SEFARI

Leading Ideas for Sustainable and Resilient Crops

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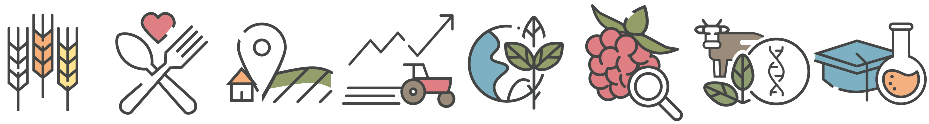
Leading Ideas on Crops: Sustainable Food Systems and Supply

The Scottish Environment, Food and Agriculture Research Institutes (SEFARI) is a collective of six research institutes, each with their own global capability, expertise and reputation.

The six institutes are:

- Biomathematics and Statistics Scotland
- James Hutton Institute
- Moredun Research Institute
- Rowett Institute
- Royal Botanic Garden Edinburgh
- Scotland's Rural College

SEFARI focuses its work under eight 'Leading Ideas'



This booklet highlights key research outputs from Scottish Government funded strategic research programme 2022-27 on sustainable food systems and supply. This includes research on sustainable food production from domestic agriculture through to sustainable and secure supplies of food, as well as supporting a safe and healthy diet. It provides elements of research relevant right through from farm to fork to contribute to the economy, people's livelihoods and the health of the nation.

One of the primary focuses is in developing resilient, high-quality crop, and food and drink industries that capture market value and contribute to Scotland's economy. There is also a focus on improving agricultural practices to develop a resilient, productive sector that is abreast of new and transformative opportunities.

Here we highlight examples of impact arising directly from the Strategic Research Programme and its crucial role in leveraging of further research funding to expand impact.

Contact us

www.sefari.scot

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info@sefari.scot

Exploiting Genetic Diversity for Food Security and Sustainability

Best Practices in Data Collection, Management, Visualization, and Sharing

Contact: Paul Shaw – Paul.Shaw@hutton.ac.uk

Climate change poses a significant threat to global food security. As weather patterns become increasingly unpredictable, farmers and plant breeders face unprecedented challenges in maintaining a reliable and nutritious food supply.

A potential solution lies within the world's vast genetic diversity. Genebanks and other plant collections hold a wealth of genetic material, including crops with resistance to pests, diseases, and climate extremes. However, unlocking this genetic potential requires efficient tools to allow researchers to search for promising plants and subsequently collect, manage and analyse the massive amounts of data generated by crop improvement research.

Innovative software solutions have been developed to address this challenge. State-of-the-art computational tools, such as Germinate, GridScore, and Helium, empower researchers to collect, organise, store, and analyse data on plant diversity and breeding experiments, streamlining the entire breeding process, from initial data collection to final variety release.

By building the software researchers need to efficiently manage and analyse data, we have contributed to the accelerated development of climate-resilient crops, ensuring a sustainable future for our crops and a brighter outlook for those that rely on them. Foundations put in place through RESAS funding have allowed us to develop computational tools that:

- promote the use (and re-use) of existing and future information.
- reduce errors in datasets.
- reduce barriers of access to publicly available datasets.
- provide a standard distribution framework and format for publishing data and results.
- optimise data exploitation.
- ensure simplified cross-working between complex datasets.

"Our innovative software that efficiently manages and analyses research data has contributed to the accelerated development of climate-resilient crops."

Root Research: Unveiling the Hidden Strength of Plants

Understanding root growth, development and root-soil relationships

Contact: Gwendolyn Kirschner - Gwendolyn.Kirschner@hutton.ac.uk

Agricultural soils are hugely varied: water, nutrients, and microbes are unevenly distributed. The distribution of roots, their architecture and anatomy are therefore crucial to optimize water and nutrient uptake and the interaction with the soil microbiome.

Roots serve multiple vital functions for plants, providing stability and anchorage in the soil, absorbing water and nutrients essential for growth and development, and interacting with the soil microbiome, which can improve stress tolerance and disease resistance. Understanding root growth and development and root:soil interactions is therefore essential for optimizing agricultural practices and ensuring plant productivity.

"Our root research is crucial to providing productive and resilient crops in a changing climate."

