

# ERA-CAPS Showcase Report



**European Research Area Network  
for Coordinating Action in Plant Sciences**  
[www.eraCaps.org](http://www.eraCaps.org)



## Overview

The European Research Area Network for Coordinating Action in Plant Sciences (ERA-CAPS) is a multilateral funding program aimed at developing and strengthening fundamental molecular plant science research in Europe through transnational and transatlantic collaborations.

The network was created in 2011 and funded by the European Commission under the 7th Framework Programme. Since August 2015, ERA-CAPS has operated as a self-sustained initiative, i.e. without the financial support of the European Commission.

This showcase report aims to provide an overview of the ERA-CAPS program to date, discussing the diverse range of plant science research supported and the benefits of multinational support for plant sciences highlighted by participating researchers.

You can learn more about ERA-CAPS by visiting [www.eracaps.org](http://www.eracaps.org).

2013  
2014  
2016 | **3**  
funding calls

**38** transnational collaborative grants awarded

  
**177** research groups supported

**18 countries involved in ERA-CAPS calls**



 **€55.6**  
million invested

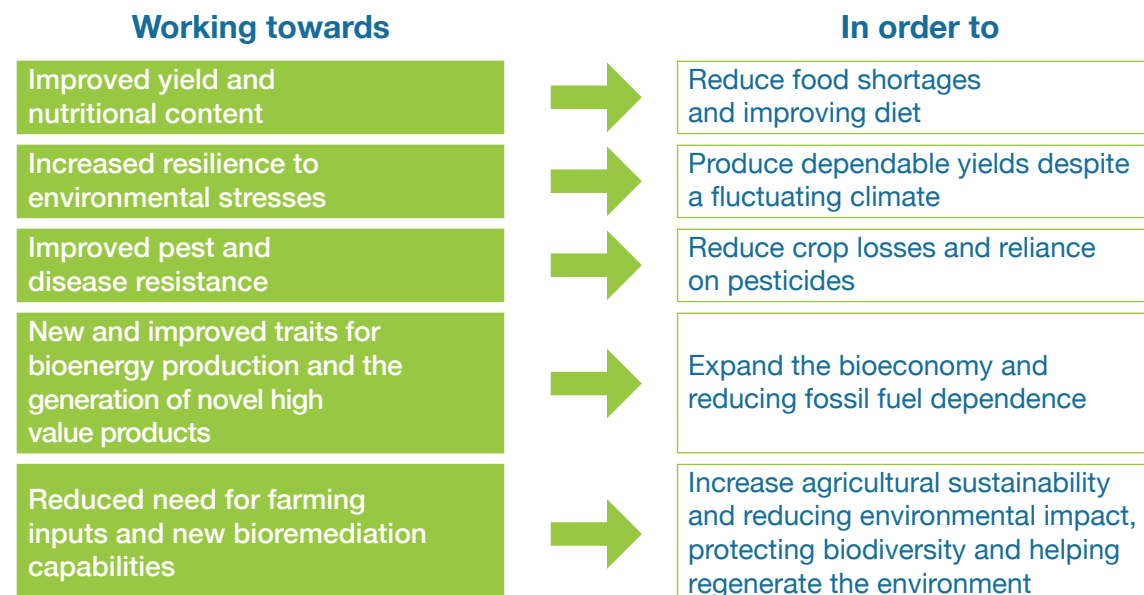
# Why plant sciences?

**Plants are essential to human life. Directly or indirectly, they produce most of the world's food and provide renewable sources of energy and materials.**

At present, we are facing global challenges associated with factors such as population growth, environmental degradation and climate change.

To help tackle these challenges and create a more sustainable future, we must improve our fundamental understanding of plant systems. New knowledge of plant systems will directly contribute to a range of possible improvements to crop species, which will help to deliver more productive, healthy, resilient and sustainable agriculture for food and the bioeconomy.

“It has brought a cohort of Early Career Researchers together who are experiencing a degree of independence and collective decision making which I believe will only help their careers as they develop.”



# Why ERA-CAPS?

Producing sustainable, resilient crops for food security and the bioeconomy requires coordinated international collaboration to engage the best people, organisations and facilities in world class research. ERA-CAPS brings together national and regional funding organisations from across Europe and beyond, who coordinate efforts to embed molecular plant sciences more firmly into national policies and processes whilst continuing to fund excellence-driven research.

## What science has it enabled?

To date, ERA-CAPS has run three funding calls and provided funding to 38 transnational projects. These projects sought to advance our fundamental understanding of plant biology and featured work in 25 different plant species, ranging from basic plant models to economically and socially important crops. The projects covered a broad spectrum of research topics and used various methodologies to tackle questions relating to food security, non-food crops, adaptation to climate change and biotic/abiotic stresses.

