The Multinational Arabidopsis Steering Committee

Annual Report 2017/2018

Nicholas Provart
nicholas.provart@utoronto.ca
MASC Inc President

Siobhan Brady
sbrady@ucdavis.edu
MASC Inc Treasurer

Geraint Parry
geraint@garnetcommunity.org.uk
MASC Inc Secretary

MASC Directors

Rodrigo A. Gutiérrez
rgutierrez@bio.puc.cl
Masatomo Kobayashi
kobayasi@rtc.riken.jp
Sean May
sean@Arabidopsis.org.uk
Blake Meyers
BMeyers@danforthcenter.org
Barry Pogson
Barry.Pogson@anu.edu.au
Xuelu Wang
xlwang@mail.hzau.edu.cn
Michael Wrzaczek
michael.wrzaczek@helsinki.fi

MASC Sub委员会 Chairs and Co-Chairs

Malcolm Bennett
Malcolm.Bennett@nottingham.ac.uk
Siobhan Brady
sbrady@ucdavis.edu
Joe Ecker
ecker@salk.edu
Fabio Fiorani
f.fiorani@fz-juelich.de
Joshua Heazlewood
jheazlewood@unimelb.edu.au
J. Chris Pires
jpires@missouri.edu
Nicholas Provart
nicholas.provart@utoronto.ca
Kazuki Saito
kazuki.saito@riken.jp
Robert Schmitz
schmitz@uga.edu
Motoaki Seki
motoaki.seki@riken.jp
Wolfram Weckwerth
walr@dfg.de
Xuehua Zhong
xuehua.zhong@wisc.edu

MASC Country Representatives

Wagner Araújo
waraujo@ufv.br
Maria Francisca Blanco
mfblando@unab.cl
Dario Bonetta
dario.bonetta@uoi.ca
Lynette Brownfield
lynette.brownfield@otago.ac.nz
Ana I. Caño-Delgado
ana.cano@crigenonica.es
Maura Cardarelli
maura.cardarelli@unimona.it
Saccio De Vries
saccio.devries@wur.nl
Maria E. Eriksson
maria.eriksson@plantphys.umu.se
Joanna D. Fresiers
jdfrieser@ucdavis.edu
Thorsten Hamann
thorsten.hamann@ntnu.no
Klaus Harter
klaus.harter@emb.zmbp.uni-tuebingen.de
Polideska Hatzopoulos
phat@aua.gr
Marie-Theres Hauser
marie-theres.hauser@boku.ac.at
Inhwan Hwang
ihhwang@postech.ac.kr
Yuling Jiao
yjiao@pku.edu.cn
Masatomo Kobayashi
kobayasi@rtc.riken.jp
Jitendra P. Khurana
khuranaj@genehome.org
Loic Lepiniec
Loic.Lepiniec@versailes.inra.fr
Minami Matsui
minami@riken.jp
José Lourdes Milcol
jmilcol@eth.es
Monika Murcha
monika.murcha@uwa.edu.au
Moritz K. Nowack
moritz.nowack@vib.be
Adriano Nunes-Nesi
nunesnesi@ufv.br
Michael Palmgren
michael.palmgren@pln.ku.dk
Catherine Perrot-Rechenmann
catherine.rechenmann@cnrs-dir.fr
Nicholas Provart
nicholas.provart@utoronto.ca
Sigal Savidl-Goldstein
sigal@technion.ac.il
Motoaki Seki
motoaki.seki@riken.jp
Charles Spillane
charles.spillane@nuigalway.ie
Kentaro K. Shimizu
kentaro.shimizu@ieu.uzh.ch
Ranamurthy Srinivasan
srinivasan53@gmail.com
László Szabados
szabados@brc.hu
Marcelo J. Yanovsky
mryanovsky@gmail.com
Viktor Zásky
viktor@natur.cuni.cz

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated figure from that article.

MASC thanks Hanne Kualheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turku.

MASC especially thanks Science des Plantes de Saclay who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.

Further information can be found on the MASC website: www.ArabidopsisResearch.org

MASC Inc is registered as a not-for-profit corporation in Canada under Corporation Number 960778-1, subject to the regulations of the Canada Not-for-profit Corporations Act

Cover design and editing

Geraint Parry MASC Secretary, GARNET, Cardiff University, UK
geraint@garnetcommunity.org.uk

Cover images taken from Open Access publications

Top Image: http://dx.doi.org/10.7554/elife.26023
Middle Image: http://dx.doi.org/10.7554/elife.23625
Bottom Image: http://dx.doi.org/10.7554/elife.34064

The MASC report 2017/18 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
  http://arabidopsisresearch.org/index.php/publications/masc-reports
> uNASC, The Nottingham Arabidopsis Stock Centre:
  http://arabidopsis.info/progreports.html
> TAIR, The Arabidopsis Information Resource:
  http://www.Arabidopsis.org/portsals/masc/masc_docs/masc_reports.jsp
> GARNet:
  http://garnetcommunity.org.uk/reports

Published by the Multinational Arabidopsis Steering Committee (MASC) June, 2018

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated figure from that article.

MASC thanks Hanne Kualheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turku.

MASC especially thanks Science des Plantes de Saclay who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.

Further information can be found on the MASC website: www.ArabidopsisResearch.org

The MASC report 2017/18 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
  http://arabidopsisresearch.org/index.php/publications/masc-reports
> uNASC, The Nottingham Arabidopsis Stock Centre:
  http://arabidopsis.info/progreports.html
> TAIR, The Arabidopsis Information Resource:
  http://www.Arabidopsis.org/portsals/masc/masc_docs/masc_reports.jsp
> GARNet:
  http://garnetcommunity.org.uk/reports

Published by the Multinational Arabidopsis Steering Committee (MASC) June, 2018

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated figure from that article.

MASC thanks Hanne Kualheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turku.

MASC especially thanks Science des Plantes de Saclay who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.

Further information can be found on the MASC website: www.ArabidopsisResearch.org

The MASC report 2017/18 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
  http://arabidopsisresearch.org/index.php/publications/masc-reports
> uNASC, The Nottingham Arabidopsis Stock Centre:
  http://arabidopsis.info/progreports.html
> TAIR, The Arabidopsis Information Resource:
  http://www.Arabidopsis.org/portsals/masc/masc_docs/masc_reports.jsp
> GARNet:
  http://garnetcommunity.org.uk/reports

Published by the Multinational Arabidopsis Steering Committee (MASC) June, 2018

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated figure from that article.

MASC thanks Hanne Kualheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turku.

MASC especially thanks Science des Plantes de Saclay who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.

Further information can be found on the MASC website: www.ArabidopsisResearch.org

The MASC report 2017/18 and previous reports are available online at:

> MASC, The Multinational Arabidopsis Steering Committee:
  http://arabidopsisresearch.org/index.php/publications/masc-reports
> uNASC, The Nottingham Arabidopsis Stock Centre:
  http://arabidopsis.info/progreports.html
> TAIR, The Arabidopsis Information Resource:
  http://www.Arabidopsis.org/portsals/masc/masc_docs/masc_reports.jsp
> GARNet:
  http://garnetcommunity.org.uk/reports

Published by the Multinational Arabidopsis Steering Committee (MASC) June, 2018

Acknowledgements

MASC is grateful to all authors for their contribution to the MASC annual report 2017/2018.

This report has been written by the members of the MASC community including the MASC directors, subcommittee chairs and co-chairs with support of subcommittee members, country representatives, project or resource directors and the wider Arabidopsis community. Throughout the report any references that are highlighted in red include an associated figure from that article.

MASC thanks Hanne Kualheim and Michael Wrzaczek for helping with arrangements for printing the MASC summary page in Turku.

MASC especially thanks Science des Plantes de Saclay who have provided funding for the printing and distribution of the MASC report and for support of the MASC annual meeting.
# Table of Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Table of Contents</td>
<td>4</td>
</tr>
<tr>
<td>Foreword and Executive Summary</td>
<td>6</td>
</tr>
<tr>
<td>Progress and Activities of MASC</td>
<td>8</td>
</tr>
<tr>
<td>Analysis and Recommendations by MASC</td>
<td>10</td>
</tr>
<tr>
<td>Reports of the MASC Subcommittees</td>
<td>12</td>
</tr>
<tr>
<td>Bioinformatics</td>
<td>12</td>
</tr>
<tr>
<td>Clone-Based Functional Genomics Resources (ORFeomics)</td>
<td>15</td>
</tr>
<tr>
<td>Epigenetics and Epigenomes</td>
<td>15</td>
</tr>
<tr>
<td>Metabolomics</td>
<td>18</td>
</tr>
<tr>
<td>Proteomics</td>
<td>19</td>
</tr>
<tr>
<td>Systems and Synthetic Biology</td>
<td>20</td>
</tr>
<tr>
<td>Arabidopsis Community Projects and Resources</td>
<td>23</td>
</tr>
<tr>
<td>Resource and Stock Centers</td>
<td>24</td>
</tr>
<tr>
<td>Arabidopsis Informatics and Data Sharing Resources</td>
<td>26</td>
</tr>
<tr>
<td>Plant Projects and Resources with Strong Participation of <em>Arabidopsis</em> Community</td>
<td>29</td>
</tr>
<tr>
<td>Summary Page</td>
<td>34</td>
</tr>
<tr>
<td>Analysis of Arabidopsis Publications</td>
<td>35</td>
</tr>
<tr>
<td>Research Highlights in 2017/18</td>
<td>36</td>
</tr>
<tr>
<td>Country Highlights</td>
<td>41</td>
</tr>
<tr>
<td>Argentina</td>
<td>42</td>
</tr>
<tr>
<td>Australia</td>
<td>43</td>
</tr>
<tr>
<td>Austria</td>
<td>45</td>
</tr>
<tr>
<td>Belgium</td>
<td>48</td>
</tr>
<tr>
<td>Brazil</td>
<td>50</td>
</tr>
<tr>
<td>Canada</td>
<td>52</td>
</tr>
<tr>
<td>Chile</td>
<td>54</td>
</tr>
<tr>
<td>China</td>
<td>57</td>
</tr>
<tr>
<td>Czech Republic</td>
<td>59</td>
</tr>
<tr>
<td>Denmark</td>
<td>61</td>
</tr>
<tr>
<td>Finland</td>
<td>62</td>
</tr>
<tr>
<td>France</td>
<td>63</td>
</tr>
<tr>
<td>Germany</td>
<td>64</td>
</tr>
<tr>
<td>India</td>
<td>66</td>
</tr>
<tr>
<td>Israel</td>
<td>69</td>
</tr>
<tr>
<td>Italy</td>
<td>70</td>
</tr>
<tr>
<td>Japan</td>
<td>73</td>
</tr>
<tr>
<td>New Zealand</td>
<td>77</td>
</tr>
<tr>
<td>Norway</td>
<td>78</td>
</tr>
<tr>
<td>South Korea</td>
<td>79</td>
</tr>
<tr>
<td>Spain</td>
<td>80</td>
</tr>
<tr>
<td>Sweden</td>
<td>81</td>
</tr>
<tr>
<td>Switzerland</td>
<td>83</td>
</tr>
<tr>
<td>United Kingdom</td>
<td>85</td>
</tr>
<tr>
<td>United States</td>
<td>87</td>
</tr>
<tr>
<td>Members of the MASC Subcommittees</td>
<td>90</td>
</tr>
</tbody>
</table>
**Forward and Executive Summary**

Thanks for being interested in the latest activities of the Multinational Arabidopsis Steering Committee (MASC). Although you will read within these pages that it has been a successful year for Arabidopsis research there is always the challenge to ensure that support is maintained for research conducted with this important model organism. To this end the report includes discussion on the future possibilities within the field, in particular to support the bioinformatics tools that are critical for the analysis of the enormous amount of data that can be generated through ‘omic technologies.

MASC started in the early 1990’s, when scientists from several countries formed an ad hoc committee to promote large-scale research with Arabidopsis. The ultimate goal was the understanding of physiological, biochemical and developmental processes of flowering plants at the molecular level, employing Arabidopsis as a model system. In order to reach this long-term goal, a commitment from the global Arabidopsis community was essential. Therefore, actively engaged researchers developed ‘The Multinational Coordinating Arabidopsis - Genome Research Project’ in 1990. Over time this changed through different versions of MASC, which in the current and hopefully long lasting version is registered in Canada as a charitable organisation.

This should ensure smooth transitions between board members and hopefully provide some small amount of financial support for future ICAR meetings, which are a key component of the Arabidopsis year. MASC and the Arabidopsis community are working toward the third decade-long roadmap document entitled ‘From Bench to Beautiful Harvests’ (Lavagzi et al., 2012, Plant Cell, 24:2240-7). The 2017/2018 annual MASC report will be the 6th published under the current road map. Over time this changed through different versions of MASC, which in the current and hopefully long lasting version is registered in Canada as a charitable organisation.

**MASC Subcommittees**

Currently eight MASC Subcommittees monitor progress and important activities as well as discuss future directions of each of their respective fields of Arabidopsis research. Members of each subcommittee are in positions to stay in close contact with the community and promote international cooperation (pages 12-21).

In the lead up to the MASC annual meeting that takes place at ICAR2018, there have been questions tabled about the future directions of these subcommittees. Therefore this will be a topic of conversation at the annual meeting.

Six of the subcommittees have contributed to the 2017-2018 annual MASC report and the activities of the Phenomics subcommittee are included in the report of international phenotyping.

**Contributing subcommittees are:**

- Bioinformatics (page 12)
- ORFeomics (page 15)
- Epigenetics and Epigenomes (page 15)
- Metabolomics (page 18)
- Proteomics (page 19)
- Systems and Synthetic Biology (page 20)

**MASC is open to discuss the evolution of the current subcommittees and community members are welcome to suggest if there is a community need for a new subcommittee. In this case please contact the permanent members of MASC (Nick Provart, Siobhan Brady or Geraint Parry) to discuss your ideas. Suggestions will be gratefully received and likely approved to the next step in the official formation of new subcommittee would be to assemble a group of individuals knowledgeable in the area who could contribute to the submission to the annual report as well as becoming involved in the possible organisation of subcommittee-related meetings.**

**Arabidopsis Community Projects and Resources**

A key component of the mature Arabidopsis research community is the variety of resources that have been developed over the course of the past 20 years. These community projects, stock centers and bioinformatic resources enable researchers to fully integrate their research from its initial phenotypic description through to full multi-omic characterisation.

Information on the progress and activities of the range of community resources can be found on pages 23-33.

**Country Highlights**

MASC is supported by individual countries through the selection of representatives that report each year on the progress that their colleagues have made. In addition, they provide an important commentary on the prospects for Arabidopsis research in their individual countries. These country reports highlight the exceptional numbers of resources that have been developed for the benefit of the global Arabidopsis community as well as highlighting where future issues might emerge that could be tackled on a global level.

In this report we are delighted to include an inaugural report from Norway whose contribution means that 25 of the 29 current member countries have reported to MASC this year (page 41-89).

We encourage researchers from other countries who are not featured in this MASC report to become involved with this process by contacting a member of the MASC Board of Directors. Providing an update for the global community not only highlights the outstanding work that is occurring in their home country but also provides an easy reference point that can be important in discussions with potential funders and other interested parties.

**Arabidopsis Scientific Highlights in 2017/2018**

According to an NCBI search, Arabidopsis researchers published over 4100 peer-reviewed papers in 2017, which is a decline from the highest numbers from 2013 and 2014. This number is buoyed by continued increase in publications from Chinese researchers. As also shown in figure 2 this reflects a plateauing in papers from many other countries.

In this report we highlight ten papers that demonstrate the breadth of research in which Arabidopsis is involved. The papers include those that tackle challenges in basic research as well as those that provide community resources as an intentional side-effect of their research.

- Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis. EMBO J http://dx.doi.org/10.15222/embj.2016.94983
- WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. PLoS Genet. http://dx.doi.org/10.1371/journal.pgen.1007177
- A small peptide modulates stomatal control via abscisic acid. Nature https://doi.org/10.1038/s41586-018-0009

MASC thanks Michael Wrazcek and the local organisers of ICAR2018 in Turku for their organisational and financial support for our activities and to all MASC members who contributed to this report.

Finally we would like to thank Science des Plantes de Saclay for providing financial support for printing and distribution of the full report.
MASC operates via three groups who receive continuous input from the whole Arabidopsis and plant community: MASC subcommittees, Arabidopsis community projects and resources and MASC country representatives.

The MASC subcommittees, proposed in 2002, were established to help tracking the progress and advances made by the international Arabidopsis community. This report includes contributions from six of the eight current subcommittees: Bioinformatics, Epigenetics and Epigenomes, ORFeomics, Metabolomics, Proteomics and Systems and Synthetic Biology.

The requirements for a subcommittee to be considered active were formulated in 2009 and remain relevant during the transition to MASC.

- Submission of an annual report
- Input at MASC annual meetings
- MASC subcommittee chair has to be nominated with a 3-year minimum term to provide continuity
- Co-chairs could help promote activity of the subcommittee
- MASC subcommittee chairs/co-chairs should confirm leadership annually. If necessary, new subcommittee chair should be found
- Chair/co-chair should confirm and represent the interest of subcommittee members.

Representatives of Arabidopsis community projects and resources attend the annual MASC meeting and contribute to the annual MASC report by submitting country reports.

MASC is delighted to welcome Thorsten Hamann as the country representative from Norway and thanks the other 24 country representatives for their valuable contributions this year.

Overall we encourage Arabidopsis researchers to become involved in MASC activities, e.g. subcommittees, projects and resources or as country representatives.

International Conference on Arabidopsis Research (ICAR)

Over the past decade the flagship ICAR meeting has rotated though global locations in Asia, North America and Europe. However the board of directors is more than happy to consider other global locations if there is a need to take the ICAR meeting to previously under-represented locations. Organisation of these meeting relies upon a committed local organising committee who might engage a conference management company to deal with the meeting details.

These are the locations for upcoming ICAR meetings:
- 29th ICAR, Turku, Finland: June 25th-29th 2018
- 31st ICAR, Seattle, USA June 22nd-26th 2020
- 32nd ICAR, Europe, June 2021.

The 28th International Conference on Arabidopsis Research (ICAR) was held in St Louis, Missouri between 19th-23rd June 2017 where the organising committee was led by Joanne Fernie. The number of attendees was less than usual, likely due to competition from the ASPB meeting in Hawaii, yet it included the usual variety of outstanding scientific sessions arguably highlighted by presentations of unpublished data from Noko Geldner and Keiko Torii.

460 people attended the 28th ICAR with and 65% of the attendees (300) submitting a poster abstract (Figure 1). On average 63% of the attendees have presented a poster during the ICARs over the last 10 years.

One strong feature of ICAR2017 were the independently organised workshops that remain an important part of the schedule. Members of MASC were involved in the organisation of workshops on Careers (Joanna Friesen, NAASC), Science Communication (Ruth Bastow, GPC), Chemical Biology (David Gilford, Minami Matsui, RIKEN) and Bioinformatics (Eva Huala, TAIR-Phoenix Bioinformatics and Chris Town Araport).

As there is no specific funding for the MASC coordinator, Dr Parry continues to manage these limited MASC activities:

- Serving as executive secretary of MASC
- Collating, writing and editing of the annual MASC report with input from MASC members
- Organising and maintaining the MASC web pages to inform the global research community about various opportunities, collaborations, large-scale activities and research progress
- Efforts of other community projects (BAR, Gramene) with strong participation of the Arabidopsis community are also presented in the report as well as a summary from the International Plant Phenotyping Community (page 31).

Country representatives attend the MASC annual meeting held during ICARs and contribute to the annual MASC report by submitting country reports.

MASC is an independent not-for-profit MASC Inc in Canada required a change in organisational structure. This includes non-paid positions of the President, Treasurer and Secretary, the current incumbents are Nicholas Provart, Siobhan Brady and Geraint Parry respectively.

In 2017 eight directors were elected for a range of term lengths. These will ultimately be for four years once the first round of rotations has ended. These MASC directors officially take up their positions at the ICAR2018 meeting and to ensure that only two directors rotate off the board the initial term lengths will be less than 4 years. This is a list of the inaugural board of directors and the length of their terms:

2018-2020: Michael Wrzaczek (Finland), Barry Pogson (Australia)
2018-2021: Vuclu Wang (China), Elizabeth Haswell (United States of America)
2018-2022: Blake Meyers (United States of America), Sean May (United Kingdom)
2018-2023: Rodrigo Gutierrez (Chile), Masatomo Kobayashi (Japan)

From 2020 two new directors will be elected for four term years. Primarily appointments these will aim to improve the gender balance on the board of directors as well as maintain geographical diversity.

