

Wheat Rust Vulnerability Mapping: Integrating variety distribution, rust resistance and rust risk for ex-ante decision-support

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Introduction

Wheat rusts, especially stripe and stem rust, are the major biotic constraints that affect wheat production on a large scale in Ethiopia. Both rusts are capable of causing devastating epidemics that can cover hundreds of thousands of hectares; causing economic losses running into hundreds of millions of dollars and negatively impacting food security. Control of recurrent wheat rust epidemics in Ethiopia is a national priority for agricultural development, as the country strives for self-sufficiency in wheat production.

The pathogens that cause the wheat rust diseases – namely *Puccinia striiformis* f.sp. *tritici* (Pst) the causal agent of wheat yellow (stripe) rust and *P. graminis* f.sp. *tritici* (Pgt) the causal agent of wheat stem rust – are both fungal pathogens that share common characteristics. They are both highly destructive, with losses of >60% typical for yellow rust and up to 100% for stem rust under favorable conditions. They are both highly mobile, capable of moving thousands of kilometers by wind-borne or accidental human-borne movements. Finally they are both highly changeable, rapidly generating new races to overcome host resistance through mutation or recombination.

Within the last decade recurrent rust epidemics and appearance of new races has severely affected wheat production in Ethiopia. In 2010/11, over 600,000 ha were affected by yellow rust and in 2013/14 a new race of stem rust caused major losses in Bale and SNNPR. Stem rust epidemics once again devastated large areas in 2014/15. In 2016, a new race of yellow rust rendered several widely grown cultivars susceptible although widespread losses were avoided by improved and timely control in key areas.

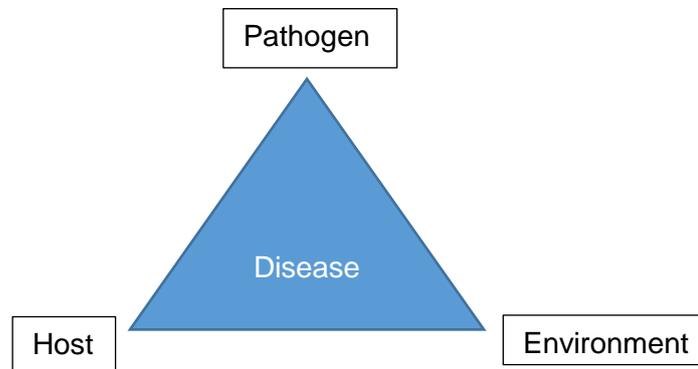
Rust epidemics are major drivers of varietal change, as farmers often seek out new resistant varieties when they experience heavy losses on existing varieties that have become susceptible.

Given the importance of wheat rusts it is no surprise that considerable investments have been made in resistance breeding and also surveillance systems. However, current information on actual variety distribution and host resistance is limited. The introduction of DNA fingerprinting at the national scale has the potential to fill some of these knowledge gaps.

The continual evolution and incursion of new races of wheat rusts means that having data-driven tools available that can highlight areas most at risk in advance and give some degree of early warning are likely to be extremely valuable for decision-making around varietal replacement and disease control strategies. This report highlights the development of such tools, with DNA fingerprinting providing critical data on variety distribution and being the foundation of the system. Work reported has largely been undertaken through external, complementary projects but does highlight a decision-support application made possible through data derived from DNA fingerprinting.

Wheat rust vulnerability mapping – conceptual approach

Disease outbreaks occur only when all the conditions of the classic disease triangle occur simultaneously; (i) susceptible host (ii) virulent pathogen (iii) suitable environment.



The vulnerability mapping approach described in this report integrates these three critical factors within a spatial framework. If we know the distribution of different varieties, the area's most suitable for different pathogens, the resistance genes present in the varieties and the virulence profile of the pathogen then we can do a weighted map overlay to identify which areas would be the most vulnerable to different rust races i.e., an area with a susceptible variety to a specific rust race coincides with highly suitable environment for the pathogen. This approach can be used for ex ante impact assessment and early warning in two main ways. Firstly, for known races already present in a country, but with a limited distribution, in order to identify areas of vulnerability if the pathogen race spreads. Secondly, for known races present in other countries, but currently absent from the country of interest, in order to identify areas of greatest vulnerability if an incursion of the new race occurs. Both scenarios would provide extremely valuable information to decision makers around variety deployment / replacement strategies and also planning and deployment of limited fungicide resources. Until recently, absence of data has been a major limiting factor restricting the application of such approaches.

As a result of several different initiatives on wheat improvement in Ethiopia, these data limitations are being reduced. Critical to the development of the rust vulnerability mapping tool approach have been: (1) The use of DNA fingerprinting in Ethiopia to enable for the first time an accurate picture of varietal distribution; (2) An increasing knowledge of the rust resistance genes present in varieties and variety field responses, obtained through the use of molecular markers, gene postulation, seedling tests and single race rust nurseries as part of on-going rust resistance breeding efforts; and (3) The creation of extensive, multi-year surveillance networks permitting areas at risk to different rust diseases and hot spots to be identified.

