

*President: Stuart Knight*

# Adding value to field crop genetic resources

A two day conference  
at the John Innes Centre, Norwich, UK  
on 25-26 April 2019



**PROGRAMME, ABSTRACTS  
and DELEGATE LIST**



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We gratefully acknowledge support given to  
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# Adding value to field crop genetic resources

at the John Innes Centre, Norwich, UK

on 25-26 April 2019

(BASIS Points will be applied for)

## PROGRAMME

For decades the world's genebanks have conserved genetic diversity and supplied stakeholders with the raw materials of basic research and breeding. Recent development of next generation gene discovery tools together with associated phenotypic and genotypic datasets based on genebank foundations have opened completely new opportunities for the interrogation of genebank resources, for the delivery of new and useful genetic variation to agriculture. This conference will highlight these exciting developments and map out next steps for the genetic resources community.

### THURSDAY 25 APRIL 2019

12:00 LUNCH and REGISTRATION

13:00 WELCOME and INTRODUCTION

NOAM CHAYUT (John Innes Centre, Norwich, UK)

13:10 **Session I: Genebank data analysis and accessibility**

Chair: CHARLOTTE ALLENDER (Warwick University, Wellesbourne, UK)

*Invited Speaker:*

**The NASC, or there and back again**

SEAN MAY (University of Nottingham, UK)

*Invited Speaker:*

**Data standards for interoperable tools/FAIR data**

ROB DAVEY (Earlham Institute, Norwich, UK)

**SeedStor: A germplasm information management system and public database**

R S P HORLER, A TURNER, P FRETTER & M AMBROSE (John Innes Centre, Norwich, UK)

**Capturing diversity in dynamic core collections**

NOAM CHAYUT, LUZIE WINGEN, SIMON GRIFFITHS, SIMON ORFORD, EVGENIA KIM,  
RICHARD HORLER & LIZ SAYERS (John Innes Centre, Norwich, UK)

14:50 TEA

15:10 **Session II: Added value from genomics**

Chair: SEAN MAY (University of Nottingham, UK)

**Elevator pitch: IDna Genetics**

STEVE CUMMINGS (IDna Genetics Ltd., Norwich, UK)

*Invited Speaker:*

**Worldwide phylogeography and history of wheat genetic diversity**

FRANÇOIS BALFOURIER, SOPHIE BOUCHET, SANDRA ROBERT, ROMAIN DE OLIVEIRA,  
HÉLÈNE RIMBERT, JONATHAN KITT, FRÉDÉRIC CHOULET, INTERNATIONAL WHEAT  
GENOME SEQUENCING CONSORTIUM, BREDWHEAT CONSORTIUM & ETIENNE PAUX  
(INRA, Clermont-Ferrand, France)

**Exploiting wheat mutant resources to uncover and validate novel variation for yield components**  
JAMES SIMMONDS, TOBIN FLORIO, PAMELA CRANE & CRISTOBAL UAUY (John Innes Centre, Norwich, UK)

***Invited Speaker:***

**Practical genotyping for the development and management of wheat breeding material**  
AMANDA BURRIDGE (University of Bristol, UK)

***Invited Speaker:***

**Using the past to resource the future: New insights into barley diversity**  
JOANNE RUSSELL (The James Hutton Institute, Dundee, UK)

**Genetic and genomic studies to enhance the value of pea germplasm resources**

CAROL MOREAU, JITENDER CHEEMA (John Innes Centre, Norwich, UK), PETER G ISAAC (IDna Genetics Ltd, Norwich, UK), TRACEY RAYNER, NOAM CHAYUT (John Innes Centre, Norwich, UK), NOEL ELLIS (University of Auckland, New Zealand) & CLAIRE DOMONEY (John Innes Centre, Norwich, UK)

17:20–17:35 TEA

18:00 **Social event: The annual Innes lectures**

**From farm field to genebank: a short history of seed keeping**

HELEN ANNE CURRY (Senior lecturer in the Department of History and Philosophy of science, University of Cambridge, UK)

19:00 **INFORMAL DINNER (JIC bar & BBQ)**

## FRIDAY 26 April 2019

09:00 **Session III: State of the art genebanking**

Chair: SIMON GRIFFITHS (John Innes Centre, Norwich, UK)

***Invited Speaker:***

**Gene-banks into genetic resource centres: helping promote complementary *in situ* conservation**  
NIGEL MAXTED, SHELAGH KELL, JOANA MAGOS BREHM, JADE PHILLIPS (University of Birmingham, UK) & EHSAN DULLOO (Bioversity International, Mauritius)

***Invited Speaker:***

**Plant genetic resources for food and agriculture maintained in the global genebanks - state of the art**

ANDREAS BÖRNER, MANUELA NAGEL (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany), MIAN ABDUR REHMAN ARIF (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; Nuclear Institute of Agriculture and Biology (NIAB), Pakistan), MONIKA AGACKA-MOŁDOCH (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; Institute of Soil Science and Plant Cultivation, Poland), MARIANN BÖRNER (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; Enza Zaden, The Netherlands), ULRIKE LOHWASSER (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany), DAVID RIEWE (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; Julius Kuehn-Institute (JKI), Germany), JANINE WIEBACH (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany; Charité – Universitätsmedizin Berlin, Germany) & THOMAS ALTMANN (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany)

