empowering future investigations into resilience. Quantitatively, over 100,000 pig records and whole-genome sequencing data will generate insights in novel candidate genes for resilience, setting a new benchmark in the field.

Economic and technological impacts:

The project will optimize breeding programs and reduce economic losses, by enabling real-time detection of perturbations in pigs and integrating farmers' feedback. Moreover, the collected data could serve as a reference population for genomic prediction of resilience in these pig populations. These innovations will enhance breeding organizations' profitability while decreasing reliance on correlated, low-heritability traits. The web application developed will be transferable to other farms, facilitating insights to improve herd management. Industry collaborations with SUISAG and Hendrix Genetics ensure direct implementation. Potential cost savings and productivity gains are significant, with estimates suggesting a 5–10% reduction in mortality rates and a 3–5% increase in feed efficiency due to early perturbation detection and refined breeding strategies.

Societal impacts:

The project will directly improve animal welfare by identifying and promoting resilience traits, reducing the prevalence of stress, disease, and mortality in pig farming. These improvements address societal demands for sustainable and ethical livestock production. Indirectly, the project contributes to global food security by enabling more efficient and sustainable pork production. Reduced environmental impacts further enhance sustainability outcomes.

Magnitude and importance of impacts:

The results are expected to benefit the livestock industry at large, including breeders, farmers, and researchers. The methodologies developed are transferable to other species, potentially impacting broader agricultural systems. The estimated economic and environmental benefits, including reduced feed costs, decreased mortality, and lower emissions can be substantial. The importance of these benefits lies in their alignment with global sustainability goals, including the United Nations' Sustainable Development Goals (e.g., SDG 2: Zero Hunger, SDG 12: Responsible Consumption and Production).

3. Quality and Efficiency of the Implementation

3.1 Quality and effectiveness of the work plan, assessment of risks and appropriateness of the effort assigned to work packages

Experimental approach and methods, milestones and expected output

This project first aims to develop a real-time prediction model utilizing preprocessed sensor data to identify perturbed pigs (WP1). Next, farmers' feedback is incorporated to predict causality and refine resilience phenotypes (WP2). These refined phenotypes are used to identify candidate genes associated with pigs' resilience (WP3). The work plan for achieving the objectives is outlined in Figure 2. Specific milestones (Mx) and deliverables (Dx) are also outlined throughout these WP. All WP rely on access to high throughput (real-time) AFS data and cooperation of farm employees for real-time feedback collection. To answer our research questions, a collaboration is set up with SUISAG, the local Swiss pig breeding organization, and Hendrix Genetics, an international breeding organization (Table 1).

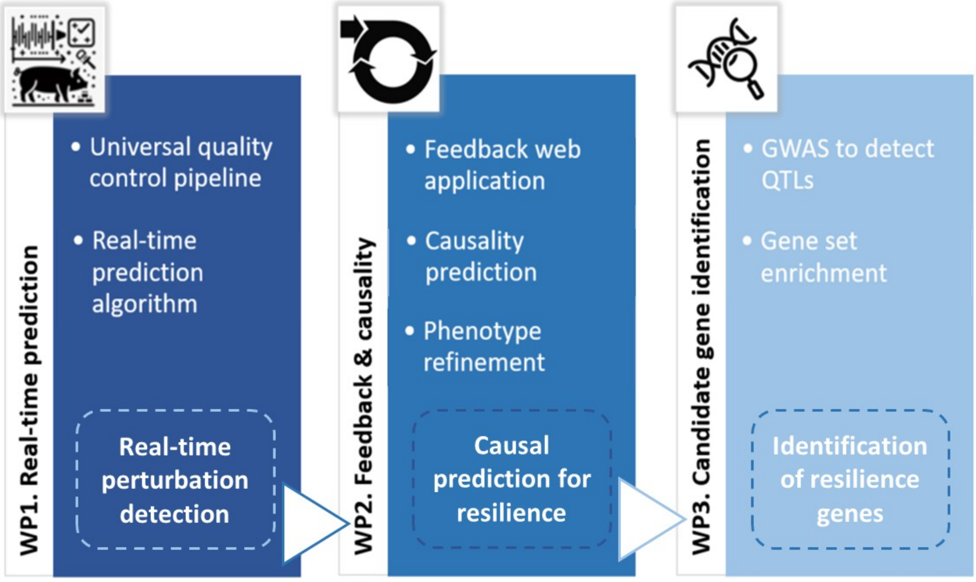


Figure 2. Schematic overview of the work plan. WP1 will lead to a real-time prediction model which will be used in WP2 to gather farmers' feedback for causal prediction for resilience. These refined phenotypes will be needed in WP3 to identify resilience genes.

