

Derailing Witchweed (*Striga*) Virulence in to Achieve Durable and Broad-Spectrum Resistance

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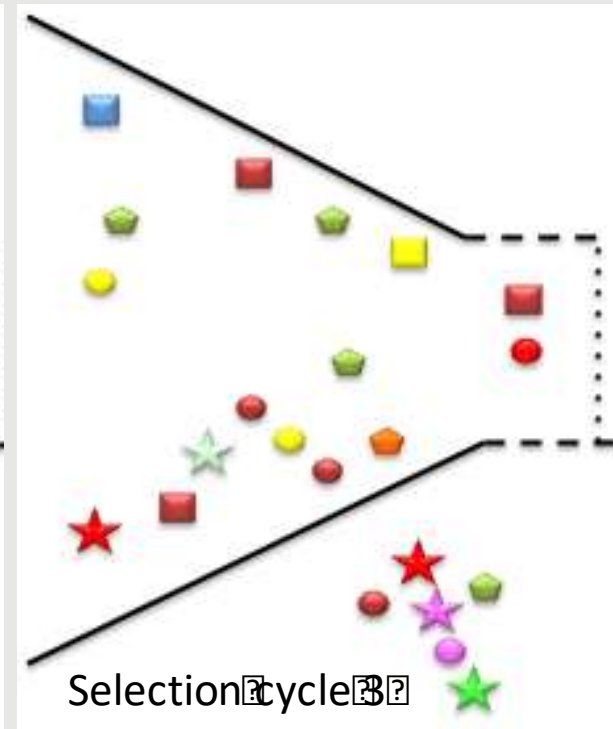
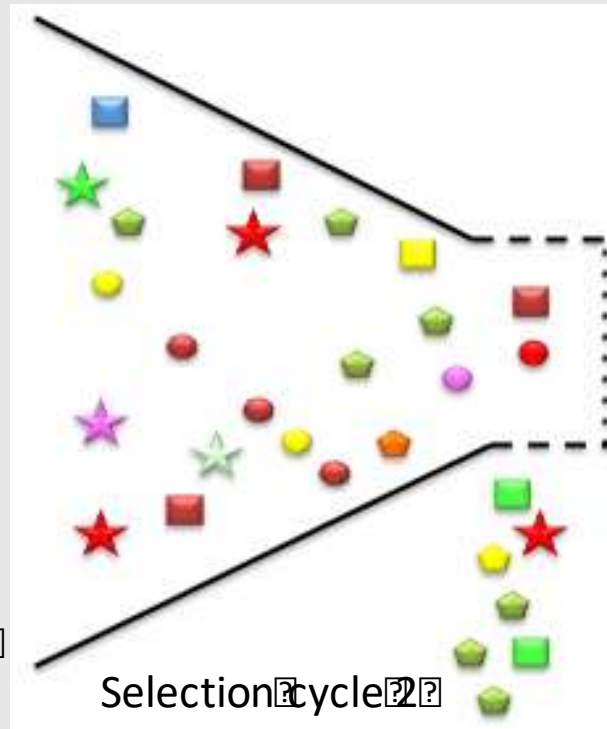
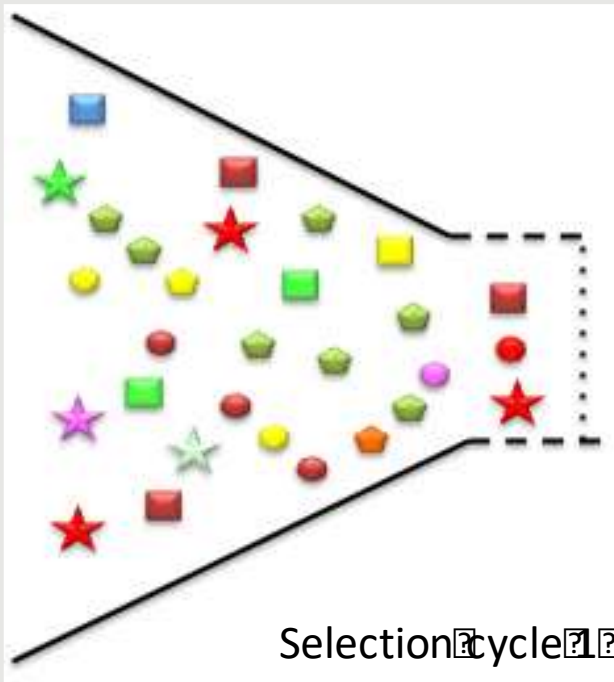
Striga resistance in wild sorghum. Sorghum's resistance to *Striga* field demonstration site. Alupe, Busia Kenya

Attack of the witch!



Hypothesis

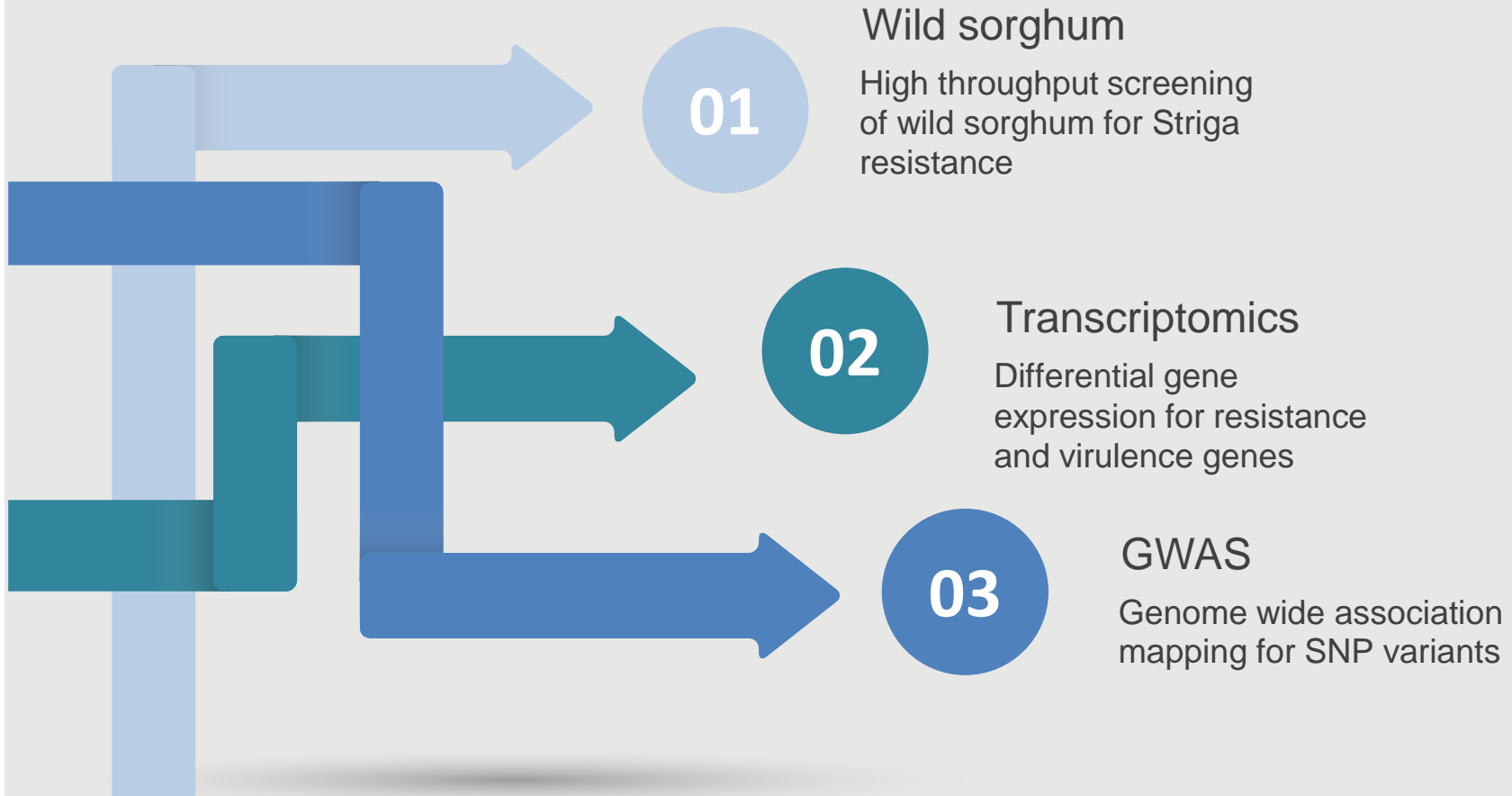
Domestication leads to loss of genetic diversity



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Approach

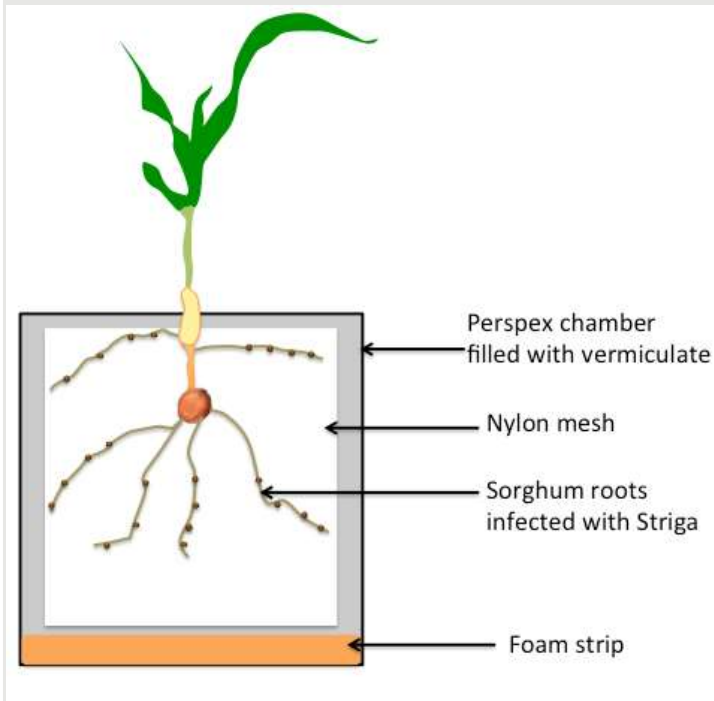
Genomic tools for identification of host resistance and pathogen virulence