09:50 **COFFEE**

10:15 ***Invited Speaker:***

**Conservation and use of plant genetic resources: the role of the UK Vegetable Genebank**

CHARLOTTE ALLENDER (Warwick University, Wellesbourne, UK)

**A toolkit for the transfer of alleles from germplasm collections to wheat breeders**

SIMON ORFORD, SIMON GRIFFITHS, LUZIE WINGEN, RICHARD HORLER, JULIE ELLWOOD (John Innes Centre, Norwich, UK), MALCOLM HAWKESFORD (Rothamsted Research Harpenden, UK), CRISTOBAL UAUY (John Innes Centre, Norwich, UK), ROB DAVEY (Earlham Institute, Norwich, UK), KEITH EDWARDS (Bristol University, UK), ALISON BENTLEY (NIAB, Cambridge, UK), IAN KING (Nottingham University, UK), JACOB LAGE (KWS, Essex, UK), CHRIS BURT (RAGT UK Saffron Walden, UK), DAVID SCHAFER (LSPB, Cambridge, UK), SIMON BERRY (Limagrain UK, Suffolk, UK), DAVID FEUREUHELM (Syngenta UK, Cambridge, UK), MICHAEL SCHMOLKE (BASF Agric Solutions, Gatersleben, Germany), MATT KERTON (DSV UK, Banbury, UK), MILIKA BUURMAN (Elsoms Wheat UK, Lincolnshire, UK) & NOAM CHAYUT (John Innes Centre, Norwich, UK)

11:10 ***Elevator pitch session***

CHAIR: NOAM CHAYUT (John Innes Centre, Norwich, UK)

1. **Genotyping Analysis by LGC**

2. **The genotyping platform in JIC**, RICHARD GORAM (John Innes Centre, Norwich UK)

3. **RevGenUK**, SALEHA BAKHT, (John Innes Centre, Norwich, UK)

11:20 **Tour to the John Innes Centre Rare Books Collection and visit the Germplasm Resource Unit**

**CONFERENCE GROUP PHOTOGRAPH**

12:00 **LUNCH (Sandwiches)**

13:15 ***Session IV: Research genebanks interface***

Chair: SIMON ORFORD (John Innes Centre, Norwich, UK)

**Identifying new and useful genetic variation in the A. E. Watkins landrace collection**

SIMON GRIFFITHS, LUZIE WINGEN, MICHELLE LEVERINGTON WAITE, SARAH COLLIER (John Innes Centre, Norwich, UK), MALCOLM HAWKESFORD, ANDREW RICHE (Rothamsted Research Harpenden, UK), KEITH EDWARDS, SACHA PRZEWIESLIK-ALLEN, AMANDA BURRIDGE, MARK WINFIELD (University of Bristol, UK), JOHN FOULKES (University of Nottingham, UK) & DANIEL MIRALLES (Universidad de Buenos Aires and CONICET, Argentina)

13:40 **The central Asian wheat breeding initiative collection**

K YERMEKBAYEV (John Innes Centre, Norwich, UK; Institute of Plant Biology and Biotechnology, Kazakhstan), Y TURUSPEKOV, S ABUGALIEVA (Institute of Plant Biology and Biotechnology, Kazakhstan), A MORGOUNOV (International Maize and Wheat Improvement Center (CIMMYT), Ankara, Turkey), S BABOEV (Institute of Genetics & Plant Experimental Biology, Uzbekistan), M OTAMBEKOVA (Tajik Agrarian University, Tajikistan), O PAKHOMEEV (Kyrgyz Agriculture Research Institute, Kyrgyzstan) & S GRIFFITHS (John Innes Centre, Norwich, UK)

**Rocket science: A case study in the utilisation and development of genetic resources**

LUKE BELL (University of Reading, UK)

**What have wheat breeders been doing for 150 years? – Analysis of pedigree and genotype data reveal patterns of breeder selection**

NICK FRADGLEY, JAMES COCKRAM (NIAB, Cambridge, UK), JAMES ELDERFIELD (NIAB, Cambridge, UK; Verifa Oy, Helsinki, Finland), KEITH GARDNER (NIAB, Cambridge, UK), JOHN HICKEY (University of Edinburgh, UK), PHIL HOWELL, ROB JACKSON (NIAB, Cambridge, UK) & IAN MACKAY (NIAB, Cambridge, UK; IMplant Consultancy Ltd., Chelmsford, UK)

**Using vegetable crop genetic resources to identify tolerance to abiotic stress and other key performance traits**

ANDREW M BEACHAM, PAUL HAND (Harper Adams University, Shropshire , UK),  
GUY C BARKER, GRAHAM R TEAKLE (University of Warwick, UK) & JAMES M MONAGHAN  
(Harper Adams University, Shropshire , UK)

**Exploiting genetic diversity of *Vicia faba***

ANNE WEBB, KRYSTYNA GOSTKIEWICZ, JANE THOMAS & THOMAS WOOD (NIAB,  
Cambridge, UK)

14:55 TEA

15:15 CLOSING DISCUSSION

Chairs: NOAM CHAYUT & SIMON GRIFFITHS (John Innes Centre, Norwich, UK)

**Discussion of challenges, opportunities, and funding pathways**

16:00 CLOSE (Safe journey home)

# **Platform**

# The NASC, or there and back again

SEAN MAY

*Nottingham Arabidopsis Stock Centre (NASC), Sutton Bonington Campus,  
University of Nottingham, Loughborough LE12 5RD, UK  
<http://arabidopsis.info@NASCarabidopsis>*

## ABSTRACT

The Nottingham Arabidopsis Stock Centre (NASC), est. 1990, is funded by the BBSRC (BBRF) as a partial cost recovery centre (since 1999), and is sister centre to the ABRC (OSU – USA).