WP1. Development of a real-time model for perturbation detection in pigs using sensor data

In WP1, historical AFS data from over 100,000 finishing pigs will be used (Table 1) to develop a real-time prediction model. This model will detect perturbations in body weight, feed intake, and feeding behavior based on data collected from finishing pigs at three farms operated by Hendrix Genetics and SUISAG.

WP1.1: Development of a quality control pipeline

Filtering out technical errors is crucial in modeling perturbations as they significantly impact result accuracy. Without proper data filtering, variability will be inflated leading to false detections of perturbations. A QC pipeline will be developed for individual pigs' body weight using the historical AFS data. An extensive literature review, building further on previous work (Garrido-Izard et al., 2022; Revilla et al., 2022; Gorssen et al., 2023), will reveal crucial parameters to consider for data filtering. In addition to previous studies, we will not only consider individual animal variability, but also observed group variability and animals' expected genetic value for daily gain and feed intake. An easy-to-use R-package will be built from this QC pipeline, which will be made publicly available under a MIT license within GitHub (**D1**).

Table 1. Overview of sample size (N) per line of pigs. Line 1 to 5 are from Hendrix Genetics (±150 AFS since 2011), Lines 6 and 7 are from SUISAG (128 AFS since 2020). The number of expected perturbations for WP2 were estimated based on the data from my previous study in line 5 (Gorssen et al., 2023), showing 4.7% perturbed pigs.

	Line 1	Line 2	Line 3	Line 4	Line 5	Line 6	Line 7
N historical records	22,000	17,500	43,000	8,500	27,000	5,000	5,000
N records per year	1,600	1,250	3,100	600	1,900	1,200	1,200
N perturbations per year	75	60	145	30	90	55	55

WP1.2: Development of a real-time prediction model to detect perturbed pigs

Building on my previous research demonstrating the heritability of resilience traits based on deviations in body weight, feed intake and feeding behavior (Gorssen et al., 2023), the aim is to develop an algorithm for real-time prediction of significant deviations in these parameters. Here, the innovative part lies in the combination of several traits (weight, feed intake and feeding behavior), which will be integrated into the algorithm using tailored statistical methods for each trait. Moreover, the developed algorithm from these traits will be transferable to other species, as patterns of eating and weight gain are linked to animals' resilience.

The prediction algorithm development to detect perturbations in pigs' performance consists of four steps. First, healthy periods are identified for a given trait (body weight, feed intake, or feeding behavior). Therefore, an iterative fitting procedure will be used (similar to Adriaens et al., 2021), starting with the complete trajectory and gradually removing outliers. Second, based on the identified healthy periods, group-level trends will be estimated to capture the influence of farm, pen, age, sex, and genetic predisposition, estimated from breeding value estimations. Third, by combining individual animal data and group-level trends, empirical Bayes techniques (Adriaens et al. 2018) are used to estimate an animal's unperturbed curve. Finally, perturbations will be detected using statistical process control methods on the residuals between the observed values and the predicted unperturbed curves.

Within this approach, different models will be evaluated for each trait, starting from simple linear regression to Gompertz growth curve modelling and polynomial quantile regression (Poppe et al., 2020). Different techniques will be tested and validated to optimize perturbation detection in the individual AFS time series. The validated prediction algorithm (**D2**) will serve as a cornerstone for subsequent work packages (**M1**). The results of WP1 will be combined in a scientific manuscript (**D3**).

WP2. A feedback loop to predict causality of resilience and improve resilience phenotyping

In WP2, the real-time prediction model (WP1) is integrated into a web application, for which a prototype has already been developed, offering a monitoring tool and allowing to directly collect farmers' feedback. This feedback offers crucial information to predict causality and provide insights into challenges affecting pigs thereby improving resilience phenotyping. Figure 3 shows the data workflow for WP2.