Some examples of projects supported through ERA-CAPS are:

- **EURO-PEC** – European plant embryology consortium
- **KatNat** – Elucidating the multifaceted functions of protein acetyltransferases in plant stress response and regulation of metabolism.
- **AI-UCIDATE** – Towards a molecular understanding of aluminium genotoxicity for crop improvement
- **EVOREPO** – Evolution of sexual reproduction in plants
- **H.I.P** – Homeostasis of isoprenoids in plants: understanding compartmentalization, flux and transport of isoprenoids in glandular trichomes for non-crop and crop species.
- **C4BREED** – Designing C4 breeding strategies using genetic enablers of C4 evolution

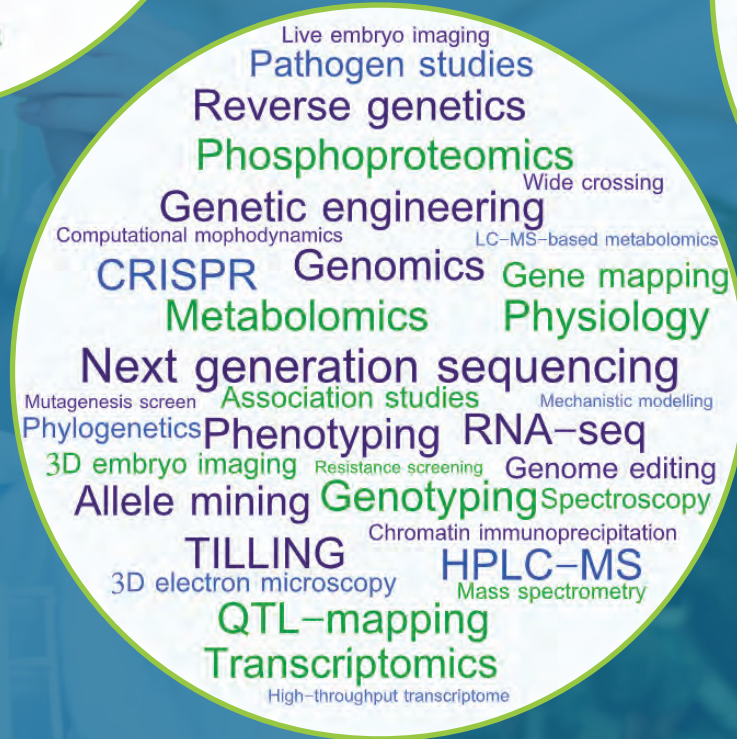
*For a full list of projects please see the annex on pages 16–18.*

To deepen and enlarge cooperation in the area of molecular plant science, ERA-CAPS has:

- Provided joint funding to a transnational research programme, to strengthen ties between international research groups.
- Facilitated the systematic exchange of information to expand the network and involve new members and affiliates.



An overview of species, research themes and methods represented within the portfolio of awards supported through ERA-CAPs



# INTREPID INvestigating TRiticeae EPIgenomes for Domestication

**The work of an interdisciplinary team from the UK, Germany and the USA will help in understand how epigenetic can be used as a source of genetic variation.**

Crop breeding is driven by genetic variation. Identifying, understanding and introducing variation into elite material through crop breeding is critical for the development of new high-performance. The INTREPID project has pioneered the methodology for analysing epigenetic variation, DNA modifications that do not change the DNA sequence, in the genome of hexaploid bread wheat. The team has uncovered a massive amount of untapped and stable epigenetic variation across a diverse collection of wheat.

The INTREPID consortium brought together international experience in epigenetics, genomics and data science to build a comprehensive view of the wheat epigenome. Using novel methodology, researchers in the UK and USA generated the first survey of the epigenome of over 100 core wheat cultivars taken from the Watkins collection, an important wheat diversity collection. Teams in UK and Germany analysed the survey data. They identified genome-wide genetic and epigenetic patterns of over 100 different types of wheat and discovered that there were both genetic and epigenetic variations

between cultivars. They also found these variations follow a geographical pattern, suggesting changes arose from environmental conditions in the areas where these cultivars normally grow. This means changes in DNA can happen due to the environment but are still inherited. A greater understanding of the role of epigenetics in plant breeding opens the possibility to improve plants to respond quickly to local conditions and could enable farmers and breeders to grow the best possible crop for their environment.

These results continue to be explored within the current teams and through international collaborations with Germany, USA, Australia, and Mexico. All the data and associated metadata is available on public databases and the Chinese Spring wheat methylation data has been added to the EMBL-EBI ensemble wheat browser. The work is being used through collaborations with breeding companies RAGT and KWS and technology developers LGC. Consortium members are also working with IBM to apply machine learn approaches to re-analyse the data.





### UK – NIAB (non-funded partner)

- Generation of new synthetic line wheat hybrids

### DE – Helmholtz-Zentrum Muenchen

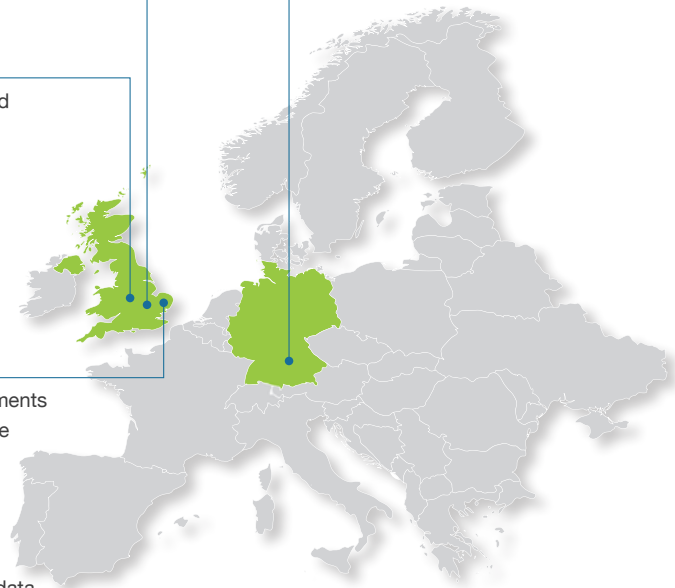
- Collaborated in the analysis of methylation data
- Developed approaches to integrate multiple data sets