Varietal Distribution

Large-scale, plot sampling (n=3909) and DNA fingerprinting undertaken in 2016/17 resulted in the most accurate picture of variety distribution currently available in Ethiopia. This data was supplemented with wheat rust survey data, undertaken by wheat experts, for 2016-2018 that included named varieties. The expert survey data was considered more reliable than farmer reports and showed reasonable spatial alignment with the DNA fingerprinting data. All variety data was aggregated at zone level, as the DNA data were representative at this level and it was considered a suitable scale for decision making. The data was rasterized using the wheat harvest area SPAM data (<https://harvestchoice.org/category/keywords/spatial-production-allocation-model-spam>) as the masking layer. This restricted the variety distribution layers solely to the main wheat growing areas within zones. The top 10 varieties by area from the DNA fingerprinting study, which accounted for over 80% of the area, were

used and zonal abundance raster layers were created for each variety. Bobicho / Senkegna was excluded due to uncertainty over varietal identification. The varieties considered and area shares are given in Table 1.

Table 1: Predominant wheat varieties identified by DNA fingerprinting in 2016/17

Variety	Year Released	Wheat area		
		Area(ha)	Individual %	Cumulative %
Kakaba	2010	301.6	27.0	27.0
Kubsa	1995	148.9	13.4	40.4
Danda'a	2010	111.4	10.0	50.4
Digalu	2005	99.9	9.0	59.3
(Bobicho / Senkegna) *	2002	51.7	4.6	64.0
Galema	1995	50.6	4.5	68.5
Pavon-76	1982	37.8	3.4	71.9
Ogolcho	2012	37.8	3.4	75.3
Arendato (durum)	1967	35.4	3.2	78.4
Hidasie	2012	30.3	2.7	81.2

- Excluded due to uncertainty over varietal identification.

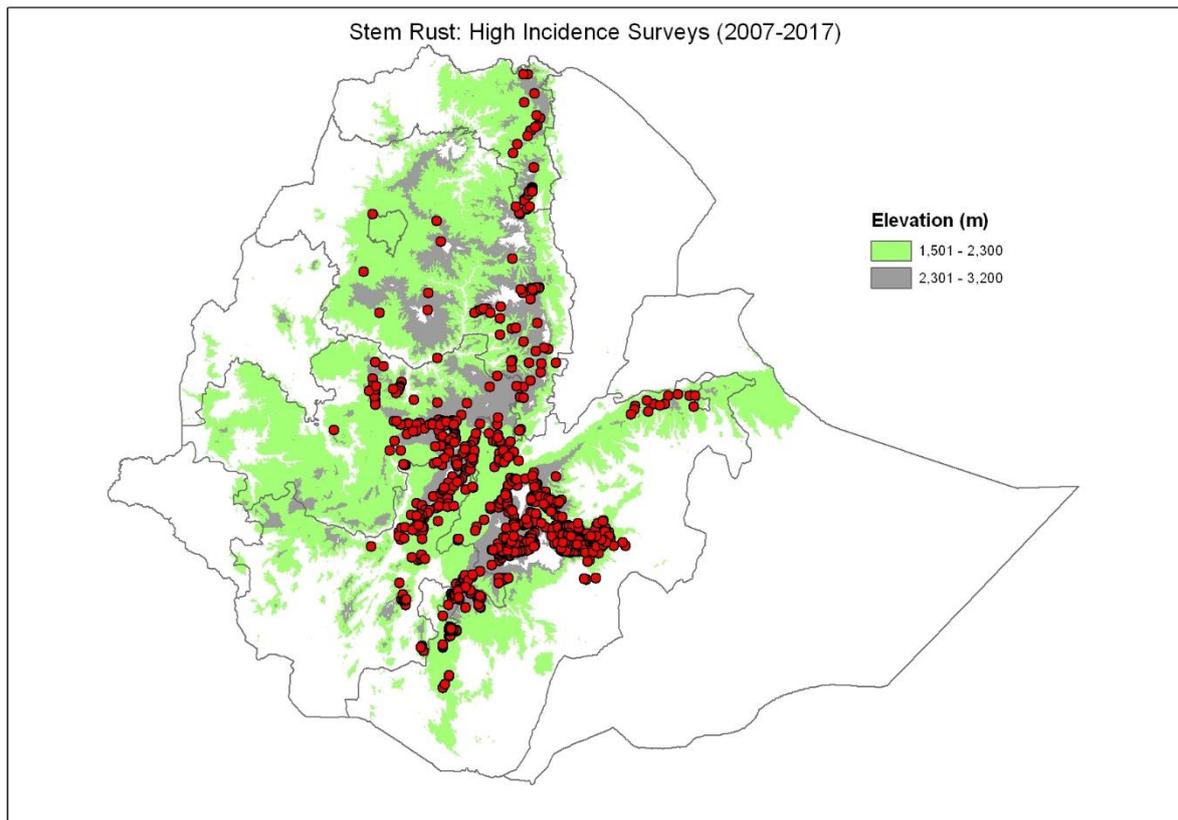
The generated raster variety zonal abundance maps are given in Appendix 1.

