

PP1530: Flowering Time Control – from Natural Variation to Crop Improvement


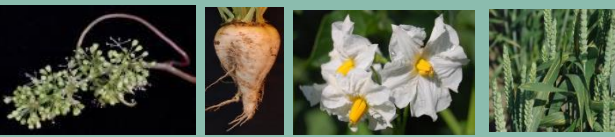
Project affiliations, Phase II

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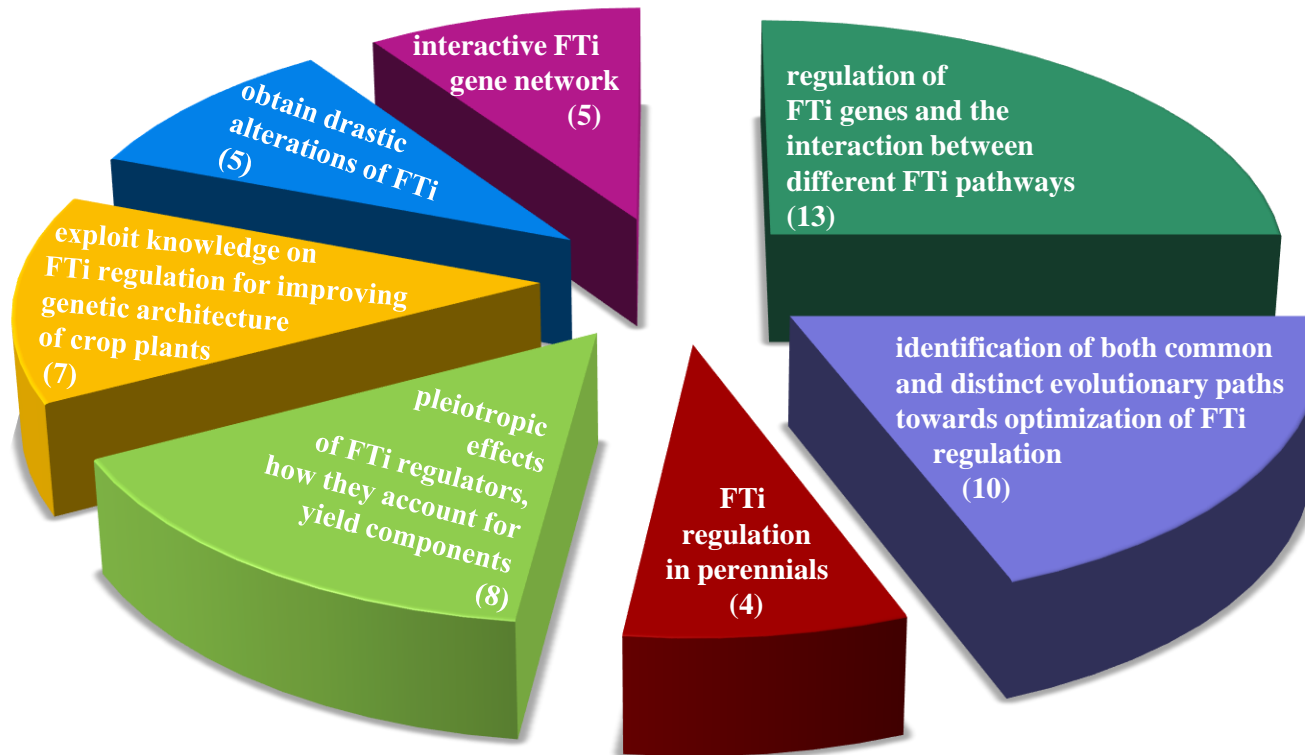


Quelle Karte: http://d-maps.com/carte.php?lib=deutschland_Lankarte&num_car=14461&lang=de



Funding by:	Deutsche Forschungsgemeinschaft (DFG) since June 2011, 2nd phase approved by DFG in October 2014
Start of phase I: Start of phase II:	July 1, 2011 July 1, 2014
Project duration:	2 x 3 years
Interdisciplinary approach:	Phase I: 19 interdisciplinary scientific projects Phase II: 18 interdisciplinary scientific projects
Disciplines:	botany, plant breeding, plant physiology, genomics, bioinformatics
International Ties:	Australia, Austria, Belgium, Chile, Canada, France, Israel, Russia, Kindom of Saudi Arabia, South Korea, Spain, Sweden, Switzerland, United Kingdom, United States of America
Plant species in focus (Phase II)	 <i>Arabis alpina, Hordeum vulgare, Arabidopsis thaliana, Brassica napus</i>  <i>Vitis vinifera, Beta vulgaris ssp. vulgaris, Solanum tuberosum, Triticum aestivum</i>
Methodology:	Genetic, genomic and molecular methods with a focus on –omics techniques
Coordination:	Christian-Albrechts-University of Kiel, Prof. Dr. Christian Jung, Dr. Martina Blümel (Administrative Manager)
Scientific steering committee:	Prof. Dr. Christian Jung, Christian Albrechts-Universität of Kiel Prof. Dr. Dorothee Staiger, Bielefeld University Dr. Maria von Korff, Max-Planck-Institut for Plant Breeding Research, Cologne Prof. Dr. Ivo Grosse, Martin-Luther University Halle-Wittenberg Prof. Dr. Klaus Pillen, Martin-Luther University Halle-Wittenberg

