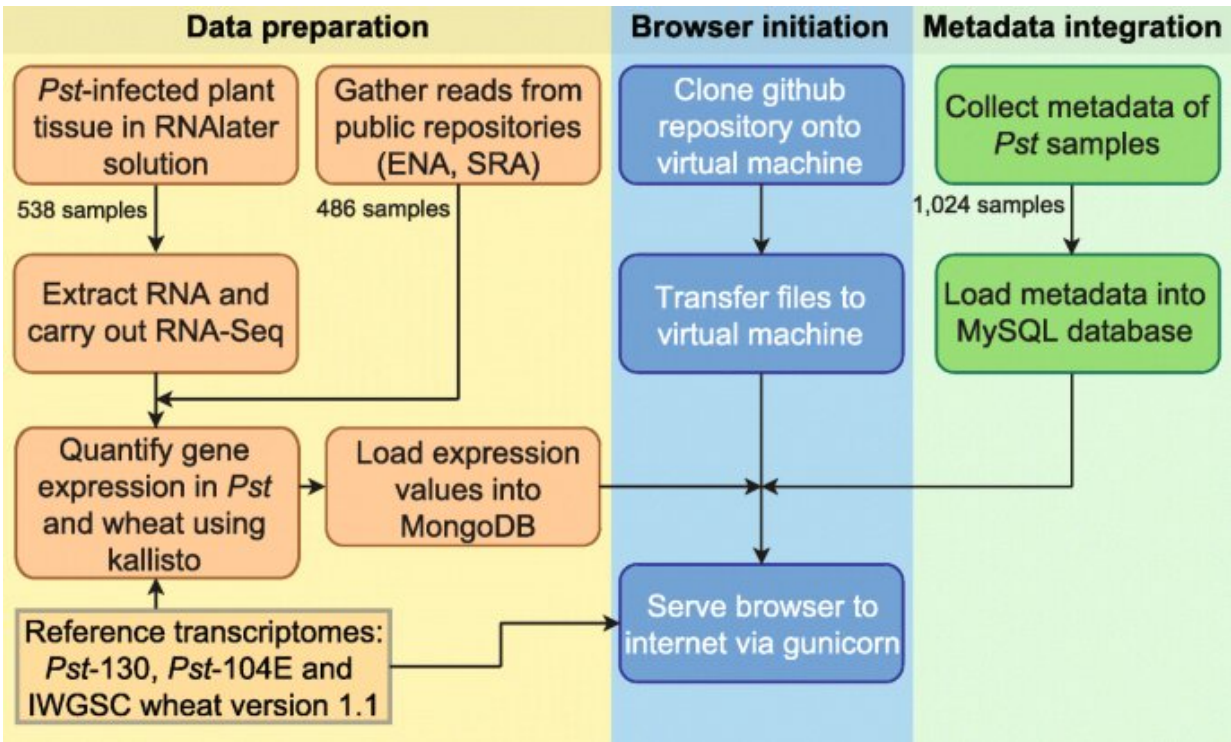


A new genomic tool for wheat rust researchers worldwide

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Flowchart illustrating the construction of the rust expression browser. RNA-Seq data was collated from 1024 *Pst* samples and pseudoaligned to the *Pst* reference transcriptomes (isolates *Pst*-130 [19] and *Pst*-104E [21]) and wheat transcriptome version 1.1 [25] using kallisto [26], generating gene expression values (“Data preparation”). Metadata was gathered for each sample and loaded into a MySQL database. Data included where available (i) host species and variety, (ii) host developmental stage, (iii) host tissue type, (iv) fungicide treatment, (v) level of infection, and (vi) collection date and location information (“Metadata integration”). The publicly available expVIP code was cloned from GitHub and transferred to a virtual machine. Metadata, gene expression values

and the reference transcriptome were then integrated into the rust expression browser, served to the internet using gunicorn (“Browser initiation”). All computer code used is available as a github repository [27, 28] and metadata files are available via figshare [29]

A new genomic tool has been launched to help the global community of wheat rust researchers.

The [Rust Expression Browser](#) – developed by John Innes Centre researchers—is the first gene expression browser to enable simultaneous interrogation of gene expression data for the notorious yellow [rust](#) pathogen and its [wheat host](#).

This new web interface currently hosts 1,024 gene expression datasets in an easy 'point-and-click' format to improve access to these valuable but complex data resources. In particular, it hosts hundreds of datasets generated by use of the revolutionary, genomic based 'field pathogenomics' technique that was developed in the Saunders Lab.

The yellow rust fungus causes devastating losses to wheat production worldwide and is a serious constraint on UK wheat production.

In a new paper published in *BMC Genomics*, researchers describe the creation of this new tool and demonstrate its utility for accelerating wheat yellow rust research.

Dr. Thomas Adams, the first author said: "We are thrilled to be able to share the wealth of data collected over the years by the lab with the wider community. We hope this will make these datasets more accessible to all researchers, regardless of access to specialist computer systems or any experience with sequencing data."

infected plant samples. d Pst-infected field plant samples were collected from 64 wheat varieties where the variety could be confirmed. Those wheat varieties with at least 3 samples are illustrated. Varieties were confirmed based on their presence in the EU crop variety database [33] or the CIMMYT pedigree database [34]

Dr. Diane Saunders, the corresponding author, commented: "The Rust Expression Browser is a fantastic resource for the global community of rust researchers. This will undoubtedly lead to exciting new insight into the intricacies of the interaction between yellow rust and its wheat host."

More information: Thomas M. Adams et al. Rust expression browser: an open source database for simultaneous analysis of host and pathogen gene expression profiles with expVIP, *BMC Genomics* (2021). [DOI: 10.1186/s12864-021-07488-3](https://doi.org/10.1186/s12864-021-07488-3)

Provided by John Innes Centre

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