WP2.1: Setting up a web application to generate real-time alerts and gather farmer's feedback

The real-time prediction model (WP1) will be applied to AFS data within the framework of SUISAG and Hendrix Genetics. A web application will be set up to communicate alerts for specific pigs to farm employees to collect their feedback (**M2**). We will optimize the frequency of alerts based on our previous findings and feedback from the farmers. The web application will send alerts to farm employees every time interval and prompt them for binary feedback on observed perturbations. Farmers will need to simply indicate whether they can detect any problem on the perturbed pig using a dropdown menu. If yes, the farmer will be asked to classify perturbations into environmental (e.g. heat stress), disease (e.g. diarrhea, coughing), social (e.g. tail biting wounds, pen aggression) and/or other challenges. Finally, the application will allow for additional input on the presumed cause, so farmers can add more detail on things that are hard to capture in relatively simple categories.

The web application will first be tested and optimized with the farmers on-site. Additionally, a protocol will be implemented for farm employees to monitor each pen of pigs biweekly minimizing the risk of undetected challenges due to technical errors. Finally, publicly available outdoor weather data (e.g. Meteostat) and the temperature and humidity inside the farm will be monitored and integrated to evaluate the impact of environmental challenges such as heat stress (Mayorga et al., 2019). Based on my previous research, we expect about 5% of pigs to show perturbations, leading to the detection of about 500 perturbed pigs per year (Table 1).

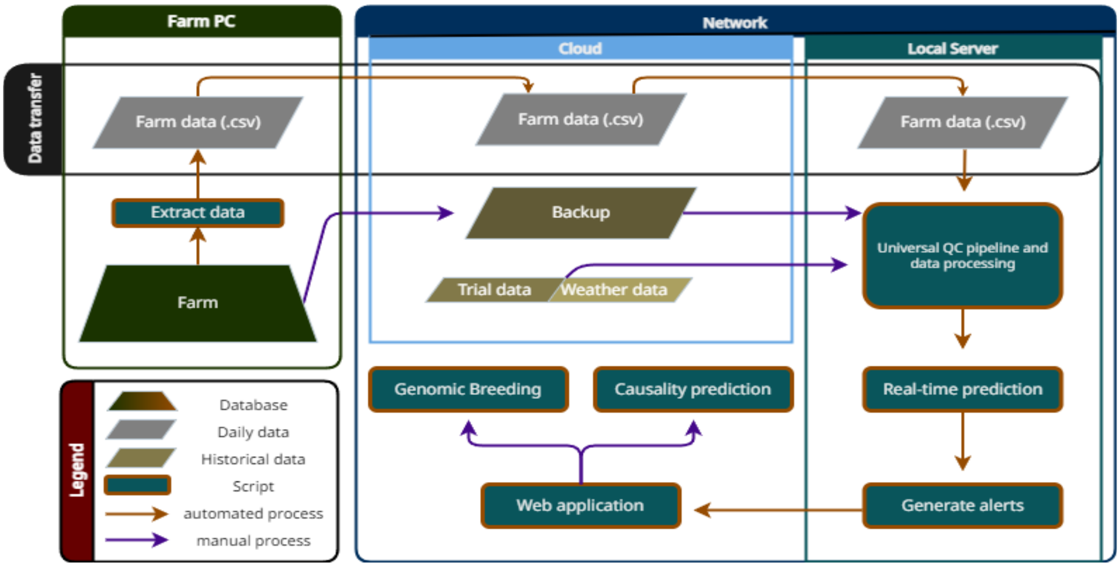


Figure 3. Data workflow for WP2.

WP2.2: Causality prediction for perturbations in pigs

This section aims to predict the causality of perturbation patterns in pigs introduced by specific challenges including disease, social stressors and/or environmental stressors. First, we will analyze the correlation between perturbation patterns for weight, feed intake and feeding behavior from AFS with the feedback. Heat stress, for example, will probably lead to a moderate perturbation in body weight and feed intake, while the number of visits to the feeder were shown to be less affected due to heat stress (Mayorga et al., 2019; Bus et al., 2021). In a next step we will develop models to classify perturbations. Different models will be evaluated, such as models based on perturbation patterns and/or machine learning (**D4**). In the final, most challenging and innovative step, we will try to extend these models to be self-learning by automatically integrating new feedback. If successful, this methodology is extremely valuable for the development of a commercial product in a later phase beyond the scope of this project application.

