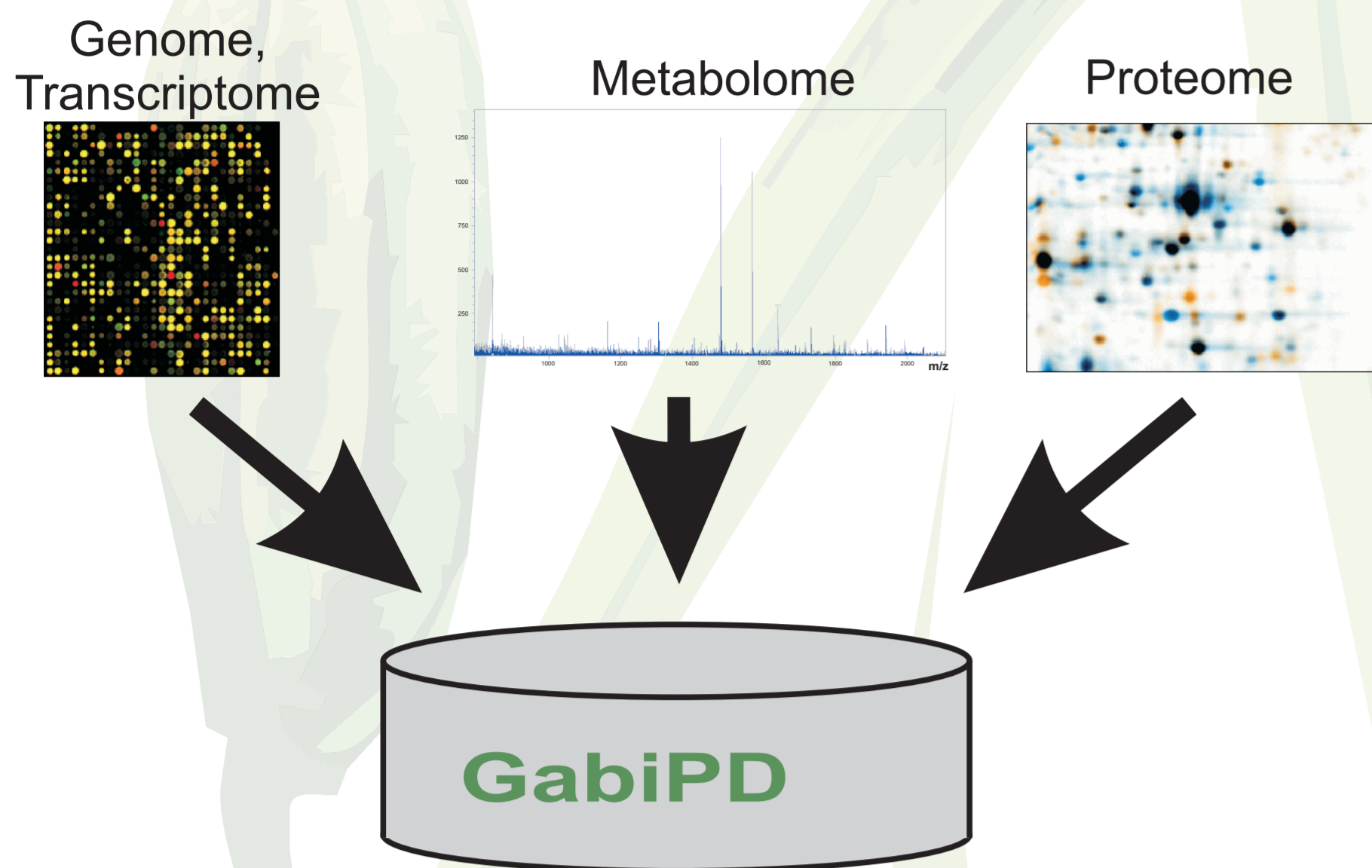


INTEGRATION OF PLANT 'OMICS'-DATA IN GENE CONTEXT <http://www.gabipd.org/gabipd@mpimp-golm.mpg.de>

Diego Mauricio Riaño-Pachón, Axel Nagel, Neigenfind J, Robert Wagner, Rico Basekow, Elke Weber, Sabrina Kleessen, Birgit Kersten
GabiPD team, Bioinformatics, Max Planck Institute of Molecular Plant Physiology, Wissenschaftspark Golm, Am Mühlenberg 1, 14476 Potsdam - Golm, Germany

1. 'omics' data



Database paper in NAR

News feed

Species list: *Populus trichocarpa*, *Populus tremula*, *Medicago truncatula*, *Arabidopsis thaliana*, *Brassica napus*, *Vitis vinifera*, *Solanum tuberosum*, *Solanum lycopersicum*, *Capiscum annuum*, *Nicotiana glauca*, *Nicotiana glauca*, *Beta vulgaris*, *Hordeum vulgare*, *Oryza sativa*

Data from different fronts (i.e., genomics, transcriptomics, proteomics and metabolomics) are integrated in GabiPD, originating from more than 20 different biological species. The GabiPD reference paper has been published in Nucleic Acid Research (Riaño-Pachón *et al.* 2009).

