WHEAT SIDE STORY

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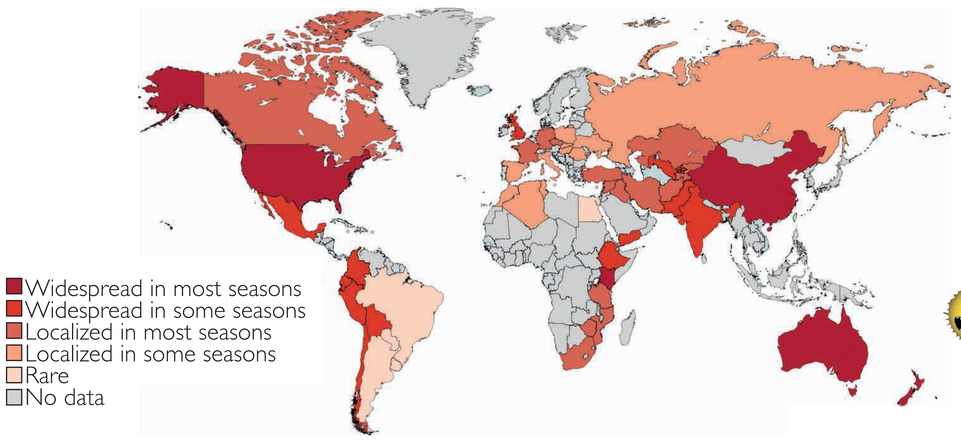
YELLOW RUST IS THREATENING GLOBAL WHEAT PRODUCTION

Yellow (or stripe) rust (YR) disease caused by the fungus ***Puccinia striiformis f. sp. tritici* (PST)** is present in all the major wheat-growing regions causing significant reductions in grain quality and yield in susceptible hosts.

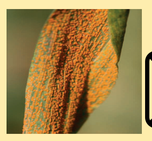
In the past, yellow rust endemics were specific to cool, wet and often high-attitude regions and **race-specific resistance (R) genes** in wheat varieties were traditionally successful to control the disease. Due to the genetic homogeneity of crops world-wide, climate change and global trade, **new more virulent PST races** adapted to warmer temperatures and drier areas have evolved and overcome the previously resistant varieties causing **devastating pandemics.**



Right now **88% of the world's wheat production is susceptible** to the disease[1].

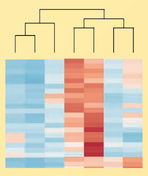
ANALYSING THE HOST RESPONSE TO YELLOW RUST

1. Host **gene expression** dynamically changes under pathogen infection.
2. A sucessful pathogen is able to **reprogramme a host plant's gene expression** to impair the plant immune response and obtain nutrients.
3. PST genotypes show seasonal and **varietal specificity.** In fact, specific wheat varieties only harbor particular PST genotypes.
4. Identifying changes in gene expression in closely related hosts will help us to understand the **wheat-rust interaction.**



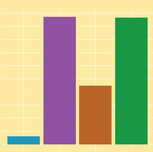
Receive PST-infected field samples. We have collected >500 samples from over 30 countries.

Use a **dual RNA-seq** approach to identify genes expressed by pathogen and host during infection.



Compare gene expression in specific wheat varieties

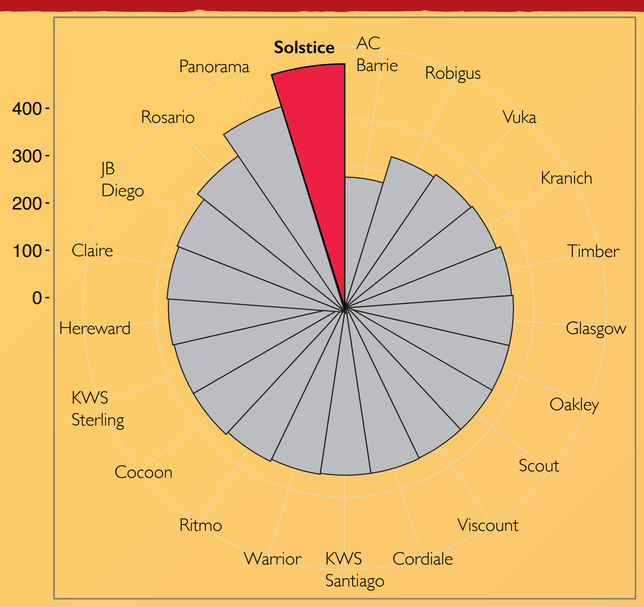
Align to reference wheat transcriptome and confirm wheat variety using SNP markers