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High through-put screening of *Striga* resistance

Striga size, number and biomass

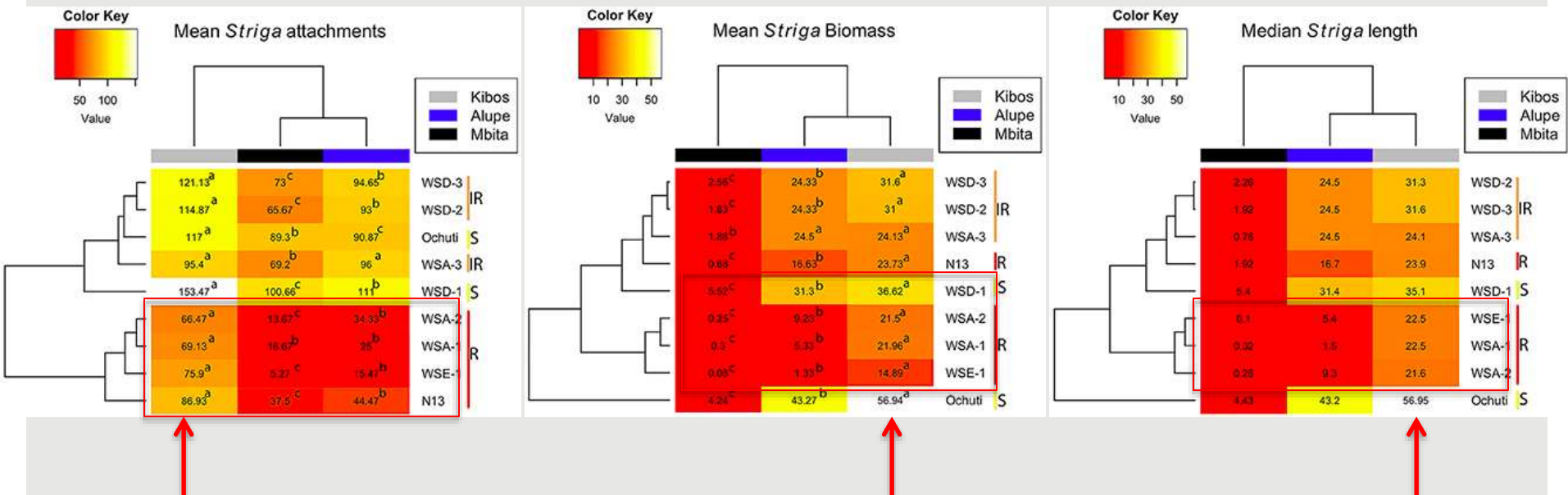


High throughput *Striga* screening facility at KU

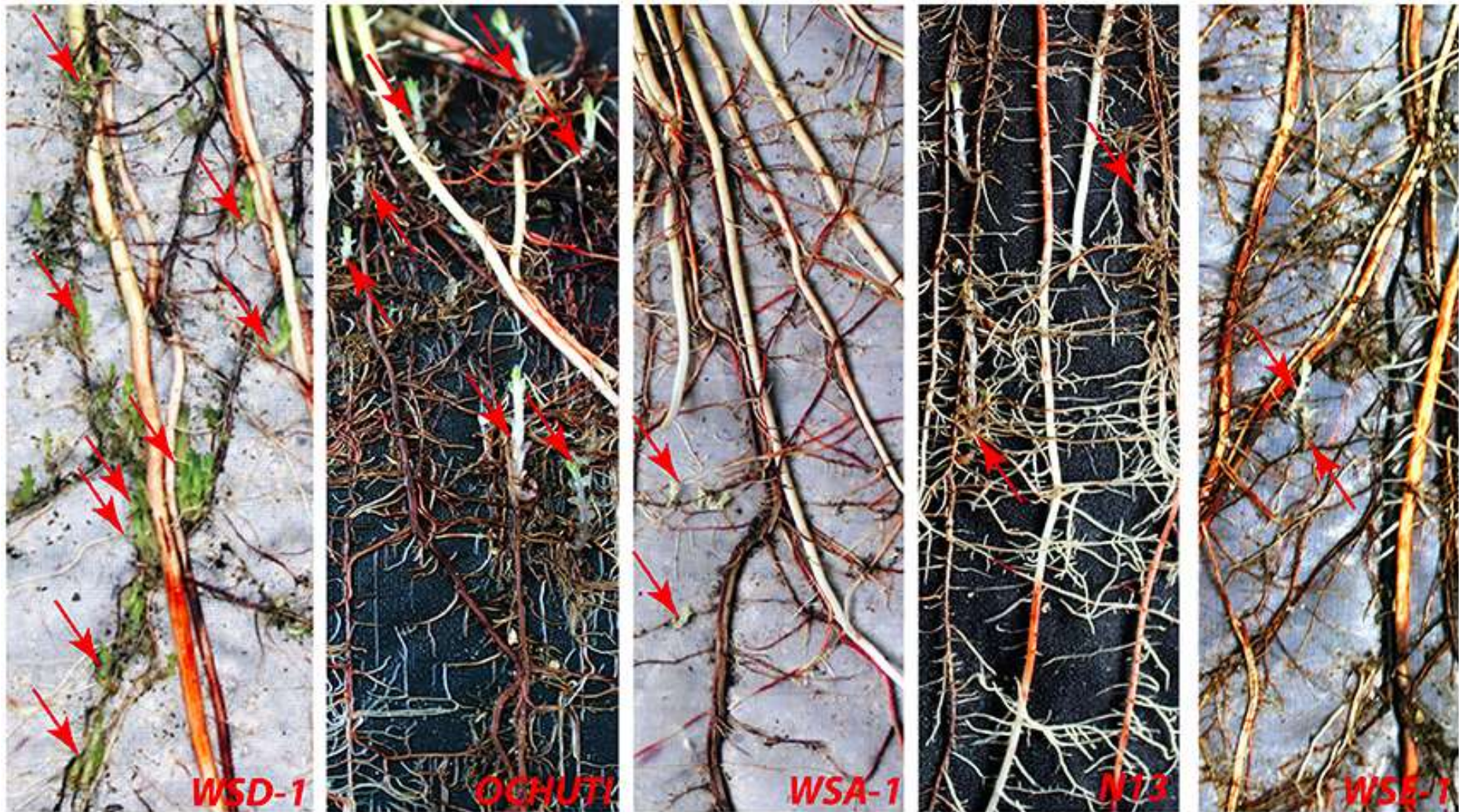


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Wild sorghum accessions show post-germination *Striga* resistance



Wild sorghum accessions show post-germination *Striga* resistance



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Mbuvi et al., *Frontiers in Plant Sciences*; 2017

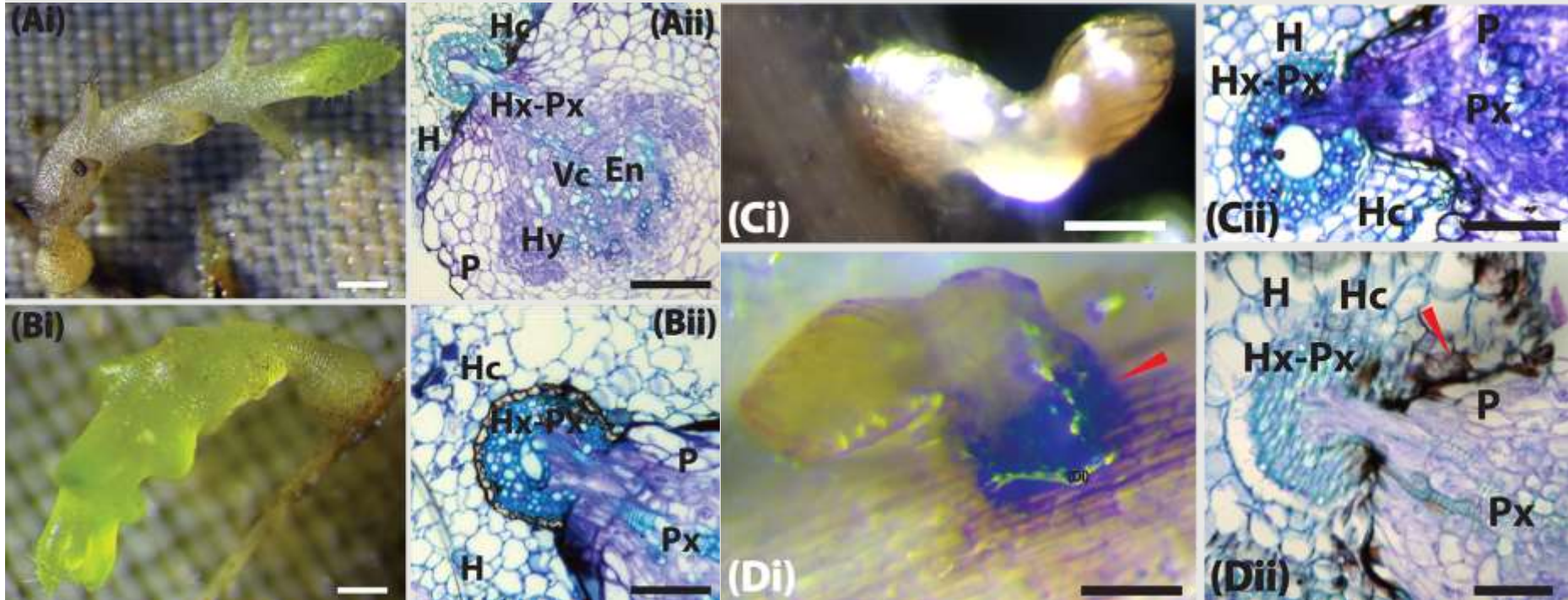
Histological analysis of host parasite interactions