NASC holds > 800,000 seed stocks representing ~ 1 million genotypes donated from a very large international community. The most populous seed donations are from GABI-kat (Germany - Bernd Weisshaar); and SALK (USA - Joe Ecker). These two insertion populations account for more than half of all stocks held by the stock centres.

We send to >50 countries (more than 100,000 tubes of seed per annum) including >15 DAC/ODA recipients (Total > 2,700 stocks in 2018). Individual stock orders have consistently increased for >15 years, but large sets (~40% of tubes set) strongly skew our geographical statistics. The UK and Germany are always top five, but China has dramatically increased orders since 2013.

NASC started with germplasm distribution but expanded into transcriptomics in 1999, launching the world's first one-stop germplasm & transcriptomic data linked genome browser in 2002. As part of several federated programs over the years (ukcrop.net, PLANET, IAIC, Araport, etc.) we have actively promoted integration of diverse domestic and international resources. As part of this process we have dropped the heterogenous datatypes that we previously aggregated locally - in favour of specialisation and inter-database connectivity through direct links and Web Services.

# Data standards for interoperable tools/FAIR data

ROB DAVEY

*Earlham Institute (EI), Norwich Research Park Innovation Centre, Colney Ln,  
Norwich NR4 7UZ, UK*

## ABSTRACT

The Designing Future Wheat consortium represents a UK-wide collaboration to deliver technologies and resources for national and international wheat improvement. This involves the development of new genomic sequences of key elite, alien, and landrace varieties, as well as computational improvements to data accessibility. The project has already made great strides to make well-described wheat data available early in the generation and publication process through a variety of databases, under open access licences, and linked to germplasm resources such as the JIC Germplasm Resources Unit.

# **SeedStor: A germplasm information management system and public database**

R S P HORLER, A TURNER, P FRETTER and M AMBROSE

*The John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK*

## **ABSTRACT**

SeedStor (<https://www.seedstor.ac.uk>) acts as the publicly available database for the seed collections held by the Germplasm Resources Unit (GRU) based at the John Innes Centre, Norwich, UK. The GRU is a national capability supported by the Biotechnology and Biological Sciences Research Council (BBSRC). The GRU curates' germplasm collections of a range of temperate cereal, legume and Brassica crops and their associated wild relatives as well as precise genetic stocks, near-isogenic lines and mapping populations. With over 35000 accessions the GRU forms part of the UK's plant conservation contribution to the Multilateral System (MLS) of the International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA) for Wheat, Barley, Oat and Pea.

SeedStor is a fully searchable system that allows our various collections to be browsed species by species through to complicated multipart phenotype criteria driven queries. The results from these searches can be downloaded for later analysis or used to order germplasm via our shopping cart. The user community for SeedStor is the plant science research community, plant breeders, specialist growers, hobby farmers and amateur gardeners and educationalists.

Furthermore, SeedStor is much more than a database, it has been developed to act internally as a Germplasm Information Management System that allows team members to track and process germplasm requests, determine regeneration priorities, handle cost recovery and Material Transfer Agreement paperwork, manage the Seed Store holdings and easily report on a wide range of the aforementioned tasks.

# Capturing diversity in dynamic core collections

NOAM CHAYUT, LUZIE WINGEN, SIMON GRIFFITHS, SIMON ORFORD,  
EVGENIA KIM, RICHARD HORLER and LIZ SAYERS

*The John Innes Centre, Norwich Research Park, Colney Lane, Norwich  
NR4 7UH, UK*

## ABSTRACT

The Germplasm Resources Unit (GRU) at the John Innes Centre (JIC), a national capability supported by BBSRC, holds > 40,000 accessions; chiefly of barley, wheat, oats and peas. To promote their exploitation, practical tools are needed for rational germplasm selection. Developing core-collections is a strategy to reduce the number of accessions with a minimal negative effect on the total genetic variation. The GRU germplasm is divided into 18 context-dependent collections, of which several were previously entirely genotyped. The genotypic characterization allows us to assess the relatedness between accessions and to generate core-collections.

For example, the JIC Pisum Collection (3004 accessions) was genotyped by Jing *et al.*, 2010 using a retrotransposon-based insertion polymorphism marker analysis. This study was followed by Buekelaer *et al.*, 2018 to exemplify the performance of Core-Hunter-3, an open source software for core-collections development. Moreover, The A.E. Watkins Stabilised Collection of Hexaploid Landrace Wheat (1063 accessions), was entirely genotyped by Wingen *et al.*, 2011 using microsatellite markers. This study facilitated the development of a core-collection (119 accessions) currently available to order via SeedStor @ [www.seedstor.ac.uk](http://www.seedstor.ac.uk).

