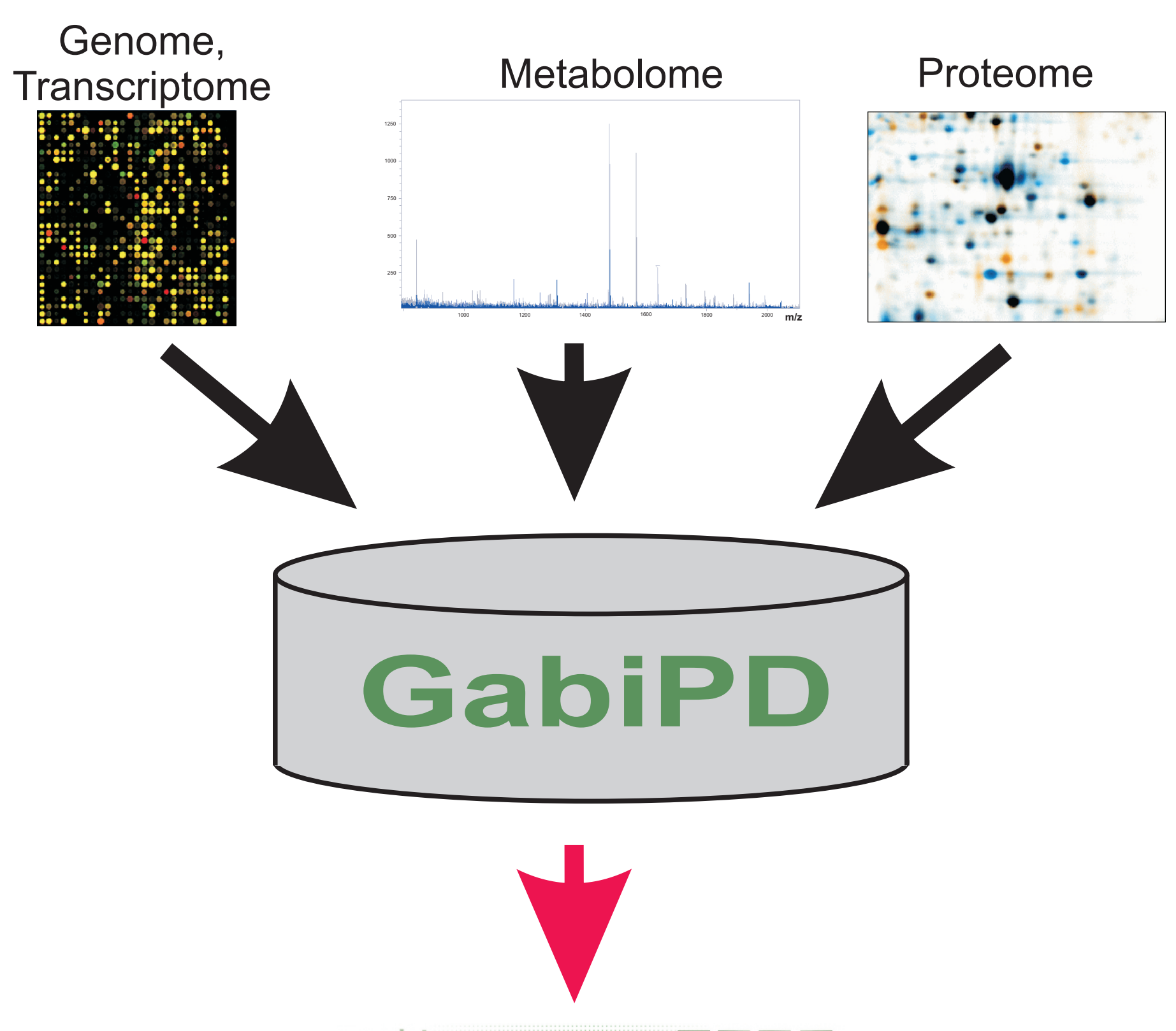


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1. 'omics' data



2. Species and data types in GabiPD

Species	Genomics, transcriptomics						Prot.	Met.	
	Clones	Sequences	Traces	SNPs	Predicted ORFs	Clusters	Expression profiling	Mascot results	Metabolic profiling
<i>Populus trichocarpa</i> Salicaceae									
<i>Populus tremula</i> Salicaceae									
<i>Medicago truncatula</i> Fabaceae							6 (12643)		
<i>Arabidopsis thaliana</i> Brassicaceae	34711	524655	6804	3160	232471	4176 (3733032)	3914	3180	
<i>Brassica napus</i> Brassicaceae	8065	8747	8747		53198	1216			
<i>Vitis vinifera</i> Vitaceae									
<i>Solanum tuberosum</i> Solanaceae	200563	202469	285	1654	38625				
<i>Solanum lycopersicum</i> Solanaceae	2133	2691							
<i>Capsicum annuum</i> Solanaceae	5	1							
<i>Nicotiana tabacum</i> Solanaceae	8	4							
<i>Beta vulgaris</i> Amaranthaceae	11358	14806			84313				
<i>Hordeum vulgare</i> Poaceae	157622	215355	3828	20	1413624	35960			
<i>Oryza sativa</i> Poaceae									

Phylogenetic tree depicting the evolutionary relationships among the species represented in GabiPD. Species in blue represent completely sequenced and annotated genomes which will be included soon in GabiPD, facilitating information transfer in a comparative genomics context. This tree reflects our current knowledge on the evolution of seed plants (references at the bottom). Few additional solanaceous species present in GabiPD are not shown in the tree: *S. bulbocastanum*, *S. demissum*, *S. phureja*, and *S. spegazzinii*.