As there is no specific funding for the MASC coordinator, Dr Parry continues to manage these limited MASC activities:

- Serving as executive secretary of MASC
- Collating, writing and editing of the annual MASC progress report with input from MASC members
- Maintaining and updating the MASC web pages to inform the global research community about various opportunities, collaborations, large-scale activities and research progress

Progress of Arabidopsis informatics and data sharing resources are highlighted in this year’s report, including updates from the International Arabidopsis Informatics Consortium (IAIC) and the Arabidopsis Information Resource (TAIR).

MASC inc Annual Report 2017/2018
8

Figure 1. Number of attendees (blue) and number of posters presented (red) at the International Conference on Arabidopsis Research since 2005, when information about posters became available.
Analysis and Recommendations by MASC

Prepared by Geraint Parry with input from Nicholas Provart.

The main objective of MASC is to promote and facilitate research in Arabidopsis, a powerful reference system for plant molecular and genetic approaches. By publishing this annual report we bring together in one place information about the remarkable progress that has been made across all facets of research in this most dynamic of plant science research communities.

In global terms, research that uses Arabidopsis as a model organism is still in good shape. In most countries the number of publications that feature Arabidopsis remains stable or is increasing that means the total productivity is not declining. As there is an increase in applied research that uses crops such as rice, maize or wheat, research funding diverted into those areas might negatively impact the amount of funding available to Arabidopsis research. However it is clear that much applied research relies on initial findings made using model organisms so it is important to maintain support at the early phase of the discovery pipeline.

Despite many years of research, 14,717 of 27,655 Araport 11 genes lack a Gene Ontology Biological Process annotation and 10,035 lack a Gene Ontology Molecular Function annotation. Clearly there is still a lot to learn and within this report the MASC ORFeomics Expert Committee (NAASC) conducted a survey where almost 700 respondents answered questions about location, content and cost.

The germplasm and bioinformatics resources available to Arabidopsis researchers are far in advance of those available to other plant systems. There are a well-known set of core community tools such as TAIR, BAR, the SIGnAL-T DNA resources and the Arabidopsis stock centres that have been developed over the past twenty years. In addition, this report highlights numerous less well known but important software tools for interrogation of Arabidopsis data. In particular the country reports from China, Japan, Australia, USA and the UK provide information about many such tools but most countries are developing their own resources that are available for use by the global community. We urge potential users to investigate these resources and to utilize those that fit their research needs.

MASC President Nicholas Provart recently conducted a survey on the future of plant-focused bioinformatic resources. The results of this can be downloaded here: (arabidopsisresearch.org/images/publications/documents_articles/2018_MASC_BioinfoSurvey.pdf). A quarter of 320 respondents would like to see a centralised website that lists all of these resources although the option favoured by almost 50% of respondents was for individual sites to be more tightly linked to other appropriate tools. This would allow a step-wise progression of data analysis and increase usage of multiple sites.

Although there are lots of available resources the community is entering a new phase regarding the future of these resources and how they can be funded over the longer term. The MASC bioinformatics survey asked about funding for community bioinformatics resources. The two favoured options were the ‘Freemium’ option currently operated by TAIR as well as the ‘Sugar daddy model’ where an extra cost was added to seed stocks ordered from the three Arabidopsis stock centres. Slightly less favourable but still popular was the ‘Sugar daddy model’ where large research centres supported resources for all and the

‘Greater Good model’ wherein resources are supported by funding agencies to ensure the research community and that users did not have directly contribute for their use (Figure 2).

Maintaining funding for community resources is clearly a challenging puzzle but hopefully discussions amongst international collaborators can develop a system that can ensure the long-term viability of the most useful resources. The pressing need to solve this challenge is highlighted by uncertainty over the future of Araport and how that resource will be maintained and whether a more international source of funding can be leveraged to support this global resource. A possible option is to consider an “OpenPlant” model whereby data sets, code, and expertise are deposited in open repositories, similar to the OpenWorm.org initiative, which is becoming widely used in the C. elegans research community.

Research in Arabidopsis spans all topics and the International Conference on Arabidopsis Research (ICAR) serves to bring together researchers from across scientific disciplines to fertilise the development of new ideas. Since 2007 ICAR has been hosted on a three-year cycle between Asia, North America and Europe. The 2016 ICAR in South Korea has almost 1000 attendees yet the ICAR2017 meeting had the lowest recent number of attendees with 420 travelling to St Louis. The reasons for this decline are complex and include competition from the ASPB meeting in Hawaii and any perceived issues regarding travel to the US from many countries. Regardless of the reduced numbers of delegates, the meeting hosted an outstanding selection of scientific sessions, workshops and posters.

To understand what people would like from future ICAR meetings the North American Arabidopsis Steering Committee (NAASC) conducted a survey where almost 700 respondents answered questions about location, content and cost.

Interestingly the most important consideration for delegates was to have the opportunity to present a research talk (unlike North American or Europeans, Asian respondents also highly valued the chance to give a poster presentation) closely followed by the wish for a diverse topic and speaker list that does not just focus on ‘big names’. This provides both food for thought for future organisers and evidence that there is an important role for large general conferences despite the increase of smaller research topic specific meetings.

Hopefully this report can provide a unique global perspective that gives important information that can reduce any unnecessary repetition of effort. We demonstrate that Arabidopsis research remains very active, efficient and innovative with thriving research communities in many countries. Many countries are developing their own community tools so the global challenge is to bring together these tools to maximise their usage and usefulness.

No doubt that as these tools are generated, federated and shared MASC will continue to promote and support these exciting resources.
Reports from MASC Subcommittees

Bioinformatics


Compiled by Nicholas Prowart with input from MASC Bioinformatics Subcommittee members and the wider Arabidopsis community.

Reports from MASC Subcommittees

Lab used pair-end sequencing of transcription start site tags (TSS tags) to identify 324,461 promoters in Arabidopsis, including many not associated with existing gene models (Tokizawa et al., 2017). The Vandepoele Lab reported differential transcript usage events – related to alternative splicing – for 6,146 Arabidopsis genes across 206 public RNA-seq data sets, with protein sequences being changed in 22% of the cases (Vanechhoute et al., 2017). The Van de Peer Lab used gene pairs resulting from whole genome duplication events to show a “remarkable” 92 homoeologous gene pairs with similar patterns of tissue-specific gene expression where one homoeolog exhibits more expression in aerial tissues and the other homoeolog exhibits more expression in tip-growth tissues (Smet et al., 2017).

Gene regulatory networks/codes: Roger Deal’s group used ATAC-seq to interrogate chromatin accessibility in stem cells and mesophyll cells to help delineate cell-type-specific gene regulatory networks acting in each (Sijacic et al., 2018). The Muday Lab identified transcriptional and receptor networks controlling root responses to ethylene (Harkey et al., 2018). Several groups published methods for inferring or exploring gene regulatory networks in Arabidopsis including GRACE (Banf and Rhee, 2017), GENEST (Balaguer et al., 2017), TF2Network (Kulkarni et al., 2018), and SeqEnrich (Becker et al., 2017). The Wigge Lab published a paper describing the G-box regulatory code in Arabidopsis to identify the set of bZIP and bHLH transcription factor networks that bind to G-boxes (ACAGTG) that are most predictive of expression of genes with G-boxes in their promoters (Ezer et al., 2017).

Other “big data”: The 1001 (Arabidopsis) Genomes Consortium continues to make the leveraging of natural variation for elucidating gene function easier than ever. The recent paper describing the global pattern of polymorphisms across 1,135 Arabidopsis accessions (1001 Genomes Consortium, 2016) provides the underlying data, while useful tools like AraGWAS – a “major new resource” that contains hundreds of thousands of linkages between phenotypes and polymorphisms (Tognolli et al., 2018) – and easyGWAS, published last year (Griff et al., 2017), enable easy identification of potentially causal SNPs. Text mining: the Sternberg lab at the California Institute of Technology published TextMiner (2017) which contains many new associations for Arabidopsis genes (Müller et al., 2018), while eGenPub selects articles that are about specific plant proteins (from 8 species) in the UniProt database (Ding et al., 2017). The Ecker lab published 8,577 interactions among Arabidopsis transcription factors (AIFTFIN-1) using a next-gen sequencing-based Y2H assay (GhY2H-seq) method they developed (Trigg et al., 2017).

Integrative tools: The ePlant tool for exploring Arabidopsis data from the kilometre- to nanometre-scale in an integrative manner was published by the Proxov Lab and collaborators (Waese et al., 2017), and is available at http://app.ePlant.org or as an “app” on Araport. A 2018 update to ePlant includes Klepikova et al.’s (2016) RNA-seq-based developmental atlas for Arabidopsis and O’Malley et al.’s DAP-Seq effort (2016) to map the binding specificity of 529 TFs in Arabidopsis – more than 2.8 million protein-DNA interactions are now viewable in ePlant’s Interaction Viewer.

GENIUS is a user-friendly web server that uses a novel machine learning algorithm to infer functional gene networks focused on specific genes and environmental conditions that are relevant to biological functions of interest, developed by the Gütlécz Lab. Try it for 8 species, including Arabidopsis at http://networks.bio.nuscigenius.

Overviews/collections: To reiterate from last year’s report, a good overview of several plant genomic databases is provided in volume 1533 of Methods in Molecular Biology (Plant Genomics Databases, edited by Aalt-Jan van Dijk, 2016), including chapters on ENSEMBL Plants, the BAR, PLAZA, Plant Promoter DB and many others. A similar collection providing a good overview of plant bioinformatic resources is available in the open-access Current Plant Biology special edition on genomic resources that Nutanithi and Van de Peer edit (2016). The 2018 Nucleic Acids Research database issue (Ridgen and Fernández, 2018) contains updates or reports on several plant databases. Of note here: Plant Chromatin State Database (Liu et al., 2018), Planteome - a portal for plant ontologies (Cooper et al., 2018), updates to PLAZA (Van Bel et al., 2018) and Gramene (Tello-Ruiz et al., 2018), and the aforementioned AraGWAS. AgrICO for Gene Ontology enrichment analyses in several plant species was also updated to version 2.0 by the Su Lab at the Chinese Agricultural University (Tian et al., 2017).

References


Reports from MASC Subcommittees

Clone-Based Functional Genomics Resources (ORFeomics)

http://ArabidopsisResearch.org/index.php/subcommittees/orfeomics

Motoaki Seki (Chair), motoaki.seki@riken.jp, RIKEN CSRS
Joe Ecker (Co-Chair), ecker@salk.edu, Salk Institute
Pascal Braun (Subcommittee Member), pascal.braun@helmholtz-muenchen.de, Helmholtz Zentrum München (HMGU)
Satoshi Iuchi (Subcommittee Member), satoshi.iuchi@riken.jp, RIKEN BRC
Debbie Christ, christ.t00@osu.edu, ABRC

Open Tools and Resources for Arabidopsis Researchers

We prepared the updated list of full-length cDNA and ORF clones that are available from Resource Centers (Please see Table 1). The revised ones are shown in red.

Recent activities of Subcommittee members.

Keeping tracking progress made towards the production of full-length cDNAs and open reading frame (ORF) clones for all annotated Arabidopsis protein-coding genes.

Future Activities of the Subcommittee.

ORFeomics subcommittee would like to propose a new project to collect all ORF (full-length cDNA) clones from every Arabidopsis protein-coding gene so as to test protein-protein, protein-DNA and protein-RNA interactions.

Our recent search showed that now about 23,000 Arabidopsis protein-coding genes have been isolated as Full-length cDNA clones. One of the last unexplored continents of Arabidopsis are the remaining 5,000 protein-coding genes. After that, only the non-coding genes remain to be isolated.

With the completion of isolating all 28,000 Arabidopsis protein-coding genes, comprehensive analysis of plant gene function will become possible by various functional analyses using transgenic and protein expression approaches.

The human whole ORFeome project is already ongoing. Arabidopsis is a model plant, thus this will represent the first big plant ORFeome project. On completion it might be possible to start synthetic biology using the whole gene set of Arabidopsis to allow functional studies of corresponding proteomes.

Reports from MASC Subcommittees

EPigenetics and Epigenomics

Xuehua Zhong
xuehua.zhong@wisc.edu
University of Wisconsin-Madison

Robert Schmitz
schmitz@uga.edu
University of Georgia

Open Tools and Resources for Arabidopsis Researchers

Enhanced Browswe Plug-ins for Epigenomic Data Visualization.
https://github.com/bhofmei/bhofmei-jbplugins

CoGe browsers for Arabidopsis, maize and soybean - online servers for plant epigenomic data.

Conferences and Workshops

2017
International Conference on Arabidopsis Research, St. Louis, MO, June 2017 (Session on Epigenetics).

Gordont Research Conference, Epigenetics. Holderness, NH, August 2017

Plant & Animal Genomes Conference, San Diego, CA, January 2017 (Session on Epigenomics of Plants International Consortium)

40th New Phytologist Symposium – Plant Epigenetics, Vienna, Austria, June 2017

2018

Plant & Animal Genomes Conference, San Diego, CA, January 2018 (Session on Epigenomics of Plants International Consortium)

Cold Spring Harbor Asia meeting on Chromatin, Epigenetics & Transcription, Suzhou, China, April 2018

(Section on Epigenetic inheritance and Plant Epigenetics)

Gordont Research Conference, Plant Molecular Biology. Holderness, NH, June 2018 (Session on Epigenetics)

Midwest Chromatin & Epigenetics meeting, West Lafayette, IN, June 2018 (Session on Plant Epigenetics)

Publications


Figure 3: A view of the ontology hierarchy around Trait Ontology term plant height (TO:0000207). Crop Ontology (CO) terms for plant height from the lentil, wheat, rice and cassava ontologies are mapped to the Trait Ontology term for data integration.


Plant Genomics Databases - Methods and Protocols | Aalt-University of Georgia

Robert Schmitz
schmitz@uga.edu

Epilepsia, 2018


Plant Genomics Databases - Methods and Protocols | Aalt-University of Georgia

Robert Schmitz
schmitz@uga.edu

Epilepsia, 2018


Plant Genomics Databases - Methods and Protocols | Aalt-University of Georgia

Robert Schmitz
schmitz@uga.edu

Epilepsia, 2018

Table 1. List of available ORF Resources. Revised numbers are shown in Red.

Table 1a. List of available ORF Resources. Revised numbers are shown in Red.

Selected Publications


Genome Biology Special issue on Plant Epigenomics included 30 articles edited by Claudia Kohler and Nathan Springer

https://www.biomedcentral.com/collections/plantepigennomics
Metabolomics

http://Arabidopsisresearch.org/index.php/ subcommittees/metabolomics

Kazuki Saito (chair) and Wolfram Weckwerth (co-chair) with contributions from subcommittee members and the wider Arabidopsis community

Open Tools and Resources for Arabidopsis Researchers

www.masc-metabolomics.org
Metabolomics subcommittee website
https://www.arabidopsis.org/portsals/metabolome/index.jsp
TAIR metabolomics Resources

http://prime.psc.riken.jp/
PRIMe, a web-based service for metabolomics, containing computational metabolomics toolbox (MS-DIAL, MS-FINDER, etc), metabolic datasets (DROP Met), metabolic modeling system (PASMet), metabolic characterization of 50 Arabidopsis mutants and the database as a functional genomics tool (MeKO), standard compounds (MetFIRD), Arabidopsis metabolome expression databases (AtMetExpress development, AtMetExpress 20 ecotypes) and a collection of literature and in-house MS spectra data (ReSpect for Ptohyochemicals).

http://gmd.mpimp-golm.mpg.de/
Golm Metabolome Database facilitates the search for and dissemination of reference mass spectra from biologically active metabolites quantified using gas chromatography (GC) coupled to mass spectrometry (MS). www.plantmetabolomics.org A web portal of Arabidopsis Metabolomics Consortium that contains data from an NSF-2010 funded project concerning metabolite profiling of a set of metabolic mutants. http://mncd.nfrram.wisc.edu/ The Madison-Qingdao metabolomics consortium database has emphasis on Arabidopsis and contains both NMR and MS data of metabolites.

http://www.ebi.ac.uk/metabolights
Metabolights, a database for metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments and is a collaborative multi-laboratory effort including groups specialising in plant metabolism.

Recent activities of Subcommittee members.

Since metabolomics is an important component of Arabidopsis omics, a continuous goal of this subcommittee will be to promote metabolomics research of Arabidopsis leading to functional genomics and systems biology. Full integration of Arabidopsis-based metabolomics research with the activities of the Metabolomics Society (http://www.metabolomicsociety.org/) is also an important goal of this subcommittee. Several members of the subcommittee are involved in drawing up the plant biology specific documentation for the Metabolomics Society. In addition, this committee will aim to establish a mechanism that allows the dissemination of metabolomics datasets to the wider Arabidopsis community and encourage and facilitate initiatives for the integration of metabolic datasets with other omic datasets. This will involve depositing metabolomic data in a usable format for data integration.

Future Activities of the Subcommittee.

To realize the goals, we aimed to establish the subcommittee website www.masc-metabolomics.org for more efficient exchange of information and dissemination of the subcommittee’s activity. The subcommittee discussion will be taken not only in the occasion of ICAR annual meeting but also in the occasions of several other metabolomics-related meetings, where the subcommittee members can join. The webinterface will provide user with a user-friendly tool to search for Arabidopsis thaliana metabolomics data in available databases. In addition, the people in plant metabolomics community actively provide open tools and resources useful for Arabidopsis researchers as indicated above.

Conferences, Workshops and Training events

2017/6/26-29 Metabolomics 2017, Brisbane, Australia
2017/7/17-19 Forsdorin Research Conference, Plant Metabolic Engineering, Waterville-Valley, NI, US
2017/7/16-20 The 4th International Conference on Plant Metabolism (ICPM 2017), Dalian, China
2018/6/18-22 MLI Metabolomics Workshop, Metabolomics Center, University of Missouri, US
2018/7/8-13 The 23rd International Symposium on Plant Lipids, Yokohama, Japan

Selected Publications


Proteomics

http://Arabidopsisresearch.org/index.php/ subcommittees/proteomics

http://www.masc-proteomics.org/
Joshua Heazlewood (chair)

Open Tools and Resources for Arabidopsis Researchers

Pep2Pro - proteo-genomic resource http://gcz.pep2pro.uzh.ch/ by Baerenfaller
ProMEX - mass spectral resource http://promex.pshl.uni-hohenheim.de/promex/ by Wieshoop and Weckwerth
GeneMap - 2-DE proteomic repository https://gelmap.de/projects-arabidopsis/ by Braun

APP - targeted proteomics (SRM) tool http://www.plantenergy.uwa.edu.au/APP/ by Taylor and Millar

SUBA - subcellular database http://suba.live/ by Millar

PPDB - plant protein database http://ppdb.tc.cornell.edu/ by van Wijk

AT_CHLORO - plastid proteomic resource http://alt-chloro.prabi.fr/at_chloro/ by Rolland and Ferro

Plant PTS1 Protein Prediction- http://ipp.gobics.de/ by Reumann

PhosPhat - phosphoproteome database http://phosphat.uni-hohenheim.de/ by Schulze

P3DB - plant phosphoproteome database http://p3db.org/ by Theilen

MASCP Gator - proteomics aggregation portal http://gator.masc-proteomics.org/ by MASCP

1001 Proteomes - non-synonomous SNPs from Arabidopsis natural variants http://1001proteomes.masc-proteomics.org/ by Heazlewood
Recent activities of Subcommittee members.

A) The subcommittee members maintain an array of Arabidopsis specific proteomic repositories. These resources currently contribute to information in the Arabidopsis Information Portal (AIP).

B) The 1001 Proteomes portal provides pre-computed nSNP data from the sequenced accessions. Data from this portal are now available in ePlant.

C) Members have ongoing interests in applying proteomic approaches in Arabidopsis to important crop species. A number of the on-line proteomic resources also provide proteomic datasets for agricultural relevant species.

D) Subcommittee members maintain extensive resources in the area of protein function in Arabidopsis, and it is expected that this information will be coordinated with the IAC.

E) Subcommittee members are involved with the initiative on Multi-Organism Proteomes (iMOP) as part of the Human Proteome Organization (HUPO) and are active members of the International Plant Proteomics Organization (INPPO). As well as many serving as active members of the International Plant Proteomics Initiative on Multi-Organism Proteomes (iMOP) as part of INPPO.

Future Activities of the Subcommittee.

A) Maintain and develop new resources for Arabidopsis focusing on protein function and proteomics.

B) Demonstrate applicability of 1001 proteome data to the research community. Update the data for the recently released accessions.

D) Continue to develop proteomic Apps for the Arabidopsis Information Portal.

E) Ensure attendance and involvement in future INPPO and HUPO activities.