However, the potential of these core-collections to improve phenotypic diversity is yet to be assessed empirically. Here we examine the probability of the 119 accessions' core-collection to intensify phenotypic diversity of wheat grain macronutrient when sampling the A.E. Watkins Collection. Since an inflexible size of a core-collection might be a restrictive factor for users, we further investigate the potency of smaller core-collections. Finally, we discuss the possibility to design accessible core-collections, dynamically sized to suite the individual.

# **Worldwide phylogeography and history of wheat genetic diversity**

FRANÇOIS BALFOURIER, SOPHIE BOUCHET, SANDRA ROBERT, ROMAIN DE OLIVEIRA, HÉLÈNE RIMBERT, JONATHAN KITT, FRÉDÉRIC CHOULET,  
INTERNATIONAL WHEAT GENOME SEQUENCING CONSORTIUM,  
BREEDWHEAT CONSORTIUM and ETIENNE PAUX

*Genetics, Diversity & Ecophysiology of Cereals, INRA Auvergne-Rhône-Alpes,  
5 chemin de Beaulieu, 63000 Clermont-Ferrand, France*

## **ABSTRACT**

Since its domestication in the Fertile Crescent ~8,000 to 10,000 years ago, wheat has undergone a complex history of spread, adaptation and selection. To get better insights into the wheat phylogeography and genetic diversity, we describe allele distribution through time using a set of 4,506 landraces and cultivars originating from 105 different countries genotyped with a high-density SNP array. Although the genetic structure of landraces is collinear to ancient human migration roads, we observe a reshuffling through time, related to breeding programs, with the apparition of new alleles enriched with structural variations that may be the signature of introgressions from wild relatives after 1960.

# Exploiting wheat mutant resources to uncover and validate novel variation for yield components

JAMES SIMMONDS, TOBIN FLORIO, PAMELA CRANE and CRISTOBAL UAUY

*Crop Genetics, John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK*

## ABSTRACT

TILLING mutant populations provide a valuable source of novel variation for researchers through both forward and reverse genetic screens. In collaboration, we exome-sequenced 1,535 EMS mutants from the tetraploid variety ‘Kronos’ and 1,200 EMS mutants from the hexaploid variety ‘Cadenza’. Over 10,000,000 EMS-induced mutations were discovered in the protein-coding regions of the wheat genome, with on average 35–40 mutations per kb in each population (Krasileva *et al.*, 2017). In addition, we have recently developed single seed descent (SSD) populations for both Kronos and Cadenza to enable forward genetic screens on more homogenous material.

We will demonstrate how we have utilised these materials in our research. Firstly, through a reverse genetics approach we identified the loss-of-function mutations in all three homoeologs of the *Grain Width and Weight 2* (*TaGW2*) gene (Wang, Simmonds *et al.*, 2018). We combined these mutations to generate triple mutants and then backcrossed them for the creation of Near Isogenic Lines (NILs). We observe increases in thousand grain weight by up to 20% over wildtype lines in both glasshouse and field trials. Secondly, we performed a forward genetic screen of the Cadenza SSD population in both normal and low Nitrogen regimes in the field for the identification of mutant lines showing stability for grain size and grain number in reduced N conditions.

A more substantial field trial is currently being carried out on lines showing good stability potential.

All mutations can be queried and investigated through public databases (<http://plants.ensembl.org/index.html>). The M<sub>4</sub> seed is deposited and can be requested through the Genetics Resource Unit ([www.seedstor.ac.uk](http://www.seedstor.ac.uk)). Predesigned KASP primers are available to validate the mutations and for their selection in downstream research and breeding applications. The Cadenza SSD population is also now available for forward genetic screens with the Kronos to follow in 2020.

## References

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- Wang W, Simmonds J, Pan Q, Davison D, He F, Battal A, Akhunova A, Trick H, Uauy C, Akhunov E. 2018.** Gene editing and mutagenesis reveal inter-cultivar differences and additivity in the contribution of *TaGW2* homoeologues to grain size and weight in wheat. *Theor Appl Genet* **131**:2463.

# **Practical genotyping for the development and management of wheat breeding material**

AMANDA BURRIDGE

*Life Sciences Building, Lab 333, University of Bristol, 24 Tyndall Avenue,  
Bristol BS8 1TQ, UK*

## **ABSTRACT**

Gene-banks provide access to important genetic resources for plant breeding, and the inclusion of genotypic and phenotypic information with this allows users to make the most of these resources. By providing genotype data alongside gene-bank material we not only reduce the duplication of effort, but allow access to the genetic diversity before the experimental design begins.

Breeders and academics alike regularly use Single Nucleotide Polymorphisms (SNP) marker based genotyping to characterise material of interest. A number of SNP-based genotyping platforms are available and their utility depends upon factors such as the available technologies, number of data points required, budgets and the technical expertise. The genotyping platforms most appropriate for large scale quality control may be inappropriate for small in-depth studies and so a common platform is unlikely. As such, we discuss the importance of designing markers and generating data that can be compared or combined across platforms, projects and institutes and ensuring that such markers are appropriate for screening the available wheat breeding material we use today.