### UK – John Innes Centre

- Generated samples and coordinated production of hybrid wheat
- Experimental design and biological interpretation

### UK – Earlham Institute

- Design and interpretation of experiments
- Developed an approach to genotype and epi-type from the same captured material
- Surveyed the epigenome and genotyped all 105 lines
- Associated analysed material with geographical position and climatic data

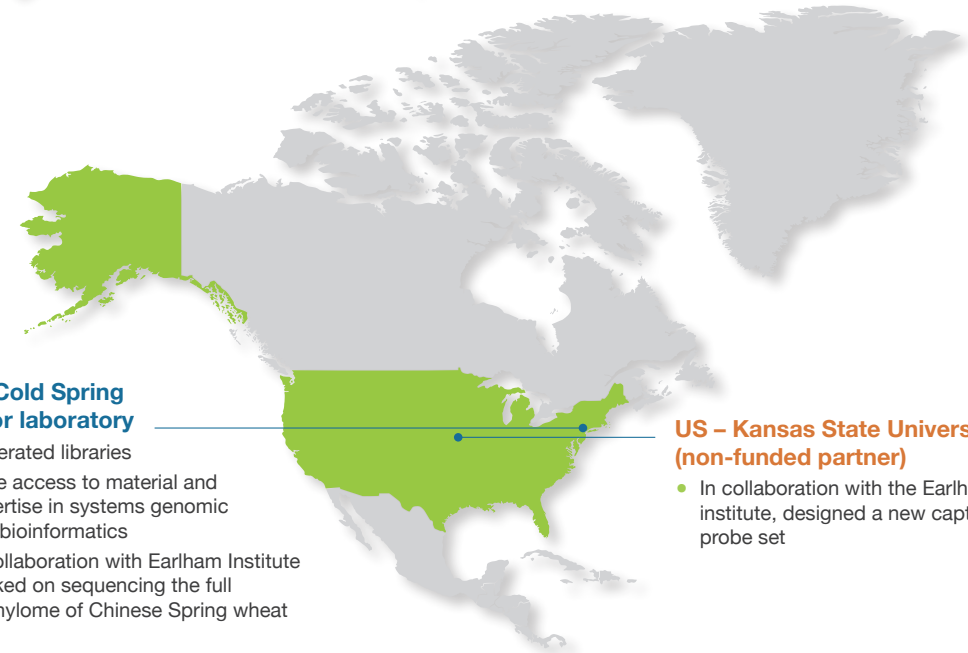


### US – Cold Spring Harbor laboratory

- Generated libraries
- Gave access to material and expertise in systems genomic and bioinformatics
- In collaboration with Earlham Institute worked on sequencing the full methylome of Chinese Spring wheat

### US – Kansas State University (non-funded partner)

- In collaboration with the Earlham institute, designed a new capture probe set



## Key impacts

- First description of the wheat epigenome
- Identified differences between epi-type and genotype, with some cultivars sharing a common epi-type but different genotype
- Associated this material with geographical position and climatic data
- Trained computational biologists now playing leading roles in academia and industry