F) Maintain an active Arabidopsis proteomics subcommittee (http://www.masc-proteomics.org)

Publications


Systems and Synthetic Biology

http://arabidopsisresearch.org/index.php/subcommittees/systems-biology

Siobhan Brady, UC Davis sbrady@ucdavis.edu
Malcolm Bennet, University of Nottingham Malcolm.Bennett@nottingham.ac.uk,
Gabriel Krouk, CNRS gkrouk@car.tn
Nicola Paton, Earlham Institute Nicola.Paton@earlham.ac.uk
Rodrigo Gutierrez, P Universidad Catolica de Chile rutierrez@bio.ucl
Pascal Falter-Braun, Helmholtz Zentrum Muenchen pascal.falter-braun@helmholtz-muenchen.de
Open Tools and Resources for Arabidopsis Researchers

GB1.0 A Digital Toolbox for Plant Synthetic Biology https://gbi1oning.opv.es

LOOP A simple, open-source system for recursive fabrication of DNA circuits https://www.biosci.org/content/early/2018/01/15/247593

OpenMTA. A simple, standardized legal tool that enables individuals and organizations to share their materials on an open basis. Developed as a collaborative effort between the BioBricks Foundation and the OpenPlant Initiative, with input from researchers, technology transfer professionals, social scientists, lawyers, and other stakeholders from across the globe, the OpenMTA reflects the values of open communities and the practical realities of technology transfer. https://www.openplant.org/opemtta/


Conferences, Workshops and Training events

Conferences and Workshops

Practical Synthetic Biology. Pretoria, South Africa, February 2017
Synthetic Biology for Natural Products. Cancun, Mexico, May 2017
SB7.0 Singapore, June 2017
Gordon Research Conference, Plant Metabolic Engineering – Plant Engineering in the Synthetic Biology Era: Waterville Valley, NH, July 2017
Open Plant. Cambridge, UK, July 2017
Genome Science/Genome10K. Norwich, UK, August 2017
Natural Products and Synthetic Biology: Paths and Pathways. Olympic Valley, California USA, January 2018
Molecular Biosystems, Puerto Varas, Chile, September 23-26, 2017
1st Latin American Workshop and Conference on Systems Biology, Mexico City, Mexico, May 2-5, 2017
Systems Biology: Networks, Cold Spring Harbor, New York, USA, March 14-18, 2017
International Conference on Arabidopsis Research, St. Louis, Missouri, USA, June 19-23, 2017, session on Modeling, Gene Regulation, Systems, Quantitative and Computational Biology.
Synbiosys Summer School, Copenhagen Plant Sciences Centre, Denmark, August 2017
The Synthetic and Systems Biology Summer School (SSBSS) Robinson College, University of Cambridge, UK, July 2017
Second International Plant Biology Course (Santiago, Chile), 2017.

Future Conferences or Workshops:

EMBO Workshop: Integrating Systems Biology, April 15-17, 2018; with prominent plant talks and Sorina Popescu and as organizers Pascal Falter-Braun, Luis Serrano and Sandra Orchard.

JPBS - First International Plant Systems Biology Meeting; September 10-14, 2018; organized by Gabriel Krouk, Pascal Falter-Braun, Siobhan Brady, Gloria Coruzzi and Rodrigo Gutierrez

SEB Interdisciplinary Sessions: The 2018 Annual Meeting of the Society for Experimental Biology will be held in Florence on the 3rd-6th July 2018. This will feature many parallel sessions including interdisciplinary sessions on “Shaping root architecture - from nutrient sensing and tropism to systemic signals and decision making” organised by Stefan Kepinski and Julia Davis.

Selections Published


Additional Information

JPBS was a direct result of activities and leadership efforts on behalf of the Systems and Synthetic Biology Subcommittee.
Arabidopsis Community Projects and Resources

The Arabidopsis community has always been very open, so today researchers and funding bodies can look back on more than 20 years of strong international collaboration and data sharing. The efforts of the Arabidopsis community have always been guided by long term plans, which have led to the establishment of many Arabidopsis community projects and resources:

The Arabidopsis genome research project (1990-2001) led to the completion of the Arabidopsis genome. During this decade two out of three stock and resource centers ABRC (Arabidopsis Biological Resource Center, US) and NASC (Nottingham Arabidopsis Stock Center, UK) were founded.

The Multinational Coordinated Arabidopsis Functional Genomics Project (2002-2011) led to the functional annotation of most of the Arabidopsis genes, in that at least providing expression data for them. Alongside, The Arabidopsis Information Resource (TAIR) was founded in 2001 to meet the needs of the growing Arabidopsis research community.

From Bench to Bountiful Harvests (2012-2021) aims to obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, to be able to build a predictive model of an Arabidopsis plant.

The directors of Arabidopsis community projects and resources have been contributing to the MASC reports for several years, by presenting their respective goals, progress and news. Since 2014, general plant projects and resources have also been included, reflecting the growing connections between researchers focusing on different plant species.

Resource and Stock Centers

Arabidopsis Biological Resource Center (ABRC) (page 24)

Nottingham Arabidopsis Stock Centre (uNASC) (page 25)

RIKEN BioResource Center (BRC) (page 26)

The Arabidopsis Information Resource (TAIR) (page 26)

International Arabidopsis Informatics Consortium (IAIC) (page 28)

Plant Projects and Resources with Strong Participation of the Arabidopsis Community

Bio-Analytic Resource for Plant Biology (BAR) (page 29)

International Plant Phenotyping Resources (page 31)

Gramene (page 32)

Besides the above listed projects and resources, there are many other international and multinational initiatives with major contributions from Arabidopsis researchers:

- The 1001 Arabidopsis Genomes Project
  www.1001genomes.org

- The Epigenomics of Plants International Consortium EPIC;
  www.plant-epigenome.org

- The Plant and Microbial Metabolomics Resource
  http://metnetdb.org/PMR/

- The SUBA4: The SubCellular Proteomic Database
  http://suba.plantenergy.uwa.edu.au/

- 1001 Proteomes
  http://1001proteomes.masc-proteomics.org/

- AraGWAS
  https://aragwas/1001genomes.org/

- GENIUS machine learning algorithm to infer functional gene networks
  http://networks.bio.puc.cl/genius

- Arabidopsis hormone database 2.0
  http://ahd.pku.edu.cn/

- PlantGSEA: a gene set enrichment analysis
  http://structuralbiology.cau.edu.cn/PlantGSEA/

- Arabidopsis Protein Phosphorylation Site Database
  http://phosphat.uni-hohenheim.de/index.html

- 3DCellAtlas
  http://www.georgebassellab.com/3d-cell-atlas/)
Reports from MASC Resources

Resource and Stock Centers

The Arabidopsis Biological Resource Center (ABRC)

www.abrc.osu.edu

David Somers, somers.24@osu.edu, ABRC Director (since April 2018)
Jelena Brkljacic, brkljacic.1@osu.edu, ABRC Associate Director
Keith Slotkin, slotkin.2@osu.edu, ABRC Director (until April 2018)

Open Tools and Resources for Arabidopsis Researchers

ABRC provides seed, clones, vectors, host strains, antibodies, cell lines and education resources for species ranging from Arabidopsis thaliana and other Brassica species to maize and other crops.

Recent activities of your project or resource.

We are pleased to announce that we secured additional support for our operation in 2017 through an NSF RAPID funding program, adding to the current CSBR NSF support (April 2016 – March 2019).

Last year we expanded and diversified the ABRC’s collection. Within Arabidopsis, we acquired a number of cutting-edge resources such as a set of HALO-tagged transcription factors (TFs) for identification of DNA-binding regions, Cy2H vectors and host strains for high-throughput yeast two hybrid assays by deep sequencing, and a comprehensive toolkit comprising 162 vectors for advanced genome engineering via CRISPR/Cas9 mutagenesis.

In addition to Arabidopsis resources, the ABRC has continued to diversify its collection through the acquisition of a soybean TF clone set, seeds from diverse Brassica species, and a comprehensive toolkit for CRISPR/Cas9 across monocots and dicots.

The ABRC has continued to expand and enhance our education and outreach program, reaching out to larger and more diverse audiences. Our education kits using Arabidopsis continue to be highly ordered and most of the kits are available free of charge. Two education papers were published (see Additional Information) and a revamped education website is about to be released (see Future Activities), making this a very good year for our education and outreach program.

Planned future activities of your project or resource.

For the past 17 years, The Arabidopsis Information Resource (TAIR) has provided services for searching and ordering ABRC stocks. For the past two years, the ABRC has been collaborating with the College of Arts and Sciences Technology Services (ASC Tech) at Ohio State to design an independent ABRC database and ordering system. The ABRC database provides superior searching capabilities and access to complete stock information, including quality control (QC) and additional features. In addition, the new system is much more flexible and provides full access to a growing number of the ABRC’s non-Arabidopsis resources. The ABRC database will be released for testing in the spring of 2018. The ABRC stock ordering will still be available through TAIR during the testing stage. After successful testing of the new database, ABRC stocks will only be available for ordering through our system, and no longer through TAIR.

We have recently received a donation of Brassica species as part of a collection of “Top 20 Brassicaceae” sequenced through the Brassicales Map Alignment Project (BMAP) sponsored by the U.S. Department of Energy Joint Genome Institute (DOE JGI). The propagation and distribution of this resource is planned for 2018.

More bioenergy-related and other Brassica species, including 100 Brassica napus stocks and a GWAS population of ~500 sequenced accessions of Boechera stricta, are expected in the near future. The ABRC plans to continue serving a wide Brassica community by providing stock propagation, maintenance and QC. In addition, our new database with a user-friendly online search tool will allow users to search exclusively for Brassica stocks, making these resources much easier to find and order.

Conferences, Workshops and Training events

The ABRC shared a booth with The Nottingham Arabidopsis Stock Centre (NASC) and participated in the bioinformatics resources workshop at the International Conference on Arabidopsis Research (ICAR) in St. Louis in 2017. The ABRC also had a booth at the annual Plant Biology meeting of the American Society of Plant Biologists (ASPB) in Hawaii. In 2018, ABRC participated in the Plant and Animal Genome conference in San Diego, by presenting a talk focused on the ABRC education program and by promoting donation and distribution of other species’ resources. Current conference plans include ICAR, ASPB and the International Plant Molecular Biology (IPMB) meeting in the summer of 2018.

Additional Information


We are very grateful to Dr. Keith Slotkin for his service as an ABRC Director and welcome Dr. David Somers, an esteemed OSU Professor, as our new Director.

The Nottingham Arabidopsis Stock Centre (uNASC)

http://www.Arabidopsis.info

Sean May
Director
Sean.May@nottingham.ac.uk

Marcus Castellanos-Uribe
Operations Manager.
marco.castellanos@nottingham.ac.uk

Another productive year sending over 150,000 tubes of seed to the worldwide plant community sees a slight change in the international profile of our users. Out of a total of 43 countries ordering from NASC during 2017, the top five countries (in order by individual stock numbers) are China (No.1 for the third year in a row), the UK, Australia (first time in the top 5), Germany, and France.

For entertainment purposes, we shared (@NascArabidopsis - Jan 2018) a map of locations in China and the UK (by institute) that had ordered seed from us in 2017.

Of course, our broader catalogue access maps for all countries can always be found at http://clustrmaps.com/map/Arabidopsis.info

For up-to-date details on stock donations or anything else that you wish to know, please do visit the NASC site, or contact curators@arabidopsis.info at any time.

If we (NASC and ABRC) can save you time, effort and promote your research impact by distributing seed on your behalf to the wider plant community then please do holler (or email) - don’t wait for us to come to you.

See you in Turku!
In addition to performing term enrichment for Arabidopsis, the tool can also be used to perform enrichment on 9 other species included in the PANTHER database: Brachypodium, Chlamydomonas, soybean, rice, Physcomitrella, poplar, tomato, sorghum and grape.

Genome and Gene Function Curation

A major goal of TAIR curation is to present the most up to date and accurate picture of the Arabidopsis genome. All gene models, assignments, computational descriptions and sequences in TAIR have been updated to Arabidopsis 11. In addition, we have updated and added thousands of T-DNA polymorphisms using genome coordinates and locus assignments provided by the Ecker Lab. Many TAIR tools, like gene descriptions and sequences, limit their data to recent updates and now use Arabidopsis 11 as the underlying data source and the remaining tools will follow. The addition of new gene models has increased the pool of ‘unknown’ or ‘unannotated’ genes slightly, as reflected in the updated genome snapshot (http://www.arabidopsis.org/portals/genAnnotation/genesnapshot.jsp).

In the updated genome we have added or updated descriptions for 147 alleles, and added or updated 147 alleles, and added or updated 662 new gene symbols to TAIR and added or updated locus assignments provided by the Ecker Lab. Many TAIR tools use gene symbols and names, links between genes and publications, and updated gene descriptions added to TAIR through 12/11/2016. The most current data and tools are available through the website, which is updated on a weekly basis. Anyone can access a limited number of pages per month; unlimited access requires a subscription. The TAIR website also provides current data in the form of quarterly releases (http://www.arabidopsis.org/download/index-auto.jsp?dir=download_files/Subscriber_Database_Releases) and can request custom data sets via our helpdesk (curator@arabidopsis.org).

Outreach: Workshops, Conferences, Presentations and Social Media

In the past year, TAIR has pioneered efforts aimed at increasing community engagement with curation, training in data management and publishing at UC Berkeley with curators from MaizeGDB. Slides from that presentation are available at http://bit.ly/2prjRjS.

TAIR is also a member of the newly formed AgBiodata consortium of Agricultural Databases (www.agbiodata.org), which aims to develop and promote standards and best practices for the acquisition, display and retrieval of genetic, genomic and breeding data. TAIR staff presented at ICAR 2017 (St. Louis, MO, USA), ASPB 2017 (Honolulu, HI, USA), and PAG 2018 (San Diego, CA, USA). TAIR curators will attend ICAR 2018 in Turku, Finland and ASPB 2018 in Montreal, Canada.

TAIR curators are also available to assist the community through our HelpDesk (curator@arabidopsis.org), and through social media on Facebook (https://www.facebook.com/tairnews), Twitter (https://twitter.com/tair_news), and YouTube (https://www.youtube.com/user/TAIRInfo).

Data Releases

In accordance with our data sharing policy, TAIR continues to publish year-old data in the form of quarterly data releases (http://www.arabidopsis.org/download/index-auto.jsp?dir=download_files/Public_Data_Releases). These data are freely available and distributed for reuse under the CC-BY4.0 license. They include all GO and PO annotations, gene symbols and names, links between genes and publications, and updated gene descriptions added to TAIR through 12/11/2016. The most current data and tools are available through the website, which is updated on a weekly basis. Anyone can access a limited number of pages per month; unlimited access requires a subscription. The TAIR website also provides current data in the form of quarterly releases (http://www.arabidopsis.org/download/index-auto.jsp?dir=download_files/Subscriber_Database_Releases) and can request custom data sets via our helpdesk (curator@arabidopsis.org).
New User Guide

We published the first major revision of our chapter in Current Protocols in Bioinformatics since 2010. Many sections received significant updates and new protocols were added including: GO Term Enrichment, Gene List Analysis with Bulk Tools, How to submit GO/PO annotations using TAIR’s Online Annotation Submission Tool, and Using the Recently Added Literature Browser. The guide is available online from Current Protocols (doi: 10.1002/cpbi.36; subscription required) or in draft form from TAIR (http://bit.ly/2Ga2w6F).

Publications


International Arabidopsis Informatics Consortium (IAIC)

Blake C. Meyers
IAIC Director, BMeyers@danforthcenter.org,
The Donald Danforth Plant Science Center
Joanna D. Friesner
IAIC Assistant, jdfriesner@ucdavis.edu,
North American Arabidopsis Steering Committee

Open Tools and Resources for Arabidopsis Researchers

The IAIC was formed in 2010 to facilitate a coordinated global Arabidopsis informatics effort to maintain and explore large-scale and advanced plant biology while creating novel opportunities for research and education and strengthening international collaborations. The primary accomplishment of IAIC with respect to globally-available resources was to facilitate the collaborative effort to establish and fund a new web-based portal, ‘Araport’, for Arabidopsis information and digital resources for the global plant biology community via NSF Award #1262414; AII Development: The Arabidopsis Information Portal, (www.nsf.gov/awardsearch/showAward?AWD_ID=1262414)

Araport enables biologists to navigate from the Arabidopsis thaliana Col-0 reference genome sequence to its associated annotation, including gene structure, gene expression, protein function, and interaction networks. Araport offers a single interface through which to access a wide range of Arabidopsis information. Araport will grow through contributions of other labs in the form of modules: data, computation, and visualization tools. (https://www.araport.org/about)

Recent activities of your project or resource.

Recent IAIC efforts have focused convening relevant attendees in a workshop that will assess the current status of Arabidopsis informatics and the needs and wishes of the Arabidopsis community. Looking forward to the next 5-10 years, The Future of Arabidopsis Bioinformatics workshop will build on the project’s previous success in enabling the establishment of ‘Araport’, the Arabidopsis community information resource funded by NSF, which has developed into a well-established portal with a broad range of data sets and functionalities. During the 4+ years since Araport went online the research community continued to generate increasing amounts of data that are challenging to store, manipulate and disseminate.

Conference, Workshops and Training events

The project’s PI and Araport/IAIC efforts entitled “Arapidopsis Informatics” at the 2018 Plant and Animal Genome (PAG) conference.

Publications

Work was completed on a “mega-app” from the BAR for Arabidopsis. ePlant is accessible from the Araport.org homepage, and from the Bio-Analytic Resource at http://bar.utoronto.ca/eplant.

The Bio-Analytic Resource is a collection of user-friendly web-based tools for working with functional genomics and other data for hypothesis generation and confirmation. Most are designed with the plant (mainly Arabidopsis) researcher in mind. Data sets include:

* 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.
* 70,944 predicted protein-protein interactions plus 36,352 documented PPIs (rice interologs also available!) and ~2.8 million protein-DNA interactions.
* 29,180 predicted protein tertiary structures and experimentally-determined structures for 402 Arabidopsis proteins.
* Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee’s site at 1001proteomes.masc-proteomics.org.
* Documented subcellular localizations for 9.3k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Recent activities of your project or resource.

Work was completed on a “mega-app” from the BAR for Araport.org, ePlant, and a publication came out in the Plant Cell describing it (Waese et al., 2017). ePlant is a zoomable user interface for exploring data across 12 orders of magnitude, from the kilometre scale down to the nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested, open source tool. ePlant is accessible from the Araport.org homepage, and from the Bio-Analytic Resource at http://bar.utoronto.ca/eplant.
International Plant Phenotyping Resources
Roland Pienuschka
Julich Plant Phenotyping Centre
r.pienuchka@ie.juelich.de

International Plant Phenotyping Network
IPPN http://www.plant-phenotyping.org/
IPPN is a non-profit association that represents the major plant phenotyping centers worldwide. The association aims to provide all relevant information about plant phenotyping. The goal is to increase the visibility and impact of plant phenotyping and enable cooperation through fostering communication between stakeholders in academia, industry, government, and the public. Within the last year, IPPN has established its basic operation by setting up a number of working groups on relevant topics, organizing workshops, meetings, and international symposia.

The next IPPN Symposium will be held in October 2-5th in Adelaide Australia (http://www.ippn2018.com.au).

With the increasing development of a global plant phenotyping community it is also essential to extend the IPPN membership base by implementing and fostering close cooperation between academia and industry partners to drive and develop innovation that delivers to academic and industry users. Thus, the IPPN General Assembly has decided to include members from industry and by mid-2018, members from industry can join the association.

EMPHASIS
https://emphasiss2020.plant-phenotyping.eu/

The European Strategy Forum for Research Infrastructure (ESRF) has identified “Plant Phenotyping” as a priority for the European research area and the project EMPHASIS has been listed on the ESFRI Roadmap as an infrastructure project to develop and implement a pan-European plant phenotyping infrastructure.

The EMPHASIS project (European Infrastructure for Multi-Scale Plant Phenotyping and Simulation for Food Security in a Changing Climate) is coordinated by the Institute of Bio- and Geosciences, IBG-2: Plant Sciences at the Forschungszentrum Jülich. In 2017 EMPHASIS has started the Preparatory Phase which is a 4-year H2020 funded project. Within the Preparatory Phase, EMPHASIS will develop a business plan embedded in a sound legal framework for a long-term operation of EMPHASIS. One of the major activities in preparation of the business plan consisted in a mapping of the plant phenotyping landscape in Europe to foster the information exchange about infrastructures, major stakeholders, projects and networks. Additionally, close interaction between national plant phenotyping communities was established and about 23 national communities have already mandated a representative, to form a link to EMPHASIS by contributing to the so-called “Support Group” and shape the development of EMPHASIS.

