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

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1 Abstract

Crop losses caused by parasitic plants of the genus *Striga* pose great danger to livelihoods of millions of smallholder farmers in Africa. The parasite attaches to host crops and siphon nutrients leading to severe retardation and crop death. *Striga* control is difficult because of the parasite's ability to produce large amounts of seeds that can stay dormant in soil for decades only germinating in response to chemical cues from the host. In recent years, breeding crops for host-based resistance has been prioritized. However, such programs have not taken into account the changes in *Striga*'s aggressiveness and severity – described as virulence. This is critical because a parasite's virulence is an important determinant of its potential to overcome host resistance and thereby expand its host and natural range. In this project, we firstly identified new sources of *Striga* resistance from wild sorghum accessions. We then used genomics tools – RNA sequencing to i) identify *Striga* resistance genes in wild sorghum and ii) *Striga* virulence genes. *Striga* resistant wild sorghum genotypes identified in the project are now available integrating *Striga* resistance in Kenya's cereal farming systems.

Fig 1. *Striga hermonthica* on maize. *Striga* infects all cultivated cereal crops including maize, millet, sorghum and rice.

2 Research plan

2.1 Hypothesis

Domestication—the process of transforming wild species into elite cultivars—inevitably leads to decreased genetic diversity in the selected crops. In some cases, the lost genetic diversity may represent the organism's capacity to adopt changes, such as pathogen resistance. Logically, pathogen virulence exhibits itself differently in resistant and susceptible hosts.

2.2 Approach

We explored the resistance interactions between wild sorghum accessions and the parasitic plant *Striga hermonthica* at the parasite's center of origin in northeastern Africa. We showed remarkable *Striga* resistance in wild sorghum accession – WSA1, WSA2, and WSE1races (Fig 2). Identified *Striga* resistance in wild sorghum makes it possible to expand the genetic basis of cultivated sorghum using genomics tools. We therefore used dualRNA sequencing (simultaneous sequencing of host and parasite tissue) to compare differential gene expression profile between wild sorghum (resistant) and cultivated (susceptible) sorghum. We further compared differential gene expression profile of Striga infecting wild sorghum with that of Striga infecting cultivated sorghum . Finally, we developed a pipeline to predict molecules that potentially aid *Striga* to overcome host immune response (effectors).

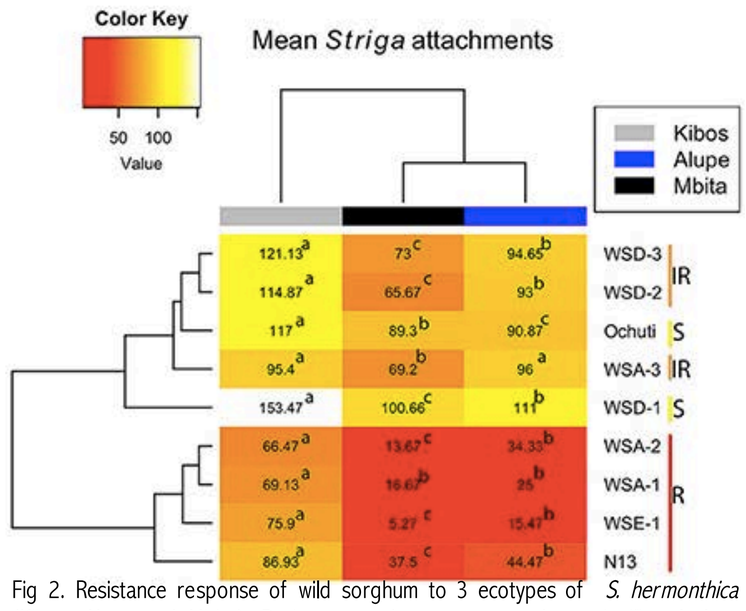

Fig 2. Resistance response of wild sorghum to 3 ecotypes of *S. hermonthica* (Kibos, Alupe and Mbita). Resistant sorghum genotypes have significantly less attachments while virulent parasite ecotypes cause more attachments.

3 Results

3.1 Host resistance genes

We found that *Striga* induced a larger number of differentially expressed genes in wild sorghum in comparison to cultivated sorghum (Fig 3a, 3b and3c). The number of differentially expressed genes in different hosts correlated with resistance level. For example, WSE1, WSA1 and WSA2 were the most resistant sorghum accessions. These accessions also had the highest number of differentially expressed genes (Fig 3c). This group of gens included: transporters, cell wall fortifying genes, as well as typical resistance genes that act to protect host cells by degrading cell wall components of pathogens (Fig 3d).

3.2 *Striga* virulence genes

We also observed that a larger number of genes were differentially expressed in *Striga* infecting wild sorghum compared to *Striga* infecting cultivated sorghum. When we subjected the differentially expressed genes in *Striga* to an analysis pipeline (Fig 3e, 3f and 3g) that is used to predict molecules that aid pathogens to overcome host immune response (effectors) i.e. sequences containing a signal peptide, a cleavage site within the first 40 amino acids, with no trans-membrane domain outside of cleaved region and not targeted to the mitochondria, we obtained a rapporteur of candidate effectors. This list included cell wall degrading enzymes as well as some homologues of pathogenic avirulence/virulence genes (Fig 3h).