Mechanism of *Striga* resistance in wild sorghum

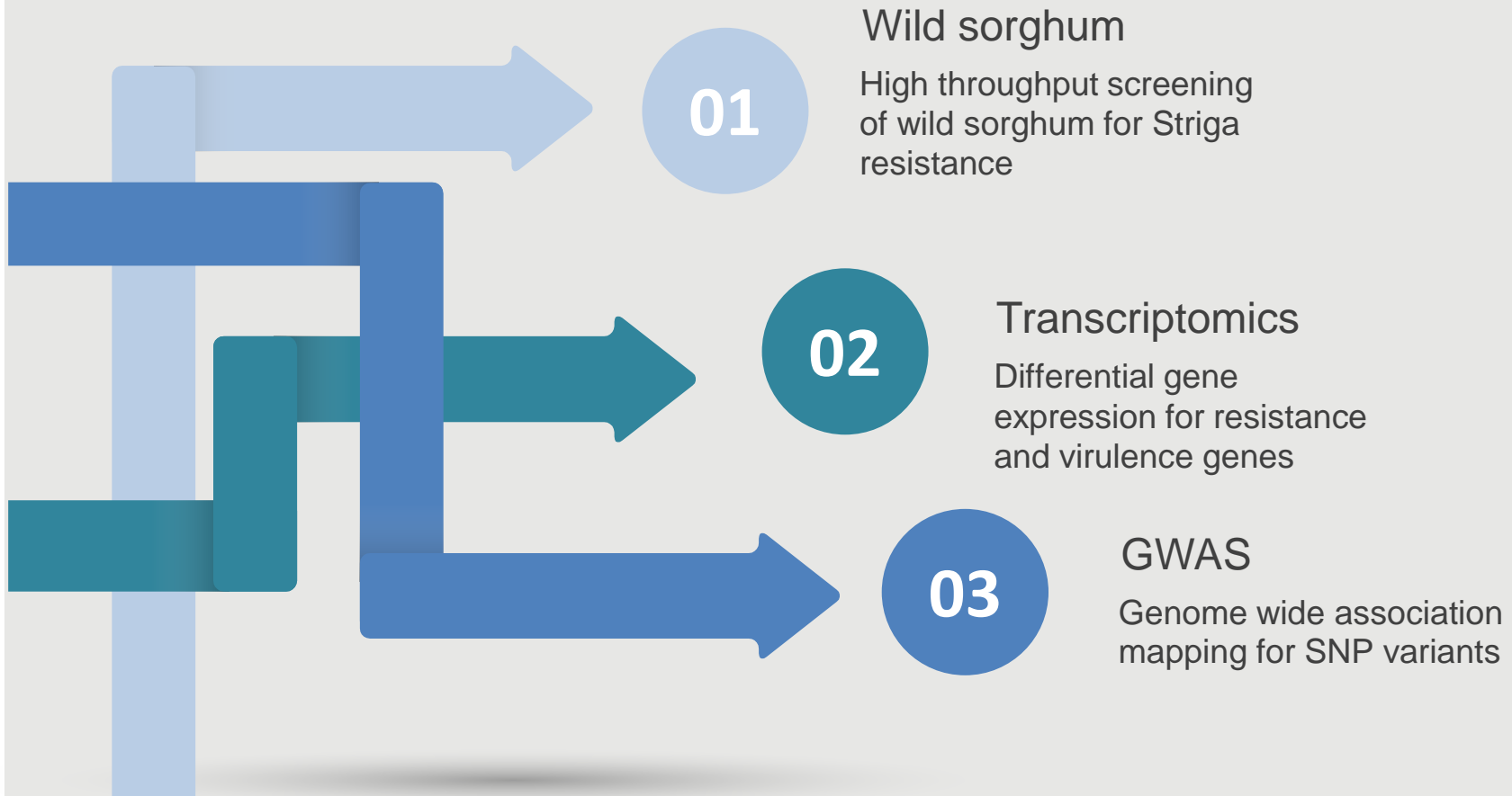
Susceptible interaction: 9DAI

Resistant interaction: 9DAI



Approach

Genomic tools for identification of host resistance and pathogen virulence



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Approach

Genomic tools for identification of host resistance and pathogen virulence

Grow *Striga* and sorghum together and extract RNA

Two different time points – early parasite development (Stage 3) and late parasite development (Stage 4). 6 wild sorghum and susceptible control

Build ILLUMINA TruSeq libraries

150 nucleotide single end

Sequence had both host and parasite tissue

– approximately 1×10^9 reads per accession

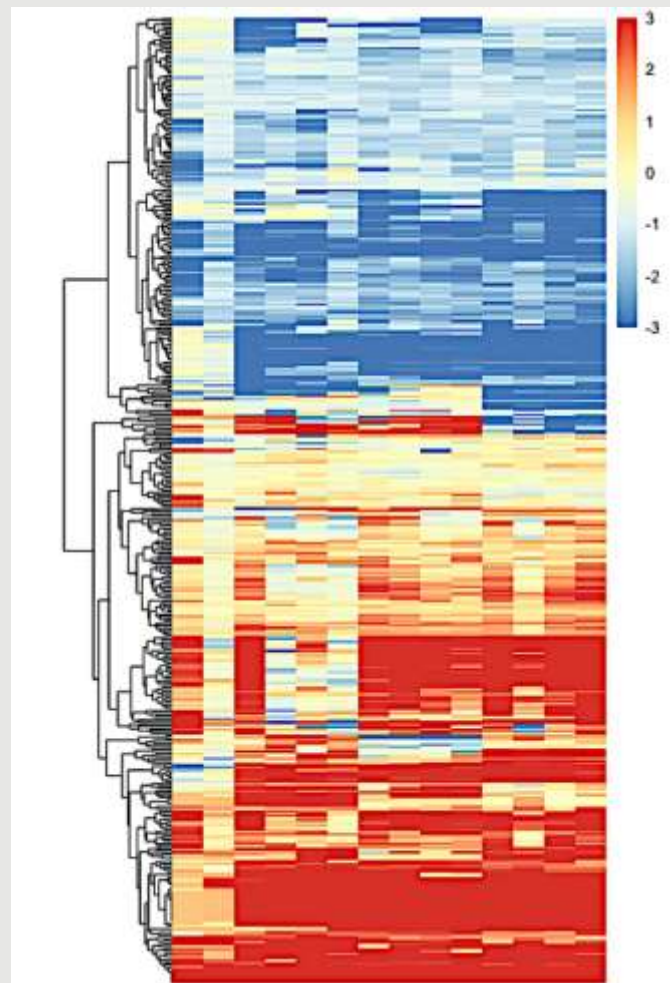
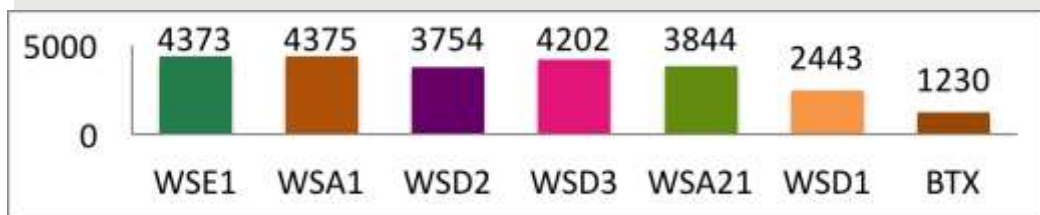
Map and separate reads clean up and analyze DE

– approximately 1×10^9 reads per accession

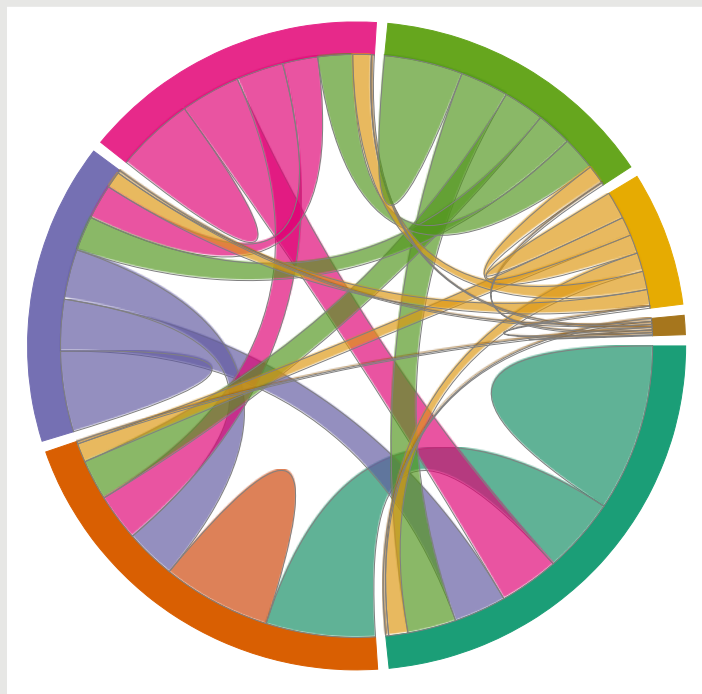


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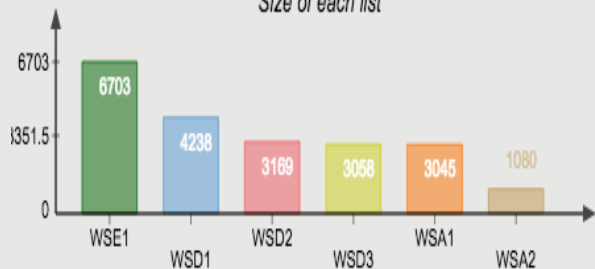
More genes differentially expressed in wild sorghum infected with *Striga*