EMPHASIS has also initiated a close interaction with the ESFRI project AnaEE (https://www.anaee.com) which offers access to experimental and modelling platforms as well as data on terrestrial and aquatic ecosystems. The activities of both projects and areas of cooperation have been outlined in a recent publication by: Roy et al (2017) European infrastructures for sustainable agriculture, Nature Plants 3, 756-758.

European Plant Phenotyping Network 2020

The EPPN2020 is a H2020 funded research infrastructure project that will provide European public and private scientific sectors with access to a wide range of state-of-the-art plant phenotyping facilities, techniques and methods and help lay the foundations of generic genomic resources available for crop improvement that represents a major scientific challenge for this coming decade. EPPN2020 specifically aims to facilitate the community progressing across the whole phenotyping pipeline, involving sensors and imaging techniques, data analysis in relation to environmental conditions, data organization and storage, data interpretation in a biological context and meta-analyses of experiments carried out on different organisms at different scales of plant organization.

Specifically EPPN2020 includes:

i) access to 31 key plant phenotyping installations;
ii) joint research activities to develop: novel technologies and methods for environmental and plant measurements, tools for statistical analysis and a European plant phenotyping information systems;
iii) networking activities to increase integration between phenotyping facilities and users within and outside of EPPN2020.

Within the first year, EPPN2020 initiated a first call for access, which resulted in 33 application. The second call for access was issued in early February 2018 with an application deadline in June 2018. New calls will be released every 6 months.
Gramene: A comparative genomics and pathways resource for plants

Marcela Karey, Tello-Ruiz (Project Manager)
mkmonaco.cshl@gmail.com
Doreen Ware (PI)
http://www.gramene.org

Open Tools and Resources for Arabidopsis Researchers

Gramene provides open access to comparative genomics and pathways data, and analysis tools. We host 53 reference genomes including Arabidopsis thaliana, A. lyrata, Brassicas, sugar beet, Solanaceae, cereals, fruits, and basal plants, each displaying functional gene annotations, genetic and structural variation, gene expression, gene-trees with orthologous and paralogous gene classification, whole-genome alignments, and synteny maps. In addition, we host 264 pathways curated in rice and inferred in 74 additional plant species (including the above) by orthology projection. Its integrated search capabilities and interactive views facilitate visualizing gene features, gene neighborhoods, phylogenetic trees, gene expression profiles, pathways, and cross-references. Our tools support comparative analyses of our data as well as data brought in by our users, and include a BLAST/BLAT sequence aligner, a sequence assembly converter, a genetic variant effect predictor, an advanced BioMart-based query interface, data analysis and visualization of OMICS data, and multi-species pathway comparisons. Together these comparative data and resources enable powerful cross-species comparisons.

Recent activities of your project or resource.

BACKGROUND - The Gramene database (http://www.gramene.org) is an integrated resource for comparative genome and functional analysis in plants. The database provides the Arabidopsis community, agricultural researchers, and plant breeders access to reference genomes, comparative resources including whole-genome DNA alignments and protein-based gene trees for 53 crops and model species including A. thaliana, A. lyrata, Brassicas, sugar beet, Solanaceae, cereals, fruits, and lower plants. In addition to 264 pathways curated in rice and inferred in 74 additional plant species (including the above), thus enabling powerful cross-species comparisons.

The Gramene project has had five data releases since 2017, of which the above), thus enabling powerful cross-species comparisons.

BACKGROUND - The Arabidopsis thaliana (dicot model crop) and Orzyza sativa (monocot staple food crop; 44 alignments). Currently, our synteny collection includes synteny maps for A. thaliana against 14 species: A. lyrata, cucumber, soybean, cotton, sunflower, lupin, cassava, tobacco, Japonica rice, common bean, poplar, peach, sorghum, and grape. SNP and structural diversity data, including individual genotypes, are available for A. thaliana, and another 11 species. The SNPs are displayed in the context of gene annotation and protein domain structure, along with predicted functional consequences (e.g. missense variant). Gramene hosts several variation data sets for Arabidopsis.

In the past year, we included the full data set (12.9 M SNPs) from the 1001 Arabidopsis Genomes Project, and linked the variants in 95 inbred lines to 107 existing phenotypes from the GWAS study by Atwell et al (2010). Genotypes from 1,179 strains from the 2012 study by Horton and collaborators using the Affymetrix 250k Arabidopsis SNP chip, and an updated data set produced through a BBSRC funded multi-institutional collaboration involving resequencing 18 Arabidopsis lines published by Clark et al in 2007 were obsoleted and archived.

For supporting Arabidopsis researchers, the annotation data hosted at Gramene was integrated with the automated GWAS workflow provided by SciApps (collaboration with the CyVerse project), a ready-to-use workflow platform, where a list of nearby genes can be automatically retrieved for the most significant associated loci.

In collaboration with the Expression Atlas project (EMBL-EBI), we provide experimental baseline expression data for 23 plant species including A. thaliana (185 experiments in various ecotypes, tissues and developmental stages) and A. lyrata (3 experiments in 3 tissues), through our Ensembl genome browser and Plant Reactome pathways interfaces.

In addition, we provide direct links to differential gene expression data on the Ensembl website for 519 experiments in A. thaliana, and 1 in A. lyrata, among a total of 720 experiments in 26 plant species. Through Gramene’s Plant Reactome, we now offer 264 curated rice pathways, as well as orthology-based pathway projections to 74 plant species including both, A. thaliana and A. lyrata.

In the past year, our integrated search database and modern user interface (http://search.gramene.org) was greatly enhanced to leverage the diverse annotations above described to facilitate finding genes through selecting auto-suggested filters with interactive views of the results. We now offer detailed views for search results featuring genomic location, gene trees and homologs lists, gene expression, and cross-references, while a pathways view is in development.

Our Blast and BioMart interfaces enable complex queries of sequence, annotation, homology, and variation data. The genomes portal of the Gramene project is developed on the Ensembl infrastructure and in collaboration with the Ensembl Genomes project (EMBL-EBI). The pathways portal of the project is the Plant Reactome (http://plantreactome.gramene.org). The project supports application programming interfaces to access the data, in addition to the graphical user interface, which supports visual displays, and download of the data in standardized formats for the genome and pathway data, as well as high-resolution, publication-ready, image files.

As we aim to reach out to a larger audience, we continue our monthly webinar series and invite the arab-gen@net.bio.net mailing list whenever topics relevant to the Arabidopsis community are covered. Recorded webinars are available for public view from Gramene’s YouTube channel https://www.youtube.com/channel/UCmtnqM20XMcCuNu4ACuQ1w

Planned future activities

We will continue with activities similar as those described above, and which aim to: 1) improve and expand our reference data collection of plant genomes and standardized comparative annotations, 2) enrich our Plant Reactome pathways data resource, 3) integrate visualization and analysis tools for exploring emerging genomic and pathway data, and 4) transform the community through communication and training opportunities.

Conferences, Workshops and Training events

In the past year, Gramene participated in 16 scientific conferences to present talks, posters, training workshops, hand out brochures and other educational materials. We organized community outreach booths for members of the AgBioData consortium at the Plant and Animal Genomes, and Plant Biology conferences. Continued to broadcast live webinars, and made the video-recordings available in Gramene’s YouTube channel.

In collaboration with CyVerse, we organized a bioinformatics workshop at the CSHL Plant Genomes and Biotechnology meeting and together with the MaizeCode project, organized a maize annotation jamboree. Other plant ecology/phytogenetics geared to K-12 students and faculty included a STEM summer camp, a DNA workshop for Science Olympics participants, and hands-on activities to celebrate Fascination of Plants Day. We plan on continuing our outreach, education and training activities in the next year.
Multinational Arabidopsis

Steering Committee
MASC Annual Report 2017/18

Country Highlights
- Australia: SUBA: The Subcellular Proteomics Database http://suba.lives/ 
- Belgium: PLAZA is an access point for plant comparative genomics centralizing genomic data. https://publiclines.versailles.inra.fr/plaza/
- Brazil: Desousa et al. (2017) BAK1 is involved in Arabidopsis-induced inhibition of root cell expansion. Plant Sci. doi: 10.1371/journal.pgen.1007053
- Canada: Continued development of BARI resource http://bari.alberta.ca
- Chile: GENUS is a user-friendly web-server that uses a novel machine learning algorithm to infer functional gene networks http://metworks.bio.pac.genes.ca
- China: Hosting ICAR2019 in Wuhan, June 16-21 2019
- Finland: Hosting 29th ICAR in Turku http://ar2018.arabidopsisresearch.org/
- France: The Versailles Arabidopsis Stock Center provides seeds useful to the international research community. http://publiclines.versailles.inra.fr/
- Germany: 5001 Genecode Project http://5001genes.org/
- Israel: Center for simulating and analyzing effects of climate change on whole plant functional trait phytoping: http://www.plant-dics.com/
- Japan: Plant Promoter Database http://ppdb.agr.gifu-u.ac.jp/ppdb/cgi-bin/index.cgi
- Norway: Eide et al. (2017) Endosperm-based hybridization barriers explain the pattern of gene flow between Arabidopsis lyrata and Arabidopsis thaliana in Central Europe. 10.1105/tpm.18.15123114
- Spain: 80 grants to support Arabidopsis research from the Spanish Ministry of Economy, Industry and Competitiveness
- Switzerland: 5.5-year joint project for Japan and Switzerland on polyploid Arabidopsis and crop species funded by Japan Science and Technology Agency
- United Kingdom: European Arabidopsis Stock Centre (uMASC) is based at the University of Nottingham: http://arabidopsis.info/

Analysis of Arabidopsis Publications

Research Outlook 2017/18

The number of Arabidopsis publications featured in PubMed that include Arabidopsis in the ‘Title’ or ‘Abstract’ continues to be the most commonly mentioned plant (Figure 3). However it is likely that 2017 is the final year that this will be the case as published research that includes rice/oryza continues to grow. The growth in this area is likely driven by support for rice research in Asian countries. This mimics the continued increase in the number of Arabidopsis publications, albeit at a slower rate, from Chinese researchers and represents continued excellent support for plant science research in that area of the world (figure 5). Other growing economies such as India and Brazil show slight increases in Arabidopsis publications (Figure 4).

Elsewhere countries that historically were in the vanguard of support for Arabidopsis research have shown a variety of trends over the past 5 years. The USA has the second

Figure 3. Papers published globally with Arabidopsis, rice/oryza or com/maize in the Title/Abstract.

Figure 4. Number of Arabidopsis publications in a variety of MASC countries. We acknowledge that using this metric to measure research productivity is not perfect but remains a useful proxy.
highest number of publications which reflects the early adoption of Arabidopsis research in this country. A slowing in the number of publications over the past 10 years might be explained by a variety of reasons not investigated here in any detail but intuitively may include a saturation on the number of articles or changes in faculty recruitment and/or grant funding policies. However the number of publication remains encouragingly high.

After 10 years of growth the number of German publications shows a very small decline over the past year and perhaps indicates that they are on a similar trajectory to the USA. Although the majority of MASC countries show a plateau in the number of publications, it is encouraging that some places, such as the Netherlands and Canada show an increase. Over the next 5-10 years we will discover whether countries with currently growing publication rates will follow the trend observed in the USA and Germany.

Overall the following Country Reports suggest a positive opinion as to the value of using Arabidopsis for discovery-led science and in the pathway to translation. The breadth of available resources places the community in an excellent position to maintain high levels of outputs.

Figure 5. Number of Arabidopsis publications in China, Germany and the USA over the past decade

Research Highlights

Over the following pages we feature a selection of outstanding Arabidopsis research that has been conducted by the global community of researchers. These manuscripts include some that use the power of Arabidopsis tools for molecular and cell biology.

In addition we highlight papers that have developed resources that are available for community use. These type of studies not only demonstrate outstanding science but facilitate the continued building of the global community of resources

Importantly each of these papers are Open Access.

Towards financially viable phytoextraction and production of plant-based palladium catalysts.


Although a promising technique, phytoextraction has yet to see significant commercialisation. Major limitations include metal uptake rates and subsequent processing costs. However, it has been shown that liquid-culture-grown Arabidopsis can take up and store palladium as nanoparticles. The processed plant biomass has catalytic activity comparable to that of commercially available catalysts, creating a product of higher value than extracted bulk metal. We demonstrate that the minimum level of palladium in Arabidopsis dried tissues for catalytic activity comparable to commercially available 3% palladium-on-carbon catalysts was achieved from dried plant biomass containing between 12 and 18 g·kg⁻¹ Pd. To advance this technology, species suitable for in-field application, mustard, miscanthus, and 16 willow species and cultivars, were tested. These species were able to grow, and take up, palladium from both synthetic and mine-sourced tailings. Although levels of palladium accumulation in field-suitable species are below that required for commercially available 3% palladium-on-carbon catalysts, this study both sets the target, and is a step toward, the development of field-suitable species that can concentrate catalytically active levels of palladium. Life cycle assessment on the phytomining approaches described here indicates that the use of plants to accumulate palladium for industrial applications has the potential to decrease the overall environmental impacts associated with extracting palladium using present-day mining processes.

Figure 6. Towards financially viable phytoextraction and production of palladium catalytic activity in Arabidopsis

Heterochromatin is marked by methylation of histone 9 on histone H3 (H3K9me). A puzzling feature of H3K9me is that this modification localizes not only in promoters but also in internal regions (bodies) of silent transcription units. Despite its prevalence, the biological significance of gene-body H3K9me remains enigmatic. Here we show that H3K9me-associated removal of H3K4 monomethylation (H3K4me1) in gene bodies mediates transcriptional silencing. Mutations in an Arabidopsis H3K9 demethylase gene IBM1 induce ectopic H3K9me2 accumulation in gene bodies, with accompanying severe developmental defects. Through suppressor screening of the ibm1 induced developmental defects, we identified the LDL2 gene, which encodes a homolog of conserved H3K4 demethylases. The ldl2 mutation suppressed the developmental defects, with suppression of the ibm1 induced ectopic H3K9me2. The ectopic H3K9me2 mark directed removal of gene-body H3K4me1 and caused transcriptional repression in an LDL2-dependent manner. Furthermore, mutations of H3K9 methylases increased the level of H3K4me1 in the gene bodies of various transposable elements, and this H3K4me1 increase is a prerequisite for their transcriptional derepression. Our results uncover an unexpected role of gene-body H3K9me2/H3K4me1 dynamics as a mediator of heterochromatin silencing and epigenome differentiation.

Figure 7. Gene-body chromatin modification dynamics mediate epigenome differentiation in Arabidopsis

Topological analysis of multicellular complexity in the plant hypocotyl


Multicellularity arose as a result of adaptive advantages conferred to complex cellular assemblies. The arrangement of cells within organs endows higher-order functionality through a structure-function relationship, though the organizational properties of these multicellular configurations remain poorly understood. We investigated the topological properties of complex organ architecture by digitally capturing global cellular interactions in the plant embryonic stem (hypocotyl), and analyzing these using quantitative network analysis. This revealed the presence of coherent conduits of reduced path length across epidermal atchiblast cell files. The preferential movement of small molecules along this cell type was demonstrated using fluorescence transport assays. Both robustness and plasticity in this higher order property of atchiblast patterning was observed across diverse genetic backgrounds, and the analysis of genetic patterning mutants identified the contribution of gene activity
towards their construction. This topological analysis of multicellular structural organization reveals higher order functions for patterning and principles of complex organ construction.

Figure 8. Topological analysis of multicellular complexity in the plant hypocotyl.

Figure 9. WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. Auxin is unique among plant hormones due to its specific mechanism mediating multiple self-organizing developmental processes. Here, we used the auxin effect on the PIN polar localization in Arabidopsis thaliana roots as a proxy for the auxin feedback on the PIN polarity during canalization. We performed microarray experiments to find regulators of this process that act downstream of auxin. We identified genes that were transcriptionally regulated by auxin in an AXR3/IAA17- and ARF7/ARF19-dependent manner. Besides the known components of the PIN polarity, such as PID and PIP5K isoenzymes, a number of potential new regulators were detected, among which the WRKY23 transcription factor, which was characterized in more detail. Gain- and loss-of-function mutants confirmed a role for WRKY23 in mediating the auxin effect on the PIN polarity. Accordingly, processes requiring auxin-mediated PIN polarity rearrangements, such as vascular tissue development during leaf veination, showed a higher WRKY23 expression and required the WRKY23 activity. Our results provide initial insights into the auxin transcriptional network acting upstream of PIN polarization and, potentially, canalization-mediated plant development.

The abundance of high-quality genotype and phenotypic data for the model organism Arabidopsis thaliana enables scientists to study the genetic architecture of many complex traits at an unprecedented level of detail using genome-wide association studies (GWAS). GWAS have been a great success in A. thaliana and many SNP-trait associations have been published. With the AraGWAS Catalog (https://aragwas.1001genomes.org) we provide a publicly available, manually curated and standardized GWAS catalog for all publicly available phenotypes from the central A. thaliana phenotype repository, AraPheno. All GWAS have been recomputed on the latest imputed genotype release of the 1001 Genomes Consortium using a standardized GWAS pipeline to ensure comparability between results. The catalog includes currently 167 phenotypes and more than 222 000 SNP-trait associations with P < 10^-4, of which 1677 are significantly associated using permutation-based thresholds. The AraGWAS Catalog can be accessed via a modern web-interface and provides various features to easily access, download and visualize the results and summary statistics across GWAS.

Figure 10. The AraGWAS Catalog; a curated and standardized Arabidopsis thaliana GWAS catalog. doi: 10.1037/journal.pgen.1007177

Figure 11. CRY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. By performing ten independent screens testing a total of 36 million binary interaction combinations, and uncovering a network of 8,577 interactions among 1,453 transcription factors, we demonstrate CRY2H-seq’s improved screening capacity, efficiency, and sensitivity over those of existing technologies. The deep-coverage network resource we call AtTFIN-1 recapitulates one-third of previously reported Arabidopsis thaliana transcription factor interactions. By extending these interactions derived from diverse methods, expands the number of known plant transcription factor interactions by three-fold, and reveals previously unknown family-specific interaction module associations with plant reproductive development, root architecture, and circadian coordination.

Figure 12. Genome-wide characterization of differential transcript usage in Arabidopsis thaliana. Genome-wide characterization of differential transcript usage in Arabidopsis thaliana.

Figure 8. Topological analysis of multicellular complexity in the plant hypocotyl.

Figure 9. WRKY23 is a component of the transcriptional network mediating auxin feedback on PIN polarity. Auxin is unique among plant hormones due to its specific mechanism mediating multiple self-organizing developmental processes. Here, we used the auxin effect on the PIN polar localization in Arabidopsis thaliana roots as a proxy for the auxin feedback on the PIN polarity during canalization. We performed microarray experiments to find regulators of this process that act downstream of auxin. We identified genes that were transcriptionally regulated by auxin in an AXR3/IAA17- and ARF7/ARF19-dependent manner. Besides the known components of the PIN polarity, such as PID and PIP5K isoenzymes, a number of potential new regulators were detected, among which the WRKY23 transcription factor, which was characterized in more detail. Gain- and loss-of-function mutants confirmed a role for WRKY23 in mediating the auxin effect on the PIN polarity. Accordingly, processes requiring auxin-mediated PIN polarity rearrangements, such as vascular tissue development during leaf veination, showed a higher WRKY23 expression and required the WRKY23 activity. Our results provide initial insights into the auxin transcriptional network acting upstream of PIN polarization and, potentially, canalization-mediated plant development.

The abundance of high-quality genotype and phenotypic data for the model organism Arabidopsis thaliana enables scientists to study the genetic architecture of many complex traits at an unprecedented level of detail using genome-wide association studies (GWAS). GWAS have been a great success in A. thaliana and many SNP-trait associations have been published. With the AraGWAS Catalog (https://aragwas.1001genomes.org) we provide a publicly available, manually curated and standardized GWAS catalog for all publicly available phenotypes from the central A. thaliana phenotype repository, AraPheno. All GWAS have been recomputed on the latest imputed genotype release of the 1001 Genomes Consortium using a standardized GWAS pipeline to ensure comparability between results. The catalog includes currently 167 phenotypes and more than 222 000 SNP-trait associations with P < 10^-4, of which 1677 are significantly associated using permutation-based thresholds. The AraGWAS Catalog can be accessed via a modern web-interface and provides various features to easily access, download and visualize the results and summary statistics across GWAS.