# Using the past to resource the future: New insights into barley diversity

JOANNE RUSSELL

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The Agronomy Institute, Orkney College, University of the Highlands and Islands,  
Orkney, UK  
University of Adelaide, Adelaide SA 5005, Australia*

## ABSTRACT

Producing enough food in a changing world has become a key global challenge. Crops need to increase yields, use resources more effectively and be resilient to changing climates. Like other major crops, bottlenecks in the selection of barley varieties have resulted in reduction of genetic diversity, however landraces and wild barleys represent important sources of alleles to respond to abiotic and biotic stresses. Because there are very large *ex situ* collections available for barley, we can explore whether and to what extent adapted landraces and wild germplasm can contribute to future crop improvements. We presume that these landraces are already adapted to a wide range of environments and are thereby amenable to mining of useful alleles. For barley, the resources that are critical to achieve this have been developed: draft barley genome sequence (IBSC, 2012; Beier *et al.*, 2017; Mascher *et al.*, 2017); physical and genetic maps (Ariyadasa *et al.*, 2014); other genomic tools, such as SNP arrays (Close *et al.*, 2009; Comadran *et al.*, 2012; Bayer *et al.*, 2017) and exome capture arrays (Mascher *et al.*, 2013). Here, using examples from collaborative work, the talk will describe how we have applied these to explore diversity and begin to understand the variation that underlies adaptive responses in barley, as well as practical exploitation in crop breeding.

# **Genetic and genomic studies to enhance the value of pea germplasm resources**

CAROL MOREAU<sup>1</sup>, JITENDER CHEEMA<sup>1</sup>, PETER G ISAAC<sup>2</sup>, TRACEY RAYNER<sup>1</sup>, NOAM CHAYUT<sup>1</sup>, NOEL ELLIS<sup>3</sup> and CLAIRE DOMONEY<sup>1</sup>

<sup>1</sup>*John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK*

<sup>2</sup>*IDna Genetics Ltd, The Centrum, Norwich Research Park, Norwich NR4 7UG, UK*

<sup>3</sup>*University of Auckland, Auckland, New Zealand*

## **ABSTRACT**

Recent advances in genetic and genomic screening technologies are rapidly accelerating the rate at which novel alleles are discovered in legume germplasm collections, alongside advances in understanding the phenotypic consequences of such variation. High-throughput screening of a wide germplasm collection for *Pisum* (pea, 2822 accessions) has led to the discovery of an accession of *Pisum elatius* which lacks the major seed trypsin-chymotrypsin inhibitors (Clemente *et al.*, 2015) and to the identification of the genetic basis for the wrinkled-seeded lines in the collection; among the latter, the majority lines were *r* mutants, with few *rb* and two which were neither *r* nor *rb* but showed a maternally-determined seed wrinkling (Rayner *et al.*, 2017).

The availability of genetic markers based on retroelements has facilitated a range of important seed and plant traits to be genetically mapped (Ellis *et al.*, 2018; Moreau *et al.*, 2018). Currently the availability of large numbers of single nucleotide polymorphic markers is enhancing the resolution of these maps greatly, particularly for populations which have been developed from cultivated accessions, in which breeders' traits are being studied (Moreau *et al.*, 2018). Improved genetic maps are being used to refine genetic loci impacting on a range of seed quality traits, including seed size and quantitative variation in amino acids.

The acceleration of breeding programmes through using genetic markers associated with desirable variant alleles coupled with advances in 'speed breeding' (Ghosh *et al.*, 2018) is now possible.

## **References**

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# **Gene banks into genetic Resource centres: helping promote complementary *in situ* conservation**

NIGEL MAXTED<sup>1</sup>, SHELAGH KELL<sup>1</sup>, JOANA MAGOS BREHM<sup>1</sup>, JADE PHILLIPS<sup>1</sup>  
and EHSAN DULLOO<sup>2</sup>

<sup>1</sup>*School of Biosciences, University of Birmingham, Edgbaston, Birmingham B15 2TT, UK*

<sup>2</sup>*Bioversity International, Rose-Hill 71368, Mauritius*

## **ABSTRACT**

Target 9 of the GSPC calls for: “70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved, while respecting, preserving and maintaining associated indigenous and local knowledge”. Such a target is necessitated by the dual challenges of unprecedented expanding human population and an unstable and changing cultivation environment. To increase food production sustainably in the face of these challenges requires significant additional plant genetic resources (PGR), beyond that currently held by *ex situ* collections. Such additional diversity is available in global plant agrobiodiversity, specifically landraces (LR) and crop wild relatives (CWR) populations held within more traditionally diverse farming systems and in nature. Historically the availability of such diversity has limited their use in crop improvement, but the use of the full breadth of plant agrobiodiversity will be required if we are to meet the challenge and feed the predicted 9.8 billion human population in 2050. The integration of global; regional and national CWR / LR conservation; of *in situ* and *ex situ* actions; of formal and informal sectors; and of conservation with use is critical to sustaining humankind. Specifically, we will need to build on existing regional and national PGR networks, where necessary establish novel networks of partners and sites that safeguards the wealth of PGR and promotes its utilization as a means of underpinning future, climate smart agriculture, food and nutritional security. To achieve this aim it will be necessary to (1) Establish PGR stakeholders, status and network best practice, (2) Enhance PGR population management and best practice, (3) Promote PGR *in situ* valuation and use, (4) Establish durable PGR network partnerships linked to broader plant diversity conservation in Europe, and (5) Promote PGR awareness and conservation product / tool dissemination. This will involve the transformation of some PGRFA gene banks into PGR centres that oversee both *ex situ* and *in situ* activities to ensure growing user needs for diversity are met.