This integrated approach allows for the estimation of the probability associated with specific challenges, enabling the evaluation of animals' responses. Implementing this methodology will advance our comprehension of resilience dynamics and contribute to more precise resilience phenotyping (**M3**). A manuscript will be written on the results of causality prediction and resilience refinement using feedback data in WP2 (**D5**). We aim to publish in a top journal, given the uniqueness and possible far-reaching implications of our proposed methodology.

WP3. Identification of candidate genes for resilience

WP3 addresses the scarcity of knowledge regarding the genetic basis of resilience in pigs. An extensive GWAS will utilize imputed whole-genome sequences and phenotype data for the animals from WP1 and WP2 to identify candidate genes associated with resilience in pigs. This analysis will encompass seven lines of purebred pigs with known pedigree and genomic information from two breeding organizations.

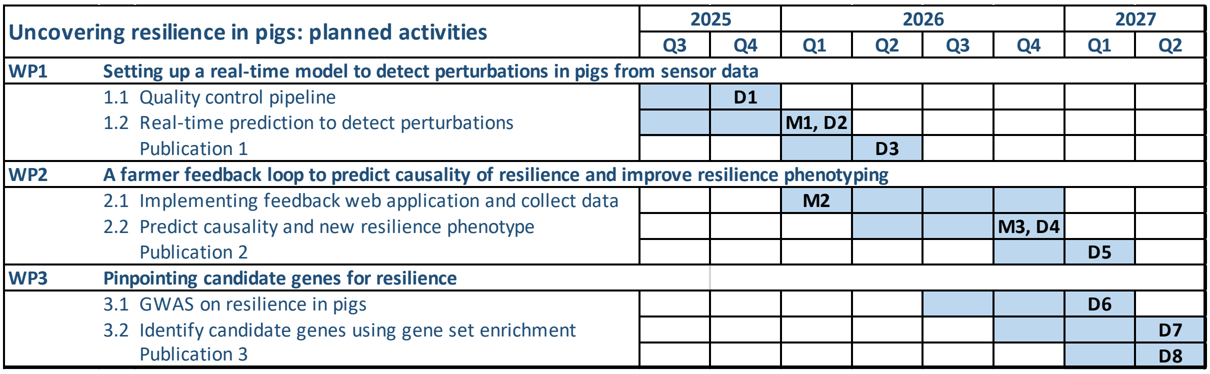
WP3.1: A genome-wide association study on improved resilience phenotypes in pigs

GWAS analyses will be performed based on resilience phenotypes generated in WP1 and WP2 and imputed WGS genotype information using GCTA software (Yang et al., 2011). In a first step, we will impute medium density single nucleotide polymorphism (SNP) data to WGS level. Medium density SNP data is available for most pigs that were phenotyped with AFS in each purebred pig line (Table 1). Moreover, >100 pigs per purebred line have been whole genome sequenced (30x) and WGS information for 1800 pigs of different breeds is also publicly available from online databases, such as https://piggtex.ipiginc.com (Teng et al., 2024). Medium density SNP data will be imputed to the sequence level via Beagle 5.4 (Browning & Browning, 2007).

Next, two GWAS strategies will be used: a case-control approach and a quantitative approach. For the case-control approach, pigs will be grouped in 'resilient' vs 'non-resilient' based on resilience phenotypes and farmers' feedback data. To classify pigs as 'resilient', we will select pigs that showed no severe perturbations and no alerts that were present in the same pen as pigs with substantial perturbations and several alerts. This is done to ensure these pigs were subjected to (environmental) stressors. For the quantitative approach, resilience phenotypes and number of alerts will be used as such, while correcting for factors such as sex, farm, herd-year-season-effects,…. Through the application of statistical methods such as Fisher's exact test and logistic regression, genetic variants associated with the phenotype will be pinpointed (**D6**).