Figure 10. The AraGWAS Catalog; a curated and standardized Arabidopsis thaliana GWAS catalog. doi: 10.1037/journal.pgen.1007177

Figure 11. CRY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. By performing ten independent screens testing a total of 36 million binary interaction combinations, and uncovering a network of 8,577 interactions among 1,453 transcription factors, we demonstrate CRY2H-seq’s improved screening capacity, efficiency, and sensitivity over those of existing technologies. The deep-coverage network resource we call AtTFIN-1 recapitulates one-third of previously reported Arabidopsis thaliana transcription factor interactions. By extending these interactions derived from diverse methods, expands the number of known plant transcription factor interactions by three-fold, and reveals previously unknown family-specific interaction module associations with plant reproductive development, root architecture, and circadian coordination.

Figure 12. Genome-wide characterization of differential transcript usage in Arabidopsis thaliana. Genome-wide characterization of differential transcript usage in Arabidopsis thaliana.
We demonstrate the power of combining large-scale untargeted metabolomics-based GWAS with time-course-derived networks both performed under different abiotic environments for identifying metabolite-gene associations, providing novel global insights into the metabolic landscape of Arabidopsis.

N-terminomics reveals control of Arabidopsis seed storage proteins and proteases by the Arg/N-end rule pathway.

The N-end rule pathway of targeted protein degradation is an important regulator of diverse processes in plants but details of its regulation regarding its influence on the proteome is lacking. To investigate the impact of the Arg/N-end rule pathway on the proteome of etiolated seedlings, we used terminal amine isotopic labelling for relative quantification of N-terminal peptides in prts, an Arabidopsis thaliana N-end rule mutant lacking the E3 ligase PROTEOLYSIS56 (PRT6). TMT-TAILS identified over 4000 unique N-terminal peptides representing c. 2000 protein groups. Forty-five protein groups exhibited significantly increased N-terminal peptide abundance in prts seedlings, including cruciferins, major seed storage proteins, which were regulated by Group VII Ethylene Response Factor (ERFVII) transcription factors, known substrates of PRT6. Mobilisation of endosperm cruciferin was delayed in prts seedlings. N-termini of several proteases were downregulated in prts, including R2D2A, R2D2A transcript, protein and activity levels were downregulated in a largely ERFVII-dependent manner. By contrast, cathespin B3 protein and activity were upregulated by ERFVII independent of transcript. We propose that the PRT6 branch of the pathway regulates protease activities in a complex manner and optimises storage reserve mobilisation in the transition from seed to seedling via control of ERFVII action.

The final paper selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modules stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betuyenku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuho Yamaguchi-Shinozaki, Kazuo Shinozaki.

Mammalian peptide hormones propagate extracellular stimuli from sensing tissues to appropriate targets to achieve optimal growth maintenance. In land plants, root-to-shoot signalling is important to prevent water loss by transpiration and to adapt to water-deficient conditions. The phytohormone abscisic acid has a role in the regulation of stomatal movement to prevent water loss. However, no mobile signalling molecules have yet been identified that can trigger abscisic acid accumulation in leaves. Here we show that the CLAVATA3/EMBRYO-SURROUNDING REGION-RELATED 25 (CLE25) peptide transmits water-deficiency signals through vascular tissues in Arabidopsis, and affects abscisic acid biosynthesis and stomatal control of transpiration in association with BARELY ANY MERISTEM (BAM) receptors in leaves. The CLE25 gene is expressed in vascular tissues and enhanced in roots in response to dehydration stress. The root-derived CLE25 peptide moves from the roots to the leaves, where it induces stomatal closure by modulating abscisic acid accumulation and thereby enhances resistance to dehydration stress. BAM receptors are required for the CLE25 peptide-induced dehydration stress response in leaves, and the CLE25-BAM module therefore probably functions as one of the signalling molecules for long-distance signalling in the dehydration response.

The page selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modules stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betuyenku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuho Yamaguchi-Shinozaki, Kazuo Shinozaki.

Mammalian peptide hormones propagate extracellular stimuli from sensing tissues to appropriate targets to achieve optimal growth maintenance. In land plants, root-to-shoot signalling is important to prevent water loss by transpiration and to adapt to water-deficient conditions. The phytohormone abscisic acid has a role in the regulation of stomatal movement to prevent water loss. However, no mobile signalling molecules have yet been identified that can trigger abscisic acid accumulation in leaves. Here we show that the CLAVATA3/EMBRYO-SURROUNDING REGION-RELATED 25 (CLE25) peptide transmits water-deficiency signals through vascular tissues in Arabidopsis, and affects abscisic acid biosynthesis and stomatal control of transpiration in association with BARELY ANY MERISTEM (BAM) receptors in leaves. The CLE25 gene is expressed in vascular tissues and enhanced in roots in response to dehydration stress. The root-derived CLE25 peptide moves from the roots to the leaves, where it induces stomatal closure by modulating abscisic acid accumulation and thereby enhances resistance to dehydration stress. BAM receptors are required for the CLE25 peptide-induced dehydration stress response in leaves, and the CLE25-BAM module therefore probably functions as one of the signalling molecules for long-distance signalling in the dehydration response.

The final paper selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modules stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betuyenku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuho Yamaguchi-Shinozaki, Kazuo Shinozaki.

Mammalian peptide hormones propagate extracellular stimuli from sensing tissues to appropriate targets to achieve optimal growth maintenance. In land plants, root-to-shoot signalling is important to prevent water loss by transpiration and to adapt to water-deficient conditions. The phytohormone abscisic acid has a role in the regulation of stomatal movement to prevent water loss. However, no mobile signalling molecules have yet been identified that can trigger abscisic acid accumulation in leaves. Here we show that the CLAVATA3/EMBRYO-SURROUNDING REGION-RELATED 25 (CLE25) peptide transmits water-deficiency signals through vascular tissues in Arabidopsis, and affects abscisic acid biosynthesis and stomatal control of transpiration in association with BARELY ANY MERISTEM (BAM) receptors in leaves. The CLE25 gene is expressed in vascular tissues and enhanced in roots in response to dehydration stress. The root-derived CLE25 peptide moves from the roots to the leaves, where it induces stomatal closure by modulating abscisic acid accumulation and thereby enhances resistance to dehydration stress. BAM receptors are required for the CLE25 peptide-induced dehydration stress response in leaves, and the CLE25-BAM module therefore probably functions as one of the signalling molecules for long-distance signalling in the dehydration response.

The final paper selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modules stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betuyenku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuho Yamaguchi-Shinozaki, Kazuo Shinozaki.

Mammalian peptide hormones propagate extracellular stimuli from sensing tissues to appropriate targets to achieve optimal growth maintenance. In land plants, root-to-shoot signalling is important to prevent water loss by transpiration and to adapt to water-deficient conditions. The phytohormone abscisic acid has a role in the regulation of stomatal movement to prevent water loss. However, no mobile signalling molecules have yet been identified that can trigger abscisic acid accumulation in leaves. Here we show that the CLAVATA3/EMBRYO-SURROUNDING REGION-RELATED 25 (CLE25) peptide transmits water-deficiency signals through vascular tissues in Arabidopsis, and affects abscisic acid biosynthesis and stomatal control of transpiration in association with BARELY ANY MERISTEM (BAM) receptors in leaves. The CLE25 gene is expressed in vascular tissues and enhanced in roots in response to dehydration stress. The root-derived CLE25 peptide moves from the roots to the leaves, where it induces stomatal closure by modulating abscisic acid accumulation and thereby enhances resistance to dehydration stress. BAM receptors are required for the CLE25 peptide-induced dehydration stress response in leaves, and the CLE25-BAM module therefore probably functions as one of the signalling molecules for long-distance signalling in the dehydration response.

The final paper selected as a research highlights is not open access but is of great interest as it introduces a new paradigm in plant hormone signaling.

Small peptide modules stomatal control via abscisic acid

Fuminori Takahashi, Takehiro Suzuki, Yuriko Osakabe, Shigeyuki Betuyenku, Yuki Kondo, Naoshi Dohmae, Hiroo Fukuda, Kazuho Yamaguchi-Shinozaki, Kazuo Shinozaki.


Major Funding Sources

Argentina

Marcelo J. Yanovsky
myanovsky@leiloi.org.ar
Fundación Instituto Leloir, CONICET.
Buenos Aires, Argentina

Use of Arabidopsis

There are more than 35 groups conducting varied research with Arabidopsis in Argentina.

They work in different Institutes and Universities scattered throughout the country in cities such as Buenos Aires, Rosario, Mar del Plata, Santa Fe, Córdoba, Mendoza and Bariloche.

The research topics and research groups include; among others, water transport (Gabriela Amodeo, Gustavo Guadelschat), responses to water deficit (Raquel Chan, Norberto Iusem), UV-B light (Paula Casati, Carlos Ballaré), oxidative stress (Nestor Carrillo, Daniel Gonzalez, Estela Valle, Diego Gomez Casati), leaf growth and development (José Estevez) carbohydrate metabolism (Graciela Salerno, Fernando Santiago Mora García, Ruben Bottini, Federico Ariel), root growth and development (José Estevez) stress (Nestor Carrillo, Daniel Gonzalez, Estela Valle, Nestor Carrillo), responses to water deficit (Raquel Chan, Norberto Iusem), light signaling and photomorphogenesis (Jorge Casal, Carlos Ballaré, Javier Botto), responses to UV-B light (Paula Casati, Carlos Ballaré), alternative splicing from RNA-seq data. ASpli, a Bioconductor package for the analysis of Kornblihtt).

Eugenia Zanetti, Flavio Blanco, Ezequiel Petrillo, Alberto Konnblhit.

New Software Tools

ASpli, a Bioconductor package for the analysis of alternative splicing from RNA-seq data.

Selected Publications

RALF4/19 peptides interact with LXR proteins to control pollen tube growth in Arabidopsis. Mecchia MA, Santos-RALF4/19 peptides interact with LRX proteins to control alternative splicing from RNA-seq data. ASpli, a Bioconductor package for the analysis of Kornblihtt).


Australia

Monika Murcha
monika.murcha@uwa.edu.au
Australian Research Council Centre of Excellence, Plant Energy Biology, The University of Western Australia.

Use of Arabidopsis

There are over 60 research groups located at most Universities across the country and within Commonwealth Scientific Research Organisation (CSIRO) facilities.

Open Resources for Arabidopsis Researchers


RICE DB: Rice DB facilitates and integrates direct comparison of rice annotations to Arabidopsis allowing parallel comparison between these two model species within one database. http://ricedb.plantenergy.uwa.edu.au/


MASC Gator: a proteomics aggregation utility that displays information from a variety of online Arabidopsis databases. http://plantenmostab.com/

MASCP Gator: a proteomics aggregation utility that displays information from a variety of online Arabidopsis databases. http://ricedb.plantenergy.uwa.edu.au/

Selected Publications

Australian researchers have published over 170 articles involving Arabidopsis. Pubmed search using keyword Arabidopsis (Title/Abstract) and Australia (affiliation) since Jan 2017-Mar 2018. Selected publications indicating the breadth of outputs are listed below.


The Virtual Plant Cell (VPC) developed by the Centre of excellence in Plant Energy Biology allows users to become immersed in and interact with a plant cell, learn about the importance of phosphate and walk through labs and facilities such as The Plant Accelerator. Aimed at primary and senior school students. https://www.youtube.com/channel/UCeIGuxGxHgKtAZP9WbXgA
Figure 16. A Heatmap summarising the patterns of relative expression for each treatment vs the untreated control, including 60 minutes of excess light (III), recovery of 60 minutes (VIII), immediate repeat of 60 minutes of excess light (IX), 24-hour recovery (X) and further repeat excess light after 24-hour recovery period. doi: 10.1105/tpc.16.00828.
Figure 17. Time-lapse recording of eight Arabidopsis root tips expressing UBQ10::YFP-PIP1;4 over the course of 38 h. (A) Maximum intensity projections of a single time point for the eight roots tracked. (B) Growth rates of the root tips were calculated from the output of the TipTracker program. The yellow and grey areas indicate when the LED illumination was on or off, respectively; (C) Cell division and elongation are visualized for the root #5. Each new cell wall is highlighted so that the original cell walls are in yellow, the second generation of the walls is in cyan, the third generation is in magenta, and the fourth generation in green. The last image of the series is shown on the right side. A stack of 14 projections of a single time point for the eight roots tracked. (B) Growth rates of the root tips were calculated from the output of the TipTracker program. The yellow and grey areas indicate when the LED illumination was on or off, respectively; (C) Cell division and elongation are visualized for the root #5. Each new cell wall is highlighted so that the original cell walls are in yellow, the second generation of the walls is in cyan, the third generation is in magenta, and the fourth generation in green. The last image of the series is shown on the right side.

Pipeline for transcriptome assemblies from short read data. This pipeline reduces the number of poorly supported, mis-assembled transcripts often arising from the high degree of inaccuracy of transcript assembly programs. www.ncbi.nlm.nih.gov/pubmed/28402429

Conferences, Workshops and Outreach events

5th European Workshop on Plant Chromatin, 22-24 June 2017
22nd Meeting of the Austrian Society of plant Biology (ATSPB), 5-7 April 2018
21st Meeting of the European Network for Plant Endomembrane Research (NPER), 4-7 Sep 2018
Open campus day at IST Austria presenting also Arabidopsis research

Selected Publications

MASC Country Reports

Belgium

Mozzit K. Nowack
nowack.mozzit@vib.be
VIB-Ugent Center for Plant Systems Biology, Ghent, Belgium

Use of Arabidopsis

Research Facilities
Arabidopsis Research Centers in Belgium:
- VIB-Ugent Center for Plant Systems Biology, www.ps.b.ugent.be
- University of Ghent https://www.ugent.be/en
- University of Leuven https://www.kuleuven.be/en
- University of Hasselt http://www.uohasselt.be
- Universite catholique de Louvain https://www.uclouvain.be


Open Resources for Arabidopsis Researchers

The Department of Plant Systems Biology (PSB) continuously develops and disseminates an exhaustive collection of destination vectors, designed for the functional analysis of genes in plant cells and compatible with the recombinatorial cloning Gateway technology (www.ps.b.ugent.be/gateway). The Yield Booster website provides the scientific community with information on genes and molecular mechanisms that govern plant growth and productivity. Data on model plants (including Arabidopsis) as well as crops are presented (www.yieldbooster.org).

PLAZA is an access point for plant comparative genomics centralizing genomic data produced by different genome sequencing initiatives. It integrates plant sequence data and comparative genomics methods and provides an online platform to perform evolutionary analyses and data mining within the green plant landscape (http://bioinformatics.psb.ugent.be/plaza/).

Other developed resources include:
- Platform for semi-automated kinematic analysis of growth in Arabidopsis root tips and leaves
- Phenotyping platforms
- Metabolomics and Enzyme activity assays for antioxidant system
- Leaf modelling platform based simulation models of Arabidopsis root tip and leaf growth.
- A collection of adventitious rooting mutants
- Marker lines for cell cycle, DNA stress, and meiosis specific events
- Marker lines for developmental cell death

Conferences, Workshops and Outreach events

Conferences and Workshops:

Outreach events:
- International Plant Biotechnology Outreach (IPBO) http://www.vib.be/en/research/scientists/Pages/IPBO.aspx
- Day of Science http://flandersbio.be/events/dag-vandewetenschap
- Day of Biotechnology http://flandersbio.be/events/dag-van-de-biotechnologie

Selected Publications


Major Funding Sources

- Flanders Institute for Biotechnology (VIB; www.vib.be)
- European Union Framework (cordis.europa.eu)
- Belgian Federal Science Policy Office (www.belspo.be)
- Institute for the Promotion of Innovation by Science and Technology in Flanders (IVWT; www.ivwt.be)
- European Research Council (erc.europa.eu)
- European Research Council (erc.europa.eu)
- European Research Council (erc.europa.eu)
Use of Arabidopsis

In Brazil at least eight institutions use Arabidopsis in their research.

Conferences, Workshops and Outreach events

VI Simpósio Brasileiro de Genética Molecular de Plantas, Ouro Preto, Minas Gerais Brazil, from May 28 to June 02, 2017.

47th Annual Meeting of the Brazilian Society for Biochemistry and Molecular Biology (SBBrq), Joinville, Santa Catarina, Brazil, May 26th to 29th, 2018

XVII Brazilian Congress of Plant Physiology, which will be held in Cuiabá, Mato Grosso Brazil, from June 9 to 12, 2019.

Selected Publications


Figure 19. Proposed model for ARALF1 perception in root cells of Arabidopsis. (A) In the absence of ARALF1, the BRI1-BL-BAK1 complex is active in the plasma membrane and the cell expands. The apoplast is acidic as the plasma membrane proton pump AHA2 is functional and FERONIA (FER) is in the cell membrane complexed with LRE-like CPL-APT (LIGGLCOREL) (LRE). (B) In the presence of ARALF1, the peptide binds FER-LLG1/LRE complex, recruits the receptor-like cytoplasmic kinase RIPK and inactivates AHA2, leading to an increase in apoplastic pH. It is proposed that the resulted apoplastic alkalinization is acidic as the plasma membrane proton pump AHA2 is functional and FERONIA (FER) is in the cell membrane complexed with LRE-like CPL-APT (LIGGLCOREL) (LRE). (C) Peptide binds FERONIA (FER) and inactivates AHA2, preventing cell expansion. AHA2 is functional and FERONIA (FER) is in the cell membrane complexed with LRE-like CPL-APT (LIGGLCOREL) (LRE). (D) In the presence of ARALF1, the peptide binds FER-LLG1/LRE complex, recruits the receptor-like cytoplasmic kinase RIPK and inactivates AHA2, leading to an increase in apoplastic pH. It is proposed that the resulted apoplastic alkalinization is acidic as the plasma membrane proton pump AHA2 is functional and FERONIA (FER) is in the cell membrane complexed with LRE-like CPL-APT (LIGGLCOREL) (LRE).

MASC Inc Annual Report 2017/2018 51
and many others, all in one easy-to-use, extensively tested, web-based tool for working with functional genomics and other data for hypothesis generation and confirmation. Most are designed with the plant (mainly Arabidopsis) researcher in mind. Data sets include:

- 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.

- 70,944 predicted protein-protein interactions plus ~2.8 million protein-DNA interactions.

- 29,180 predicted protein tertiary structures and 36,352 documented PPIs (rice interologs also available!)

- 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.

- Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee’s site at 1001proteomes.org, myc-masc-proteomics.org.

- Documented subcellular localizations for 9.1k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Work was completed on a “mega-app” from the BAR for Araboport.org, ePlant, and a publication came out in the Plant Cell describing it (Waese et al., 2017). ePlant is an “eFP overview” provides a table of pictographs to get a feeling for where expression is the strongest or weakest. Released hundreds of new protein-protein interactions for the extra-cellular domains of leucine-rich repeat receptor kinases into our ePlant and Arabidopsis Interaction Viewer tools (Smakowska-Luzan et al., 2018).

For translational researchers, publications came out for eFP Browser views announced last year: a Developmental Map for Brachypodium distachyon from Marek Mutwil and colleagues (Silhau et al., 2017; http://bar.utoronto.ca/ efp_brachypodium/), a Maize Root view, part of the Maize eFP Browser, from Stefan Hey and colleagues (Hey et al., 2017; http://bar.utoronto.ca/efp_Maize/cgi-bin/efpWeb.cgi), and a Classification SuperViewer for Medicago truncatula genomics (Herrbach et al., 2017; http://bar.utoronto.ca/ntools/cgi-bin/ntools_classification_superviewer_medicago.cgi).

Open Resources for Arabidopsis Researchers

Bio-Analytic Resource for Plant Biology (BAR)
http://bar.utoronto.ca

The Bio-Analytic Resource is a collection of user-friendly web-based tools for working with functional genomics and other data for hypothesis generation and confirmation. Most are designed with the plant (mainly Arabidopsis) researcher in mind. Data sets include:

- 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.

- 70,944 predicted protein-protein interactions plus ~2.8 million protein-DNA interactions.

- 29,180 predicted protein tertiary structures and 36,352 documented PPIs (rice interologs also available!)

- 150 million gene expression measurements (75 million from A.th.), plus “expressologs” (homologs showing similar patterns of expression in equivalent tissues) for many genes across 10 species. View expression patterns with our popular eFP Browser or new ePlant tool.

- Millions of non-synonymous SNPs from the 1001 Arabidopsis Genomes project, delivered through the MASC Proteomics Subcommittee’s site at 1001proteomes.org, myc-masc-proteomics.org.

- Documented subcellular localizations for 9.1k proteins, predicted localization for most of Arabidopsis proteome, from the SUBA database at the University of Western Australia.

Work was completed on a “mega-app” from the BAR for Araboport.org, ePlant, and a publication came out in the Plant Cell describing it (Waese et al., 2017). ePlant is a zoomable user interface for exploring data across 12 nanometre scale, encompassing at least 20 different kinds of genome-wide data covering gene expression, subcellular localization, 3D molecular structure, chromatin states, and many others, all in one easy-to-use, extensively tested, open source tool. ePlant is accessible from the Araport.org homepage, and from the Bio-Analytic Resource at http://bar.utoronto.ca/eplant.