**Keywords:** *Plant genetic resources, crop wild relative, crop landrace, in situ, ex situ*

## **Short Biography of Nigel Maxted**

Nigel Maxted (Senior lecturer in Genetic Conservation at University of Birmingham, UK) has professional expertise in *in situ* and *ex situ* plant genetic conservation, he has published over 350 scientific papers and 22 books. He led/leads national,

European and international crop wild relative and landrace conservation research projects in Europe, Asia and Africa for various international agencies (FAO / ITPGRFA / CGIAR / Crop Trust / World Bank / United Nations). Successful coordination of four large EC funded projects (EU Biotech ESIN, FP5 PGR Forum, FP7 PGR Secure, H2020 Farmer's Pride) and regularly works as a consultant for the leading international conservation agencies. He is International Scientific Advisor for Bioversity International; Co-Chair of the IUCN SSC Crop Wild Relative Specialist Group; Chair of Wild Species Conservation in Genetic Reserves WG; Co-Chair for genetic resources for the Ecosystem Services Partnership; and Chair of the U.K. Plant Genetic Resources Group.

# Plant genetic resources for food and agriculture maintained in the global genebanks - state of the art

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## ABSTRACT

Plant genetic resources play a major role for global food security. The most significant and widespread mean of preserving plant genetic resources is *ex situ* conservation. Today about 1,750 *ex situ* genebanks world-wide maintain 7.4 million accessions. The largest numbers of accessions stored are of wheat (855,000), rice (775,000), barley (465,000) and maize (325,000). Other large germplasm holdings include bean, sorghum, soybean, oat, groundnut and cotton.

One of the ten largest *ex situ* collections of our globe is located at the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany, conserving 150,000 accessions from 3,200 plant species and 780 genera. Since the majority of genebank holdings globally is maintained as seed, seed storability is of exceptional importance for germplasm conservation.

At IPK research on seed longevity was initiated for a range of crops and wild relatives stored over decades. Historical germination data accumulated during 35 years of seed germination monitoring were analysed to predict species specific seed longevities. The study considered 75 species comprising 79,075 accessions and 157,402 observations. Beside interspecific differences variation was also detected within species and genetic analyses were initiated using long term stored and experimental aged materials. The complex trait seed longevity was studied exploiting classical quantitative trait locus analysis and association genetics. Results obtained for wheat, barley, oilseed rape and tobacco are presented.

In addition, mass spectrometry based untargeted metabolite profiling experiments were performed in order to detect biochemical changes coinciding with loss in seed germination. GC-MS analysis of the polar metabolome of wheat and barley identified glycerol and related intermediates as highly correlated to germination rate. Therefore, the lipidomic composition of a wheat panel was investigated using high-resolution liquid chromatography-mass spectrometry (LC-MS). A high proportion of tentative oxidized lipids was detected, suggesting lipid oxidation as the causal trigger for membrane degradation.

# **Conservation and use of vegetable genetic resources: The role of the UK Vegetable Genebank**

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## **ABSTRACT**

Vegetable crops make a significant contribution toward nutritionally diverse and healthy diets. In order to support and increase vegetable production and consumption, plant breeders must deliver new varieties suited to lower input and more sustainable production systems. This includes resilience in less than optimal growing environments and better resistances to pests and pathogens. Crop genepool diversity if the raw material used by plant breeders and collections of plant genetic resources such as genebanks are tasked with the conservation of this diversity and its distribution to the user community. The UK Vegetable Genebank (UKVGB) holds a collection of approximately 14,000 samples of a range of vegetable crops including brassicas, carrot, lettuce and onion. As well as collection management and conservation, the UKVGB is a partner in the Vegetable Genetic Improvement Network. This network aims to provide a pipeline to enable the genetic variation present in the genebank collections to be deployed more easily by plant breeders through the development of diversity sets, mapping collections and other specific resources as well as the key phenotyping screens required to identify useful material for uptake by breeding programmes. The various approaches taken will be discussed and examples provided.

# A toolkit for the transfer of alleles from germplasm collections to wheat breeders

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*Collectively the Designing Future Wheat Selection Panel*

## ABSTRACT

The Designing Future Wheat (DFW) Breeder Tool Kit (BTK), collection is curated in the Germplasm Resources Unit at the John Innes Centre. DFW-BTK germplasm is an opportunity for the research community to test the latest developed material and findings by the breeding industry in a multisite scale. The BTK principle is that DFW research groups produce agronomically advantageous material that is trackable and comparable. Trackability is achieved by molecular markers associated with the traits. Comparability is achieved by transferring the advantageous candidate loci into a standard unified genetic background. Ultimately the commercial breeding industry will introduce the advantageous alleles into their breeding programmes and thus widening the diversity that they select from.