Functionally annotate interesting genes to look for enrichment of specific pathways involved in disease response

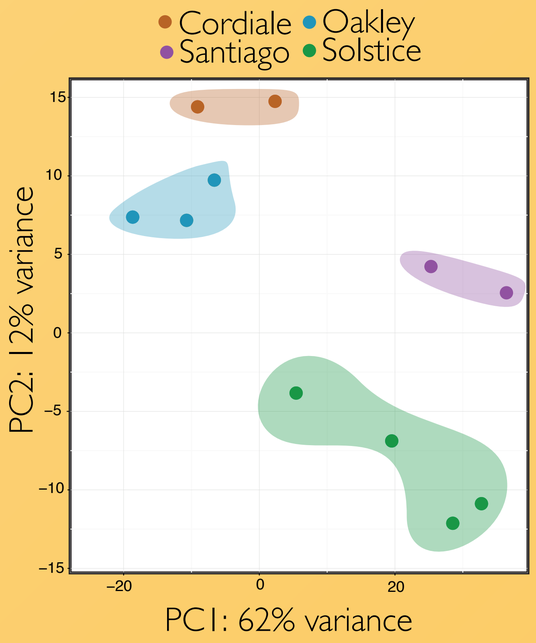
Validate differential expression in controlled conditions by inoculating wheat plants with different PST isolates .

I. Confirm wheat variety using SNP markers



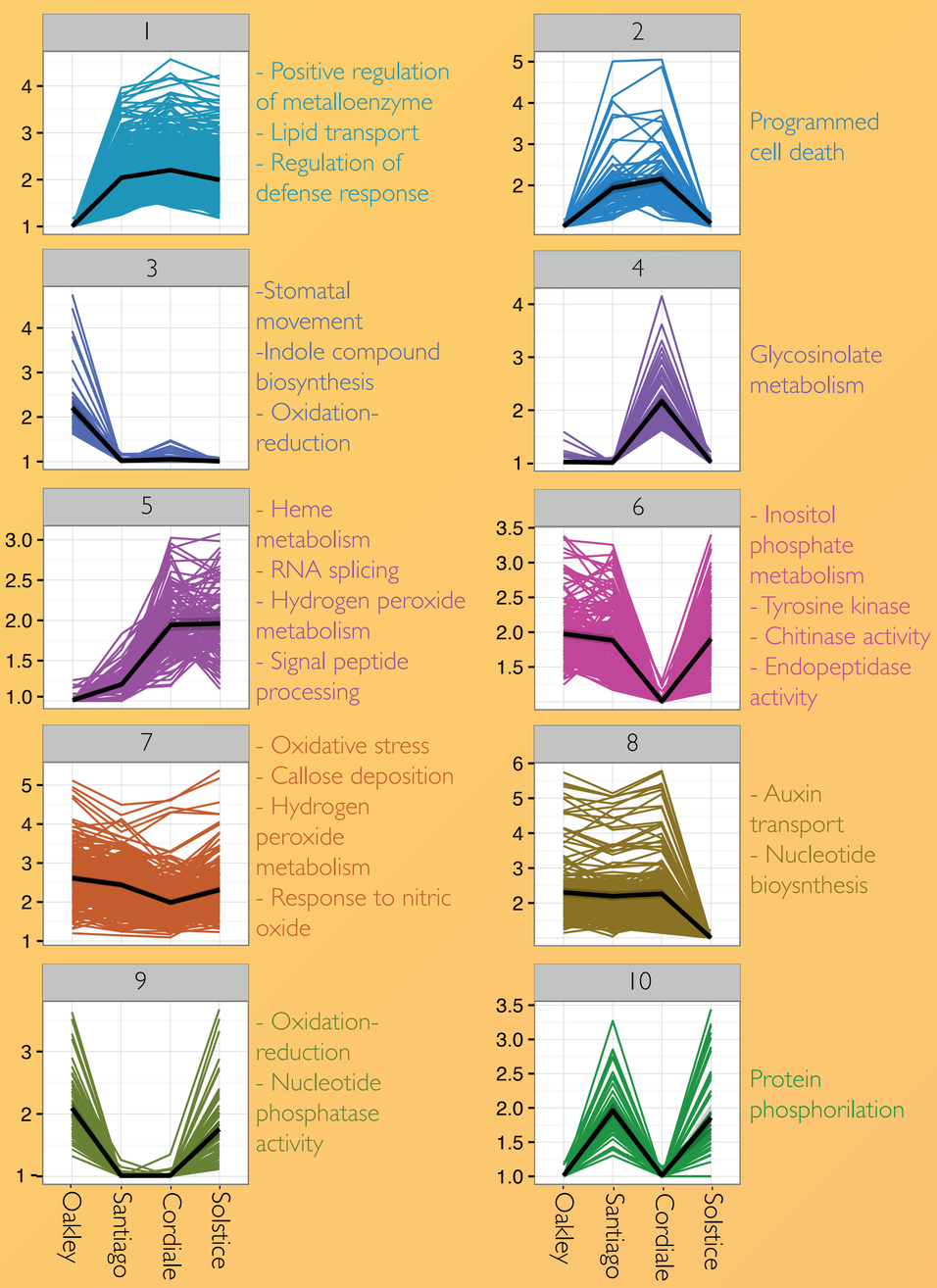
We obtained transcriptomic data from PST-infected samples and verified the wheat variety for over 20 sampled hosts. We assigned a score to each field sample using over 20,000 SNP markers with the highest score identifying/describing the host variety.