To enhance water and nutrient uptake, it is essential to adapt root system architecture, which includes the length, angle number, and types of roots; and root anatomy, which includes the root diameter, tissue composition, and the presence of root hairs.

A significant challenge in root research is that roots are hidden in the soil, making them difficult to analyse. Traditional phenotyping methods are often destructive, complicating the study of root systems. To overcome this, advanced phenotyping methods for use in both controlled environments and under field conditions have been developed. We have examined barley, potato and legume populations for different root phenotypes under varying soil moisture conditions, and tillage versus no-till and measured plant performance in relation to the root phenotype. This will lead to the discovery of new genes that regulate root system architecture and anatomical traits.

These innovative approaches provide insights into root biology, leading to the development of crops with optimized root systems for better water and nutrient uptake, improved resilience, and higher yields. Understanding and enhancing the hidden half of plants paves the way for more sustainable and productive agricultural systems.

Micronutrient Efficient Barley

Exploring previously untapped genetic variation for future sustainability

Contact: Kelly Houston - Kelly.Houston@hutton.ac.uk

Barley underpins Scottish agriculture and is worth £7.1 billion each year to the UK economy. However, there is a pressing need to establish an environmentally benign and sustainable supply of locally produced, high quality barley grain to safeguard the food, feed and drink sector. Modern crops (elite varieties) have been selected for high yield under high inputs and a stable climate, therefore the major challenge faced by plant breeders is to develop new varieties that maintain yields whilst establishing more sustainable and resilient production.

Natural diversity is a rich source of novel variation that has the potential for improving the resilience of modern crops. Our strategy is to explore and utilise variation within landrace barleys; ancient, locally adapted crops that yield efficiently under limiting conditions.

Bere landrace is one of oldest and most widely grown barleys in Scotland; tolerance to poor soils and a northerly climate made it a valuable staple for centuries. Collaborative SEFARI research has identified Bere barley lines that are tolerant to the nutrient-deficient soils on Orkney and which have much higher concentrations of manganese in the leaves (which is crucial for plant growth and health) compared with modern (elite) varieties.

> **"Improving our understanding of untapped genetic diversity will help us learn how to safeguard Scotland's barley production."**

Characterizing the superior capacity of Bere barleys to acquire and allocate Manganese allowed us to identify the unique associated gene combinations and transfer them into modern elite varieties. Using this targeted approach, we identified a candidate genome region and developed novel breeding lines tailored to growing on marginal nutrient-depleted soils.

Our work demonstrates that landraces provide an invaluable source of untapped genetic variation that can be explored to unravel complex sustainability traits, securing optimal and resilient crop productivity. With the potential for marginal land being co-opted into arable farming due to climate change, climate change mitigations, and land degradation, identifying combinations of genes responsible for efficient uptake and internal distribution of micronutrients will underpin the ability of barley to maintain crop yield in the challenging and variable conditions that lie ahead.

Practical IPM measures, resulting from fundamental and applied SEFARI research, in conjunction with precision agriculture innovations, will continue to have impact in maintaining or improving food- production during the transition to lower-input agricultural systems.

Coping with Climate Change: Considering Protein Yield Resilience

Examining the effect of crop mixtures on protein yield

Contact: Pietro Iannetta - pete.iannetta@hutton.ac.uk

"Crop mixtures can result in protein yields which significantly exceed those of monocrops."

Dependence on the import of high-protein legume grain has placed Scottish producers in an unattractive position financially, and environmentally. However, high import prices and price-volatility can be avoided by producing high protein legume crops such as peas and beans 'at home'. This approach offers environmental benefits, as legume crop residues help to realise regenerative crop rotations, enhanced soil quality, and reduced greenhouse gas emissions.

The potential of legumes is underpinned by 'biological nitrogen fixation', a process whereby atmospheric nitrogen is 'fixed' into biologically useful forms. This is a function of the symbiosis between legumes and soil bacteria termed 'rhizobia'. The benefits of high protein grain production are allied to soil-enriching crop residues which remain in-field.

Data obtained from plot-scale field trials showed that crop mixtures can result in protein yields which significantly exceed those of monocrops and offer protein yield-resilience. The highest protein yields were obtained from winter and spring mixtures, as either whole-crop or grain, respectively. Furthermore, the best performing winter and spring mixtures, were achieved in the absence of synthetic (mineral) nitrogenous fertiliser being applied.