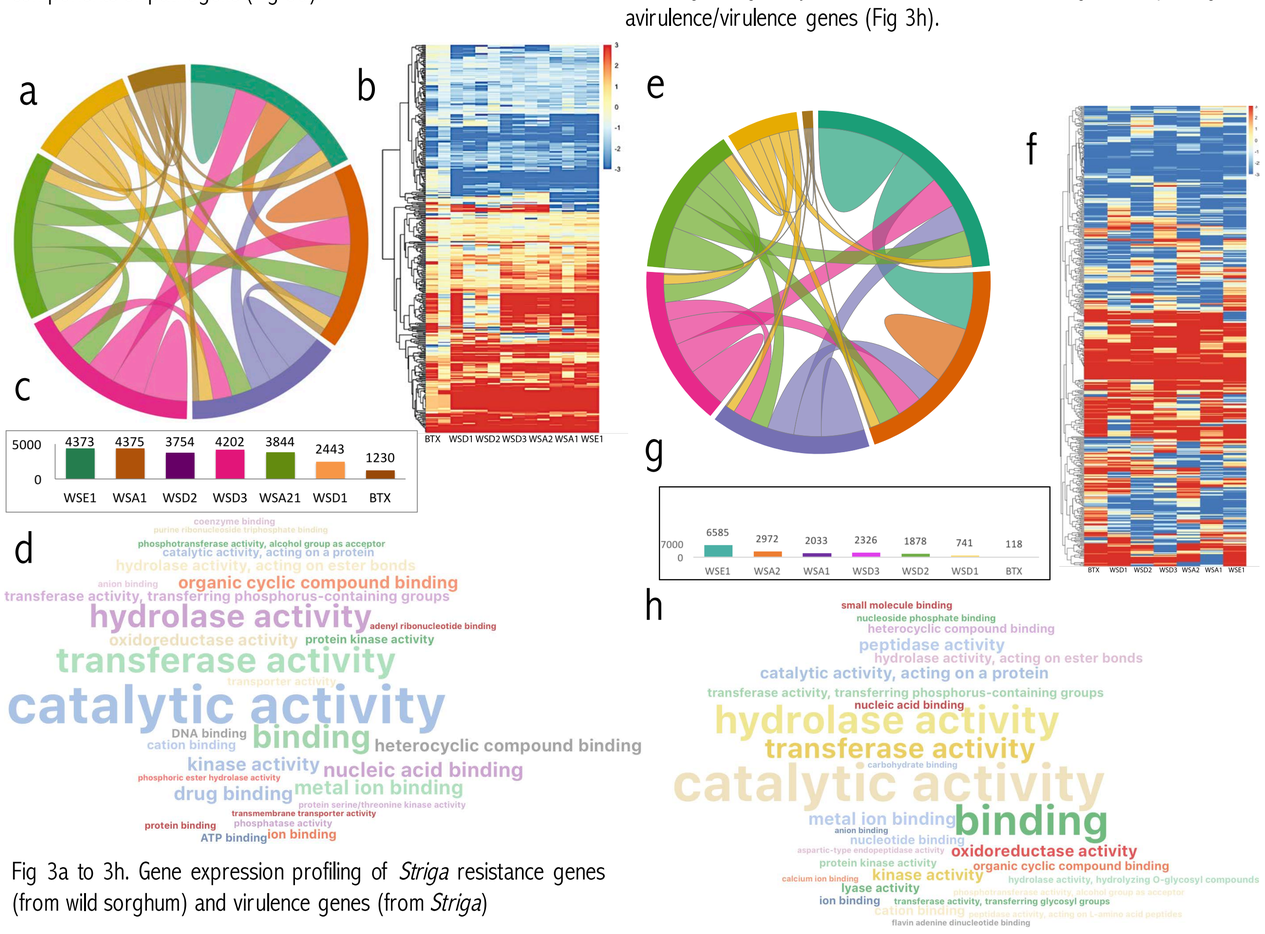

Fig 3a to 3h. Gene expression profiling of *Striga* resistance genes (from wild sorghum) and virulence genes (from *Striga*)

4 Impact

4.1 Conservation and sustainable utilization of wild sorghum

To demonstrate and influence policy on conservation and utilization of wild sorghum genetic resources, we set up a field demonstration site for *Striga* resistant wild sorghum at Alupe in Western Kenya (Fig 4). This field site was set up in a *Striga* endemic area and shows the diversity of wild sorghum relatives and their potential to elevate biotic and abiotic constrains of sorghum production.

Fig 4. Diverse sorghum genotypes that can act as reservoirs for disease resistance genes in a demonstration field site in Alupe, Western Kenya. The field site also serves as a genebank for conservation.

4.2 Genomic aided selection of *Striga* resistant cereals

We have described a platform for developing resistance in sorghum against *Striga* based on marker assisted selection of resistance from wild sorghum. This process will expand the genetic basis of cultivated sorghum to cope with evolving *Striga* virulence. Fig 5.

5 Dissemination

1. Runo S, Kuria, E. Habits of a Highly Successful Cereal Killer, *Striga*. PLoS Pathogens, 2018. 14(1): e1006731.

2. Mbuvi, D. A., Masiga, C. W., Kuria, E., Masanga, J., Wamalwa, M., Mohamed, A., Timko, MP, Runo, S. Novel Sources of Witchweed (*Striga*) Resistance from Wild Sorghum Accessions. Frontiers in Plant Science, 2017 8, 271.

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