Strategic Aims



Work packages

WP 1: Gene expression networks and signaling pathways

WP 2: Control of flowering time in perennials

WP 3: Integration of endogenous and environmental factors

WP 4: Pleiotropic effects of FTi genes and impact on adaptation and speciation

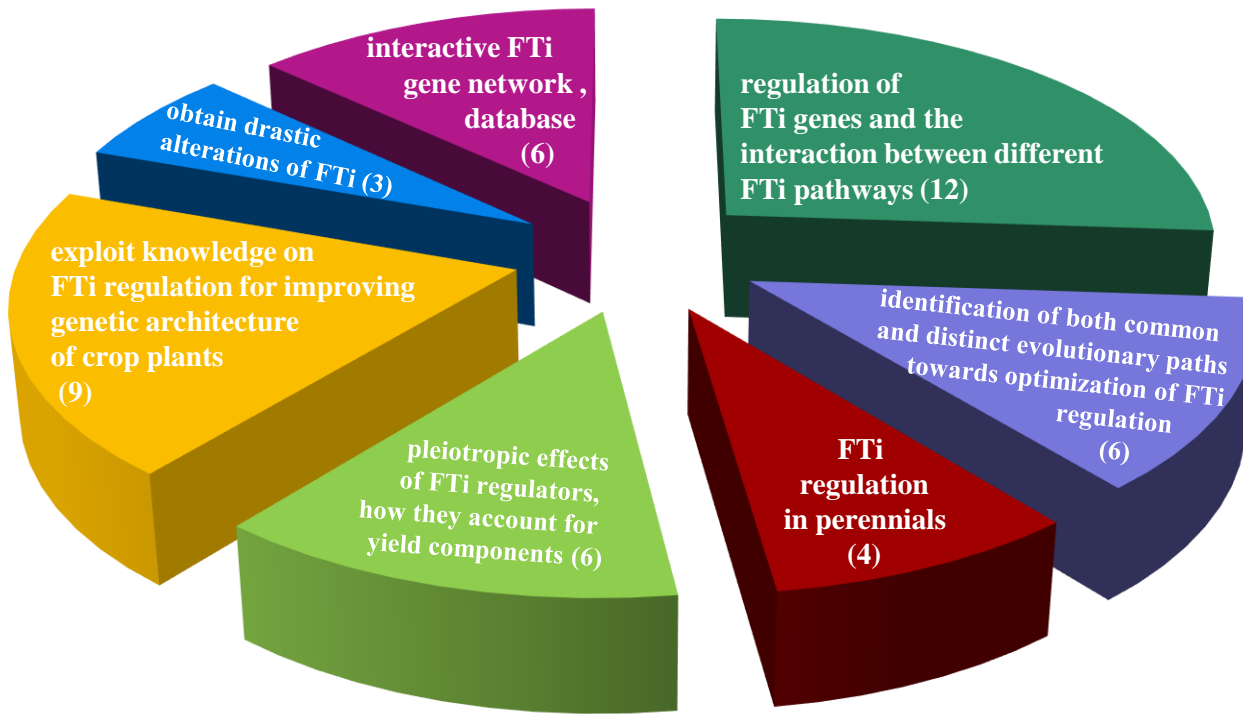
WP 5: Genetic variation for FTi genes and application for crop improvement

Numbers in brackets indicate the number of projects addressing the respective strategic aim

FTi: Flowering Time



Strategic Aims



Work packages

WP 1: Gene expression networks and signaling pathways

WP 2: Control of flowering time in perennials

WP 3: Integration of endogenous and environmental factors

WP 4: Pleiotropic effects of FTi genes and impact on adaptation and speciation

WP 5: Genetic variation for FTi genes and application for crop improvement

Numbers in brackets indicate the number of projects addressing the respective strategic aim