## Key figures

**105** wheat lines from the Watkins collection where screened for epigenetic variations and genotyped

The wheat genome is **5** times the size of the human genome

# HotSol

## Future-proofing potato: mechanisms and markers for global-warming tolerant ideotypes

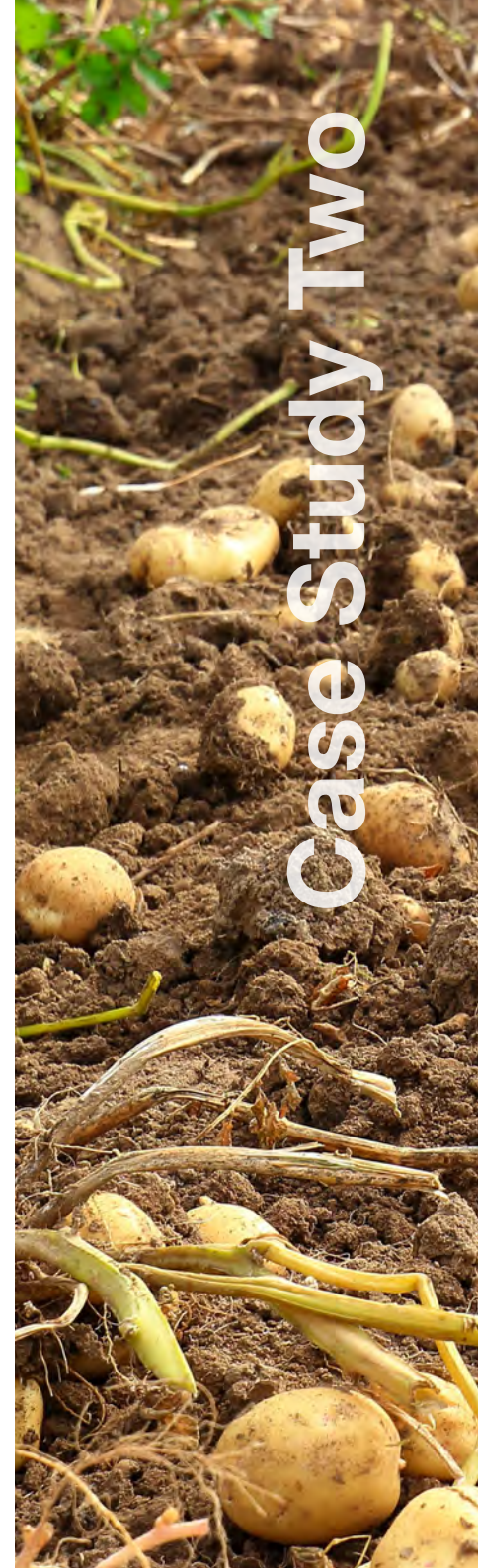
Heat can be detrimental to crops. In potatoes, high temperatures reduce or prevent tuberization and affect tuber quality and storage. These effects set in well below 30°C, adding to the long list of challenges posed by climate change. The problem of increasing temperatures now threatens to severely limit potato harvests in Europe and elsewhere.

The HotSol project set out to analyze the impact of elevated temperatures on potato tuber development, tuber quality (e.g. starch accumulation) and tuber dormancy by combining physiological studies, genetics and natural variation studies into an integrated approach towards understanding the underlying molecular mechanisms that cause heat sensitivity.

### The projects major findings include:

- 1 At elevated temperatures (>29°C during the day, >27°C at night) a small RNA (SES) blocks the formation of potato tubers by inhibiting the expression of the protein SELF-PRUNING 6A (SP6A). The project team managed to successfully switch off SES, which resulted in potato plants better able to form tubers at higher temperatures.
- 2 At moderate temperatures, the SP6A protein moves from leaves to the stolons (belowground modified stems), inducing tuber formation to prepare for periods of cold. At higher temperatures, the signal is switched off by the mechanism described above and the plant switches to making more shoots and leaves and fewer/no tubers. Further details of this so-called source-sink regulation have also been elucidated by HotSol.
- 3 Identification of a specific allelic variant of the Hsc70 protein that also confers greater heat tolerance when expressed in potato or tobacco.

Knowing the regulatory mechanisms can now help to overcome the problem of pronounced heat sensitivity of tuber formation in potato varieties that we currently grow. The next step will be testing of newly developed heat resistant potato plants under field conditions.



