

**sDiv workshop**
**sEpiDiv**
**Towards understanding the causes and consequences of  
epigenetic diversity**


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The workshop will take place from 2<sup>nd</sup> to 6<sup>th</sup> March 2015 at **iDiv, Deutscher Platz 5, 04103 Leipzig** according to the following program:

<b>Monday 2<sup>nd</sup> March</b>	
12:00 am	Registration
12:30 pm	Lunch
1:30 pm	<b>Opening &amp; Introduction</b> - <i>Chairs: Katrin Heer &amp; Lars Opgenoorth</i>
2:30 pm	<b>Discussion of the glossary</b> - <i>Chairs: Christian Lampei &amp; Marie Mirouze</i> <ul style="list-style-type: none"> <li>Theoretical Considerations on Epigenetics (Sonja Prohaska)</li> </ul> <i>Protocol: Conchita Alonso</i>
3:30 pm	Coffee Break
3:45 pm	<b>Epigenetic mechanisms</b> - <i>Chair: Claude Becker</i> <ul style="list-style-type: none"> <li>Small RNAs: introduction and blot-based sRNA detection (Etienne Bucher, 30 min)</li> <li>SmallRNA-seq (Ovidiu Paun, 15 min)</li> <li>RNA interference (Christina Richards, 30 min)</li> <li>Combined discussion on the small RNA session (15 min)</li> <li>DNA methylation: introduction to the methods and their (dis)advantages (Claude Becker, 15 min)</li> <li>MSAPs (Walter Durka, 15 min)</li> <li>DNA methylation in the context of transposable elements and its role in genome stability (Marie Mirouze, 30 min)</li> <li>Histone modifications (Ilkka Kronholm, 30 min)</li> </ul> <i>Protocol: Etienne Bucher &amp; Marie Mirouze</i>



<i>7 pm</i>	<i>Dinner</i>
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<b>Tuesday 3<sup>rd</sup> March</b>	
8:15 am	<b>Ecological Epigenetics: Central questions</b> - <i>Chairs: Oliver Bossdorf &amp; Koen Verhoeven</i> Protocol: Christina Richards
9:45 am	<i>Coffee Break</i>
10:00 am	<b>Study systems</b> - <i>Chair: Koen Verhoeven</i> <ul style="list-style-type: none"> <li>• Translating tools/knowledge from Arabidopsis to other systems (Etienne Bucher)</li> <li>• (epi)genetic control of plant mobilomes (Marie Mirouze)</li> <li>• Comparing epigenomic variation between plant species (Emiliano Trucchi, Thomas von Gulp &amp; Koen Verhoeven)</li> <li>• Conceptual issues relating to sexual-asexual study systems (Koen Verhoeven)</li> </ul> Protocol: Claude Becker & Maria Colome Tatche
12:30 pm	<i>Lunch</i>
1:30 pm	<b>Study designs</b> - <i>Chair: Conchita Alonso</i> Relevance of the ecological context in the analysis of epigenetic variation at different scales <ul style="list-style-type: none"> <li>• Which ecological context may select for epigenetic rather than genetic variation? (Christian Lampei)</li> <li>• Relevant spatial and temporal scales of epigenetic variability (Maria Colome Tatche)</li> </ul> Adaptive phenotypes and appropriate designs to uncover their epigenetic "control" <ul style="list-style-type: none"> <li>• Identification of relevant phenotypic traits (measurable, ecologically relevant &amp; under epigenetic control) (Conchita Alonso)</li> <li>• How to establish the autonomy of epigenetic effects? (Emiliano Trucchi)</li> </ul> Protocol: Walter Durka & Vit Latzel
3:45 pm	<i>Coffee Break</i>

4:00 pm	iDiv public seminar <b>"Causes and Consequences of Epigenetic Diversity"</b> by Maria Colome Tatche & Koen Verhoeven
6:00 pm	<i>Dinner</i>