The first major update to ePlant was released in January 2018, and included a new Plant eFP view for Kleipikova et al. (2016) RNA-seq-based developmental atlas, updated subcellular localization data using SUBA4 data, an ePlant Navigator to easily view expression patterns of homologs in other species, and the highlighting of gene parts in the Gene view.

“eFP-Seq Browser” was released for exploring the 113 RNA-seq data sets used to reannotate the Arabidopsis genome for the Araport11 build, or the RNA-seq data sets generated for Kleipikova et al.‘s (2016) developmental atlas, both as read maps and pictographs summarizing the expression levels in various tissues, easily sortable by any desired column: http://bar.utoronto.ca/eFP-Seq_Browser/.

In addition to simply sorting the table by expression level, an “eFP overview” provides a table of pictographs to get a feeling for where expression is the strongest or weakest. Released hundreds of new protein-protein interactions for the extra-cellular domains of leucine-rich repeat receptor kinases into our ePlant and Arabidopsis Interaction Viewer tools (Smakowska-Luzan et al., 2018).

For translational researchers, publications came out for eFP Browser views announced last year: a Developmental Map for Brachypodium distachyon from Marek Mutwil and colleagues (Silhau et al., 2017; http://bar.utoronto.ca/ efp_brachypodium/), a Maize Root view, part of the Maize eFP Browser, from Stefan Hey and colleagues (Hey et al., 2017; http://bar.utoronto.ca/efp_Maize/cgi-bin/efpWeb.cgi), and a Classification SuperViewer for Medicago truncatula genomics (Herrbach et al., 2017; http://bar.utoronto.ca/ntools/cgi-bin/ntools_classification_superviewer_medicago.cgi).

Outlook on Arabidopsis Research

Funding for Arabidopsis research is largely from NSERC, one of the three federal funding agencies in Canada. The federal government has recently committed additional funding to support basic research through the NSERC Discover Grant program.

Conferences, Workshops and Outreach events

The BAR participated in the 2017 American Society of Plant Biology (ASPB) Plant Biology conference in Hawaii, as part of the Plant AgData Outreach booth; and Plant and Animal Genomes (PAG) XXVI at the start of 2018 in San Diego, California. It also gave a talk in the Arabidopsis Informatics workshop at IACR2017 in St. Louis, Missouri.

Major Funding Sources

National Science and Engineering Research Council (NSERC)
http://www.nserc-crsng.gc.ca

Genome Canada
http://www.genomecanada.ca/en/
Paulo Canesas’s Using RNAseq of plants infected with Botrytis cinerea and after data analysis and integration, we expect to determine the global transcriptional impact on B. cinerea when infecting plant tissue, but also to generate information relative to the genome-wide expression profile of A. thaliana upon light stimulation when the wild-type fungus, or one that is sensing the environment in an altered manner (Δbcwcl1) are interacting with the plant tissue.

Pablo Figuerola’s lab research goal is to contribute to understanding the connection between Jasmonate and abiotic stress such as high salinity. Jasmonate (JA) is an essential hormone involved in plant defense against herbivory and in responses to abiotic stress. However, the relationship between the salt stress response and the JA pathway in Arabidopsis is not understood at a molecular and cellular level. In this work, we investigated the activation of JA signaling by NaCl and its effect on primary root growth. We found that JA-responsive JAZ genes were upregulated by salt stress in a COI1-dependent manner in the roots.

Rodrigo A Gutiérrez’s lab goal is to understand how nitrogen signaling interacts with other signaling networks to control plant growth and development. This is essential to improving nitrogen use efficiency in plants or the amino acid content of seeds, important issues for health, agriculture and human nutrition.

Michael Handford’s lab is interested in the study of Arabidopsis sugar alcohol metabolism. Sugar alcohol (polyols) like sorbitol and mannitol perform various roles in vivo. In plants, they are a means of long-distance phloem carbon transport, of redistributing boron and as compatible solutes in abiotic stress. Arabidopsis possesses low basal levels of sorbitol and other sugar alcohols, in addition to low specificity sugar alcohol transporters. By reverse genetics, we identified ARDH in this species which oxidizes sorbitol, and atsdh- mutants are more resistant to drought stress.

Loreto Holuigue’s lab research is focused on determining the substrate specificity of sRNA-controlled networks influence root phenotypical, molecular and physiological response to external cues such as nutrient availability over the plant life cycle.

New Software Tools

GENIUS is a user-friendly web server that uses a novel machine learning algorithm to infer functional gene networks focused on specific genes and experimental conditions that are relevant to biological functions of interest. These functions may have different levels of complexity, from specific biological processes to complex traits that involve several interacting processes. GENIUS also enriches the network with new genes related to the biological function of interest, with accuracies comparable to highly discriminative Support Vector Machine methods. Availability and Implementation: GENIUS currently supports eight model organisms and is freely available for public use at http://networks.bsc.puc.cl/GENIUS/.

Conferences, Workshops and Outreach events


Workshop: “Applied Plant Biology II: Expression of gene regulation in plant development and fruit ripening”

Organizers: Universidad de Talca

November 30th to December 2nd, 2017

Signal Workshop on Environmental Regulation of Plant Development. This workshop will be held at P. Universidad Católica de Chile in Santiago from

Organizers: SIGNAT, Horizon 2020 European Union funding for Research & Innovation
China

Yuling Jiao yljiao@genetics.ac.cn
Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China

Use of Arabidopsis

There are a large number of Chinese research institutions that conduct Arabidopsis research. Because of the large size of the country, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.

Whereas there are dedicated grants to basic and applied research in universities, it is difficult to precisely estimate the exact number of research labs using Arabidopsis, although the number must be over 500. This can in part be reflected by the large number of Arabidopsis related posters and talks at each annual National Congress of Plant Biology.

Not surprisingly, research topics range from developmental and hormone biology to abiotic and biotic stress, and to evolution. Hence, Arabidopsis is the model plant of choice to many groups. However, only a small portion of these labs is solely dedicated to Arabidopsis research or using Arabidopsis as the main model plant, which may vary from different many other countries. A major reason behind this would be the current funding priority.
Although a number of high-profile international conferences, including ICAR, have chosen China as their meeting venues, Chinese scientists are clearly underrepresented in some international conferences, such as the ICAR. For example, only one speaker from China talked at the recent ICAR2017. This underrepresentation will likely negatively influence Chinese researchers’ enthusiasm for attending ICAR.

Selected Publications

During 2017, Chinese researchers authored over 500 plant science papers with a portion involved work on Arabidopsis.


Major Funding Sources

National Natural Science Foundation (NSFC). (http://www.nsc.gov.cn/publish/portal11/)

Ministry of Science and Technology (MOST). (http://www.most.gov.cn/erj/programmes/index.html)

Czech Republic

Viktor Žárský
viktor@natur.cuni.cz

Use of Arabidopsis

There are 10 institutions (five universities, two centers and three institutes of the Academy of Sciences of the Czech Rep.) and about 30 labs within these institutions using Arabidopsis as a model plant for the research.

Open Resources for Arabidopsis Researchers

BRNO - CEITEC - Central European Institute of Technology Proteomics Core Facility
http://www.ceitec.eu/ceitec-mu/proteomics-core-facility/8

The Core Facility is part of Czech National Affiliated Centre of INSTRUCT. All CEITEC core facilities are available to external users (academia and companies). Czech and international researchers from universities and research institutes interested in accessing core facilities can benefit from support of CEITEC – open access project funded by the Ministry of Education, Youth and Sports of the Czech Republic.

Figure 22. RALF4 and RALF19 are pollen tube–expressed and are required for pollen tube integrity. The figure shows Aniline Blue staining of wild-type (WT) and ralf4 ralf19 pollen tubes in WT pistils at 20 hours after pollination. http://dx.doi.org/10.1126/science.aao3642

Figure 23. Structural models of the PSII megacomplexes (a–m) Photosystem II (PSII) megacomplexes fitted with the proposed PSII crystalline structure, as published by Caffarri et al. (2009). Individual PSII subunits are colour coded in the following manner: pale green, core complex; blue, M trimer; orange S trimer; magenta, additional LHCII trimers; yellow, Lhcb4; green, Lhcb5; red, Lhcb6. https://doi.org/10.1111/tpj.13325


**Conferences, Workshops and Outreach events**

Last year 2017:
- ENPER meeting 2017, Prague, “20th European Network for Plant Endomembrane Research” meeting, September 12-15, 2017, Prague

This year 2018:
- ACPD2018 - “Auxins and Cytokinins in Plant Development”, July 1-5, 2018, Prague

**Selected Publications**


**Major Funding Sources**

Both major funding agencies for basic research - Czech Science Foundation (GACR) and Ministry of Education of CR (MSMT CR) - support regularly projects based on the use of Arabidopsis as a model plant.

1. Czech Science Foundation/GACR, Prague http://www.gacr.cz


Both institutions support also bilateral projects with selected countries. Targeted or applied research is since recently supported also by the Technology Agency of the Czech Republic (TACR) and Arabidopsis model is accepted as a driver for applications.


4. Ministry of Agriculture, National Agency for Agricultural Research (NAZV) might support projects using Arabidopsis as a driver for the applied research https://goo.gl/jPGvIO

**Use of Arabidopsis**

Arabidopsis research in Denmark primarily takes place at University of Copenhagen. Arabidopsis research is also carried out at University of Aarhus. Copenhagen Plant Science Centre (CPS) is a new initiative at University of Copenhagen scheduled to be inaugurated in 2017. CPS will be rooted in the Department of Plant and Environmental Sciences and will include up-to-date facilities for Arabidopsis research.

**Current Arabidopsis Projects**

There are no dedicated Arabidopsis consortia or centers in Denmark, but Arabidopsis is commonly used by plant biologists as a model organism. The Danish National Research Foundation funds a number of major Centers of Excellence. In one such center Arabidopsis is employed as a model organism: Center for Dynamic Molecular Interactions (Dynamic) directed by Prof. Barbara Ann Halkier.

In Denmark it is becoming increasingly difficult to obtain funding for basic research on Arabidopsis as the general trend is shifting towards supporting applied research.

**Selected Publications**


Use of Arabidopsis

Largest users of Arabidopsis in research: University of Helsinki, University of Turku, University of Oulu
The number of labs depends on definition and many plant labs even focusing on other plant species will use Arabidopsis as a tool.

Open Resources for Arabidopsis Researchers


New Software Tools

Groups at the University of Helsinki are developing PhenomotoR, an R package to integrate different phenotypic data from different sources (several phenotyping platforms as well as data from conventional approaches) with mathematical normalization of repeats and other features. A manuscript is currently in preparation approaches) with mathematical normalization of repeats and other features. The software will be available as R package.

Conferences, Workshops and Outreach events

Finland is organizing the International Conference on Arabidopsis Research 2018 in Turku, Finland, from June 25 to 29. All information about the conference can be found at the website: http://icar2018.arabidopisreseach.org/
The conference is organized by groups from the Universities in Helsinki, Turku and Oulu.

Selected Publications


Major Funding Sources

- Research organizations such as CNRS, INRA, CEA or Universities provide recurrent funding to their laboratories in addition to payment of salaries of permanent researchers and technicians.
- The French national research agency, ANR (http://www.agence-nationale-recherche.fr/en/about-anr/about-the-french-national-research-agency3), provides funding for project-based research. The main calls deal with societal issues that do not very well support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is decreasing, although a new ANR call (2017) was dedicated to fundamental mechanisms.

European funding:
- ERC http://erc.europa.eu/funding- and-grants
- Marie-Curie research programmes http://erc.europa.eu/research/mariecurieactions/
- EMBO http://www.embo.org/funding-awards

Selected Publications


Major Funding Sources

- Research organizations such as CNRS, INRA, CEA or Universities provide recurrent funding to their laboratories in addition to payment of salaries of permanent researchers and technicians.
- The French national research agency, ANR (http://www. agence-nationale-recherche.fr/en/about-anr/about-the- french-national-research-agency3), provides funding for project-based research. The main calls deal with societal issues that do not very well support fundamental research in general, including in plant biology. Funding on Arabidopsis projects is decreasing, although a new ANR call (2017) was dedicated to fundamental mechanisms.

European funding:
- ERC http://erc.europa.eu/funding- and-grants
- Marie-Curie research programmes http://erc.europa.eu/research/mariecurieactions/
- EMBO http://www.embo.org/funding-awards
Germany

Klaus Harter
klaus.harter@znbp.uni-tuebingen.de
University of Tübingen, Tübingen

Use of Arabidopsis

Arabidopsis research in Germany is performed in all corners of the country and this wide distribution also reflects the high diversity of topics explored by German scientists. The major sites hosting Arabidopsis researchers are Universities, Max Planck Institutes, Helmholtz Centers and Leibniz Institutes.

In order to maintain and enhance collaborations and communication, German Arabidopsis researchers count on the coordinating activities of the ‘Arabidopsis Functional Genomics Network’ (AFGN). Established in 2001 following the completion of the Arabidopsis genome sequencing, the AFGN was funded by the German Science Foundation (DFG) until 2010. Today the AFGN operates under the umbrella of the German Botanical Society (DBG) and its actions include the maintenance of a mailing list for advertising events, job postings, inquiries on seeds, plasmids and resources, as well as any other topic of interest for the plant community in Germany and Europe http://www.dbg-afgn.de/.

Open Resources for Arabidopsis Researchers

1001 Genomes Project
http://1001genomes.org/

German Plant Phenotyping Network
http://www.dppn.de/dppnEN/Home/home_node.html

The Arabidopsis Protein Phosphorylation Site Database
http://phosphat.uni-hohenheim.de/index.html: In addition to the database, the PhosPhAt offers a plant-specific phosphorylation site predictor

GABI Primary Database
http://www.gabipd.org/

Plant Genome and Systems Biology Databases
http://pgb.helmholtz-muenchen.de/plant/plantsdb.jsp

Plant Transcription Factor Database
http://plnftd.bio.uni-potsdam.de/v3.0/

The AraGWAS Catalog: a curated and standardized Arabidopsis italiana GWAS catalog
https://aragwas.1001genomes.org

New Software Tools

qPortal: A large set of software tools and portlets are accessible via the recently established web-based science portal of the Quantitative Biology Center (QBIC) of the University of Tübingen (https://portal.qbic.uni-tuebingen.de/portal/web/qbic/software). qPortal provides users with an intuitive way to create, manage, and analyze quantitative biological data and comprises front-end solutions to give users access to data management and easy-to-use analysis options. qPortal provides solutions for biological projects, providing up to date analysis pipelines, quality control workflows, and visualization tools. Appropriate data models build the foundation of qPortal’s biological data management system and provide possibilities to annotate data, query existing metadata for statistics and future re-analysis on high performance computing systems via coupling of workflow management systems.

nQuire: a statistical framework for ploidy estimation using next generation sequencing. nQuire is implemented as a stand-alone Linux command line tool in the C programming language and is available at https://github.com/cchgegn/nQuire.

findGSE: estimating genome size variation within human and Arabidopsis using k-mer frequencies. The R package of findGSE is freely available at https://github.com/schneebergerlab/findGSE and supported on linux and Mac systems.

myTAI: evolutionary transcriptomics with R. The myTAI package is available at https://github.com/HajidmyTAI and https://cran.r-project.org/web/packages/myTAI/index.html

Conferences, Workshops and Outreach events

Conferences
6th International Meeting on Plant Genome Stability and Change, 03. – 06.06. 2018, Gatersleben, Germany
1st Cologne Conference on Food for Future, 05. – 07. September 2018, Cologne, Germany
12th Conference Molecular Biology of Plants, 18. – 21. February 2019, Daringhausen, Germany
11th Tri-National Arabidopsis Meeting, 10. – 12. April 2019, Zürich, Switzerland
International Plant Science Conference (BotanikerTagung), 15. – 19. September 2019, Rostock, Germany

Workshops and Summer Schools
Dresden Summer School in Systems Biology, 11. – 18. August 2018, Dresden, Germany

de.NBI Summer School 2018, 03. – 07. September 2018, Braunschweig, Germany
1st Black Forest Flagellated Plant Workshop, 17. – 20. September 2018, Feldberg, Germany
1st Greifswald Summer School on Mathematics of Evolution, 16. – 22. September 2018, Greifswald, Germany
Workshop on Genome-Wide Analysis of Selection Signatures and Genotype-Phenotype Associations, 22. – 26. October 2018, Berlin, Germany

Outreach Events
The PLANT2030 is an initiative from the German Federal Ministry of Education and Research (BMBF) that fosters research projects within public-private partnerships (http://www.pflanzenforschung.de/plant-2030/)

German institutions are very active in communicating plant science to the general public. Max Planck Institutes, for instance, offer guided tours, events and informative booklets for people of all ages. Some examples are below.

- Wissenschaftsscheune, “The Science Barn” (http://www.wissenschaftsscheune.de/)
- Open House of the Tübingen MPI (http://www.mpi-molgen.mpg.de/institute/information-for-the-public.html)
- Frag die Erbe, “Ask the Past” booklet series (http://www.mpimp-golm.mpg.de/22409/Frag_die_Erbe_Booklet)
Selected Publications


Major Funding Sources

The German Science Foundation (DFG) is the major source financing Arabidopsis research in Germany.

Contact: Catherine Kister: catharine.kister@dfg.de

Open Resources for Arabidopsis Researchers

The researchers working on Arabidopsis now meet regularly and hold an annual meeting, where they share their work and whatever resource material they have been generating they are willing to share. Some teachers of undergraduate colleges have shown keen interest and generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share. Some teachers of their work and whatever resource material have been generated they are willing to share.
Additional Information

The major thrust in research on Arabidopsis in India continues to be on unravelling molecular mechanisms involved in the development of plant organs, plant pathogen interaction, abiotic stress tolerance, light, hormone and sugar signaling.

The I2ZIP transcription factor, HY5, is known to be a key player in light signaling in Arabidopsis. Jiten Khurana’s group has shown that one of the rice ortholog of AtHY5, OsDIZIP48, although complements AtHY5 mutant in Arabidopsis but, unlike HY5, it is stable in dark and causes semi-dwarfism when over-expressed in rice, indicating that OsDIZIP48 has acquired novel functions in rice during the course of evolution.

In addition, Sourav Datta’s group has shown that the zinc finger transcription factors, BBX21 and BBX24, regulate HY5 activity post-transcriptionally, in opposite ways, and may be involved in executing contrasting functions in phomomorphogenesis. In collaboration with Sadip Chatterpadhyai, Ashish Nandi’s lab has highlighted the role of GBF1 in both light and defense signaling. His group has also identified GSTT2 as a critical component of SAR signaling during pathogenesis. Using a diverse range of Arabidopsis accessions, Jagreet Kaur’s lab showed that these accessions exhibit variable response, from complete resistance to high susceptibility to Alternaria brassicae; resistance to pathogens could also be attributed to multiple regions on the genome by GWAS.

Scientists from NRCPII and IBBT collaborated and characterized two novel mutants associated with the process of gametogenesis in Arabidopsis. Mutation in the Arabidopsis Coproporphyrinogen III oxidase gene (AHEMN1), which adversely affected silique length, ovule number, and seed set. A block in tetrapyrrole biosynthesis in the AtHEMN1 mutant resulted in increased ROS activity in floral tissues, thereby resulting in nonviable pollen and embryo sacs with unused polar nuclei. Another mutation in a TRAF-like gene resulted in fewer ovules, pollen and reduced seed set. The mutation exhibited altered Megaspore Mother Cell (MMC) specification, and delayed programmed cell death in meigaspores and the tapetum. This work establishes a novel link between a TRAF-like gene and reproductive development in plants.

Figure 26. Showing abnormalities in pre-fertilized and post fertilized ovules of Athemn1 mutants of Arabidopsis. A, Ovule in a wild-type. B, An Athemn1-1 mutant ovule. C, An Athemn1-2 mutant ovule. D, An ovule from Athemn1-1 mutant complemented with the GNAt (AHEMN1) gene. E, Post-fertilized ovule of a wild-type plant stage embryos. F and G, Post-fertilized ovules from the Athemn1-1 mutant. H, Aborted seed in a mature silique from an Athemn1-1 mutant (the degenerated globular embryo is marked with dotted lines). APC, Antipodal cell; CC, central cell; E, embryonic; EC, egg cell; ESN, endosperm nucleus; SC, synergid cell; UPN, unfused polar nuclei.

https://doi.org/10.1104/pp.16.01482


Major Funding Sources

Department of Biotechnology (DBT), Government of India http://dbt.india.nic.in/

Department of Science & Technology (DST), Government of India http://www.dst.gov.in/

Science and Engineering Research Board (SERB), Government of India http://www.serbonline.in/

Council of Scientific and Industrial Research (CSIR), New Delhi http://www.csir.res.in/

Indian Council of Agricultural Research (ICAR), New Delhi http://www.icar.org.in/

University Grants Commission, New Delhi https://www.ugc.ac.in/
Italy

Maura Cardarelli
maura.cardarelli@uniroma1.it
IBPM-National Research Council (CNR),
c/o Sapienza University of Rome,
Department of Biology and Biotechnology, Rome.