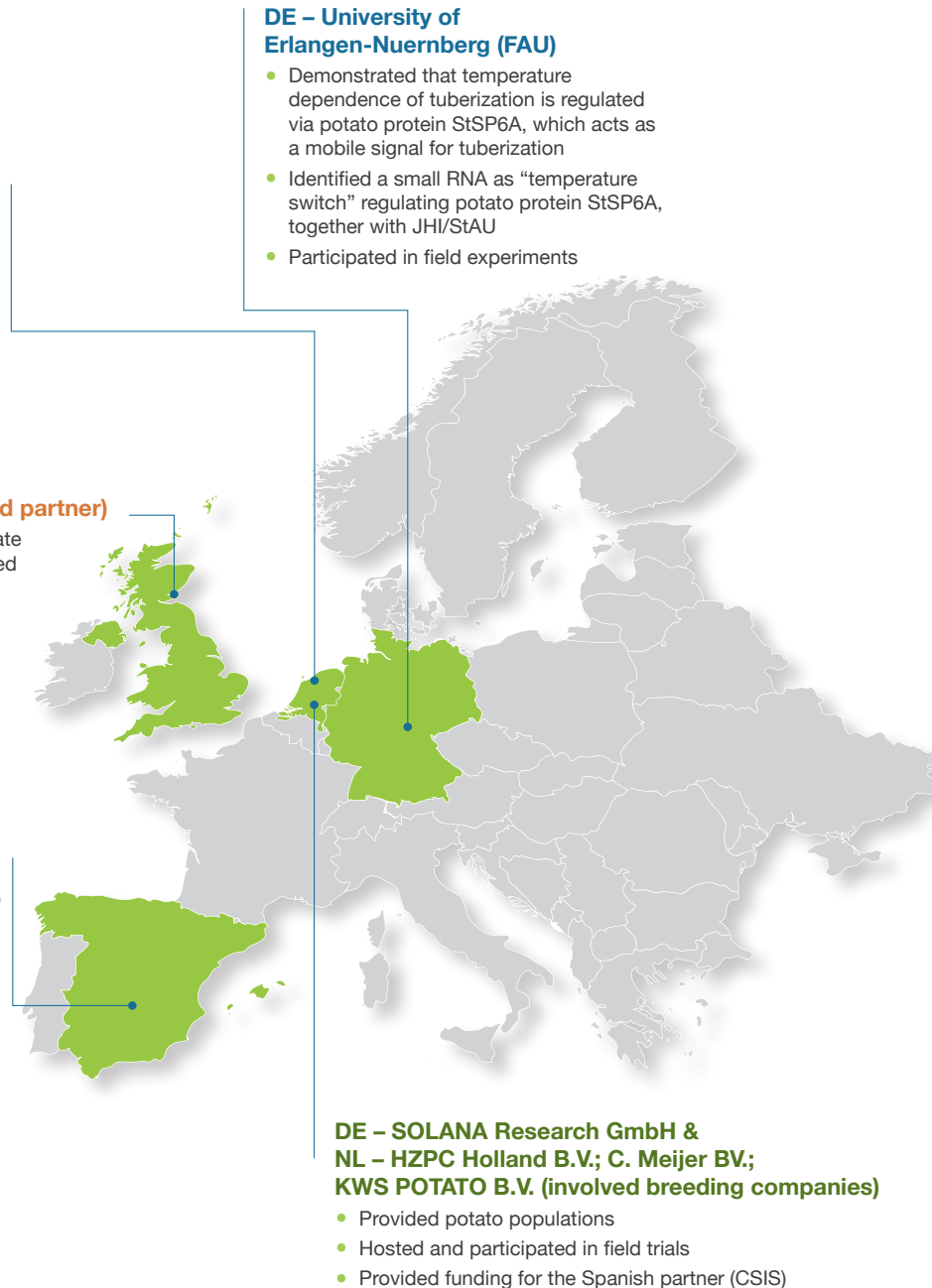


# Key impacts

- Identified a small RNA of 19 nucleotides involved in temperature regulation of potato tuber formation
- Elucidated source-sink regulation in potato via the SP6A protein and the sugar transporter SWEET11
- Identified an allelic variant of the potato Hsc70 protein that confers heat tolerance

# Key figures

- 5** academic partners
- from **4** different countries and
- 4** breeding companies involved
- 8** peer-reviewed articles published



## NL – Wageningen University

- Showed that potato protein StSP6A interacts with a SWEET sugar efflux transporter to facilitate starch formation from sucrose in tubers
- Participated in field experiments

## UK – St. Andrews University & James Hutton Institute (non-funded partner)

- Identified an allele of Heat Shock Cognate protein 70 (HSC70) that confers improved heat tolerance in a potato
- Helped identify a small RNA as “temperature switch” regulating potato protein StSP6A (together with FAU)
- Participated in field experiments

## ES – CSIS (non-funded partner)

- Supported small RNA analysis in potato
- Identified StSP5G as a negative regulator of StSP6A
- Provided transgenic plants overexpressing StSP6A/StSP5G
- Participated in field experiments

## DE – University of Erlangen-Nuernberg (FAU)

- Demonstrated that temperature dependence of tuberization is regulated via potato protein StSP6A, which acts as a mobile signal for tuberization
- Identified a small RNA as “temperature switch” regulating potato protein StSP6A, together with JHI/StAU
- Participated in field experiments

## DE – SOLANA Research GmbH & NL – HZPC Holland B.V.; C. Meijer BV.; KWS POTATO B.V. (involved breeding companies)

- Provided potato populations
- Hosted and participated in field trials
- Provided funding for the Spanish partner (CSIS)

# Root Barriers

**A multidisciplinary team from UK, Germany, France, Denmark, and the Netherlands shed light on how plants modulate their nutritional and water uptake via their root barrier system.**

Plants absorb nutrients and water from the soil through their roots. The flow of water and minerals outside of cells in the cell wall is blocked by Casparian strips, which form a tight seal between cells that controls the movement of nutrients and water into the plants vascular system for transport to the shoots. Suberin, a waxy coating covering endodermal cells, further controls the entrance of nutrients and water along the root. Together, Casparian strips and suberin block solutes moving into the plant's vascular system through the free space between cells and prevent solute backflow.

The international team pooled their expertise in molecular plant science, cell biology, analytical chemistry, plant physiology and modelling to dissect the biology of Casparian strips and endodermal suberin. Using the plant genetic model *Arabidopsis thaliana*, the researchers identified several genes essential for the formation of both Casparian strips and suberin and created mutants which had lost or damaged root barriers. They then tested how nutrient transport pathways behaved in different physiological conditions, such as in deficiency or excess of essential minerals, to see how plants compensated for a damaged barrier.

Plants were able to respond to leaky root barriers in several ways, e.g. by relocating transporters of ammonia which is a major source of soil nitrogen, across root layers to ensure shoots received the right amount of nitrogen. Plants were also shown to sense minerals leaking through damaged Casparian strips and responded by deactivating water channels, by depositing suberin to block the leakage, and by reducing transpiration in leaves. All these events, triggered by the damage in the Casparian strips, rebalanced solute and water uptake.