<b>Wednesday 4<sup>th</sup> March</b>	
8:30 am	<b>Experimental Designs</b> – <i>Chair: Vit Latzel</i> <ul style="list-style-type: none"> <li>• Environmental variables and compare field vs common garden experiments (Christian Lampe)</li> <li>• Designs, traits and phenotyping methods used in ecological epigenetic studies (Vit Latzel)</li> </ul> Protocol: Emiliano Trucchi & Andreas Gogol-Döring
9:30 am	<b>Bioinformatics I</b> – <i>Chairs: Andreas Gogol-Döring &amp; Ivo Große</i> <ul style="list-style-type: none"> <li>• Whole-genome BS-seq, differential methylation and ChIP-Seq analysis (Claude Becker)</li> </ul>
10:00 am	Coffee Break
10:30 am	<b>Bioinformatics I</b> – <i>Chairs: Andreas Gogol-Döring &amp; Ivo Große</i> <ul style="list-style-type: none"> <li>• Methylation mapping, DMR calling, correlation to expression (Peter Stadler)</li> <li>• RAD-Seq and BS-RAD-Seq analysis (Emiliano Trucchi)</li> <li>• Exome capture BS-seq; Histone modification ChIP-Seq analysis (Stefan Rensing)</li> </ul> Protocol: Kristian Ullrich & Sonja Prohaska
12:30 am	<i>Lunch</i>
1:30 pm	<b>Breakout groups I - ETN</b> – <i>Chairs: Oliver Bossdorf &amp; Koen Verhoeven</i>
4:00 pm	<i>Coffee Break</i>



4:15 pm	<b>Synthesis of discussion in outbreak groups</b> Protocol: Ovidiu Paun
7:00 pm	<i>Dinner</i>

<b>Thursday 5<sup>th</sup> March</b>	
8:30 am	<b>Introduction to work in Breakout groups II</b> – Chairs: Katrin Heer/ Lars Opgenoorth <ul style="list-style-type: none"><li>• Introduction ETN</li><li>• New Phytologist Symposium</li><li>• Methods Guide, organisation</li></ul>
10:00 am	<i>Coffee Break</i>
10:15 am	<b>Breakout groups II</b> <ul style="list-style-type: none"><li>• ETN</li><li>• Bioinformatics</li></ul>
12:15 pm	<i>Lunch</i>
1:15 pm	<b>Synthesis breakout groups</b>
2:00 pm	<b>Bioinformatics II</b> – Chairs: Andreas Gogol-Döring & Ivo Große <ul style="list-style-type: none"><li>• Detection of genome wide chromatin states (Maria Colome Tatche)</li><li>• Epigenetic modeling (Sonja Prohaska)</li><li>• de-novo (transcriptome) assembly and transcriptome completeness (Kristian Ullrich)</li><li>• Histone modification ChIP-Seq analysis (Claude Becker)</li></ul> Protocol: Christian Lampei
4:00 pm	<i>Coffee Break</i>
4:15 pm	<b>Breakout groups III</b> <ol style="list-style-type: none"><li>1) New Phytologist</li><li>2) Paper</li><li>1) "Bold ideas" &amp; funding sources</li></ol>



5:00 pm	<b>Synthesis of Breakout groups II &amp; III and coordination of tasks after the workshop –</b> Protocol: Claude Becker
7 pm	<i>Dinner</i>

<b>Friday 6<sup>th</sup> March</b>	
9:00 am	<b>Breakout groups V</b> <ul style="list-style-type: none"><li>• ETN: concepts and experiments</li><li>• ETN: non-academic partners &amp; PhD education</li></ul>
11 am	<i>Coffee Break</i>
11:15 am	<b>Final discussion and work in Breakout groups as needed – Chairs: Katrin Heer &amp; Lars Opgenoorth</b> Protocol: Oliver Bossdorf
1:00pm	<i>Lunch</i>
	Departure