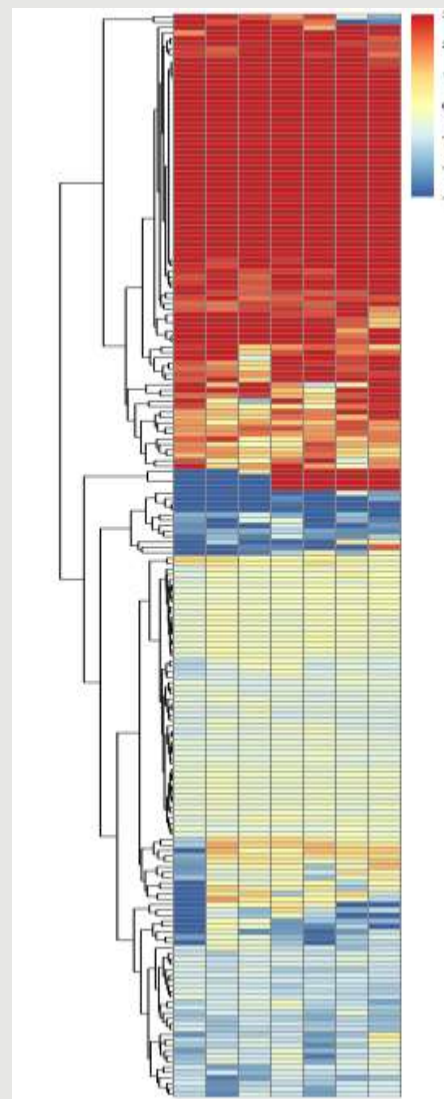
More *Striga* genes are differentially expressed in *Striga* infecting wild sorghum



Size of each list



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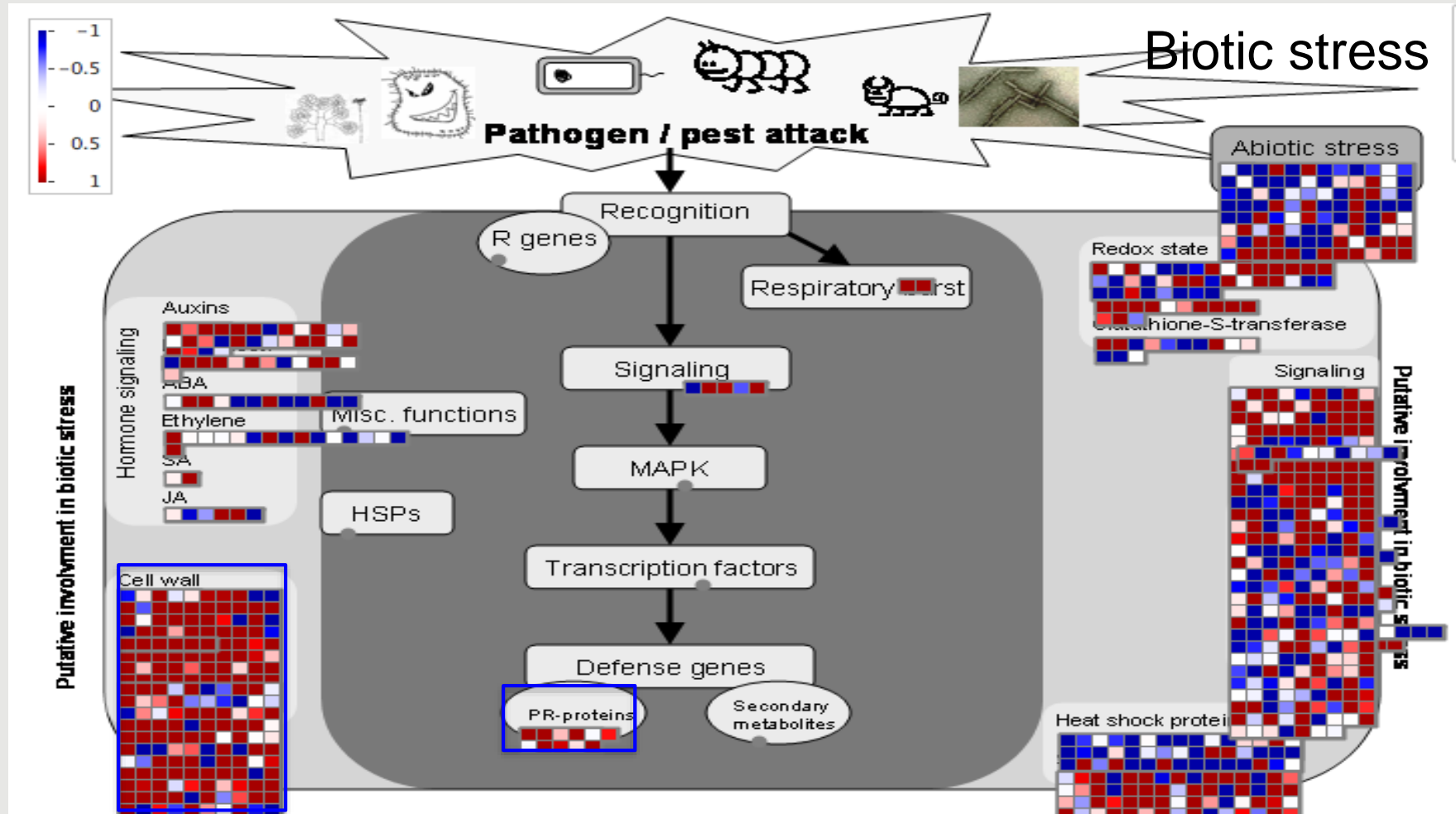


Runo et al 2018 (manuscript in preparation)

Cell wall, signaling, defense and transport genes are up regulated

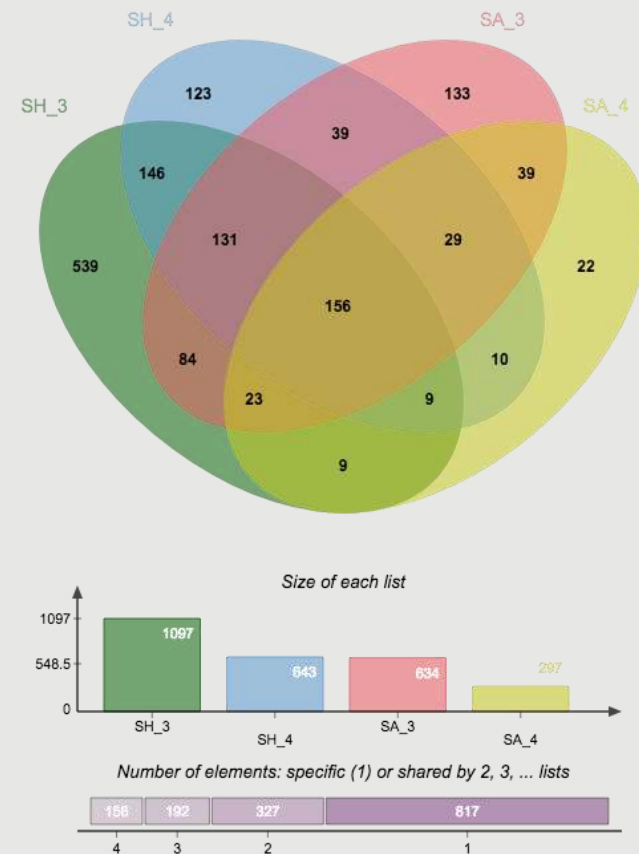
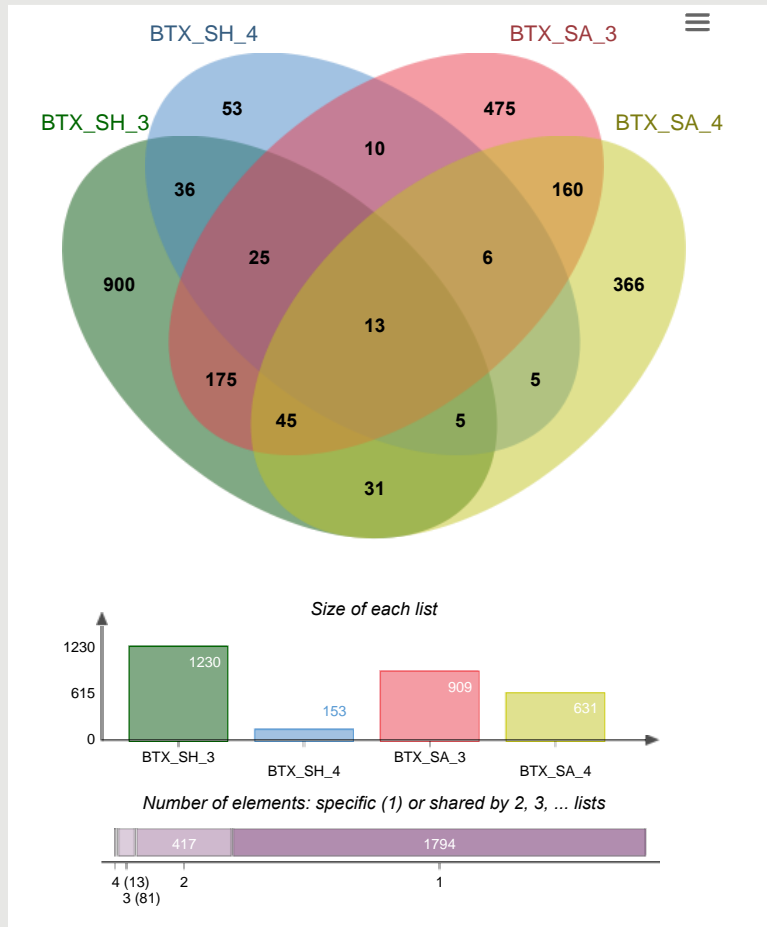
GOBP_Term	Fold Enrichm	Bonferroni	Benjamini	FDR
GO:0044092~negative regulation of molecular function	4.36179291	3.55E-07	3.55E-07	3.55E-07
GO:0006865~amino acid transport	4.44821538	5.31E-07	2.65E-07	5.30E-07
GO:0046942~carboxylic acid transport	4.11777652	6.44E-07	2.15E-07	6.43E-07
GO:0015849~organic acid transport	4.11777652	6.44E-07	2.15E-07	6.43E-07
GO:0015837~amine transport	4.3818241	7.61E-07	1.90E-07	7.60E-07
GO:0043086~negative regulation of catalytic activity	4.27028676	3.28E-06	6.55E-07	3.27E-06
GO:0044042~glucan metabolic process	2.95526468	4.42E-06	7.36E-07	4.41E-06
GO:0007018~microtubule-based movement	3.86292388	1.39E-05	1.99E-06	1.39E-05
GO:0007047~cell wall organization	2.28930536	2.51E-05	3.14E-06	2.51E-05
GO:0045229~external encapsulating structure organization	2.24445106	2.68E-05	2.98E-06	2.68E-05
GO:0007167~enzyme linked receptor protein signaling pathway	2.98098864	4.63E-05	4.63E-06	4.62E-05
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	2.98098864	4.63E-05	4.63E-06	4.62E-05
GO:0007017~microtubule-based process	3.00861113	1.05E-04	9.56E-06	1.05E-04
GO:0006073~cellular glucan metabolic process	2.93582215	1.89E-04	1.58E-05	1.89E-04
GO:0007049~cell cycle	2.30850972	2.63E-04	2.03E-05	2.63E-04
GO:0005976~polysaccharide metabolic process	2.35938218	2.70E-04	1.93E-05	2.70E-04
GO:0009250~glucan biosynthetic process	3.44469799	0.00115008	7.67E-05	0.00114887
GO:0030243~cellulose metabolic process	3.61331957	0.00188836	1.18E-04	0.00188706
GO:0044264~cellular polysaccharide metabolic process	2.51641898	0.00284351	1.67E-04	0.0028429
GO:0015833~peptide transport	3.35522531	0.00643621	3.59E-04	0.00644633
GO:0006857~oligopeptide transport	3.35522531	0.00643621	3.59E-04	0.00644633
GO:0007166~cell surface receptor linked signal transduction	2.3629788	0.01155552	6.12E-04	0.01160327
GO:0006260~DNA replication	2.57779506	0.01878315	9.48E-04	0.01892924
GO:0033692~cellular polysaccharide biosynthetic process	2.73630025	0.0231982	0.00111707	0.02343069
GO:0051301~cell division	2.27957955	0.02485032	0.00114318	0.02512032
GO:0022402~cell cycle process	2.47227128	0.0278457	0.0012271	0.02819095
GO:0000271~polysaccharide biosynthetic process	2.63400866	0.04412546	0.00187859	0.04504525