Unravelling the biology of root barriers across disciplines will enable a molecular manipulation of Casparian strips and endodermal suberin. This could help develop crop varieties with improved nutrient and water use, and enhanced resistance to root pathogens, salinity and water stress.



Case Study Three

### DE – Leibniz Institute of Plant Genetics and Crop Plant Research

- Studied the contribution of different nutrient transport pathways
- Quantified how nitrogen is transported across the roots in different mutants for suberin and Casparian strip

### DK – University of Copenhagen

- Developed a new protocol for bioimaging that preserves ions in their native cellular environment
- Tested how mutants for Casparian strips and suberin react to deficiency and excess of minerals

### NL – Wageningen University

- Tested how mutants for Casparian strips and suberin react to deficiency and excess of minerals

### UK – University of Nottingham

- Characterized the molecular machinery involved in the formation of Casparian strips
- Established and distributed mutants to partners for further experiments

### FR – INRA, Montpellier

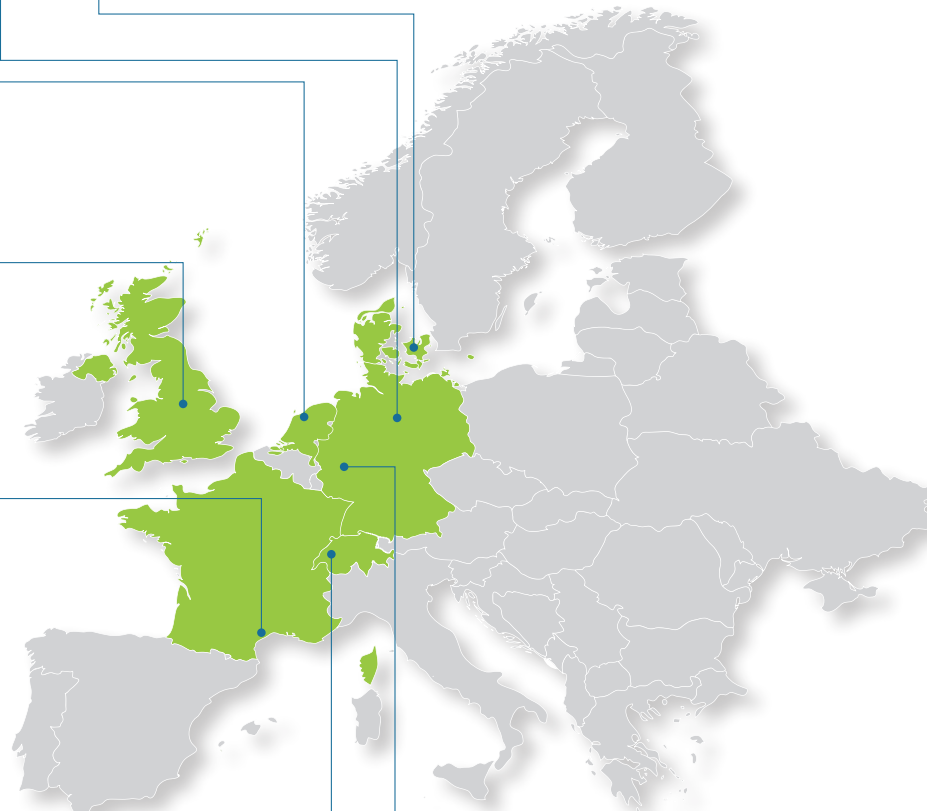
- Quantified the impact of defective Casparian strips on water and nutrient uptake
- Tested how mutants for Casparian strips and suberin react to water stress and salinity level
- Developed mathematical models of root and whole plant water transport

### CH – University of Lausanne (non-funded partner)

- Prof Niko Geldner, one of the leading experts in Casparian strip biogenesis, and members of his group actively participated in the bi-yearly consortium workshops
- Provided reagents, technical advice and mutants, and contributed to publications on the impact of root barriers on ammonium transport, and plant-parasitic nematode infection and a whole water plant transport

### DE – University of Bonn

- Selected genes involved in the biosynthesis of suberin, established mutants and distributed to partners for further experiments
- Tested the role of Casparian strips and suberin in response to plant-parasitic nematode infection



# Key impacts

- Increased understanding of a basic plant root barrier system that could have important applications in crop science
- Root nematode infection damages the endodermis leading to the activation of endodermal suberin biosynthesis to limit infection and feeding
- Produced a predictive model of root and whole plant water transport that integrates Casparian strip and endodermal suberin properties

# Key figures

- 7** partners from **5** countries
- 19** peer-reviewed articles published
- 2** protocols developed and shared worldwide (multi-element bioimaging and a nematode infection assay)
- 7** genes identified and characterised
- 32** *A. thaliana* mutants were used to test the formation and adaptive role of Casparian strips and suberin

## Root Barriers



# Benefits and outcomes from ERA-CAPS projects

## 1 Research

We asked ERA-CAPS project leaders and grant holders what they thought the main benefits from ERA-CAPS were. Access to unique expertise and facilities, potential for novel discoveries, student training, long lasting partnerships, and improved professional networking were some of the benefits mentioned. A common denominator in all the responses was that without ERA-CAPS as a funding programme these projects would not have been possible due to difficulties linking and exchanging expertise across different countries.