FTi: Flowering Time



PP 1530: Projects, Phase I

Project title	Principal Investigator	Institute
Identification and molecular characterization of genes involved in the perennial flowering of <i>Arabis alpina</i>	Maria Albani	MPI Cologne
Mechanistic analysis of the transition from juvenility to maturity in perennial <i>Arabis alpina</i> and comparison with <i>Brassica</i> crop species	George Coupland	MPI Cologne
Directing floral timing through genetic variation in the plant circadian clock	Seth Davis	MPI Cologne
Is the immune system required to adapt to flowering time change ?	Juliette de Meaux	WWU Münster
Development of an early flowering system for poplar breeding and biosafety research	Matthias Fladung	TI Grosshansdorf
Bioinformatics support for RNA-seq experiments	Ivo Große	MLU Halle-Wittenberg
A final step of speciation? Changes in flowering time and their genetic and ecological background within three closely related diploid <i>Hordeum</i> species from Patagonia	Frank Blattner	IPK Gatersleben
Genomic dissection of floral transition in <i>Brassica napus</i> towards crop improvement by life cycle adaptation and hybrid yield increase	Christian Jung	CAU Kiel
Allele mining in wild barley: finding new exotic genes which control flowering time in the barley nested association mapping (NAM) population HEB-25	Klaus Pillen	MLU Halle-Wittenberg
Regulation of flowering time by Trehalose-6-Phosphate signaling	Markus Schmid	MPI Tübingen
Identification of flowering time genes in barley using next generation sequencing of bulked segregants	Korbinian Schneeberger Maria von Korff	MPI Cologne MPI Cologne
Mechanisms of flowering time control by the novel flowering time genes GNC and GNL	Claus Schwechheimer	WZW@TU Munich
Flowering time, development and yield in oilseed rape (<i>Brassica napus</i>): sequence diversity in regulatory genes	Rod Snowdon Wolfgang Friedt	JLU Gießen
Unraveling the role of a novel autonomous pathway component in FTi control by small RNA profiling and cross-species comparison	Dorothee Staiger	Bielefeld University
Analysis of the genetic variation of flowering time genes and their control network in grapevine	Reinhard Töpfer Bernd Weisshaar	JKI Siebeldingen Bielefeld University
Unraveling a mechanism for floral transition control in annual, biennial and perennial <i>Beta</i> species	Conny Tränkner	CAU Kiel
Analysis of genetic variation for flowering time in wild barley grown under different environmental conditions	Maria von Korff Benjamin Kilian	MPI Cologne IPK Gatersleben
Comparative analysis of miRNA networks regulating flowering	Detlef Weigel	MPI Tübingen
Genetic dissection of flowering time in wheat by high-density genome-wide association mapping	Tobias Würschum	Hohenheim University



PP 1530: Projects, Phase II

Project title	Principal Investigator	Institute
Identification and molecular characterization of genes involved in the perennial life cycle	Maria Albani	MPI Cologne, Cologne University
Genetic and molecular analysis of epistatic interactions in flowering time pathways identified in a barley multi-parent advanced generation intercross (MAGIC) population	Agim Ballvora, Jens Leon	FWU Bonn
Metabolite regulation of cryptochrome activity and flowering time	Alfred Batschauer	PU Marburg
Mechanistic analysis of the transition from juvenility to maturity in perennial <i>Arabidopsis alpina</i> and comparison with <i>Brassica</i> crop species	George Coupland	MPI Cologne
Central Data Analysis Platform for the PP-1530 Consortium	Ivo Große	MLU Halle-Wittenberg
Unravelling a genetic network for bolting time regulation in Beta species to breed winter sugar beet	Christian Jung	CAU Kiel
StPCP1: an IDD transcription factor involved in sugar-induced flowering and tuberization in <i>Solanum tuberosum</i>	Christina Kühn Vanessa Wahl	HU Berlin MPI Potsdam-Golm
Evolutionary Transcriptomics of Floral Transition	Marcel Quint Ivo Große Bernd Weisshaar	IPB Halle MLU Halle-Wittenberg Bielefeld University/CeBiTec
Allele mining in wild barley: finding new exotic genes controlling flowering time in the barley nested association mapping (NAM) population HEB-25	Klaus Pillen Jochen Kumlehn	IPK Gatersleben MLU Halle-Wittenberg
Regulation of Flowering Time by Trehalose-6-Phosphate Signaling	Markus Schmid Vanessa Wahl	MPI Tübingen MPI Potsdam-Golm
The function of cytokinin in regulating flowering time	Thomas Schmülling	FU Berlin
Development and implementation of advanced methods for the identification of barley flowering time genes using next generation sequencing	Korbinian Schneeberger Maria von Korff	MPI Cologne MPI Cologne/HHU Düsseldorf
Temperature-dependent control of flowering by the gibberellin pathway and interactions between DELLA proteins and APETALA1/VRN1 MADS-box factors	Claus Schwechheimer	WZW @ TU Munich
Flowering time, miRNA regulation and climatic adaptation - Variation in <i>Brassica napus</i> idiotypes under drought stress	Rod Snowdon	JLU Gießen
The function of an autonomous pathway component in flowering time control in Arabidopsis and barley	Dorothee Staiger	Bielefeld University
Analysis of the genetic variation of flowering time genes and their control network in grapevine	Reinhard Töpfer Bernd Weisshaar Detlef Weigel	JKI Siebeldingen Bielefeld University/CeBiTec MPI Tübingen
Quantitative effects of vernalization requirement, day length and temperature on flowering time of oilseed rape	Christian Möllers	GAU Göttingen