Comparative seed biology will lead the way: Evolutionary conservation and biodiversity of physiological mechanisms that control germination.

Celery seed (days to emergence):
Theophrastus of Eresos 39-50
ISTA germination tests 10-28

ISTA: Uniformity in Seed Testing

Modern Seed technologies / treatments

Seed germination ✓
Seed dormancy ✓
Seed after-ripening ✓
Seed priming ✓
Seed longevity ✓
Comparative seed biology will lead the way: Evolutionary conservation and biodiversity of physiological mechanisms that control germination.
Comparative seed biology will lead the way: Evolutionary conservation and biodiversity of physiological mechanisms that control germination.

Plant hormone ethylene as seed vigor marker.
Importance to consider specific seed tissues.

Petruzelli et al. (2003, 2000, 1999)

see www.seedbiology.eu for references


ISTA: Uniformity in Seed Testing

Modern Seed technologies / treatments
Comparative seed biology will lead the way:
Evolutionary conservation and biodiversity of physiological mechanisms that control germination

Distinct effects of plant hormone ethylene on seed germination and seedling establishment


ISTA: Uniformity in Seed Testing
Comparative seed biology will lead the way:
Evolutionary conservation and biodiversity of physiological mechanisms that control germination

ABA-ethylene antagonism:
- Abscisic acid (ABA)
- Ethylene (precursor ACC)
- Pericarp (Fruit coat)

Importance of natural + artificial seed covers!

ISTA: Uniformity in Seed Testing

Beta vulgaris (sugar beet)
Operculum
Pericarp
Radicle
Outer + Inner testa
1. Evolution of seed quality from MYA until today

MYA = Million Years Ago


Arabidopsis thaliana (mouse-ear cress, Brassicaceae):
Establishment of the first model plant of the molecular era

Genetic map
Mutants and transgenic plants
Genome project (completed in 2000)
Microarrays, ‘omics’
NSF 2010 project
Genomics decade

INSIDE ARABIDOPSIS
The Arabidopsis 2010 project has linked thousands of the plant’s genes and proteins to their biological function.

Arabidopsis publications (total, all research areas)

Number of publications per year (ISI Web of Knowledge)

Inside Arabidopsis:
- Studied microRNAs and the regulatory networks that control flower development
- Identified more than 350 genes with an essential role in seed development
- Analysed the expression of 27,013 specific sections of DNA
- Identified more than 4,000 gene mutations that cause defects in photosynthesis, chloroplast metabolism and development
- Studied transcription factors involved in responses to infection
- Mapped gene expression in developing roots

‘a simple weed...’

www.seedbiology.de
1. Evolution of seed quality from MYA until today

MYA = Million Years Ago

1. Evolution of seed quality from MYA until today

MYA =
Million
Years
Ago


Arabidopsis thaliana (mouse-ear cress, Brassicaceae): Establishment of the first model plant of the molecular era

- Genetic map
- Mutants and transgenic plants
- Genome project (completed in 2000)
- Microarrays, ‘omics’
- NSF 2010 project
- Genomics decade

Next decade:
- Post-genomics
- Phylo-genomics
- Model systems
- Systems biology
  ... ???

Arabidopsis publications (total, all research areas)

Seed development + germination + dormancy = 26490 = 100%

Seed development + germination + dormancy + Arabidopsis = 3370 = 13%

ca. 23% (2010)

Year
0 1000 2000 3000 4000 5000 6000
Number of publications per year (ISI Web of Knowledge)

www.seedbiology.de
1. Evolution of seed quality from MYA until today

Importance of seed tissue interactions in germination control!

Origin of seed habit ⇒ diversity of angiosperm seed mechanisms

2. Mechanisms of germination: Lettuce as example

*Lactuca sativa* (Asteraceae)


2. Mechanisms of germination: Lettuce as example

**Lactuca sativa** (Asteraceae)

(1) **Seed germination:**
Endosperm weakening + embryo growth potential!

(2) **Seedling establishment:**
Distinct developmental and molecular regulatory program (≠ seed germination)!