Cell wall, signaling, defense and transport genes are up regulated

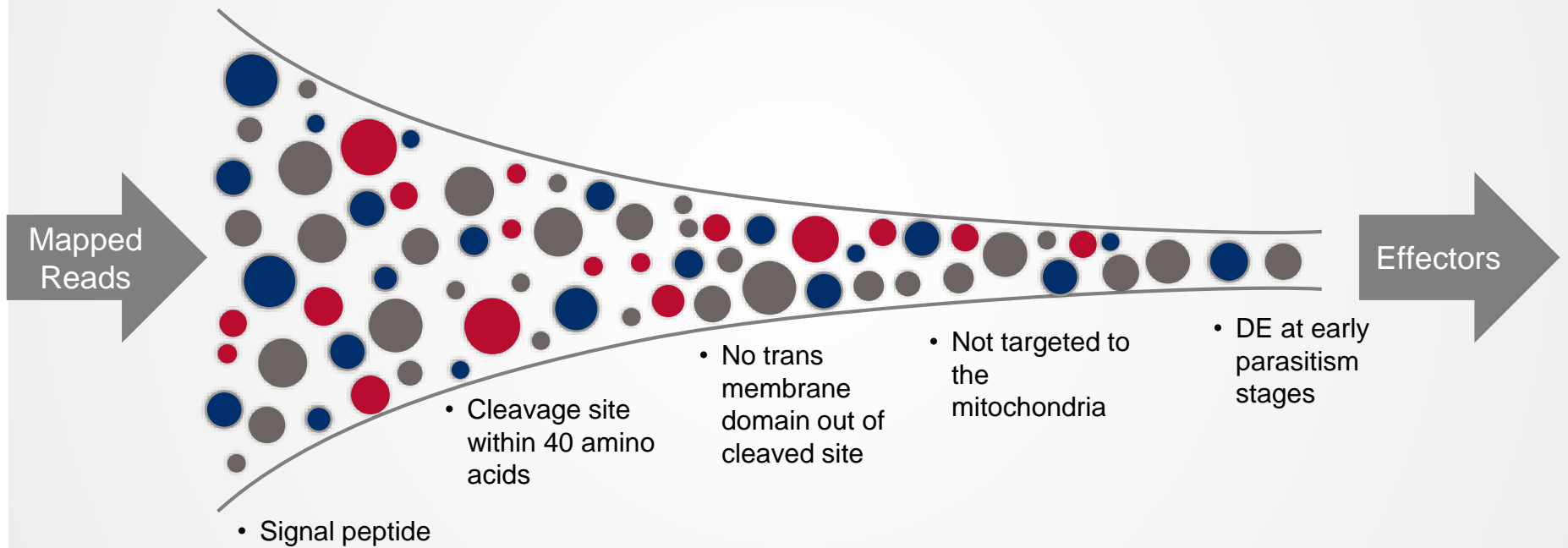


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Derailing the witchweed: Mining for *Striga* effectors



Pipeline for *Striga* effectors identification



ARTICLE

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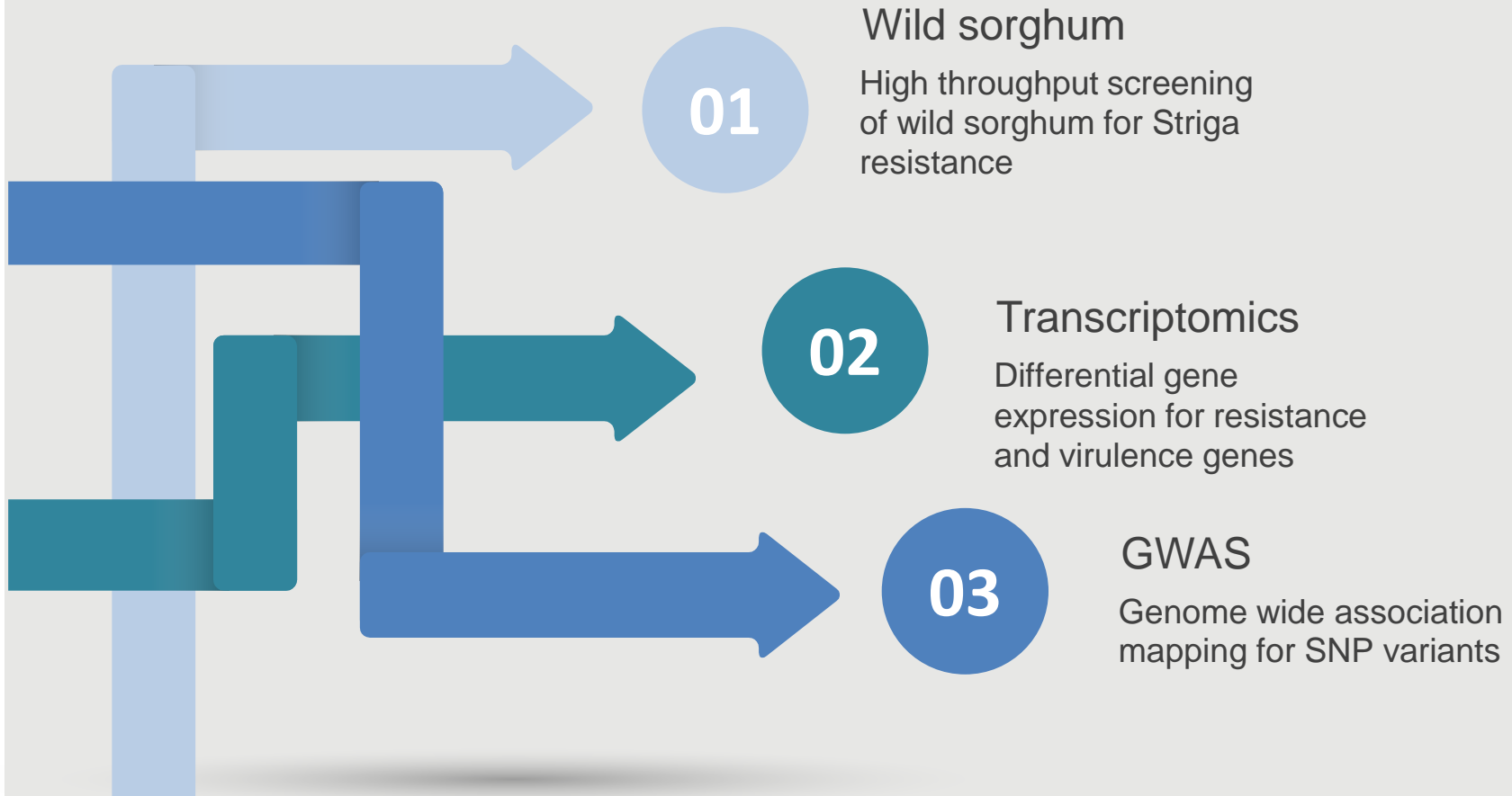
The fungal-specific β -glucan-binding lectin FGB1 alters cell-wall composition and suppresses glucan-triggered immunity in plants