3. All roads lead to the Gene's GreenCard

Clone GreenCard
Clone: MPZ02000103Q
Genotype (Genotype): Arabidopsis thaliana
Species: Arabidopsis thaliana
Type: cDNA
Common name: Arabidopsis thaliana
Library: Arabidopsis thaliana (Arabidopsis thaliana)

Transgenic line GreenCard
Plant: 24A203 (T-DNA line)
Genotype (Transgenic): Arabidopsis thaliana
Species: Arabidopsis thaliana
Type: T-DNA
Common name: Arabidopsis thaliana
Library: Arabidopsis thaliana (Arabidopsis thaliana)

Gene GreenCard
Gene: AT5G14590.1
Genotype (Genotype): Arabidopsis thaliana
Type: wTc-type
Common name: Arabidopsis thaliana
Library: Arabidopsis thaliana (Arabidopsis thaliana)

Proteomics data
SpotInfo:
X-Coordinate: 597
Y-Coordinate: 567
Spot initially identified as AT5G14590.1
Info for AT5G14590.1:
Molecular Weight: 54197 Da
pI: 5.1203
Length: 486 a.a.
Protein identified on 2D gel: Arabidopsis thaliana (Arabidopsis thaliana)

Data integration is achieved mainly through the Gene's GreenCard.

Clone and Plant (transgenic line) GreenCards point to the Gene GreenCard through BLAST searches. The "Related with" section lists the best BLAST hits to different sources (e-value 10^{-10}, 70% identity, 50% aligned region).

Identified proteins on 2D gels, are linked through their original MASCOT result.

Gene GreenCards provide links to all related data, making effective bidirectional links. GreenCards are linked to other GABI (e.g., GABI-KAT), as well as external resources (e.g., PhosPHAT).

4. Barley's maps, and a new unigene set

BarleyChromosome_1
Marker (SNP): GBS0546
Species: Barley
Chromosome: 1
Position: 7.2 cm
Related to Sequence: corresponding to BioObject: HF19G17
Sequence: HF19G17
submitter: Dr. Nils Stein
GenBank: BU289993
IPK CR-EST: HF19G17

27K UniGene set
UniGene EST_Sequence EST_Blast ClusterInfo ContigMembers Consensus_Blast Consensus_Description
1 HA01A10 HA01A10f LOC_Os09g01719.1 10888.1 1 OS206 OS206, Oryza (DESC: Putative transcriptional activator; Oryza sativa (japonica cultivar-group) lax3947 (SIZE: 335 AA, 37488 MW)
2 HA01A13 HA01A13f LOC_Os09g01719.1 17269.1 2 OS206 OS206, Oryza (DESC: Putative transcriptional activator; Oryza sativa (japonica cultivar-group) lax3947 (SIZE: 335 AA, 37488 MW)
3 HA01B01 HA01B01f LOC_Os09g01719.1 17272.1 3 OS206 OS206, Oryza (DESC: Putative transcriptional activator; Oryza sativa (japonica cultivar-group) lax3947 (SIZE: 335 AA, 37488 MW)
4 HA01B02 HA01B02f LOC_Os09g01719.1 293.1 38 OS419 OS419, Oryza (DESC: Putative transcriptional activator; Oryza sativa (japonica cultivar-group) lax3947 (SIZE: 335 AA, 37488 MW)

Barley genetic maps are linked to ESTs through the respective markers. A clone list, enriched for full length cDNAs, representing a new 27K unigene set, was made in cooperation with the Institute of Plant Genetics and Crop Plant Research in Gatersleben (IPK). This Unigene set was built using the EST assembly programs CAP3 and TGICL, to obtain: 27729 cluster contigs, 14897 CAP3 singlets and 26956 TGICL singlets. This list and its corresponding sequences are available from the GabiPD web site.

5. New data in GabiPD

- + List of Barley cDNA clones from the IPK representing a new 27K UniGene Set
- + Barley EST sequences from GABI-PLANT
- + GenBank Accession numbers for 39000 Barley EST sequences from GABI-SEED and GABI-PLANT
- + Updated GABI-KAT T-DNA insertion lines and sequences (v23, 30.11.2007)
- + TAIR v7.0 Arabidopsis genome annotation
- + TAIR v7.0 BLAST hits for all GabiPD sequences from Arabidopsis

6. Future perspectives

- Ⓛ Potato SNP data from GABI-CONQUEST 2
- Ⓛ Condensed species-specific data overviews in order to ease navigation through the data
- Ⓛ Extend database structure, user interfaces and download functionalities for new types of GABI-FUTURE data
- Ⓛ Continuously integrate GABI-FUTURE data
- Ⓛ Arabidopsis 2DE data from GABI trilateral SARA
- Ⓛ Vitis vinifera genetic maps from the BMELV
- Ⓛ SNP data of different Arabidopsis accessions from GABI-EVAST
- Ⓛ Upgrade the 2-DE interface
- Ⓛ Perform new types of data analysis, e.g. domain analysis in proteins

References

APG. 2003. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG II. *Bot J Linn Soc.* 141:399-436
Bohs L. 2005. Major clades in *Solanum* based on ndhF sequence data. pp 27-49 in Keating RC, Hollowell VC, and Croat TB (eds.), A festschrift for William G. D'Arcy: the legacy of a taxonomist. *Monographs in Systematic Botany from the Missouri Botanical Garden, Vol. 104*. Missouri Botanical Garden Press, St. Louis, MO
Knapp S. 2002. Tobacco to tomatoes: a phylogenetic perspective on fruit diversity in the Solanaceae. *J Exp Bot.* 53:2001-22.
Sol Genomics Network (http://www.sgn.cornell.edu/about/about_solanaceae.pl)
Soltis PS and Soltis DE. 2004. The origin and diversification of angiosperms. *Am J Bot.* 91:1614
The Tree of Life (<http://www.tolweb.org/angiosperms>)