II. Comparing gene expression in samples from different varieties



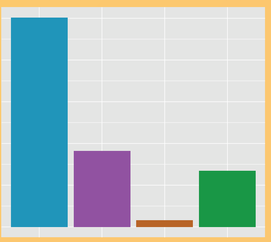
We looked at the differential gene expression of European field samples. **Samples from the same variety cluster well in terms of gene expression** and therefore can be used as **replicates** to mask the effect of the environment on the samples.

We compared the expression profiles of different wheat varieties using a clustering approach to group genes with similar levels of expression. We identified **10 different clusters** of differentially expressed host genes that were used for **functional annotation.** These genes might help elucidate the PST varietal specificity.



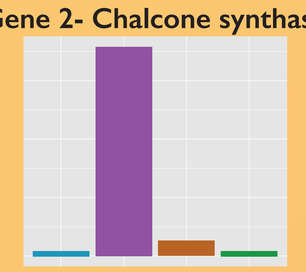
III. Variety-specific genes are involved in disease response

Gene 1- Chitinase



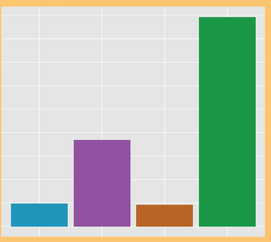
Involved in the chitin catabolic pathway. Chitin is a structural component of fungal cell walls.[2]

Gene 2- Chalcone synthase



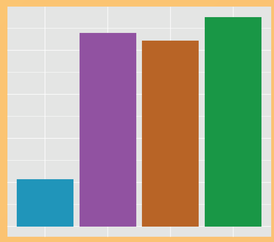
Role in plant resistance resulting in the production of antimicrobial compounds. [3]

Gene 3- Serine/threonine protein kinase (STK)



One of the important proteins responsible for defense signal transduction.[4]

Gene 4 - Phospholipase A



Involved in the accumulation of fatty acids derivatives (as oxylipins) in response to biotic aggressions. [5]

TAKE HOME MESSAGES

1- We use **transcriptomic data from PST-infected field samples** to identify host genes involved in disease response.

2- SNP markers can be used to **identify the wheat variety** in field samples.

3- Different wheat varieties have different gene expression profiles. We short-listed differentially expressed **genes** potentially **involved in disease response.**

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References

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