2. Updates in the Gene GreenCard

Gene: LOC_Os02g01010.1

Alternative names: LOC_Os02g01010, LOC_Os02g01010.1

Genotype (Genotype): species: *Oryza sativa japonica*, name: (Japanese rice), type: wildtype

Gene function: OsPDI1-4 - Oryza sativa protein disulfide isomerase, expressed (TIGR 5.0) 12002.m05451 protein OsPDI1-4 - Oryza sativa protein disulfide isomerase, expressed highly similar to (558)AT3054960] Symbols: ATPDIL1-3 [ATPDIL1-3 (PDI-LIKE 1-3), thiol-disulfide exchange intermediate | chr3:20374491-20377799 REVERSE weakly similar to (197)PDI_VHEATP protein disulfide-isomerase precursor - Triticum aestivum (Wheat) not assigned PDI_a_PDI_a_PDI_a_family Thioredoxin PDI_a_P5_PDI_a_ERp38 PDI_a_MPDI1 like PDI_a_PDIR PDI_a_ERp46 PDI_a_TM3 TRX_family PDI_a_ERdj5_C_PDI_a_TM3_PDI_a_ERp44 COG3118 PDI_a_QSOX PRK10996 PDI_a_APS_reductase ybN PDI_b_family PDI_b_family PDI_a_ERF5 Functional annotation

Gene Ontology

GO term	Identifier	Type
catalytic activity	GO:0003824	molecular function

MapMan Annotation: BIN 21.1: redox.thioredoxin, BIN 21: redox.regulation

Related with: HU07N24, HCO2809, HCO4A19, HCO2J23, HDP15005, HDP23821, MPM5g2010.H15104, Contig2400_at

Orthologues and co-orthologues identified by INPARANOID: AT5G06040.1 *Arabidopsis thaliana*

External resources: Michigan State University - Rice Genome Annotation, Aramemnon, Gramene, PlantFDB, HOP (LOC_Os02g01010), HOP (12002.m05451)

Sequence: LOC_Os02g01010.1
submitter of sequence: public data
length: 2164
description: cDNA sequence (TIGR 5.0)

Sequence features and Clone alignments (BLAST):

Exon-exon junction, Link to cDNA clone, Link to PFAM protein domain

Gene Ontology

GO term	Identifier	Type
response to abiotic stimulus	GO:0009628	biological process
response to stress	GO:0006950	biological process
catalytic activity	GO:0003824	molecular function

MapMan Annotation: BIN 4.11: glycolysis.phosphoglycerate mutase, BIN 4: glycolysis

Related with: HU04H01, HU14N13, HV13C10, H000607, H001017, HDP31007, GW003009, GC100024446, Contig15430_at

A Currently we have integrated Gene Ontology and Mapman ontology annotation into the Rice and Arabidopsis Gene GreenCards and into the GreenCards describing Barley affymetrix gene probes.

B Every gene in GabiPD is related to experimental data types. In the figure users can easily identify related cDNA clones and affymetrix probes in the Barley1 microarray.

C Orthologues between Arabidopsis and Rice were identified using INPARANOID, this will ease the transfer of functional information between this species.

C The new cDNA display allows users to identify cDNA clones that map to special regions of their gene of interest (e.g., UTRs, protein domains).

3. Barley gene expression data and a road for the transfer of functional annotation

MapMan Web

Sample (probe) GreenCard

Gene expression data visualized in MapManWeb is linked bidirectionally to the underlying probes, in a way that users can easily find in the probe GreenCard information about all experiments in which this probe is differentially expressed.

Barley affymetrix probes and cDNAs were similarity-based mapped to Rice genes in order to allow for the transfer of functional information.

Gene expression data on barley grain development and maturation (Sreenivasulu *et al.*, 2008) has been integrated in GabiPD, twelve assays can be visualized in MapManWeb.