Within the context of environmental impact reduction, resource use efficiency and climate-impact yield resilience, the potential of both winter- and spring-sown pulse-based crop mixtures (with cereals) is highlighted as offering a means by which grain and whole crop yields may be obtained whilst adapting to the variable weather characteristic of climate change.

This SRP research was also supported by the HDRF (Hannah Dairy Research Foundation), and the EC-funded project www.econutriproject.eu; and carried out partnership with the Processors and Growers Research Organisation (PGRO), Harbro Ltd, LS Plant Breeding, and Scotston (organic) Farm.

Genome-Enabled Growth Simulation Models to Predict Crop Performance

Improving breeding approaches to safeguard crop performance in a changing climate

Contact: Joanne.Russell@hutton.ac.uk

Improving the genetic potential of seeds is the most effective way to introduce the innovation in agriculture needed to meet the UN Sustainable Development Goals. Using barley as both a crop and a genetic model, the aim is to deliver new breeding strategies and toolkits for maintaining barley production under anticipated future climatic conditions. This work accelerates beyond conventional breeding through the application of precision phenotyping, the interrogation of relevant, deep genomic information, and high-resolution genetics in conjunction with bioinformatics and crop growth simulation models.

An extensive set of well characterised barley genotypes was used to derive combinations of genomic prediction (GP) and crop simulation models (CSMs) that could be used to improve current predictive breeding approaches. We focused on adaptation to European agro-climatic zones, factors predicted to provide resilience to climate change, and disease resistance.

Sustainability and resilience traits including water- and nitrogen-use efficiency, culm architecture, disease resistance, and flowering time were examined using genomic data and state of the art analytical tools and approaches, and agronomic performance was evaluated under different growth conditions, including ambient and elevated [CO2]. These data were used to improve the predictive models and new plant populations were developed as breeding resources to contribute to future food, feed and fibre security.

Populations were analysed in multiple environments for variation in a wide range of phenotypic traits and molecular diagnostics developed for variation in adaptation-associated genes, allowing selection for combinations of variants that control specific plant developmental transitions. We developed models that used the data from the molecular diagnostics to predict those combinations that would be needed to maintain barley production in target future environments. Embedding commercial organisations in the research encouraged deployment of the outcomes in breeding across the sector.

CPC Diversity

Genomics/genetics

Breeding

Future-Proofing Potato: The UK's Second Most Important Crop

Understanding and deploying resistance to key traits

Contact: Ingo Hein – Ingo.Hein@hutton.ac.uk

Potato is the second most important food crop in the UK and ranks third globally, playing a critical role in food security by providing a reliable supply of nutritious food. Unique among major crops, potatoes offer all essential amino acids, produce 2–4 times more food per hectare than cereals, and yield more food per unit of water than any other major crop. Rich in nutrients, potatoes are a cornerstone of diets worldwide.

The crop contributes £4.3 billion annually to the UK economy, including £1.6 billion from Scotland. However, the UK potato industry faces significant challenges, including multiple stresses associated with climate change, pests, diseases, and the need for sustainable production practices.

To address these challenges, SEFARI research employs cutting-edge genomics, genetics, molecular pathology, and physiology, while also leveraging the genetic diversity held in the Commonwealth Potato Collection (CPC). This work has been translated into practical solutions through close collaboration with key industry partners, delivering pathogen and climate resilience.

Our research focuses on understanding and deploying tolerance and resistance to key pests and diseases, such as late blight, viruses, and potato cyst nematodes, as well as abiotic stresses, including drought and waterlogging. By studying pathogen infection processes, we are developing novel crop protection mechanisms and exploring tuberisation pathways to enhance environmental resilience. We aim to develop resource-efficient cultivars that require less water and fertilizer, advancing food security in a sustainable manner.

New technologies, including precision breeding techniques, and state-of-the-art facilities for speed breeding and rapid crop phenotyping provided by the Advanced Plant Growth Centre, will further accelerate our capacity to deliver future-proofed potato varieties.

"SEFARI uses cutting edge technology and resource of the Commonwealth Potato Collection to support the sector's £4.3billion contribution to the UK economy."