2. Mechanisms of germination: Seed tissue interactions

- Mechanical restraint, e.g. inhibition of endosperm weakening
- Prevention of inhibitor leakage, e.g. abscisic acid (ABA)
- Interference with water uptake or gas exchange, e.g. O\textsubscript{2} (sugar beet pericarp)*

Covering layers or envelopes:

Testa and pericarp  Lateral endosperm  Micropylar endosperm

Restraint weakening

Embryo (radicle, hypocotyl):

Growth potential increase

- Gibberellin (GA) - Abscisic acid (ABA) antagonism: Endosperm weakening and embryo growth potential!
- Ethylene - ABA antagonism: Ethylene promotes weakening!**

2. Mechanisms of germination: Seed tissue interactions

- Mechanical restraint, e.g. inhibition of **endosperm weakening**
- Prevention of inhibitor leakage, e.g. abscisic acid (ABA)
- Interference with water uptake or gas exchange, e.g. O$_2$ (sugar beet pericarp)

**Covering layers or envelopes:**
- Testa and pericarp
- Lateral endosperm
- Micropylar endosperm

**Restraint weakening**
- Growth potential
- Cotyledons
- Radicle

**Embryo (radicle, hypocotyl):**
- Growth potential increase

- Thermoinhibition lettuce: narrow temperature causes switch at high temperature $\Rightarrow$ ABA up, GA down, ethylene down
- Thermotolerance lettuce: Natural variation temperature switch $\Rightarrow$ QTL for lettuce thermotolerance $\Rightarrow$ QTG for ABA production

2. Mechanisms of germination: **Seed technology interactions**

- Mechanical restraint, e.g. inhibition of **endosperm weakening**
- Prevention of inhibitor leakage, e.g. abscisic acid (ABA)
- Interference with water uptake or gas exchange, e.g. $O_2$ (sugar beet pericarp)*

Covering layers or envelopes: 

- Testa and pericarp
- Lateral endosperm
- Micropylar endosperm

Seed biotechnologies and enhancements improve seed quality:

- Seed priming, seed coating/pelleting (artificial envelopes), ...
- Seed treatments: Fungi-, Insect-, Nematicides, Plant hormones

2. Mechanisms of germination: Lettuce seedling uniformity
3. Hormonal control endosperm rupture: Solanaceae

- Endosperm weakening studied in Asterales (lettuce), Solanales (tomato, tobacco)
- Two-step germination *Nicotiana* spp.: Testa rupture $\Rightarrow$ Endosperm rupture

![Diagram of seed development and germination](image_url)
3. Hormonal control endosperm rupture: Solanaceae

- Endosperm weakening studied in Asterales (lettuce), Solanales (tomato, tobacco)
- Two-step germination *Nicotiana* spp.: Testa rupture $\Rightarrow$ Endosperm rupture
4. Endosperm in mature seeds: Evolution and functions

Martin’s tree of structural seed types (1946) based on embryo-endosperm morphology of > 1287 mature seeds
Martin (1946), Baskin and Baskin (2004)

Darwin’s tree of life (1837)
Darwin’s evidence: Structure
ANGIOSPERM SEED PHYLOGENY

EMBRYO TO SEED RATIOS = E:S

Forbis et al. (2002)
Evolution 56: 2112-2125

Trollius (Ranunculaceae)

Lactuca (Asteraceae)

Iris (Iridaceae)

Triticum (Poaceae)

Chenopodium (Amaranthaceae)

Cucumis (Cucurbitaceae) C↓ (perisperm)

Lepidium (Brassicaceae) C↓ GA↓ Ethylene↓ ABA↑

Arabidopsis (Brassicaceae)

Syringa, Fraxinus (Oleaceae) C↓ GA↓

Solanaceae: Solanoideae, Cestroideae

Coffea (Rubiaceae) C↓ GA↓ ABA↑ (biphasic)

Lactuca (Asteraceae) C↓ GA↓

Apium (Apiaceae)

Chenopodium (Amaranthaceae)

Trollius (Ranunculaceae)

Iris (Iridaceae) C↓

Triticum (Poaceae) C↓

ROSID ENDOSPERM SYSTEMS:

Solanaceae: Solanoideae, Cestroideae

Cestroideae:
- Lycopersicon C↓ GA↓ ABA↑ (?)
- Capsicum C↓ GA↓
- Datura, Solanum

Cestroideae:
- Nicotiana, Petunia

ASTERID ENDOSPERM SYSTEMS:

Cucumber (Cucurbitaceae)

Coffea (Rubiaceae) C↓ GA↓ ABA↑ (biphasic)