Use of Arabidopsis

A few groups mainly in the Universities and in the CNR (National Research Council) laboratories continue to utilize Arabidopsis as a model organism for plant biology research and their results are published in high impact journals. Research is mainly focused on root and flower development, seed germination, xylem differentiation, ion transport in plant vacuoles, plant defense responses and plant responses to environment.

Open Resources for Arabidopsis Researchers

In all combined laboratories we have resources for molecular, physiological, histological and cellular techniques.

An innovative use of isolated Arabidopsis vacuoles as an heterologous system for the functional characterization of animal intracellular channels and transporters has been developed.

Different single and multiple Arabidopsis T-DNA insertion lines, as well as overexpressing lines, GUS- YFP- and GFP-tagged lines described in publications are available.

New Software Tools

Image software for light microscopy and epifluorescence.

Conferences, Workshops and Outreach events

Summer course 2018: Plant Functional Phenotyping; from basic research to crop production

CropSym: Crop Abiotic Stress workshop. May 16-18, 2017, Faculty of Agriculture of the Hebrew University (Rehovot).

10th Symposium of the International Society of Root Research (SSR10), 8-12 July, 2018, Kityat Yavrin.

Publications

About 60 research articles employing Arabidopsis were published since the beginning of 2017 and until March 2018.

Major Funding Sources

The Israel Science Foundation (ISF). http://www.isf.org.il/
European Research Council (ERC) (erc.europa.eu)

Selected Publications


Major Funding Sources

The Italian Ministry of Education, University and Research funded:
- Project (PRIN 2014-2017) on ‘Genetic and epigenetic control of ovule number and fertility in Arabidopsis’. Coordinator Lucia Colombo;
- Project FIRB (Futuro in Ricerca 2014-2017) for young researcher. Principal investigator Raffaele Dello Ioso, Sapienza University of Rome;
- Project SIR (2015-2018) for independence of young researcher, on ‘NADS box transcription factor SHORT VEGETATIVE PHASE, understanding the molecular mechanism and involvement in sense and antisense transcription regulation’. RBSI14BTZ. Coordinator Veronica Gregis;
- Local funding: from Sapienza University of Rome and University of Milan

Other funding:
- European Commission’s 7th Framework Programme ERA-CAPS ERA-NET- grant “SEPS: Decoding ligand-receptor specificities of LysM-proteins in plant immunity and symbiosis”
- Project Promotion of consumer health of the National technological cluster AgriFood. Participant Ida Ruberti.

Additional Information

In the last years Arabidopsis research in Italy is getting little financial support. However in 2018 National basic research programmes will be re-funded, and this will give to some groups working on Arabidopsis the possibility to continue research.

Japan

Motoaki Seki, motoaki.seki@riken.jp
RIKEN CSRS
David Gifford, david.gifford@riken.jp
RIKEN CSRS
Masatoshi Kobayashi
masatoshi.kobayashi@riken.jp
RIKEN BRC

Use of Arabidopsis

The number of labs in Japan that use Arabidopsis: 350

The Leading Research Institutes and Universities:

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS) (http://www.cns.riken.jp/). CSRS (Director Kazuo Shinozaki), established in 2013 to conduct basic research integrating plant scientists, chemists and chemical biologists to work for solutions to critical scientific, technical and social issues with special focus on sustainable production of natural resources and useful, resilient agriculture under climate change. CSRS contributes to many goals of the United Nations Sustainable Development Goals (SDGs) and COP21 Paris Agreement goals by applied research through interdisciplinary R&D for sustainable production of energy, efficient engineering and production of useful plant biomass, renewable chemical materials and bioplastics, efficient catalysts, as well as crop production under climate change. In the next phase of CSRS, data science and chemical biology become more important for the advancement of plant science. In addition to Arabidopsis, CSRS uses other plant species such as Brachypodium, cassava, rubber, sorghum and others.

RIKEN National Science Institute - BioResource Center (BRC) (http://epd.brc.riken.jp/en/), (plant@brc.riken.jp).

The Experimental Plant Division (Masatoshi Kobayashi) collects, preserves and distributes plant resources developed in Japan. The project is funded by the Japanese government through the National BioResource Project (NBPR, http://www.nbpr.jp/index.jsp). The Arabidopsis resources in RIKEN BRC include seeds (mutants, transgenic lines, and natural accessions), DNA materials (full-length cDNA clones, ORF clones of transcription factors, TAC clones, and vectors), and cultured cells (T87 and At wt cell lines). The center also distributes full-length cDNA clones and cultured cells of model plants such as rice, Brachypodium distachyon and tobacco to the international research community.

Kazusa DNA Research Institute (http://www.kazusa.or.jp), Laboratory of Plant Genomics and Genetics, Plant DNA Analysis Group, Metabolomics Team, Bioresearches team, Biomass Team. Genome Informatics Group developed the portal site Plant Genome DataBase Japan PGDB (http://pgdb.jinsen.info), integrating databases related to plant omics studies. Manually curated literature information on DNA markers of 65 plants.

Creation of fundamental technologies contribute to the elucidation and application for the robustness in plants against environmental changes" Started 2015, Core Research for Evolutional Science and Technology (JST- CREST) (http://bit.ly/1I7yozD) coordinated with PRESTO (Sakigake). This project will continue to 2022. CREST is led by Satoshi Tahata (Kazusa DNA Research Inst.). Two PRESTO programs are led by Kiyotaka Okada and Masashi Ninomiya, respectively.


University of Tokyo, Multidimensional Exploration of Logic of Plant Development (2012-2017) (http://logicis. plantdev.biol.s.u-tokyo.ac.jp/). Project to delineate systems coordinating intracellular and intercellular signals,
functions of key differentiation genes, and control of metabolism, under combined efforts of 9 core research groups, 4 supporting facilities/teams, and 19 research groups (2013-2017) using multiple model species not only Arabidopsis but also a new model of land plants, Marchantia polymorpha. Led by Hirokazu Tsuchiya, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Nara Institute of Science and Technology. Principles of pluripotent stem cells underlying plant vitality (2017-2022)(http://www.plant-stem-cells.jp/). This project aims to answer the key questions: How do plants augment stem cell populations, and how do plants maintain them over long periods of time? The project members investigate the machinery of stem cell division and the regulatory system underlying maintenance of pluripotency and genome integrity. Led by Masaaki Umeda, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

National Institute for Basic Biology. (2017-2022)(http://photosynthesis.nibb.ac.jp/). Project goal is to elucidate the regulatory mechanisms of photosynthesis by incorporating a new perspective, the regulation of the proton motive force into basic photosynthesis research with the goal of improving photosynthetic efficiency. We expect to establish strategies to re-optimize the photosynthetic machinery under any environment. Led by Jun Minagawa, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.


Additional Information

Current Arabidopsis Projects

- Kazusa DNA Research Institute
- Kazusa Metabolomics Database (KOMICS) web portal to databases, tools and other information was developed

functions of key differentiation genes, and control of metabolism, under combined efforts of 9 core research groups, 4 supporting facilities/teams, and 19 research groups (2013-2017) using multiple model species not only Arabidopsis but also a new model of land plants, Marchantia polymorpha. Led by Hirokazu Tsuchiya, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

Nara Institute of Science and Technology. Principles of pluripotent stem cells underlying plant vitality (2017-2022)(http://www.plant-stem-cells.jp/). This project aims to answer the key questions: How do plants augment stem cell populations, and how do plants maintain them over long periods of time? The project members investigate the machinery of stem cell division and the regulatory system underlying maintenance of pluripotency and genome integrity. Led by Masaaki Umeda, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.

National Institute for Basic Biology. (2017-2022)(http://photosynthesis.nibb.ac.jp/). Project goal is to elucidate the regulatory mechanisms of photosynthesis by incorporating a new perspective, the regulation of the proton motive force into basic photosynthesis research with the goal of improving photosynthetic efficiency. We expect to establish strategies to re-optimize the photosynthetic machinery under any environment. Led by Jun Minagawa, Grant-in-Aid for Scientific Research on Innovative Areas from MEXT.


related TAIR gene models and annotations, by specifying a Resource ID, a TAIR AGI code or a keyword. All SABRE resources are available from the core facilities of NBRPR (National BioResource Project) (http://sabre.epd.brc.riken.jp/).

RIKEN National Science Institute - Center for Sustainable Resource Science (CSRS)
Metabolome platform using GC-MS, LC-MS, CE-MS and NMR (Kazuki Saito, Masami Hirai, Jun Kikuchi, Tetsuya Sakurai). CSRS established the Arabidopsis metabolomics platform (http://pmr.cs.riken.jp/), consisting of mass spectrometry-based untargeted metabolomics, mass spectrometry-based widely-targeted metabolomics, and NMR-based metabolomics.


Plant-PrAS (Plant-Protein Annotated System) (A. Kuratomi, Y. Yamada, AA. Tokmakov, Y. Kuroda, Y. Fukami, K. Shinozaki, T. Sakurai) Analyzed predicted multiple physicochemical and secondary structural parameters for homologous genes searched, together with Arabidopsis information. Plant resources SABRE2: database connecting plant EST/Full-Length cDNA clones with homologous genes are searched, together with Arabidopsis information. Plant resources through plant metabolomics studies of Daisuke Shibata, including integration of transcriptome and metabolome data on metabolic maps, a plant metabolome database, co-expressed gene search tools and regulatory network research. (http://www.kazusa.or.jp/komics/en)/

AIST Bioproduction Research Institute, Gene Regulation Research Group
CRES-T was applied to more than 1,600 Arabidopsis transcription factors and most T2 seeds were harvested individually. For transcriptional repressors, the group produced more than 300 VP16-fused constructs and harvested individual T2 seeds. The group also prepared Gateway entry clones of ca. 2,000 transcription factors (without stop codon) in collaboration with M. Matsui group in RIKEN. The group developed yeast one-two hybrid library using the entry clones and established high-throughput screening system. (http://bit.ly/1Q4jpJ9).

RIKEN National Science Institute - BioResource Center (BRC)
SABRE2: database connecting plant EST/Full-Length cDNA Clones with Arabidopsis information, Plant resources with homologous genes are searched, together with related TAIR gene models and annotations, by specifying a Resource ID, a TAIR AGI code or a keyword. All SABRE resources are available from the core facilities of NBRPR (National BioResource Project) (http://sabre.epd.brc.riken.jp/).

Hormone platform and RIKEN Plant Hormone Research Network: (Hitoshi Sakakibara, Mutsunori Seo) CSRS established highly sensitive high-throughput phytohormone quantification platform consisting of a mass spectrometry-based technology. Platform is conducting a wide range of collaborative research in plant hormone biology (http://hormones.psc.riken.jp/).

JST-NSF “Metabolomics: Advancing the Scientific Promise to Better Understand Plant Specialized Metabolism for a Low-Carbon Society” (http://bit.ly/2YUScSc), research led by Lloyd W. Sumner (The Samuel Roberts Nobel Foundation) and K. Saito (RIKEN), Oliver Feihe (Univ. of California at Davis) and M. Arita (NIG).

U. Tokyo, RIKEN, JIRCAS, with others of IRRI, CIAT, CIMMYT, Embrapa DREB project: Application of Arabidopsis stress-related genes to molecular breeding of drought tolerant rice and wheat supported by MAFF and JIRCAS. (http://bit.ly/257FR1r) (Kazuko Yamaguchi, Shinozaki U. Tokyo, Kazuo Shinozaki RIKEN, Kazuo Nakashima JIRCAS and others of IRRI, CIAT, CIMMYT, Embrapa) After identifying and applying DREB genes in Arabidopsis, DREB gene function in stress tolerance were recognized as well conserved in important crops. Project develops stress-tolerant soybean, rice and wheat. Recently, transgenic rice lines with Arabidopsis GA/S2 gene were shown to produce higher amount of seeds than non-transgenic rice in the dry field conditions.

New Zealand

Lynette Brownfield
lynette.brownfield@otago.ac.nz
University of Otago, Department of Biochemistry, Dunedin

Use of Arabidopsis

Arabidopsis is used as a research tool in approximately eight institutions in New Zealand (University of Auckland, University of Otago, Massey University, University of Canterbury, Lincoln University and Victoria University, AgResearch Ltd, Plant and Food Research Ltd.)

Conferences, Workshops and Outreach events

AustralAsia Genetics Society Meeting, July 3-6, 2017, Dunedin, New Zealand.

Plant Science Central, 4-6 July, 2017, Palmerston North, New Zealand.

Queenstown Molecular Biology Meeting (including a Plant Satellite) August 28-31, Queenstown, New Zealand.

Selected Publications


Major Funding Sources

- The Marsden Fund administered by the Royal Society of New Zealand (http://www.royalsociety.org.nz/programmes/funds/marsden/)
- Ministry for Business, Innovation and Employment (MBIE; http://www.mbie.govt.nz/)
- Core funding to Crown Research Institutes
- The Catalyst Fund (http://www.mbie.govt.nz/info/services/science-innovation/investment-funding/current-funding/catalyst-fund/)
- The Agricultural and Marketing Research and Information Service (http://www.mbie.govt.nz/)
- The Agricultural and Marketing Research and Information Service (http://www.mbie.govt.nz/)

- Core funding to Crown Research Institutes
- The Catalyst Fund (http://www.mbie.govt.nz/info/services/science-innovation/investment-funding/current-funding/catalyst-fund/)
- The Agricultural and Marketing Research and Information Service (http://www.mbie.govt.nz/)

- Core funding to Crown Research Institutes
- The Catalyst Fund (http://www.mbie.govt.nz/info/services/science-innovation/investment-funding/current-funding/catalyst-fund/)
- The Agricultural and Marketing Research and Information Service (http://www.mbie.govt.nz/)
MASC Country Reports

Norway

Thorsten Hamann
Norwegian University of Science and Technology

Use of Arabidopsis

In 2017 the Norwegian plant biology community held their national conference in Hamar in central Norway with around 60 attendees from all Norwegian universities and research institutes as well as invited speakers from eight different countries. The scientific program during the two-day event covered a diverse range of topics in lectures as well as workshops and public panels where questions like “how to inspire the next generation of plant scientists?” or “Public and political acceptance for genome editing in plant based food production” were discussed. In parallel Karin Metzlaff from the European Plant Science Organization (EPSO) gave a presentation introducing the organization, its aims and activities.

The scientific program was quite diverse illustrated by the examples like: heritable phenotypic changes induced by epigenetic reprogramming; gene and genome dosage on hybridization barriers in Arabidopsis lyrata and A.arenosa; PP2A as a regulator of methionine metabolism by epigenetic reprogramming; gene and genome dosage organization, its aims and activities.

Selected Publications

With respect to publication activities, 2017 was a very good year with more than 30 articles having been published that contain contributions from members of the Norwegian Arabidopsis community. Here attention is being drawn to just a few representative publications in journals like PNAS, J. Exp. Bot. and Plant. Cell and Environment, which illustrate nicely the breadth of Arabidopsis research in Norway. The articles cover topics like endosperm-based hybridization barriers explaining gene flow (Lafon-Placette et al., 2017); peptide-based signaling processes during stress response and abscission (Vie et al., 2017) and the impact of protein phosphatase 2A methylation on environmental stress responses (Creighton et al., 2017).


Major Funding Sources

Research Council of Norway

www.rrc.no

The annual plant biology conference was also financially supported through grants by the Norwegian research council and the Scandinavian Plant Physiology Society www.spps.se

South Korea

Jinwhan Hwang
jwhwang@postech.ac.kr
Pohang University of Science and Technology

Use of Arabidopsis

100 Institutions and 500 labs

Conferences, Workshops and Outreach events

- Plant Winter Conference of Korean Society of Plant Biologists
- Annual meeting of Korean Society of Plant Biologists
- Annual meeting of Korean Society of Molecular and Cell Biologists
- The first Asian conference on Plant-based Pharmaceuticals

Selected Publications


Major Funding Sources

- Systems & Synthetic Agronomicência (≤ 10 MD/yr) by Rural Development Administration, Korea.
- Agricultural Life Science Center (≤ 10 MD/yr) by Rural Development Administration, Korea.
- System understanding of plant senescence and life history (≤ 9 M/yr) by Institute of Basic Research.
- Wooloongchoon Project focusing on carbon metabolism (≥ 10 M/SD/yr for 5 years) supported by Rural Development Agency, Korea.
Spain
José Luis Micó
jmicot@umh.es
Universidad Miguel Hernández, Elche, Spain;

Use of Arabidopsis
About 100 laboratories.

Conferences, Workshops and Outreach events
The “XV Spanish - Portuguese Congress on Plant Physiology” was organized by plant biologists lead by Prof. Teresa Altabella in Barcelona (June 26-30, 2017).

Selected Publications
Authors from laboratories studying Arabidopsis in Spain published about 400 papers in the last year.


Selected Publications

Selected Publications


Applied research (pruce)

Sweden
Maria E. Eriksson
maria.eriksson@umu.se
Umeå University, Umeå Plant Science Centre, Umeå

Use of Arabidopsis
At least ten farmers use Arabidopsis as one of their main plant model species.

Open Resources for Arabidopsis Researchers

• Max Lab hosted by Lund University; https://www.maxiv.lu/se

• Dedicated to high-throughput, nanovolume characterization and quantification of biological macromolecules

• Science for Life Laboratory (SciLifeLab) is a national resource center dedicated to large scale research in molecular biosciences and medicine with two sites: in Stockholm and Uppsala. The major funding for SciLifeLab comes from strategic grants from the Swedish government, http://www.scilifelab.se

• Umeå Plant Science Centre has developed and maintains platforms of genomics, proteomics, metabolomics, quantification of plant growth regulators and wood analysis http://www.upsc.se, found under “resources”

• The Swedish Metabolomics Centre in Umeå is a national resource, http://www.swedishmetabolomicscentre.se/

New Software Tools

The PlantGenie platform; web portals for enabling in-depth exploration of poplar, Norway spruce, and Arabidopsis http://plantgenie.org/

Computational Genetics Division Uppsala University, Carlberg Lab http://www.computationalgenetics.se/

Meetings in 2018: The European Congress on Photosynthesis Research, organized by the International Society for Photosynthesis Research, June 25 – 28, Uppsala, Sweden

The 13th European Nitrogen Fixation Conference 2018, August 18 – 21, Stockholm, Sweden

Fascination of Plants Day’ is celebrated at most major plant science centres across Sweden, which also regularly host outreach activities to highlight research on plants.

Additional Information
Prof. Carmen Fenoll was elected President of the Spanish Society of Plant Physiology.

Figure 31. (a) Inflorescences of 7-week-old plants are shown. opr3-3 mutants are sterile, and (A) treatment (bracket) rescues male fertility. Scale bar, 1 cm. http://dx.doi.org/10.1038/nchembio.2540
Agriculture and Forestry (http://www.ksla.se) promotes sustainable growth by effective innovation systems.

- The Swedish Agency for Innovation Systems (VINNOVA; http://www.vinnova.se) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.

- The Wallenberg Foundations (http://www.wallenberg.org/en) private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.

- Carl Tryggers Foundation for Scientific Research (http://www.carltryggersstiftelse.se,) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.

- The Kempe Foundations (http://www.kempe.com) private foundations devoted to support scientific research in Northern Sweden


**Major Funding Sources**
- The Swedish Research Council (VR, http://www.vr.se) supports basic research and need-driven research in the areas Environment, Agricultural Sciences and Spatial Planning.
- The Wallenberg Foundations (http://www.wallenberg.org/en) private foundations supporting researcher initiated basic research as well as larger centers of excellence devoted to functional genomics and other strategic areas.
- Carl Tryggers Foundation for Scientific Research (http://www.carltryggersstiftelse.se,) is a private foundation supporting research within the areas of agriculture, forestry, biology, chemistry and physics.
- The Kempe Foundations (http://www.kempe.com) private foundations devoted to support scientific research in Northern Sweden
- Stiftelsen Olle Engkvist Byggmästare (http://www.oleengkviststiftelserna.se/)
- Sven and Lily Lawski’s foundation for research in Natural Sciences (Biochemistry and Genetics); http://www.lawskistiftelsen.se/ A private foundation supporting basic science research.
- Functional Genomics Center Zurich - The Neuchâtel Platform of Analytical Chemistry (the Mass Spectrometry and Metabolomics Unit and the Nuclear Magnetic Resonance Unit, http://www.unine.ch/mpu) - Bio-molecular Analysis Platform (collaborative basis, http://bipvg.unige.ch/services/fma/) - Genetic Diversity Center (e.g. genome-wide polymorphisms of Arabidopsis halleri)
- Stiftelsen Olle Engkvist Byggmästare (http://www.oleengkviststiftelserna.se/)
- Sven and Lily Lawski’s foundation for research in Natural Sciences (Biochemistry and Genetics); http://www.lawskistiftelsen.se/ A private foundation supporting basic science research.