Stephan Wawra^{1,*}, Philipp Fesel^{1,*}, Heidi Widmer¹, Malte Timm², Jürgen Seibel², Lisa Leson¹, Leona Kessler¹, Robin Nostadt³, Magdalena Hilbert³, Gregor Langen¹ & Alga Zuccaro^{1,3}

β -glucans are well-known modulators of the immune system in mammals but little is known about β -glucan triggered immunity *in planta*. Here we show by isothermal titration

Approach

Genomic tools for identification of host resistance and pathogen virulence

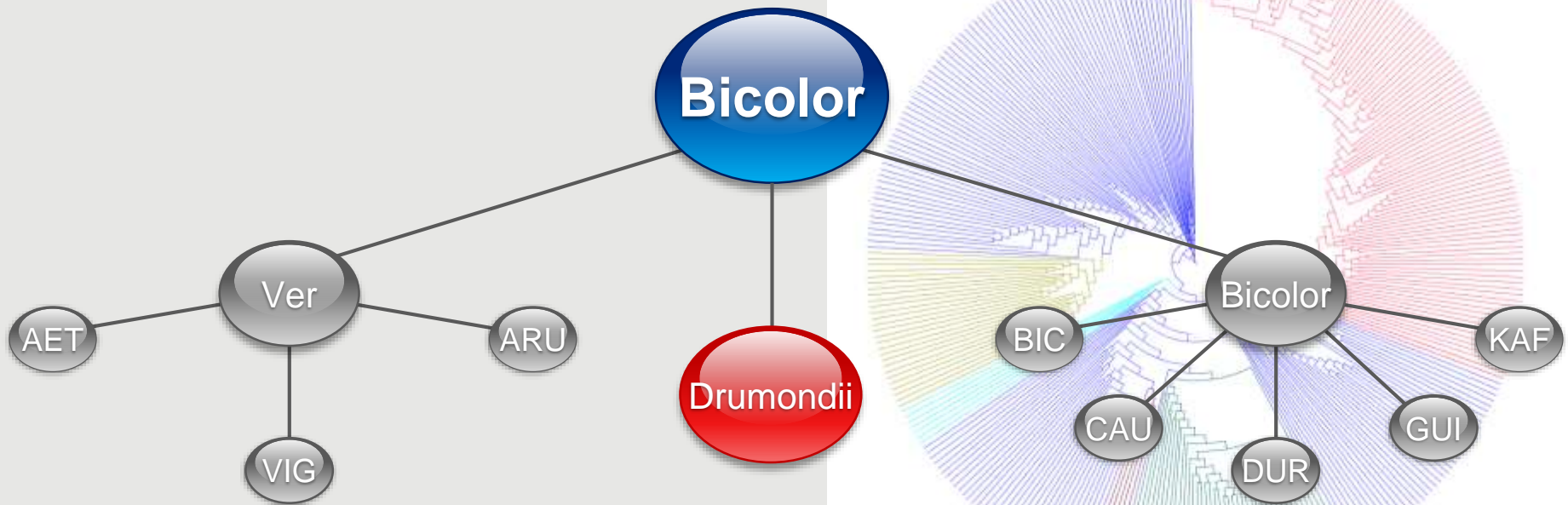


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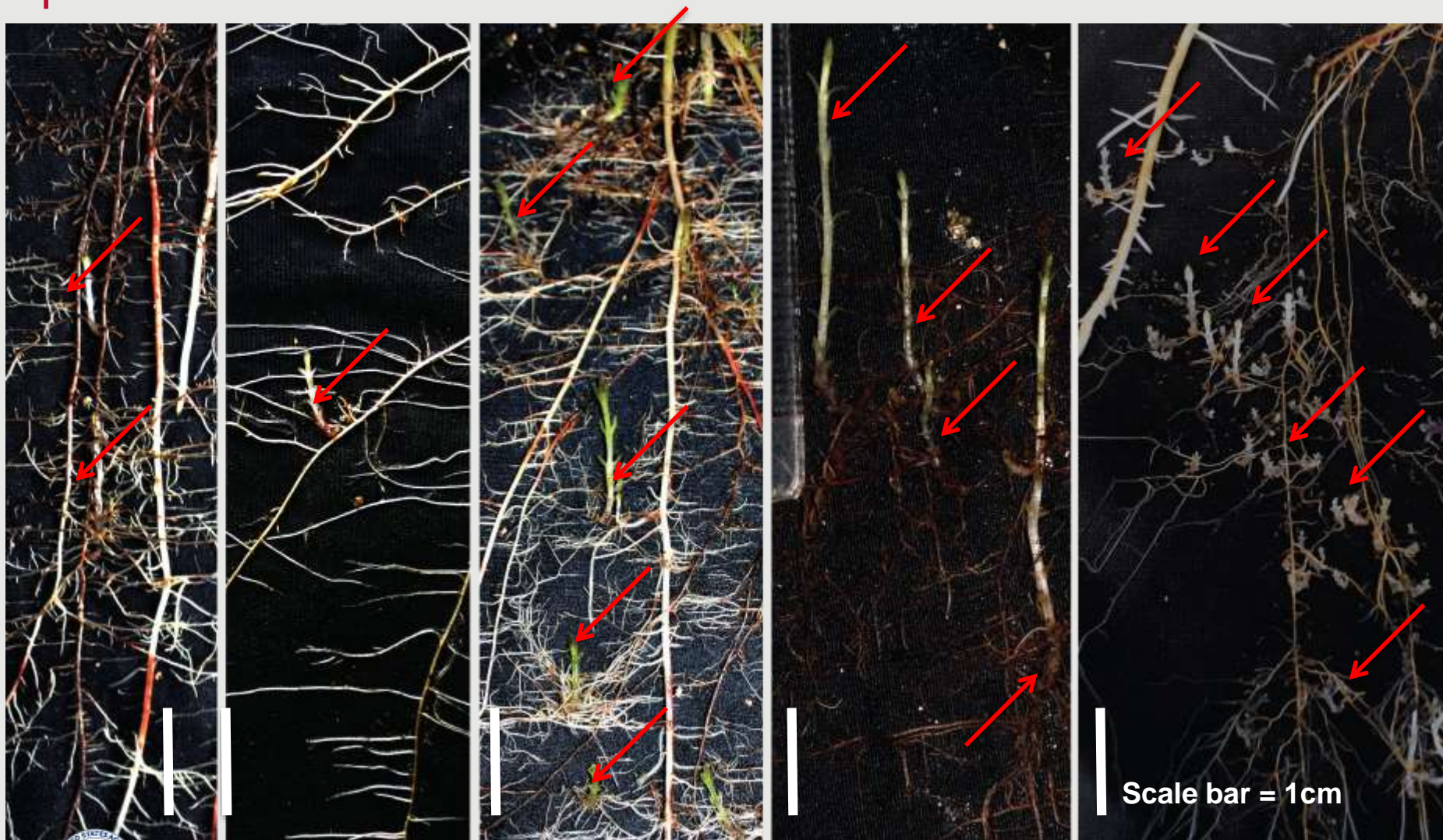
Genome wide association mapping of Striga resistance in a global diversity panel