Solanoideae:
- Lycopersicon C↓ GA↓ ABA↑ (?)
- Capsicum C↓ GA↓
- Datura, Solanum

Cestroideae:
- Nicotiana, Petunia

Puncture force:
C↓ = decrease (control)
GA↓ = GA promotes
ABA↑ = ABA inhibits
5. Comparative seed biology: DFG weakening project Le720/6

DFG endosperm weakening project (2006-2009):

Lepidium (cress) ↔ Arabidopsis
- comparative approach enables to identify evolutionary conserved mechanisms for seed germination
- ⇒ Talk by Ada Linkies
- Advantages of both seed systems
- Establish or apply technologies to cress was not always easy...
5. Comparative seed biology: DFG weakening project Le720/6

DFG endosperm weakening project (2006-2009):

Collaborators:
Bill Finch-Savage (Warwick)
Karl Morris (Warwick, UK)
James Lynn (Warwick, UK)
Francoise Corbineau (Paris)
Miroslav Strnad (Olomouc, CZ)
Veronika Tureckova (Olomouc)
Ada Linkies         Kerstin Müller
Meike Wenk, Tina Carstens (Diploma students)

DFG endosperm weakening project (2010-2012):

Collaborators:
Dr. Ada Linkies (postdoc)
Antje Schulz (PhD student)
Magdalena Jura (PhD student)
Dr. Krystyna Oracz (AvH-stipend)
Claudia Waack (Diploma student)

ERA-NET PG vSEED: Karin Weitbrecht, Sebastian Busch
5. Comparative seed biology: The European vSEED project

The ‘virtual SEED’ project (9.2009-8.2012):

“This interdisciplinary project will analyse the comparative biology of the closely related Brassicaceae species *Arabidopsis thaliana* and *Lepidium sativum* (garden cress), using engineering, imaging, identification of key transcriptome networks, modelling, and post-genomics approaches to develop a virtual germinating seed.”

Seed biomechanics: puncture-force technique

Mike Holdsworth (Nottingham)
John King (Nottingham)
Andy Wood (Nottingham)
Nichola Everitt (Nottingham)
Paul Knox (Leeds)
Leonie Bentsink (Wageningen)
Gerhard Leubner (Freiburg)
Thomas Speck (Freiburg)
Some methods applied to *Lepidium sativum* (garden cress):

- Seed tissue-specific **transcriptome (cross-species microarrays)** (Linkies et al. 2009)*, proteome (Müller et al. 2010) and hormone (Antje Schulz, Karin Weitbrecht) analysis
- **Tissue-specific** subtractive suppression hybridization (SSH) (Linkies et al. 2010)
- Quantitative (real time) pRT-PCR (superior reference genes) (Ada Linkies, Kai Gräber)
- Genetic transformation Brassicaceae, transgenic cress seeds (Ada Linkies, Kai Gräber)
- Tissue-specific **cell-wall** and ROS analyses (Müller et al. 2009) (Krys Oracz, Magda Jura)
- Gene, cDNA, promoter cloning from various **Brassicales** species
- Biomechanical and imaging techniques (Karin Weitbrecht, Sebastian Busch)

A. Hierarchical 'whole-seed' dormancy classification (Baskin and Baskin, 2004)

1. Class - **Physiological dormancy (PD)**
   - Level - PD deep
   - Level - PD intermediate
   - Level - PD non-deep > Type 1 to 5
   
   - Brassicaceae: *Arabidopsis thaliana*, *Lepidium* ssp.
   - Solanaceae: tomato, tobacco
   - Asteraceae: lettuce, sunflower
   - Poaceae: barley, wheat, wild oat

2. Class - **Morphological dormancy (MD)**
   
   - *Apium graveolens* - celery (“underdeveloped” embryo)

3. Class - **Morphophysiological (MPD)**
   
   - *Trollius* spp., *Fraxinus excelsior* (MD+PD combined)

4. Class - **Physical dormancy (PY)**
   
   - *Nelumbo nucifera* - sacred lotus (water-impermeable palisade cell layers in seed or fruit coat)

5. Class - **Combinatorial dormancy (PY+PD)**
   
   - *Geranium* spp., *Trifolium* spp.

---

Seed dormancy is a block to the completion of germination of an intact viable seed under favourable conditions.