The Germplasm Resource Unit acts as custodians for this material from all Institute donors. Initially it is referred to as a Tool Kit (TK) collection, meaning all developed material from academia. Currently this holds material from Synthetic Hexaploids, Alien Introgressions, Mutagenesis and Landrace donor backgrounds. These TK lines

are then selected from annually by a panel of DFW Platform Leaders, Institute Representatives, and members of the commercially breeding industry as nominated BTK Lines. The selected lines are then tested across multiple commercial sites to give highly statistically proven data. The panel sits twice a year, with a second meeting focussing on what traits consortium groups should be focussing their efforts on developing.

The DFW BTK has been developed for researchers to see their work tested at the highest level of commercial breeding context and to improve research to breeding industry genetic gain delivery. Please contact the BTK coordinator, [simon.orford@jic.ac.uk](mailto:simon.orford@jic.ac.uk) if you feel this may be of interest to you or for further details and guidelines to material production and curation. Visit [www.seedstor.ac.uk](http://www.seedstor.ac.uk) to see what is on offer so far.

# Identifying new and useful genetic variation in the AE Watkins landrace collection

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## ABSTRACT

The AE Watkins wheat landrace collection was assembled in the early twentieth century and was highly valued as a unique source of genetic diversity. However, there was relatively little deployment of this diversity in wheat breeding. How that might be changed for the better presents an interesting challenge in genebank stewardship. The UKs Wheat Improvement Strategic Programme (WISP) put in place a gene discovery strategy for Watkins germplasm with the intention of building resources that would expedite the transfer of beneficial alleles into breeding. This strategy, the resultant resources, and examples of their use in QTL discovery and validation will be discussed here. The modern collection comprises just 827 accessions, after SSD this increased to 1050 to capture heterogeneity within some accessions. From a genotypically defined core set we developed 96 F4 recombinant inbred line (RIL) populations in a nested association mapping design with the UK spring wheat Paragon as a common parent. Populations were genotyped and genetic maps produced. UK coordinated efforts in field phenotyping identified numerous QTL of potential agronomic use, with the Watkins allele putatively beneficial. Selected alleles were introgressed into Paragon by backcrossing to produce NILs for QTL validation and pre-breeding. NAM sub sampling has been attempted, with some success, as one way to use exploit this resource without growing 12000+ RILs! It is hoped that these resources will provide users with multiple points of access to Watkins diversity that can be mixed and matched to fit specific research objectives.

# Central Asia-UK relationships to kick off the wheat germplasm exchange for better bred wheat

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## ABSTRACT

Due to the fact that Kazakhstan occupies huge area of 2,724,900 km<sup>2</sup> and thus, is the ninth largest country in the globe, its agronomic potential is enormous. Wheat is the main crop grown in the country. Almost half of the arable land, 12 million hectares, is used to meet about 15–20 million tonnes total wheat production, half of which is for the export. However, 1 t h<sup>-1</sup> average wheat yield has not changed since 1970s. Hence, it is a time to attempt to manipulate final grain quality and yield via improving genetic potential and resilience to stress using advanced breeding approaches. The research focus of this PhD project is the genetics of wheat adaptation in Kazakhstan and neighbouring Central Asian countries.

In our research, we are attempting to better understand the genetic bases of complex traits of Kazakh bread wheat, which might be defined with unique allelic combinations, and compare it with other Central Asian wheat collections. With this purpose a mapping population Pamyati Azieva (Russian cultivar certified in Kazakhstan) × Paragon (UK) was developed, consisting from 94 recombinant inbred lines. So far, by studying this mapping population, we have identified many QTL (quantitative trait loci) associated with important agronomic traits of wheat. One of the most interesting ones of which were QTL controlling plant height.

We have also assembled a panel consisted of wheat accessions from Kazakhstan (276 spring, 64 winter and three facultative wheat varieties), Uzbekistan (30 winter), Kyrgyzstan (19 winter and 11 facultative), Afghanistan (seven spring), Tajikistan (nine winter), Russia (25 winter and one facultative), Turkey (30 winter), Ukraine (two winter) and others (12 winter) as a result of Central Asian Workshop, funded by BBSRC, which took place in Astana and Almaty in May 2018, Kazakhstan. Therefore, new germplasm panel has been named after the Central Asian Wheat Breeding Initiative (CAWBIn). The whole panel is currently stored at JIC and we hope this can become a public resource available from genebanks including the Genetic Resource Unit (GRU) of the John Innes Centre. Before this, it will be subjected to single seed descent to decrease the level of heterogeneity and heterozygosity present in the gene pool. Colleagues at the University of Bristol will then conduct genetic fingerprint with Axiom 35K platform.

During the meeting it was also agreed to grow the panel in different locations to carry out association analysis to find out new genes, important for breeding in Central Asia, underpinning complex traits of wheat. These leads will inform new crosses with the final aim of creating new pre-breeding germplasm for these target environments. Thus, launched successful collaboration between the UK and Central Asian wheat geneticists, biochemists and wheat breeders, and exchange of material are important for both countries as for each country to exploit new genetic recourses from the other it is essential that key genes controlling adaptation are identified so that the best adapted alleles can be fixed early in the breeding process.