Climate Adaptation and Sustainability of Soft Fruit Production

Linking plant spectral responses with plant stress

Contact: Susan McCallum – Susan.McCallum@hutton.ac.uk

SEFARI research is currently focused on raspberry, blackcurrant and blueberry, with other crops of interest in Scotland, particularly cherry, blackberry and honeyberry also being explored. The focus is on establishing the genetic control of key traits through the integration of genomic techniques with targeted phenotyping methods.

The two main categories of interest in soft fruit are:

1. Understanding and tackling stress. A range of abiotic and biotic stresses, including climate adaptation (winter chilling, spring frost tolerance, water and heat stress, ability to cope with rapid changes in season) and the key biotic pest and diseases.

2. Economic production and sustainability. This includes addressing yield, fruit quality, resource use efficiency, reducing the use of agrochemicals and other inputs including labour.

Work to identify the genes underlying these complex traits is underpinned by the development of a reference transcriptome dataset, and the assembly of three draft reference genomes from key raspberry varieties. This allows the development of high-resolution gene expression analysis, and the identification of variants of interest at a genomic level. The aspiration is to develop such resources for all key soft fruit crops.

"State of the art research is safeguarding the future of many of Scotland's soft fruit crops"

As increasingly complex traits are studied, the need for an underpinning physiological and biochemical understanding of trait components becomes more significant in support of gene discovery and marker identification. To achieve this, a physiological and biochemical understanding is linked with high throughput image analysis technologies to reduce the phenotyping bottleneck.

A pioneering platform and know-how for field-based 'real environment' phenotyping has been developed along with methodology to support its use and further developments in this area will be important. Work is linking spectral responses detected using the imaging platform, to underlying plant stress to help understand climate adaptation and promote a sustainable soft fruit industry.

The EORNA Barley Database

Opening gene expression data to the research community

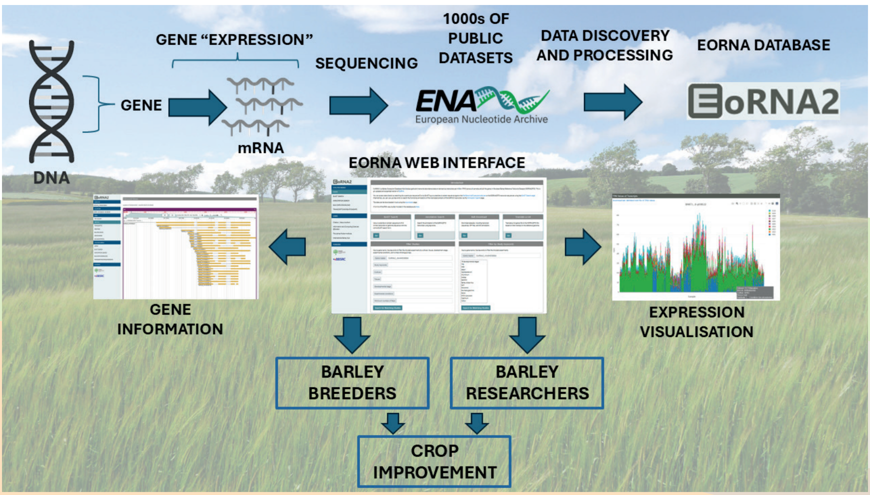
Contact: Micha Bayer – micha.bayer@hutton.ac.uk