**Switzerland**

Kentaro K. Shimizu Kentaro.shimizu@ieu.uzh.ch
Misako Yamaizaki misako.yamaizaki@ieu.uzh.ch
University of Zurich Zurich-Basel Plant Science Center info@plantscience.ethz.ch
Swiss Plant Science Web coordination-spw@unibas.ch

**Use of Arabidopsis**

c. a. 12 institutions and c. a 100 labs.

**Open Resources for Arabidopsis Researchers**
- Swiss-Prot database contributes to TAIR database
- Genevestigator (https://genevestigator.com/gv/)

As a facility or database, we have these resources below.

- Functional Genomics Center Zurich
- The Neuchâtel Platform of Analytical Chemistry (the Mass Spectrometry and Metabolomics Unit and the Nuclear Magnetic Resonance Unit, http://www.unine.ch/mpu)
- Bio-molecular Analysis Platform (collaborative basis, http://bipvg.unige.ch/services/fma/)
- Genetic Diversity Center (e.g. genome-wide polymorphisms of Arabidopsis halleri)

**Conferences, Workshops and Outreach events**

**Conferences**
- PSC Summer school 2017, Understanding Risks and Resilience in Plant Systems, 2 May – 2 June 2017, Einsiedeln
- PSC Symposium 2017, Dynamics of Plant Development & Evolution 30 November - 1 December 2017, Zurich
- SwissPLANT 2018 Symposium, 31 January - 2 February 2018, Meiringen
- Lausanne Genomics Days 2018, 5 – 6 February 2018, Lausanne

**Selected Publications**


- PSC Summer School 2017, Responsible Research and Innovation in Plant Sciences 10-14 September 2017, Einsiedeln, Switzerland

- PSC Symposium 2018, Working Title: 20th Anniversary Symposium Zurich-Basel Plant Science Center – Breathtaking in Plant Sciences – From the laboratory to the world, 5 December 2018, Zurich

- Workshops Molecular studies in nature - How plants sense and react in the nature, 19 February 2018, Zurich

- Plant Development and Evolution from molecules to ecosystems, 20-22 February 2018, Zurich

- PSC Discovery Program for Youth – new Agora project In collaboration with educators of the ETH MINT Lernzentrum, the Zurich-Basel Plant Science Center (PSC) offers workshops for school classes at the secondary school level.

- PSC Summer School 2018, Responsible Research and Innovation in Plant Sciences 10-14 September 2018, Einsiedeln, Switzerland

- PSC Symposium 2018, Working Title: 20th Anniversary Symposium Zurich-Basel Plant Science Center – Breathtaking in Plant Sciences – From the laboratory to the world, 5 December 2018, Zurich

- Workshops Molecular studies in nature - How plants sense and react in the nature, 19 February 2018, Zurich

- Plant Development and Evolution from molecules to ecosystems, 20-22 February 2018, Zurich

- PSC Discovery Program for Youth – new Agora project In collaboration with educators of the ETH MINT Lernzentrum, the Zurich-Basel Plant Science Center (PSC) offers workshops for school classes at the secondary school level.

- Selected Publications


Additional Information

Highlight 2018

- Switzerland has had regularly a high-quality publications (e.g. Andersen et al., Nature 2018, Meccchia et al., Science 2017).
- A 5-year joint project for Japan and Switzerland on polyploid Arabidopsis and crop species was funded by Japan Science and Technology Agency (JST) (PI, Kentaro Shimizu).

Major Funding Sources

1. Swiss National Science Foundation (SNSF) http://www.snf.ch/en/Pages/default.aspx
2. European Research Council (ERC), http://erc.europa.eu/
8. Japan Science and Technology Agency (JST), Core Research for Evolutional Science and Technology (CREST), https://www.jst.go.jp/kyokai/crest_en/

Use of Arabidopsis

The United Kingdom has approximately 45 academic departments and research institutes that are actively conducting Arabidopsis research. The BBSRC is the major funder of Arabidopsis research, which includes institutional support for the John Innes Centre, IIBERS in Aberystwyth and Rothamsted Research.

Open Resources for Arabidopsis Researchers

- The European Arabidopsis Stock Centre (EuNASC) is based at the University of Nottingham. http://arabidopsis.info/

New Software Tools

- The Centre for Integrative Biology based at the University of Nottingham has developed a range of open source software, hardware and other resources. https://www.cib.unimanchester.ac.uk/tools-resources/
- The Bassal Lab at the University of Birmingham have developed tools for analysis of gene expression and interaction networks in Arabidopsis. https://www.georgebassellab.com/online-tools/
- In addition they have developed 3DCellAtlas that describes a computational approach to perform digital single cell analyses in 3D plant organs. http://www.georgebassellab.com/3d-cell-atlas/
- The Millar lab at the University of Edinburgh has developed BioDare2 as a repository for circadian, biological data, providing a platform for data sharing and period analysis. https://biodare2.ed.ac.uk/welcome
- Research at the John Innes Centre have developed Leaf-GP (Growth Phenotypes) an open and automated software application for measuring growth phenotypes for Arabidopsis and wheat https://github.com/Crop-Phenomics-Group/Leaf-GP/releases
- The Tsaftaris lab at the University of Birmingham have developed Phenotiki is an affordable, easy-to-use, maintain and deploy image-based plant phenotyping platform. https://phenotiki.com/
- The Cell Architect program has been developed by researchers at the John Innes Centre and is designed to recognise microtubule (MT) and measure MT pattern changes induced by different chemicals https://github.com/TeamMacLean/CellArchitect

Conferences, Workshops and Outreach events

In 2017 and 2018 GARNet have and will organise conferences and workshops attended by Arabidopsis researchers:

- SEB-GARNET meeting on From Proteome to Phenotype: role of post-translational modifications: University of Edinburgh December 11th-13th 2017 http://www.sebology.org/events/event/from-proteome-to-phenotype

Selected Publications

The majority set of UK publications that feature Arabidopsis are documented on the GARNet blog. http://blog.garnetcommunity.org.uk/arabidopsis-research-roundups/

- Plant Methods published in the UK have collated a set of resources entitled 'Plants in Computer Vision': https://www.biomedcentral.com/collections/PCV
- The Cell Architect program has been developed by researchers at the John Innes Centre and is designed to recognise microtubule (MT) and measure MT pattern changes induced by different chemicals https://github.com/TeamMacLean/CellArchitect
Figure 34. AtPIN1 protein immunolocalization in wild-type, pin1-613, and pin1-4 mutants. (A) AtPIN1 protein accumulation in wild-type Ler inflorescence apex shows polar PIN protein at the sites of initiating organs (asterisks), and during vein patterning below the apex (arrow). (B) No AtPIN1 protein is detected in pin1-613 null mutant pinned apexes. (C) Abundant AtPIN1 protein is detected in pin1-4 pinned apexes, primarily in provascular tissues below the meristem apex (arrow). Box shows region of detail in (D). (D) Detail of boxed area shown in (C). AtPIN1 protein in pin1-4 accumulates in a perinuclear domain (arrow). All samples are 9 µm longitudinal sections. Scale bars: 25 µm in A, and 5 µm in D.


Major Funding Sources
Biotechnology and Biological Sciences Research Council (BBSRC) http://www.bbsrc.ac.uk/

The Gatsby Charitable Foundation
http://www.gatsby.org.uk/

European Research Council
http://ec.europa.eu/research/era/index_en.htm

Natural Environment Research Council
http://www.nerc.ac.uk/

The Gates Foundation
http://www.gatesfoundation.org/

Additional Information
The GARNet YouTube channel includes interviews with academics about recent papers. https://www.youtube.com/channel/UCgB90HOImou5SBrqFhNz7hQ


United States of America

https://www.araport.org/community/group/naasc

Joanna Friesner jdfriesner@ucdavis.edu

University of California, Davis, NAASC Coordinator, with input from the North American Arabidopsis Steering Committee (NAASC); Doris Wagner, NAASC President (University of Pennsylvania); Rick Vierstra (Washington University in St Louis); Sarah Assmann (Penn State University); Erin Grotewold (Michigan State University); Elizabeth Haswell (Washington University in St Louis); Jose Dimmenny, NAASC Treasurer (Stanford University); Roger Innes (Indiana University); Peter McCourt (University of Toronto- Canada); Jean Cutler (University of California, Riverside); and Jennifer Nemhauser (University of Washington, Seattle);

Use of Arabidopsis

It’s not straightforward to get accurate numbers of Arabidopsis users in the United States. However, according to two major resources, The Arabidopsis Information Resource (TAIR) and the Arabidopsis Biological Resource Center (ABRC), estimates are that there are approximately 4,700 labs that use Arabidopsis resources registered in the US, and 12,500 people.

Open Resources for Arabidopsis Researchers

There are a large number of US institutions, companies, and facilities that conduct Arabidopsis research and it would be impossible to list them all. Therefore, we list the primary resource entity, ABRC https://abrc.osu.edu/seed-handling, the US stock center which, in partnership with the European Stock Centre (NASC, UK) and RIKEN BioResourceCenter (Japan), provide valuable Arabidopsis seed and other resources to the global community.

The Arabidopsis Biological Resource Center collects, preserves, reproduces and distributes diverse seed and other stocks of Arabidopsis thaliana and related species. Resources are donated by researchers from around the world. ABRC has been providing Arabidopsis and related species seed and other resources for research and education since 1991. At present ABRC has about 4,000 characterized mutant and 2,000 transgenic lines.

Overall the seed collection is approaching half a million (~490,000) counting all the characterized and uncharacterized T-DNA lines, as well as the natural accessions. More than 100,000 samples are shipped annually to researchers and educators from 60 countries.

ABRC holdings include: Arabidopsis seed stocks and clones, Arabidopsis cell lines and protein chips, seed and clone resources from related species, Cloning vectors and host strain, Education kits.

New Software Tools


(2) GRACE (Gene Regulatory network inference ACCuracy Enhancement); Enhancing gene regulatory network inference through data integration with markov random fields. Michael Banta, J and Seung Y. Rhee. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5286517/

(3) GENIST is an algorithm to infer gene regulatory networks from spatial and temporal datasets. https://github.com/madelux/GENIST


(8) http://araport.org The Arabidopsis Information Portal, started through work by the International Arabidopsis Informatics Consortium in 2012. The new portal has been online since April 2014. While not a new tool, this is a key contribution by the US Arabidopsis community.

(9) https://www.araport.org: TAIR have successfully moved to a subscription-based model, and their non-profit organization, Phoenix Bioinformatics, continues TAIR’s annotation work. Open access is available after one year, and TAIR continues to provide free access for students using TAIR in their coursework upon request from the course organizer. While not a new tool, this is a key contribution by the US Arabidopsis community.
The North American Arabidopsis Steering Committee (NAASC) hosted the 28th International Conference on Arabidopsis Research (ICAR): “Arabidopsis Research in 2017 and Beyond,” June 2017 in St. Louis, Missouri, USA. 470 attendees from 20 countries participated in 29 sessions including 4 keynote lectures, 16 plenary and concurrent sessions, and 7 workshops. The program focused especially on female and early-career speakers: of 46 invited speakers, 46% were female (including 3 of 4 Keynotes, and 41% were ‘early-career’ speakers at the level of assistant professor or earlier. Of 10 concurrent session chairs, 5 were female and 6 were early-career invited speakers, providing exposure and a diverse program since chairs selected the 50 talks from submitted abstracts.

Platform sessions featured nearly 100 oral presentations and there were nearly 350 poster presentations. NAASC encouraged session chairs to prioritize early-career researchers and diversity in submitter gender and location. NAASC developed for ICAR 2017 new career-building and enhancing activities that proved to be successful.

Three pre-ICAR skills-based workshops were developed in collaboration with the Danforth Plant Sciences Center and funded by an award from the US National Science Foundation (NSF). Two additional early-career-focused workshops were held during ICAR 2017. The skills-based workshops included (1) “Data Carpentry”: an example-driven workshop on basic concepts, skills and tools for working more effectively with data via short tutorials alternated with hands-on practical exercises, (2) “ATAC-seq Hands-on Workshop on mapping chromatin accessibility and TF footprints”: a wet-lab and computational introduction to the ATAC-seq process, (3) “Hackathon for High-throughput Phenotyping”: an activity that expanded on the introduction to genomics data and data management and analysis for genomics research.

The career-exploration panel workshops were, firstly, “Careers Beyond the Academy” including Working in Science Communication; Career Development for Success in Industry and Elsewhere; Working at USDA and Other Government Jobs; Working at a PUI (Primarily Undergraduate Institution); Advocating for Plant Science and Careers in Science Policy; Careers for Scientists in Intellectual Property (IP) Law; and Industry Job Search in US and France; and secondly, “Careers in Industry” featuring panelists from NewLeaf Symbiotics, BioGenerator, CONVIRON, and Monsanto. In the workshops, four of seven, and three of four panelists, respectively, were female.

Several community-organized workshops at ICAR 2017 addressed impacts on scientists including “Communicating Your Science to Peers and Beyond”, and “Overcoming the Imposter Phenomenon in Academic Science – an Interactive Workshop to Combat Imposter Thoughts.” As a bit of extra fun, science and networking, the ICAR 2017 party was hosted by the Danforth Center which generously opened its doors with an open house, including site tours, for conference attendees. NAASC and Danforth staff collaborated to develop a scientific and social program that enabled science exchange in an informal setting. The activities concluded with a party featuring VO5, a live 9-piece disco band, and lots of great local food and dancing.

Planning for ICAR 2020- US- is underway. NAASC members assembled an international External Advisory Board (EAB) for ICAR 2020 which is scheduled to return to the US after rotations in Europe and Asia. The EAB began discussions and meetings in winter 2017 to envision new approaches, sessions, and activities for the US-located ICAR to ensure the meeting stays relevant and valuable to the international Arabidopsis community. The discussion by the EAB has primarily involved considering new and exciting scientific plant biology topics, an invigorated focus on bringing in new voices from the community, and novel approaches and activities to enhance collaboration, participation, and information sharing. NAASC members are expected to announce the selected date and location for ICAR 2020 during ICAR 2018 in Finland.

Selected Publications


Major Funding Sources

US Arabidopsis Research is primarily supported by funding through the Federal Government via the National Science Foundation (NSF):

http://www.nsf.gov/

Additional support may come from these sources:

US Department of Agriculture (USDA):

http://www.usda.gov/

US Department of Energy (DOE):

http://energy.gov/

National Institutes of Health (NIH):

http://www.nih.gov/
Members of the MASC subcommittees

Bioinformatics
Nicholas Provart
University of Toronto, Canada
nicholas.provart@utoronto.ca (Chair)
Sébastien Aubourg
INRA, Evry, France
aubourg@envy.inra.fr

Segen Mayer
University of Nottingham, UK
segm@arabidopsis.info

Klaus Mayer
Helmholtz Zentrum Münch, Germany
kmayer@gsf.de

Yasukazu Nakamura
Kazusa DNA Research Institute, Japan
yn@kazusa.or.jp

Yves Van Den Peer
VIB / Ghent University, Belgium
yvdp@psb.ugent.be

Christopher Town
J. Craig Venter Institute, US
cttown@jcvi.org

Tetsuro Toyoda
RIKEN BASE, Japan
toyoda@base.riken.jp (Chair)

Clone-Based Functional Genomics Resources (ORFeomics)
Motoaki Seki
RIKEN Center for Sustainable Resource Science (CSRS), Japan
motoaki.seki@riken.jp (Chair)

Joe Ecker
The Salk Institute for Biological Studies, US
ejck@ucsd.edu (co-chair)

Pascal Braun
Technische Universität München, Germany
pascal.falk@helmholtz-muenchen.de

Satoshi Iuchi
RIKEN Bioresource Center, Japan
satoshi.iuchi@riken.jp

Debbie Crist
ABRC, Ohio State University
crist.30@osu.edu

Natural Variation and Comparative Genomics
J. Chris Pires
University of Missouri, US
jcp@missouri.edu (Chair)

Brian P. Dilkes
Purdue University, US
bdilken@purdue.edu (Co-Chair)

Justin Borevitz
Australian National University, Australia
justin.borevitz@anu.edu.au

John Doonan
Aberystwyth University, UK
john.doonan@aber.ac.uk

Joe Ecker
Salk Institute, US
ecker@salk.edu

Pheonomics
Fabio Fiorani
Forschungszentrum Jülich, Germany
fabio.fiorani@fz-juelich.de (Chair)

Christine Granier
INRA-UPAGRO, France
granier@upago.inra.fr (Co-Chair)

Rob Last
Michigan State University, US
rlast@msu.edu

Basil Nikolou
Iowa State University, US
bdimas@iastate.edu

Joshua Heazlewood
Lawrence Berkeley National Laboratory, US
jheazlewood@lbl.gov (Chair)

Katja Bärenfaller
Federal Institute of Technology, Switzerland
katja.barenfall@eth.ch

Sacha Baginsky
University of California-Davis, US
sacha.baginsky@ucdavis.edu

Hans-Peter Braun
University of Heidelberg, Germany
hans.peter.braun@uni-heidelberg.de

Harvey Millar
The University of Western Australia, Australia
harvey.millar@uwa.edu.au

Satoshi Iuchi
RIKEN Bioresource Center, Japan
saito@riken.jp

Scott Peck
University of Missouri, US
scott.peck@missouri.edu

Loïc Rajjou
AgroParis Tech, France
loic.rajjou@versailles.inra.fr

Sigrun Reumann
University of Stavanger, Norway
sigrun.reumann@ui.no

Norbert Rolland
C.E.A, Grenoble, France
norbert.rolland@cea.fr

Verónica Santoni
INRA, France
santoni@supagro.inra.fr

Waltraud Schulze
University of Hohenheim, Stuttgart, Germany
waltraud.schulze@uni-hohenheim.de

Nicolas Taylor
The University of Western Australia, Australia
ntaylor@cyllene.uwa.edu.au

Julian Whitelegge
University of California, US
jpw@chem.ucla.edu

Stefanie Wienkoop
University of Vienna, Austria
stefanie.wienkoop@univie.ac.at

Systems and Synthetic Biology
Siobhan Brady
University of California, US
sbrady@ucsd.edu

Malcolm Bennett
University of Nottingham, UK
malcolm.bennett@nottingham.ac.uk

Leah Band
University of Nottingham, UK
leah.band@nottingham.ac.uk

Pascal Falter-Braun
Technische Universität München, Germany
pfalter@tu-muenchen.de

Rodrigo A. Gutiérrez
P. Universidad Católica de Chile, Chile
gutierrez@bio.puc.cl

Gabriel Krouk
CNRS, France
krouk@ipsl.upmc.fr

Nicola Patron
Earlham Institute, UK
nicola.patron@earlham.ac.uk
French Graduate School of Research: research, teaching, training and innovation in plant sciences

Understanding the genetic, molecular and cellular mechanisms controlling the physiology and development of plants, as well as their interactions with fluctuating biotic and abiotic environments
- Over 50 plant sciences research teams from 5 laboratories in the Paris area
- About 700 staff members (400 permanent positions, 150 postdocs and PhD students)
- Over 200 publications per year

Developing high-tech resources and cutting-edge technologies
- 14 scientific platforms: imaging, cytology, biochemistry, chemistry, metabolism, genomics, epigenomics, transcriptomics, proteomics, protein-protein interactions, plant culture, biological stock centers
- 5500 m² of greenhouses / About 100 growth chambers / Different biosafety levels

Training plant sciences researchers, engineers and leaders of tomorrow
- About 12,000 hours of innovative theoretical and experimental teaching and training
- More than 100 training opportunities in SPS laboratories per year
- State of the art equipment for the practical training of students

Going from basic research to a socio-economic and environmental impact
- Applications in: Plant breeding and biotechnologies / Plant adaptation to the environment / Seeds and yield / Feed, food and nutrition / Cosmetics and health / Bioenergy and bio-based materials
- More than 70 ongoing contracts, including 20 with private partners

www.saclayplantsciences.fr