B. Components of dormancy:

- **CD** = coat dormancy caused by testa, endosperm, pericarp restraint (excised embryos grow)
- **ED** = embryo dormancy caused by block to embryo extension (excised embryos do not grow)

C. Genes involved in dormancy:

- Unspecific, also affecting other traits, e.g. pleiotropic *aba1* mutant
- Specific, not affecting vegetative traits, seed-specific like *DOG1*

---

Arabidopsis thaliana:

- PD non-deep Type 1, **CD**
- Complex GA-ABA antagonism

---

6. Molecular mechanisms of dormancy: *Arabidopsis DOG1*

- Natural variation for seed dormancy among *Arabidopsis* ecotypes (Ler, Cvi, ...)
- Seed dormancy is a quantitative trait that can be approached by QTL analysis
- *DOG1 (Delay Of Germination1)* is the first QTG cloned for seed dormancy

**Graph:**

- Germination (%) vs. Seed dry storage (days)
- Line graphs for Ler and Cvi
  - Ler: Black line
  - Cvi: Red line

**Work of the group of Maarten Koornneef (MPI Köln):**
- Bentsink et al. (2006) Proc Natl Acad Sci USA 103: 17042-17047

QTL = Quantitative Trait Locus; QTG = Quantitative Trait Gene
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**QTL = Quantitative Trait Loci mapping for Arabidopsis seed after-ripening** (Alonso-Blanco et al. 2003)

1. **QTL analysis for dormancy using RILs = Recombinant Inbred Lines for Ler/Cvi**

<table>
<thead>
<tr>
<th>QTL</th>
<th>DOG2</th>
<th>DOG3</th>
<th>DOG6</th>
<th>DOG5</th>
<th>DOG4</th>
<th>DOG1</th>
<th>DOG7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chrom.</td>
<td>1</td>
<td>1</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>% (days)</td>
<td>12% (+25d)</td>
<td>10% (-12d)</td>
<td>4.4% (-13d)</td>
<td>5.4% (-19d)</td>
<td>8% (-22d)</td>
<td>12% (-29d)</td>
<td>4.4% (-15d)</td>
</tr>
</tbody>
</table>

2. **Fine-mapping using NILs = Near Isogenic Lines for Ler/Cvi** (representative NILs are shown)

Work of the group of Maarten Koornneef (MPI Köln):
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QTL = Quantitative Trait Loci mapping for Arabidopsis seed after-ripening (Alonso-Blanco et al. 2003)

1. QTL analysis for dormancy using RILs = Recombinant Inbred Lines for Ler/Cvi

<table>
<thead>
<tr>
<th>QTL</th>
<th>DOG2</th>
<th>DOG3</th>
<th>DOG6</th>
<th>DOG5</th>
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<tbody>
<tr>
<td>Chrom.</td>
<td>1</td>
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2. Fine-mapping using NILs = Near Isogenic Lines for Ler/Cvi (representative NILs are shown)

3. QTG = Quantitative Trait Gene cloning of *DOG1 = Delay Of Germination1* (Bentsink et al. 2006)


*DOG1 (At5g45830)* dormancy gene encodes an unknown protein

BLAST search: No DOG1-related sequences in the database (2006)
6. Molecular mechanisms of dormancy: *Arabidopsis DOG1*

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- Natural variation for seed dormancy among Arabidopsis ecotypes (Ler, Cvi, ...)
- Seed dormancy is a quantitative trait that can be approached by QTL analysis
- DOG1 (Delay Of Germination1) is the first QTG cloned for seed dormancy

**Arabidopsis thaliana** ecotypes Ler and Cvi (natural variation for seed dormancy)

![Graph showing germination percentage over seed dry storage days](image)

**DOG1** (At5g45830) dormancy gene encodes an unknown protein

BLAST search: No DOG1-related sequences in the database (2006)
6. Molecular mechanisms of dormancy: *Lepidium* dormancy

- *Lepidium* spp. monophyletic clade
- Adaptation to distinct environments
- *Lepidium* spp. physiological dormancy
  - CD = Coat dormancy
  - ED = Embryo dormancy
  - ND = Non-dormant
- *Lepidium* spp. *DOG1* genes found in dormant and non-dormant species

Collaborations (*Lepidium*, dormancy genes):
Klaus Mummenhoff (University Osnabrück)
Wim Soppe, Kazumi Nakabayashi (MPI Köln)

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Deutsche Forschungsgemeinschaft

DFG Le720/7

*DOG1* project

Kai Graeber

---

6. Molecular mechanisms of dormancy: *Lepidium* dormancy

(A) Non-dormancy in *Lepidium* spp. seed accessions

Lepidium sativum

Lepidium ruderale

Lepidium draba

![Graphs showing endosperm rupture over time for different treatments and species.]