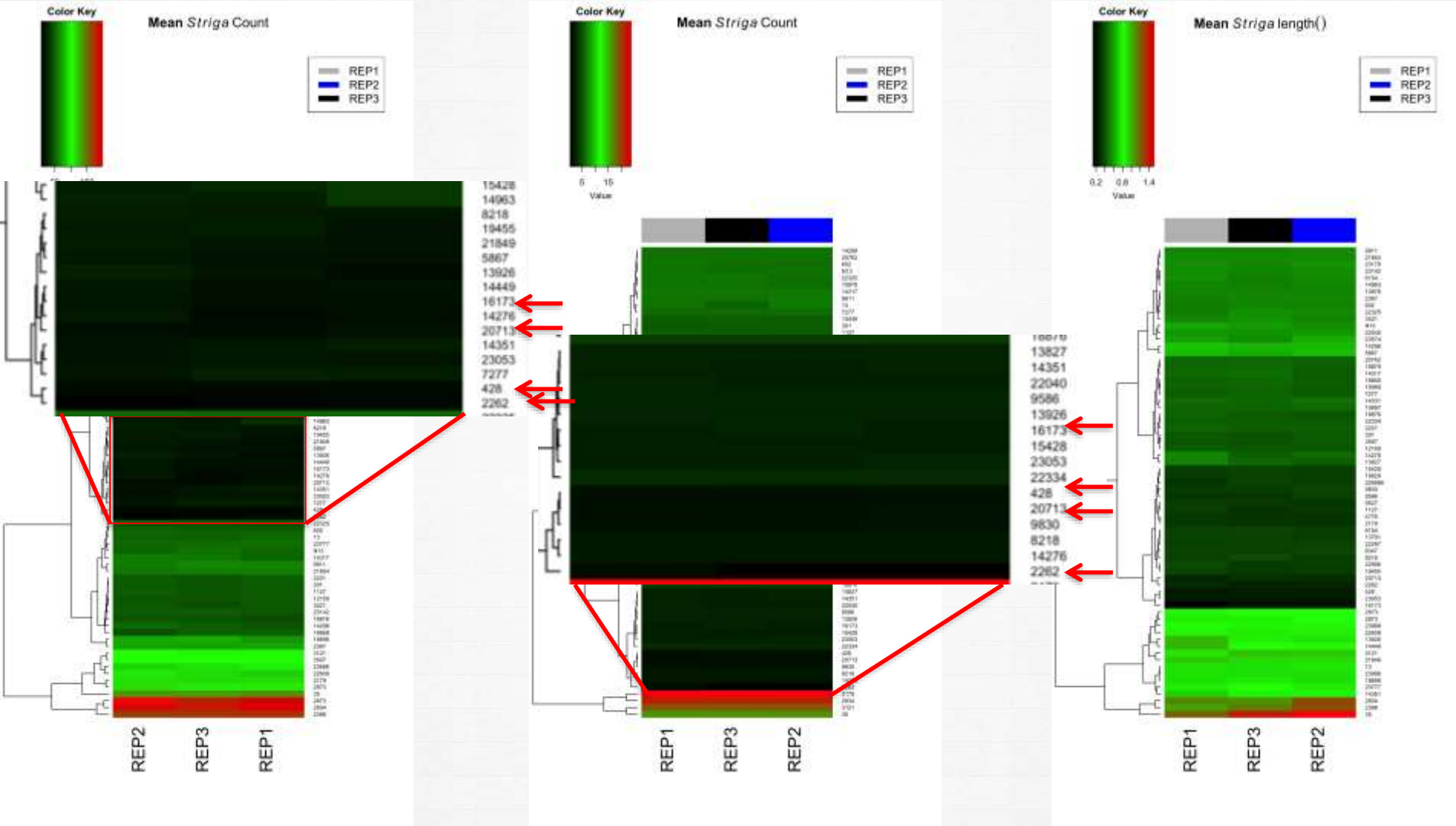
Genome wide association mapping of *Striga* resistance in a global diversity panel



Diverse resistance *Striga* resistance response in the diversity panel

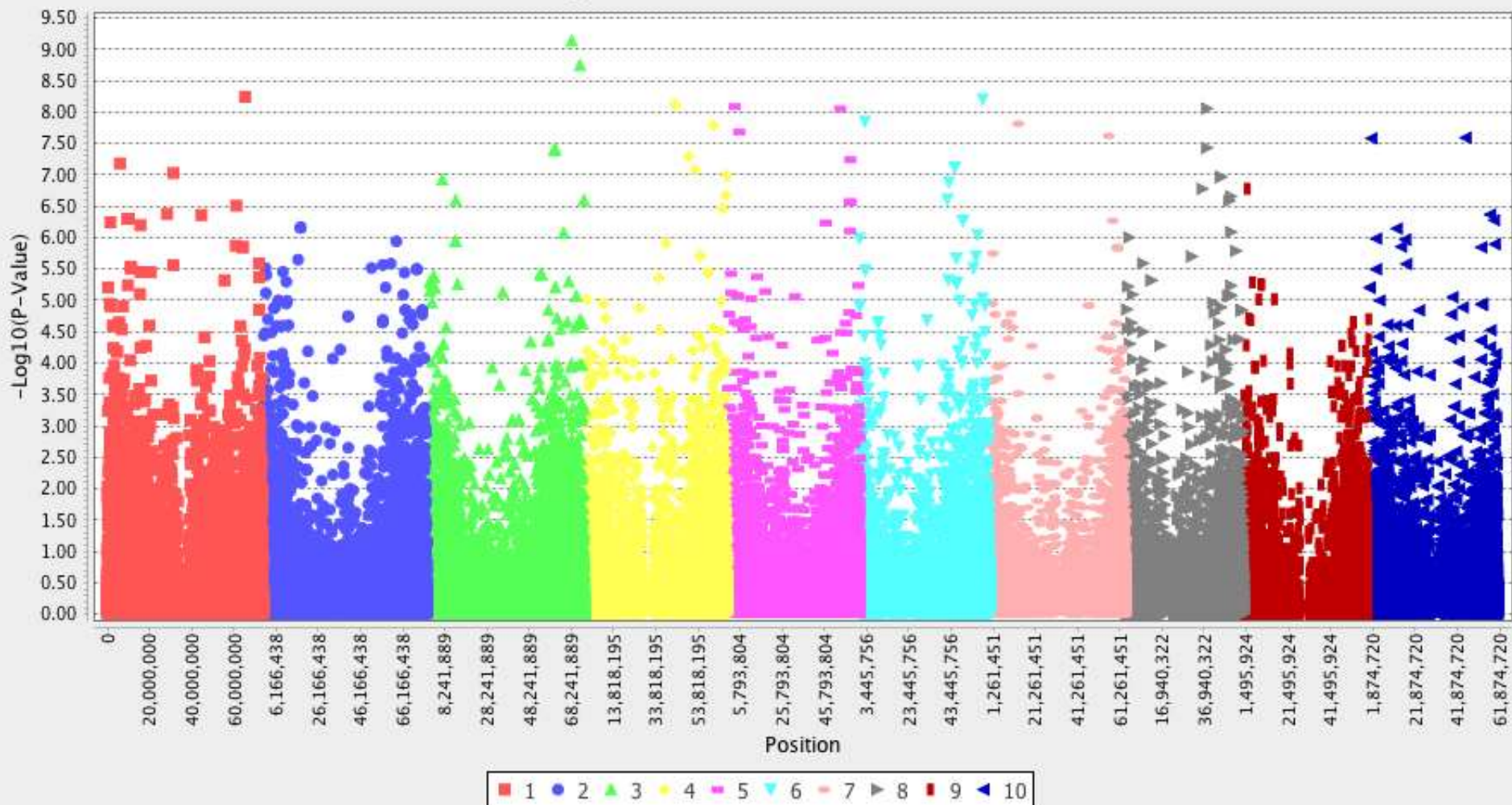


GWAS identifies of *Striga* resistance in a global diversity panel



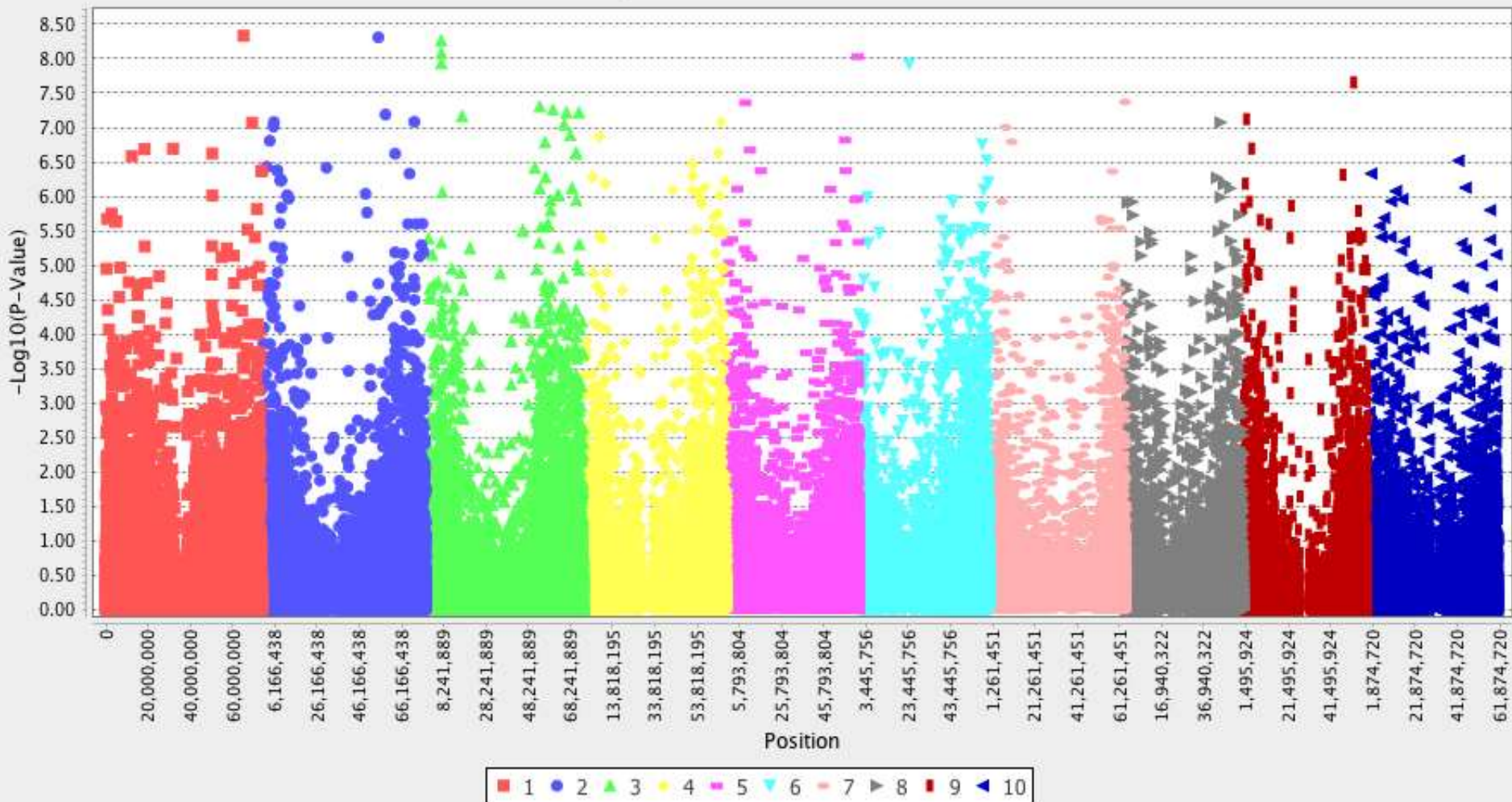
GWAS “pinpoints” *Striga* resistance loci