### Quotes:

- *'The ERA-CAPS program provided academic freedom (working on a defined research question without all kind of requirements, such as involvement of companies, linkage to applications, etc.) and a great opportunity to collaborate with high quality labs within the EU. The project was very successful, and its output was very important for my career and to obtain personal grants'*
- *'The programme brought together different expertise in molecular phytopathology to tackle a common goal - durable resistance in cereal crops. Based on this consortium a number of joint publications arose, and in some instances, collaborations last beyond the time of the actual funding.'*
- *'Synergistic and timely collaborative research with European colleagues. This type of nimble project is not the same as that achieved with larger EU framework programmes and is more versatile than bi-lateral funding arrangements between countries.'*

## Key themes

- Novel discoveries
- Academic freedom
- Improved network in area
- Long-lasting collaborations
- Access to expertise that does not exist with one country's borders
- Students and postdoc exchanges
- Access to facilities

## 2 Early career researchers

Postdocs from partners labs learned new skills, shared workload, learned to experience a junior leadership role, took on responsibilities for collecting and sharing datasets, learned how to work with international partners and benefited from interdisciplinary working.

Students were exposed to techniques in partner countries that would not have been used within their home institution, with transnational projects expanding the training opportunities available to early career researchers.

### Quotes:

- *'The post doctoral researcher has gone on to establish his own company as a spin out.'*
- *'Great opportunity for the post docs involved and for the leading PI to get experience with coordinating an international program.'*
- *'Within the collaborations, we have trained both new postdocs and students. In both cases they have been exposed to and introduced to techniques they would not have been using if individual projects would have been designed within single groups. There has also been information and expertise transfer between the people funded by the ERA-CAPS project and other people in the groups.'*



### 3 Research outputs

Common research outputs included: genetic resources, software tools to conduct quantitative genetic studies, mathematical models and phenotypic information.

#### Quotes:

- *'We established a model species for diaspora heteromorphism, no molecular system for this was available. The principles of the SeedAdapt data sharing are to treat our research data as a public resource and to make them openly available to the maximum extent possible. Our publications are therefore published with Open Access licence. The large-scale datasets will be available via user-friendly browsers.'*
- *'Phenotypic information about cultivars within a Brassica napus diversity set has been obtained'*
- *'New genetic resources'*
- *'Various detailed genome-wide gene expression data sets, new bioinformatics tools to search for patterns in gene expression and chromatin modifications and new technology to study processes at cellular level'*
- *'The database is both a resource and a tool. It is useful not only for groups working on the evolution of sexual reproduction, but also on plant evolution in general.'*





# Concluding remarks

**ERA-CAPS aimed to strengthen fundamental molecular plant science research in Europe and to ensure plant science research can contribute towards a more sustainable bioeconomy, environment and global food security.**

For plant sciences to address these these long term goals there remains a range of key challenges that international collaboration can help address, some examples of which were noted by ERA-CAPS grant holders:

- The translation of fundamental research into work with practical applications and impact.
- Improved integration of all levels of data, e.g. from different ‘-omics’ technologies, molecular and phenotyping/physiology research
- Development of additional model systems to represent the diversity of plant species.
- The development of future leaders through interdisciplinary training of early career researchers, enabling them to develop the skills and professional networks needed to build plant science career pathways and to pursue exciting new avenues of research in the future.

Feedback from ERA-CAPS grant holders suggests that this programme has helped towards tackling these challenges, by developing a collaborative network of researchers working across a range of molecular plant science topics.



# Annex

## Projects funded by the three ERA-CAPS calls

### Call 1

Acronym	Project Title	Countries Involved
<b>ABCEED</b>	Identifying and exploiting genetic variation controlling seed yield and quality in oilseed crops	UK, Germany, France
<b>BARLEY-NAM</b>	BARLEY-NAM: Locating exotic genes that control agronomic traits under stress in a wild barley nested association mapping (NAM) population	Germany, Israel, UK
<b>BENZEX</b>	Biosynthesis, transport and exudation of 1,4-benzoxazin-3-ones as determinants of plant biotic interactions	Germany, Denmark, UK
<b>DeCOP</b>	Delineating the crossover control networks in plants	Austria, UK, Germany
<b>DURESTrit</b>	Functional characterisation and validation of nonhost components in Triticeae species for durable resistance against fungal diseases	Germany, UK, Netherlands, USA
<b>EURO-PEC</b>	European Plant Embryology Consortium	Netherlands, Germany, Austria
<b>Evo-Genapus</b>	Evolution of genomes: Structure-function relationships in the polyploid crop species <i>Brassica napus</i>	UK, France, Germany
<b>FLOWPLAST</b>	Plasticity of flowering time in response to environmental signals in <i>Arabidopsis thaliana</i>	Germany, UK, Netherlands, Poland
<b>H.I.P.</b>	Homeostasis of Isoprenoids in Plants: understanding compartmentalization, flux and transport of isoprenoids in glandular trichomes for non-crop and crop species	Germany, Belgium, Israel, Netherlands
<b>HotSol</b>	Future-proofing potato: Mechanisms and markers for global-warming tolerant ideotypes	Germany, Netherlands, Spain, Germany, UK
<b>N-vironment</b>	The role of the N-end rule pathway in controlling plant response to the environment	UK, Austria, Germany, Italy
<b>PER ASPERA</b>	Plant Endoplasmic Reticulum Architecture and Seed Productivity - ERA	UK, France, Austria
<b>RootBarriers</b>	Plant root diffusional barriers: genesis and implications for nutrient efficiency and stress tolerance	UK, Netherlands, France, Germany, Denmark
<b>SeedAdapt</b>	Dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments	UK, Austria, Germany, Netherlands