(B) Coat-dormancy

Lepidium oxytrichum

(C) Embryo dormancy

Lepidium pedicellatum

(D) Tetrazolium test

Lepidium sativum

Lepidium pedicellatum

---

6. Molecular mechanisms of dormancy: *Lepidium DOG1*

Brassicaceae *DOG1* orthologous genes *AtDOG1, LesaDOG1, BrDOG1*:
- Putative DOG1 proteins similar in size and high sequence similarity (85-88%)
- Introns and 5’- and 3’-non-coding regions ca. 50% pairwise identity
- Promoter regions *AtDOG1* Cvi contains *cis*-acting elements for ABA regulation:
  - RY repeat (CATGCA; -500 from ATG) for seed- and ABI3-mediated expression
  - ABRE motifs (TACGTGTC; -1671 and -1650) for ABI5-mediated responsiveness
- RY and ABRE motifs in *BrDOG1* promoter - *Is LesaDOG1 regulated by ABA?*
- *DOG1* in Brassicaceae - *What is the evolutionary origin of the DOG1 gene?*

*AtDOG1*: Bentsink et al. (2006) Proc Natl Acad Sci USA 103: 17042-17047
*LesaDOG1* and *BrDOG1*: Graeber et al. (2010) *Plant Molecular Biology* 73: 67-87
6. Molecular mechanisms of dormancy: *Lepidium DOG1*

- **LesaDOG1** transcription is ABA inducible upon seed imbibition
- **LesaDOG1** transcript abundance ~ endosperm cap weakening
- **DOG1** has role(s) in germination timing of non-dormant seeds

*LesaDOG1* and *BrDOG1*: Graeber et al. (2010) *Plant Molecular Biology* 73: 67-87
6. Molecular mechanisms of dormancy: *Lepidium DOG1*

- Two DOG1 paralogs found in the genomes of two *Lepidium* species
- High similarity in putative exon regions of the *Lepidium DOG1* genes
- Putative exon regions used to investigate phylogenetic relationships
- The two DOG1 paralogs LesaDOG1a and LesaDOG1b of *L. sativum* are more similar to DOG1 of other Lepidium species than to each other

LesaDOG1 and BrDOG1: Graeber et al. (2010) *Plant Molecular Biology* 73: 67-87
6. Molecular mechanisms of dormancy: Brassicaceae DOG1

- “Phylogenetic DOG1 gene walking”
- Complementation Arabidopsis dog1 mutant

Evidence for Brassicaceae DOG1 genes
6. Molecular mechanisms of dormancy: Brassicales DOG1

- “Phylogenetic DOG1 gene walking”
- Complementation Arabidopsis dog1 mutant

Brassicales (Rosid clade)

Family includes species with endospermic seeds

Possible model systems for endosperm-limited seed germination (P, FA2 = seed types)

<table>
<thead>
<tr>
<th>Family</th>
<th>Type</th>
<th>Examples</th>
</tr>
</thead>
<tbody>
<tr>
<td>Akaniaceae</td>
<td>endospermic</td>
<td></td>
</tr>
<tr>
<td>Tropaeolaceae</td>
<td>non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Moringaceae</td>
<td>non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Caricaceae</td>
<td>(Carica) endospermic</td>
<td></td>
</tr>
<tr>
<td>Setchellanthaceae</td>
<td>non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Limnanthaceae</td>
<td>non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Koeberliniaceae</td>
<td>slightly endospermic</td>
<td></td>
</tr>
<tr>
<td>Bataceae</td>
<td>?</td>
<td></td>
</tr>
<tr>
<td>Salvadoraceae</td>
<td>non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Pentadiplandraceae</td>
<td>seeds small</td>
<td></td>
</tr>
<tr>
<td>Gyrostromonaceae</td>
<td>(excessively endospermic, Tersonia, Codonocarpus)</td>
<td></td>
</tr>
<tr>
<td>Resedaceae</td>
<td>± non-endospermic</td>
<td></td>
</tr>
<tr>
<td>Emblingiaceae</td>
<td>slightly endospermic</td>
<td></td>
</tr>
<tr>
<td>Tovariaceae</td>
<td>thinly endospermic</td>
<td></td>
</tr>
<tr>
<td>Capparidaceae</td>
<td>(Capparis, P)</td>
<td>endospermic or non-endospermic</td>
</tr>
<tr>
<td>Cleomaceae</td>
<td>(Cleome, P)</td>
<td>endospermic or non-endospermic</td>
</tr>
<tr>
<td>Brassicaceae</td>
<td>(Lepidum, FA2)</td>
<td>endospermic or non-endospermic</td>
</tr>
</tbody>
</table>