P-Values by Chromosome for Attachements



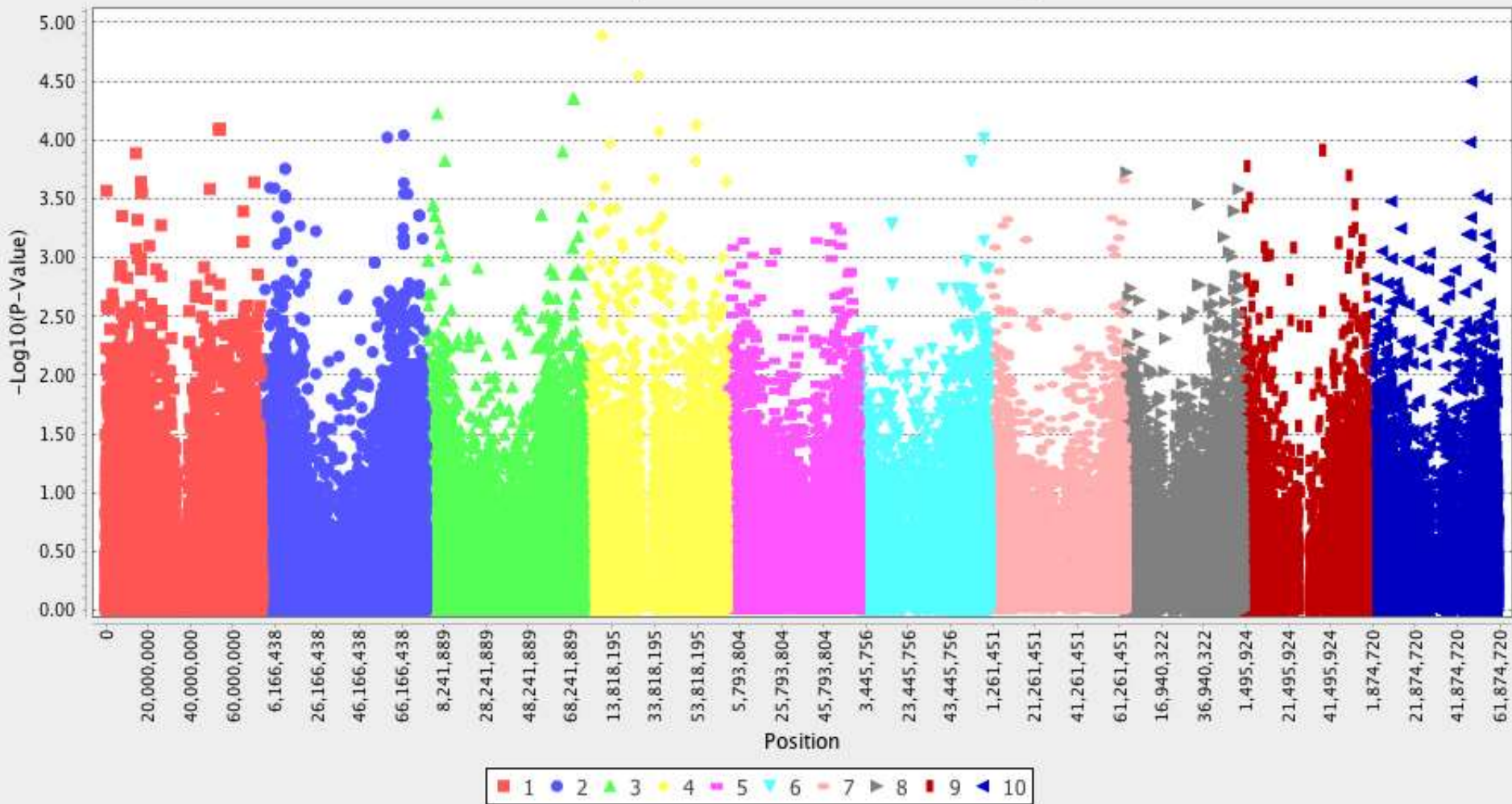
GWAS “pinpoints” *Striga* resistance loci

P-Values by Chromosome for biomass

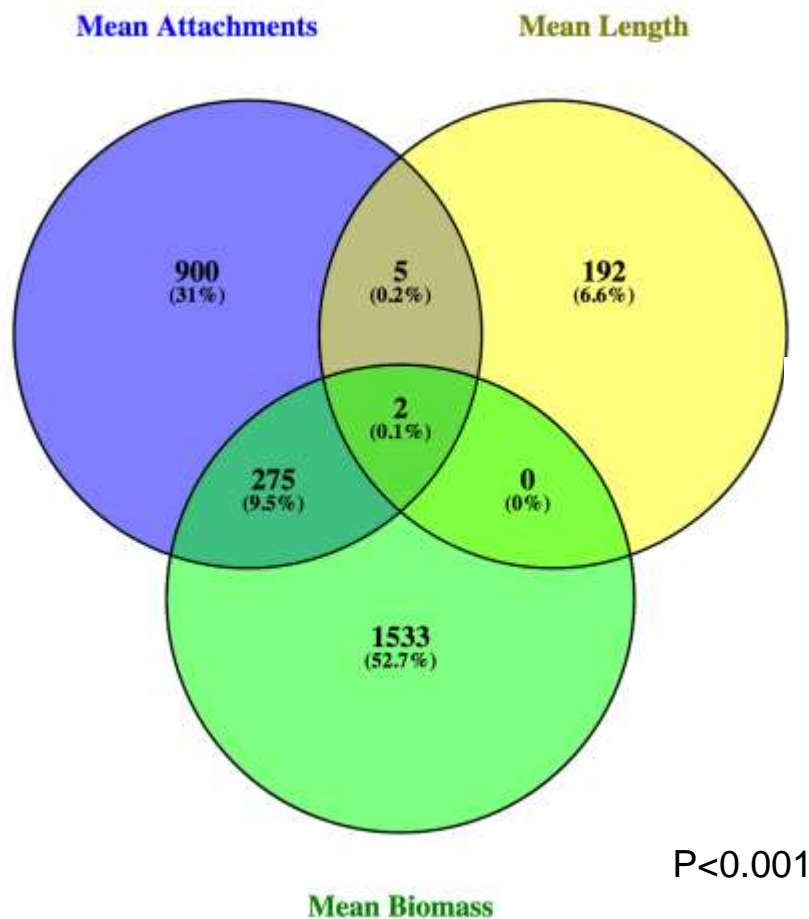


GWAS “pinpoints” *Striga* resistance loci

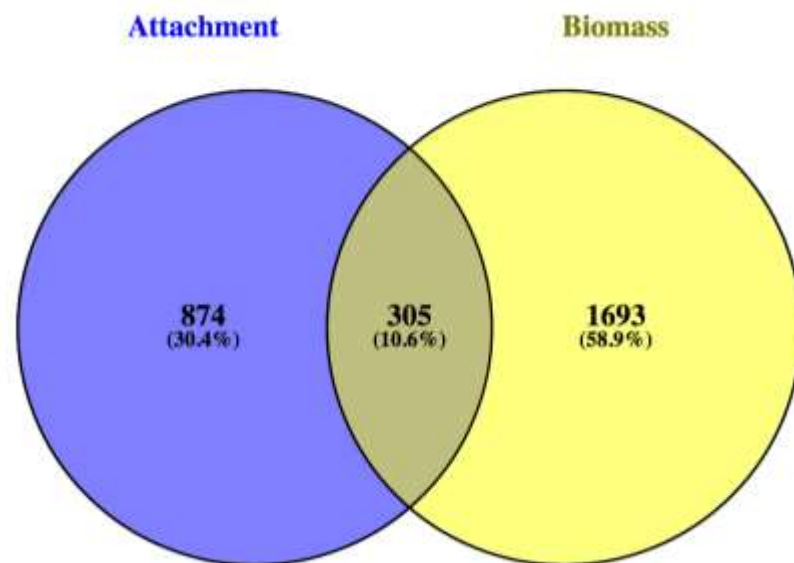
P-Values by Chromosome for Length



GWAS “pinpoints” *Striga* resistance loci



Cystein Synthase
Senescence Specific Cystein
Protease
Membrane-associated kinase
regulator 2
Clathrin heavy chain 1 (CHC1)
gene promoter



GWAS “pinpoints” *Striga* resistance loci

The receptor-like kinase SERK3/BAK1 is a central regulator of innate immunity in plants

Antje Heese^{*†}, Dagmar R. Hann[‡], Selena Gimenez-Ibanez[‡], Alexandra M. E. Jones[‡], Kai He[§], Jia Li[§], Julian I. Schroeder[¶], Scott C. Peck^{‡§}, and John P. Rathjen^{†‡}

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Communicated by David Baulcombe, The Sainsbury Laboratory, Norwich, United Kingdom, June 6, 2007 (received for review May 25, 2007)



Research

Cysteine homeostasis plays an essential role in plant immunity

Consolación Álvarez, M. Ángeles Bermúdez, Luis C. Romero, Cecilia Gotor and Irene García

Instituto de Bioquímica Vegetal y Fotosíntesis, Consejo Superior de Investigaciones Científicas and Universidad de Sevilla, Avda. Américo Vespucio, 49, ES-41092 Sevilla, Spain

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- PPGP
- RIKEN
 - Ken Shirasu
- University of Wageningen
 - Harro Bouwmeester

PEER supplement : Enhanced Utilization and conservation of wild sorghum genetic resources



Striga resistance in wild sorghum. Sorghum's resistance to *Striga* field demonstration site. Alupe, Busia Kenya