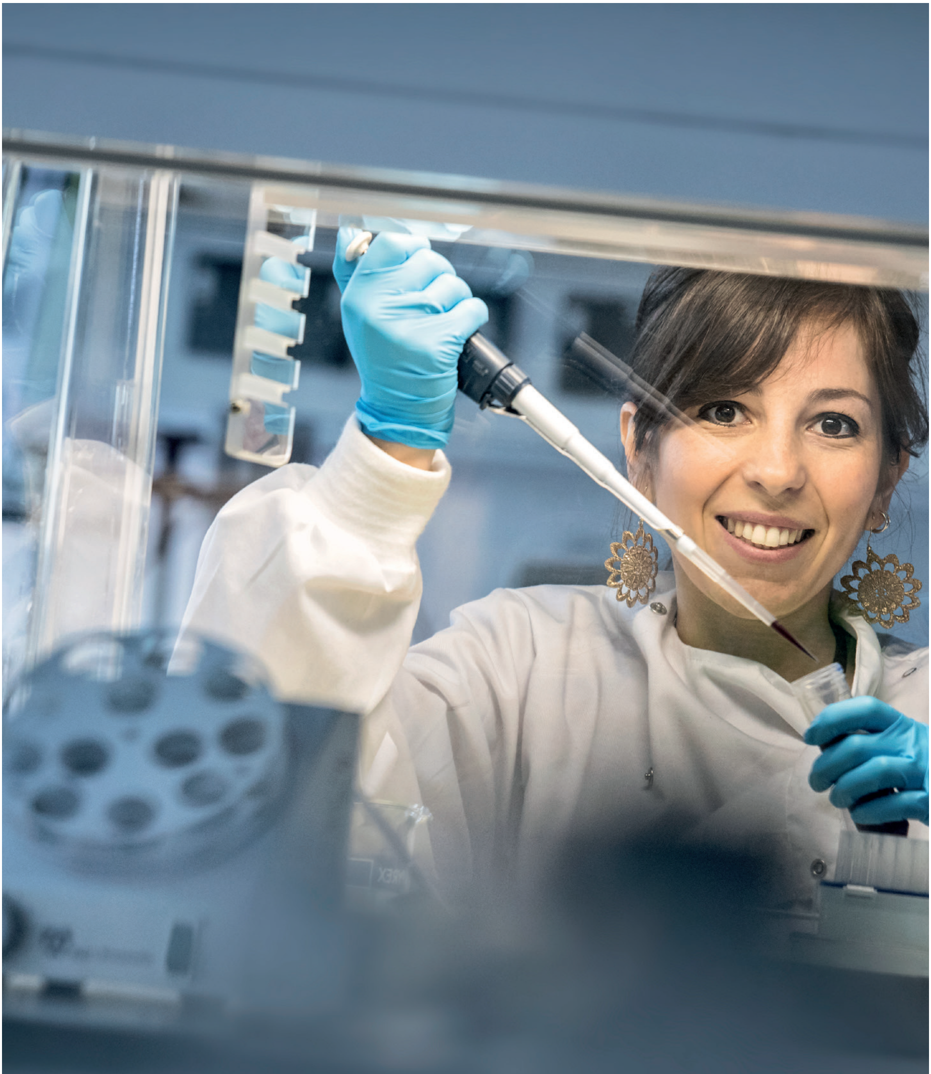
The expression of a gene – i.e. the transcription of DNA sequence into RNA -- is one of the most fundamental processes underlying life and is found in all known life forms. Information about the level of gene expression for a particular gene allows researchers to link the expression of the gene to specific tissues, environmental stresses, or genetic variants. Having a comprehensive atlas of gene expression in relation to these factors is an invaluable resource for both fundamental and applied research.

Barley is Scotland's most important cereal crop, and the fourth most important cereal crop globally. Thousands of barley researchers around the world rely critically on centralised data resources for their research, and our mission was to create a gene expression resource that barley researchers both in Scotland and worldwide could use. We were also aiming to create a computational infrastructure that researchers working on other species can use to replicate our work for their own purposes.

The first version of our barley gene expression database was published in 2021. Named EORNA , after the Scottish Gaelic word for barley, it featured gene expression level data for 843 barley samples covering a total of 22 published studies. The EORNA database proved popular and received approx. 87,000 hits in its first three years alone.

Building on this success we successfully leveraged further funding from BBSRC, resulting in the current EORNA2 database. For EORNA2, we produced code that allows the fully automated discovery, download and quantification of samples from the European Nucleotide Archive (ENA). All available public barley RNA-Seq samples were catalogued with this novel pipeline, resulting in a total of 6,726 samples from 191 studies. Additionally, users can now subset the data with search terms specifying cultivar names, environmental conditions or tissues. EORNA2 is currently under development, but we now have a beta release that is currently subject to user testing.





“Data science is being used both in Scotland and globally to underpin research into barley – our most important cereal crop”

Charles Bestwick
Director
SEFARI Gateway

Kenneth Loades
Soils and Crops
Knowledge Broker

Contact us

www.sefari.scot

@SEFARIscot
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info@sefari.scot