Papaya: Carica papaya DOG1 ???
Caper: Capparis spinosa DOG1
Spider flower: Cleome hassleriana DOG1
Brassicaceae: Arabidopsis, Lepidium, Brassica, Sisymbrium, Aethionema DOG1

LesaDOG1 and BrDOG1: Graeber et al. (2010) Plant Molecular Biology 73: 67-87
Evolution of seed quality from MYA until today...

<table>
<thead>
<tr>
<th>Time Period</th>
<th>Class</th>
<th>Example</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cenozoic</td>
<td>Pinopsida / Coniferopsida</td>
<td>Megagametophyte (n)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gnetopsida</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cycadopsida</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Gympnospermae</td>
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<tr>
<td></td>
<td></td>
<td>Volziales</td>
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<td></td>
<td></td>
<td>Cordaitales</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lycopsida</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Lycopsida</td>
</tr>
<tr>
<td></td>
<td></td>
<td>“Progynnosperms”</td>
</tr>
<tr>
<td>Paleozoic Era</td>
<td>Aneurophytales</td>
<td>Archaeopteridales</td>
</tr>
</tbody>
</table>

Importance of seed tissue interactions in germination control!

Origin of seed habit ⇒ diversity of angiosperm seed mechanisms

Evolution of seed quality from MYA until today...

Importance of seed tissue interactions in germination control!

Evolution of seed quality from MYA until today...

Importance of seed tissue interactions in germination control!


7. Comparative seed biology will lead the way...

Phylogeny-driven comparative seed biology that utilizes model plants in interdisciplinary cross-species approaches

Next decade (2010-2020):
Post-genomics
Phylo-genomics
Model systems
Systems biology
... ???

Seed development
+ germination
+ dormancy
= 26490 = 100%

Others
Cucurbitales
Fabales (legumes)
Brassicales (crucifers)
Solanales (tomato, tobacco)
Asterales (lettuce, sunflower)
Caryophylales (sugar beet)
Poales (cereal grains)

Begonia
Pea
7. Comparative seed biology will lead the way...

Model plants ↔ Horticultural plants
Information from model species can be applied to improve seed quality also of “smaller crops”
7. Comparative seed biology will lead the way...

- Transcriptome
- Proteome
- Metabolome
- SSH
- qPCR
- QTL-QTG
- TILLING
- Imaging
- Biomechanics
- Math. modeling

Model plants ⇔ Horticultural plants
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- Transcriptome
- Proteome
- Metabolome
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- Qualifications for seed job market?
- Life-long learning!
- Interaction and interdisciplinarity!
- Funding and positions!
- Evolution here?

Model plants ↔ Horticultural plants
Information from model species can be applied to improve seed quality also of “smaller crops”
PD Dr. Gerhard Leubner  
Albert-Ludwigs University  
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Elisa Petrollini (PhD, research visit)  

Dr. Krystyna Oracz (postdoc AvH)  
Magdalena Jura (PhD DFG, pectin)  
Claudia Waack (Diplom, pectin)  

Karin Weitbrecht (PhD vSEED)  
Sebastian Busch (postdoc, vSEED)  

Kai Gräber (PhD DFG, seed dormancy)  
Dominique Jacquemoud (MSc, allelopathy)  
Linda Kern (Diplom, phytopathology)  

Prof. Charles A. Knight (sabbatical visit, evol.)  
Dr. Annette Büttner-Mainik (postdoc, KWS)  

Dr. Kerstin Müller (postdoc in Canada)  
Prof. Bill Finch-Savage (Warwick, UK)  
Prof. Klaus Mummenhoff (Osnabrück)