# Annex (cont.)

## Call 2

Acronym	Project Title	Countries Involved
<b>AbioSen</b>	Molecular mechanisms of abiotic stress-induced senescence in plants	Germany, Belgium, Poland, Switzerland
<b>AI-UCIDATE</b>	Towards a molecular understanding of Aluminium genotoxicity for crop improvement	Belgium, Germany, Poland, USA
<b>BEAN_ADAPT</b>	Evolution in a changing environment: the genetic architecture of adaptation outside centers of domestication of Phaseolus vulgaris and P. coccineus	Italy, Germany, USA
<b>DesignStarch</b>	Designing starch: harnessing carbohydrate polymer synthesis in plants	Germany, UK, Switzerland
<b>EfectaWheat</b>	An Effector- and Genomics-Assisted Pipeline for Necrotrophic Pathogen Resistance Breeding in Wheat	UK, Denmark, Germany, Norway, Australia
<b>EVOREPRO</b>	Evolution of Sexual Reproduction in Plants	Portugal, UK, Germany, Austria, USA
<b>INTREPID</b>	Investigating Triticeae Epigenomes for Domestication	UK, Germany, USA
<b>MAQBAT</b>	Mechanistic Analysis of Quantitative Disease Resistance in Brassicas by Associative Transcriptomics	UK, Denmark, Germany, Poland, Netherlands
<b>PHYTOCAL</b>	Phytochrome Control of Resource Allocation and Growth in Arabidopsis and in Brassicaceae crops	UK, Germany, USA
<b>RegulaTomE</b>	Regulating Tomato quality through Expression	UK, Germany, USA, Israel
<b>SIPIS</b>	DECODING LIGAND-RECEPTOR specificities of LysM-Proteins IN PLANT IMMUNITY AND SYMBIOSIS	Germany, Denmark, Italy, Netherlands
<b>SOURSI</b>	Simultaneous manipulation of source and sink metabolism for improved crop yield	UK, Germany, Switzerland



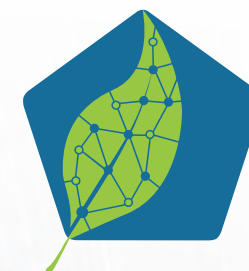


# Annex (cont.)

## Call 3

Acronym	Project Title	Countries Involved
<b>1001G3</b>	1001 Genomes Plus	Austria, UK, Germany
<b>AUREATE</b>	AUgmented REsilience After Transmission of Epimutations	Germany, Switzerland, Austria
<b>BARN</b>	BARley yield associated Network	Germany, USA, UK
<b>C4BREED</b>	Designing C4 breeding strategies using genetic enablers of C4 evolution	Germany, UK, USA
<b>Exosomes</b>	Role of extracellular vesicles in plant-microbe interactions	USA, France, Denmark
<b>Flux4LIVES</b>	Thylakoid ion flux-Linking photosynthetic efficiency with osmotic stress response	Germany, USA, Spain
<b>Genes2Shape</b>	From genes to shape: Towards development of a computable flower	UK, USA, Germany, France
<b>KatNat</b>	Elucidating the multifaceted functions of protein acetyltransferases in plant stress response and regulation of metabolism.	Germany, France, UK, Finland
<b>MEIOREC</b>	Meiotic Recombination in Plants: controlling the transition of DNA double-strand breaks to genetic crossovers	UK, France, Germany, USA, Austria
<b>MURINAS</b>	Mechano-purino signalling in abiotic stress	UK, France, USA
<b>SICOPID</b>	Activation and regulation of plasma membrane receptor signalling complexes controlling plant development and immunity, and their connection to downstream signalling cascades	Switzerland, France, USA, Germany, UK (now Austria)
<b>V-Morph</b>	Unravelling how the mechanical regulation of local variability shapes reproducible plant organs	France, Poland, Germany





ERA-CAPS

### ERA-CAPS Coordination Office

Dr Megan Rafter (UKRI-BBSRC, UK) | [eracaps@bbsrc.ac.uk](mailto:eracaps@bbsrc.ac.uk)

### ERA-CAPS Communication Office

Dr Florence Quist (F.R.S.-FNRS, Belgium) | [florence.quist@frs-fnrs.be](mailto:florence.quist@frs-fnrs.be)

For contact information of the ERA-CAPS partners and observers, please refer to the 'Partners' page of our website:

[www.eracaps.org](http://www.eracaps.org)