# **Rocket science: A case study in the utilisation and development of genetic resources**

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## **ABSTRACT**

Rocket salad (*Eruca sativa*) is a popular leafy vegetable across the world. Until recently, the crop was a niche product with little breeding or selection for advanced quality traits. In 2009 a breeding program for rocket salad was established at Elsoms Seeds Ltd. with the expressed purpose of utilising germplasm collections to screen for novel traits that would enhance and add value to commercial cultivars. Nearly ten years after initiation, new and improved cultivars are coming to market with improved shelf life quality, taste and flavour. These improvements have been achieved by screening gene bank accessions for glucosinolates, and other phytochemicals, in tandem with sensory and consumer studies, to better understand the factors driving acceptance and rejection of leaves. Next generation sequencing and sensory analyses are now being combined to understand the genetic mechanisms underpinning taste, flavour, and nutritional properties of rocket leaves. The knowledge gained will inform further improvements, and add both economic and nutritional value to rocket salad.

# What have wheat breeders been doing for 150 years? – Analysis of pedigree and genotype data reveal patterns of breeder selection

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## ABSTRACT

Fragmented information regarding wheat (*Triticum aestivum*) variety pedigrees and genetic resources limits their efficient exploitation. We present an analysis of a wheat pedigree database including over 3,000 genotypes originating from 38 countries, representing over a century of breeding and variety development (Fradgley *et al.*, 2019). Recently developed software (Shaw *et al.*, 2014) enables visualisation and navigation of the key developments in UK wheat breeding, and highlights the wide genetic background of the UK wheat gene pool. Ancestry of most modern elite varieties can be traced back to landraces originating from a broad range of geographic regions.

A combination of pedigree and genetic marker data was employed to investigate effects of breeder selection over time. Estimates of marker- and pedigree-based kinship were found to correlate well, and enabled identification of errors in the pedigree or marker data. Genedropping simulations were used to estimate probabilities of variety genotypes based on genotyped founders and Mendelian inheritance. These results showed that, as a result of breeders' selection on many offspring, varieties are generally more closely related than expected by simulations to the superior parent which contributes more favourable alleles. Simulations over the pedigree, using 110 genotyped founders released before the year 2000 to predict the distribution of marker alleles in a set of 45 derived varieties released after 2000, found evidence for selection on genetic regions linked to specific markers. One such region co-localised with a genetic locus recently identified as containing a gene for increased spikelet number per ear. Further evidence for selections was supported by greater linkage disequilibrium in observed compared to simulated genotypes, with the difference being greater at closer genetic distances. These results suggest that selection by breeders has conserved linked haplotype blocks containing beneficial gene/allele assemblages.

This pedigree resource will enable more efficient management of genetic resources for research and commercial breeding and will be freely available, and regularly updated, via the NIAB resources webpage:

<http://www.niab.com/pages/id/326/Resources/>

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# Using vegetable crop genetic resources to identify tolerance to abiotic stress and other key performance traits

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## ABSTRACT

Changing climatic conditions are placing constraints on agricultural production and so breeding to provide new environmentally-durable varieties with increased tolerance of abiotic stresses and low nutrient availability is required. The development of pre-breeding genetic resources such as the Vegetable Genetic Improvement Network (VeGIN) Diversity Fixed Foundation Sets (DFFSs) and mapping populations provides the opportunity to identify new sources of genetic material for downstream breeding programmes. We have phenotyped the response of lines of the VeGIN vegetable brassica (*Brassica oleracea*) populations to a range of single and combined abiotic stresses. Significant ( $P \leq 0.05$ ) response variation was found across the populations for drought, waterlogging and salinity stress and tolerant lines have been identified. Abiotic stress assays are now being used to phenotype VeGIN lettuce (*Lactuca sativa*) populations and are being adapted for the screening of carrot (*Daucus sativa*) and onion (*Allium* spp.) populations. Future studies will expand the investigation of responses to multiple simultaneous stresses. Such populations have also been used to investigate a range of traits including establishment, post-harvest discolouration, tipburn resilience and pathogen resistance. The results are promising for the future development of more robust vegetable varieties.

# Exploiting genetic diversity of *Vicia faba*

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## ABSTRACT

Field- or broad bean (*Vicia faba* L.) is grown worldwide as an important protein crop for animal feed and human consumption. In the UK field beans have been grown on approx. 150,000 ha in 2017 and the production area is predicted to increase (PGRO, annual report 2017). However the genetic diversity of field bean has been insufficiently explored. Recent genotyping of six current recommended list UK bean varieties with 24 Simple Sequence Repeat markers developed at NIAB suggests high genetic similarity between these elite cultivars. As part of the Defra Pulse Crop Improvement Network (PCGIN) and related projects we have assessed a diverse collection of *V. faba* landraces and varieties from Europe, North Africa, the Middle East and South Asia for multiple valuable traits, including resistance to chocolate spot, *Ascochyta* pod spot and downy mildew, and valuable agronomic traits like pod set stability and seed weight. A panel of 150 inbred Single Seed Descent lines, representing wide phenotypic and genotypic variation has been developed from international land races and cultivars and forms the basis for generating mapping populations for identifying QTLs contributing to important traits (Webb *et al.*, 2016) as well as establishing recombinant inbred lines which are made available to facilitate plant breeding. In parallel valuable genomic resources, including an annotated transcriptome of *V. faba* "Hedin", derived from RNA libraries from multiple tissues has been generated, providing new resources for investigating differential gene expression for key traits.

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