A power calculation was done based on Goddard and Hayes (2012). Using sequence data and a heritability of 20% (Gorssen et al., 2023), QTLs who explain up to 3% of trait variance can be detected with a sample size of 5,000 pigs, which is available for all lines. For specific lines (Table 1) with >20.000 records, QTLs explaining 1% variance can be detected. To further increase power of these detected QTLs, GWAS results will be compared between statistical methods (case-control vs quantitative), different traits (perturbations in weight, feed intake and/or feeding behavior) and the seven different genetic lines over two breeding organizations. QTLs appearing over different genetic lines for multiple traits and both statistical methods will be linked to general resilience mechanisms.

GANTT chart



Uncovering resilience in pigs: planned activities		2025		2026				2027	
		Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2
WP1	**Setting up a real-time model to detect perturbations in pigs from sensor data**								
	1.1 Quality control pipeline	▨	▨ **D1**						
	1.2 Real-time prediction to detect perturbations	▨	▨	**M1, D2**					
	Publication 1			▨	▨ **D3**				
WP2	**A farmer feedback loop to predict causality of resilience and improve resilience phenotyping**								
	2.1 Implementing feedback web application and collect data			▨ **M2**	▨	▨	▨		
	2.2 Predict causality and new resilience phenotype				▨	▨	**M3, D4**		
	Publication 2						▨	**D5**	
WP3	**Pinpointing candidate genes for resilience**								
	3.1 GWAS on resilience in pigs					▨	▨	**D6**	
	3.2 Identify candidate genes using gene set enrichment						▨	▨	▨ **D7**
	Publication 3							▨	▨ **D8**

WP: work package, Q: Quartile, GWAS: Genome wide association study, M: milestone; D: deliverable

WP3.2: Identify candidate genes using gene set enrichment analysis

In a following step, gene set enrichment analysis will be used to identify candidate genes, following Cheng et al. (2022). Each identified QTL-region will be expanded with one additional mega basepairs on both sides of the QTL region to ensure no important associated genes will be overlooked in this analysis. BioMart (Smedley et al., 2009) will be used to identify genes located in every expanded QTL region, utilizing gene annotation databases such as ENSEMBL (Sscrofa11.1). Next, gene set enrichment analysis will be done based on available data sources containing information from published QTLs in pigs, such as Animal QTL database (Hu et al., 2007), a pig transcriptome data, such as the Porcine Signature Database (Van Renne et al., 2018) and a gene ontology database, such as the Molecular Signatures Database (Subramanian et al. 2005). Using these three libraries, a sliding window approach will be used to assign specific features to each window for each resilience trait and per pig line. This approach will result in a dataset of underlying candidate genes for pigs' resilience (**D7**). The results of WP3 will be combined in a scientific manuscript (**D8**).

3.2 Quality and capacity of the host institutions and participating organisations

Addressing current and emerging challenges to ensure the long-term sustainability of agricultural production and food systems to meet human needs is a core mission of the Institute of Agricultural Sciences. Improving the resilience of farm animal-based food production systems is paramount to meet the globally rising demand for animal-based food while minimizing environmental impacts and improving resource efficiency. This proposal tackles the challenging research questions how the resilience of farm animals can be improved genetically. This is an extremely important research question that is currently not addressed in the Animal Genomics group. **Therefore, this project would be a highly valuable complementary addition to the research portfolio of the Animal Genomics group, which is also central to the mission of the Institute of Agricultural Sciences.**

The Animal Genomics group is a shareholder at the Euler high-performance computing cluster of ETH Zürich, ensuring that **sufficient compute and storage capacity are available to store and process large datasets obtained from automated feeding stations**. The group also has extended experience in establishing efficient and highly parallelized computing workflows in Snakemake, which will be beneficial for the project to ensure reproducibility of the computational aspects of the project.

ETH Zurich offers comprehensive support services, including workshops on advanced bioinformatics techniques, data management, and soft skills like project management and communication. Additionally, I will benefit from the institutional support provided by the ETH Career Center and Technology Transfer Office, which assists with career development and intellectual property management. The Animal Genomics group's strong collaborations with industry partners, such as SUISAG, enhance the project's relevance and applicability. **The group's well-established infrastructure, logistical support, and collaborative networks ensure that I will be well-positioned to achieve the project's ambitious goals.**

4. References

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