4. New released applications

SATlotyper

http://www.gabipd.org/projects/satlotyper/; Neigenfind *et al.* 2008

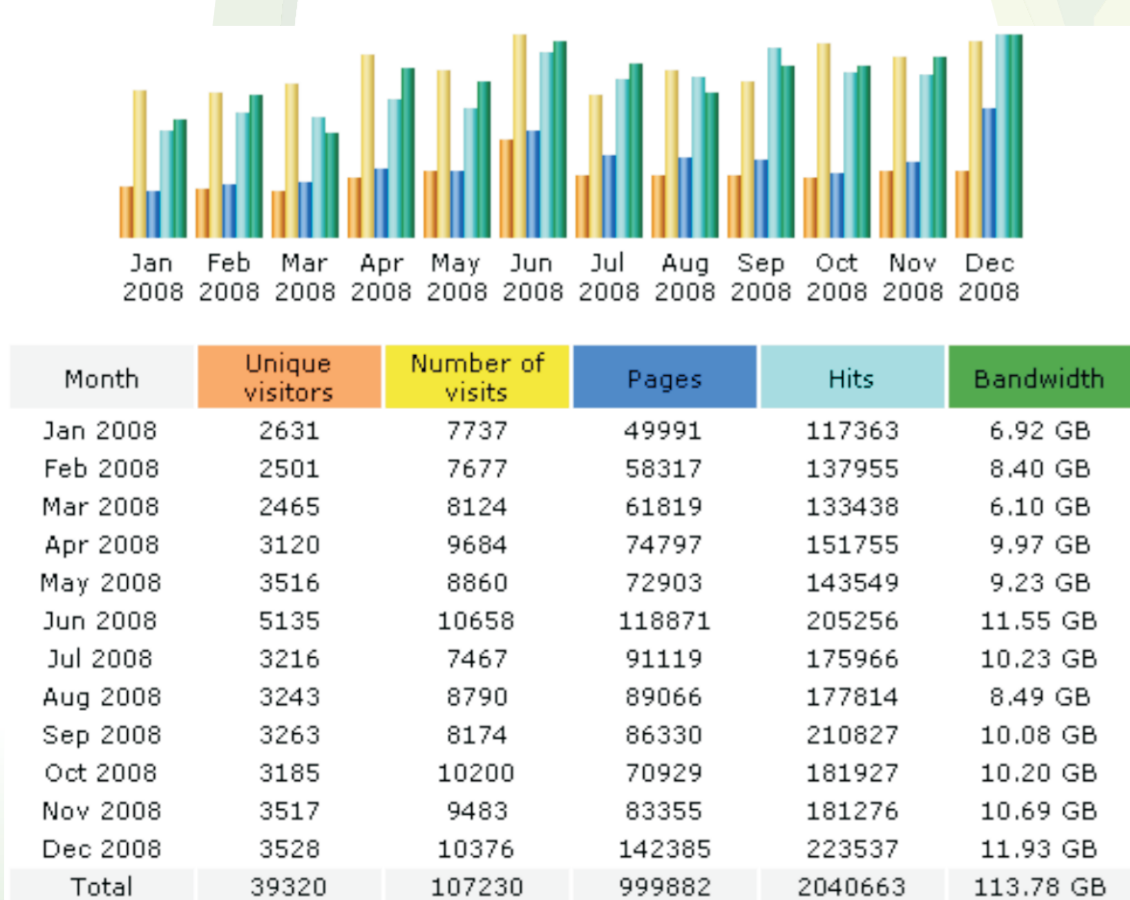
QuantPrime
qPCR primer design tool

http://www.quantprime.de/, developed in cooperation with Uni Potsdam; Arvidsson *et al.* 2008

5. New data in GabiPD

- Partial sequences of 91 Barley BAC clones from GABI-BARLEX
- Potato SNP data for 21 loci from GABI-CONQUEST2
- About 2.800 Sugar beet ESTs from Sugar Beet Seed
- 2815 Sugar beet GSS sequences from GABI BeetSeq
- TIGR v5.0 Rice (subsp. japonica) genome annotation
- TIGR v5.0 Rice cDNA hits of all Barley sequences in GabiPD
- Identified protein domains for all Arabidopsis and Rice Genes

6. Access to GabiPD



References

- Arvidsson S, Kwasniewski M, Riaño-Pachón DM, Mueller-Roeber B. 2008. **QuantPrime - a flexible tool for reliable high-throughput primer design for quantitative PCR.** *BMC Bioinformatics*. 9:465.
- Neigenfind J, Gyetvai G, Basekow R, Diehl S, Achenbach U, Gebhardt C, Selbig J, Kersten B. 2008. **Haplotype inference from unphased SNP data in heterozygous polyploids based on SAT.** *BMC Genomics*. 9:356.
- Riaño-Pachón DM, Nagel A, Neigenfind J, Wagner R, Basekow R, Weber E, Mueller-Roeber B, Diehl S, Kersten B. 2009. **GabiPD: the GABI primary database—a plant integrative 'omics' database.** *Nucleic Acids Res.* 37(Database issue):D954-9.
- Sreenivasulu N, Usadel B, Winter A, Radchuk V, Scholz U, Stein N, Weschke W, Strickert M, Close TJ, Stitt M, Graner A, Wobus U. 2008. **Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by new MapMan/PageMan profiling tools.** *Plant Physiol.* 146(4):1738-58.

7. Future perspectives

- Integrate Arabidopsis SNP data from Clark *et al* 20087, Ossowski *et al* 2008 and from GABI-EVAST
- Provide Condensed species-specific data overviews in order to ease navigation through the data
- Continuously integrate GABI-FUTURE data
- Arabidopsis 2DE data from GABI trilateral SARA
- Vitis vinifera* genetic maps from the BMELV
- Upgrade the 2-DE interface
- Provide upcoming information on Arabidopsis phosphorylation sites.