Distribution of stem and yellow rust in Ethiopia

Extensive rust surveillance systems have been created that provide accurate information on the pathogen. Since 2008, standardized rust surveys have been undertaken by EIAR, Regional Agricultural Research Centers and CIMMYT with approximately 1200 fields surveyed every year.

A summary of the distribution of stem rust is given in Fig. 1. High incidence stem rust records (>40% of a surveyed field infected with disease, N=1474) recorded on surveys undertaken between 2007 and 2017 are shown in relation to the main elevation zones for wheat production. Stem rust is most prevalent in the southern half of the country and there is also a tendency for stem rust to be recorded in the lower elevation zones.

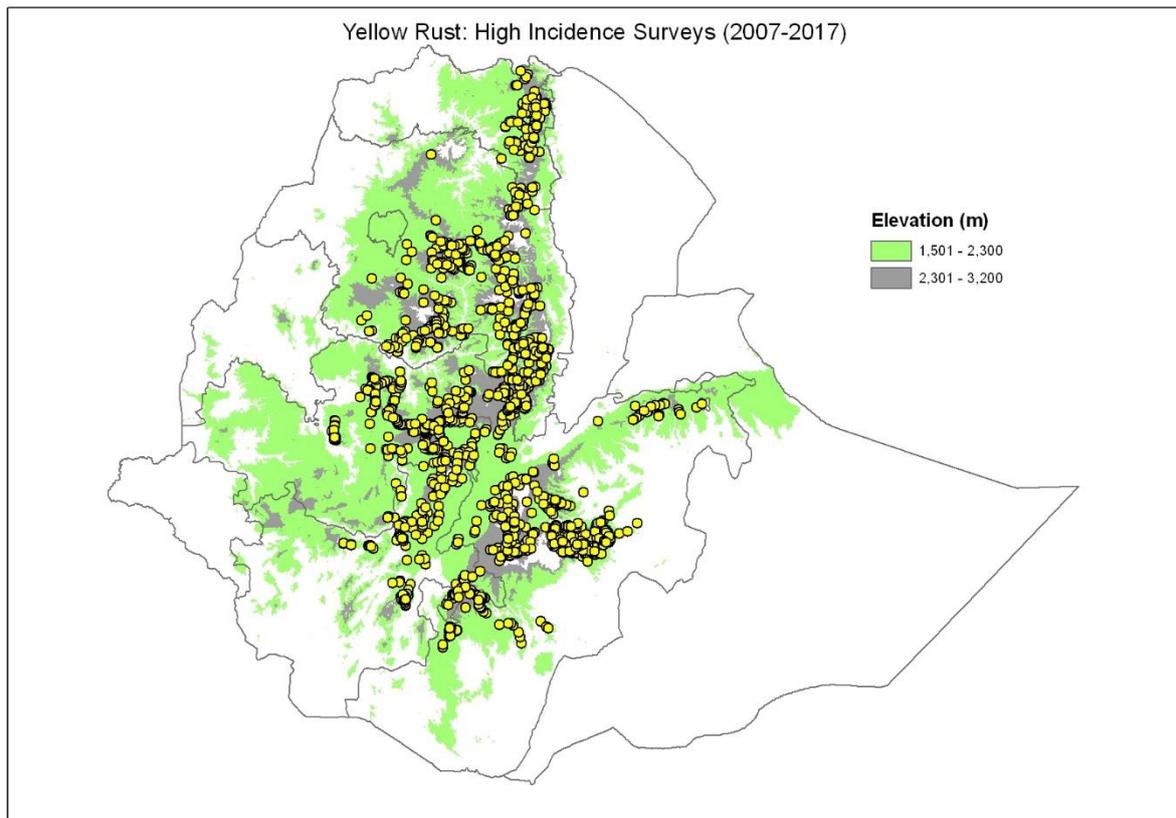
Fig. 1: The distribution of high incidence stem rust records based on surveys undertaken during 2000-2017



The distribution of yellow rust based on survey records is illustrated in Fig. 2. High incidence yellow rust records (>40% of surveyed field infected with disease, N=2069) recorded on surveys undertaken between 2007 and 2017 are shown in relation to the main elevation zones for wheat production. In contrast to stem rust, yellow rust shows a much wider distribution throughout Ethiopia, and is aligned much more to the higher elevation zones.

For both stem and yellow rust it should be noted that the actual distribution and occurrence of disease varies by year and season. Environmental factors in addition to the presence of susceptible hosts and virulent pathogens all play a strong role in determining the occurrence and severity of disease outbreaks.

Fig. 2: The distribution of high incidence yellow rust records based on surveys undertaken during 2000-2017



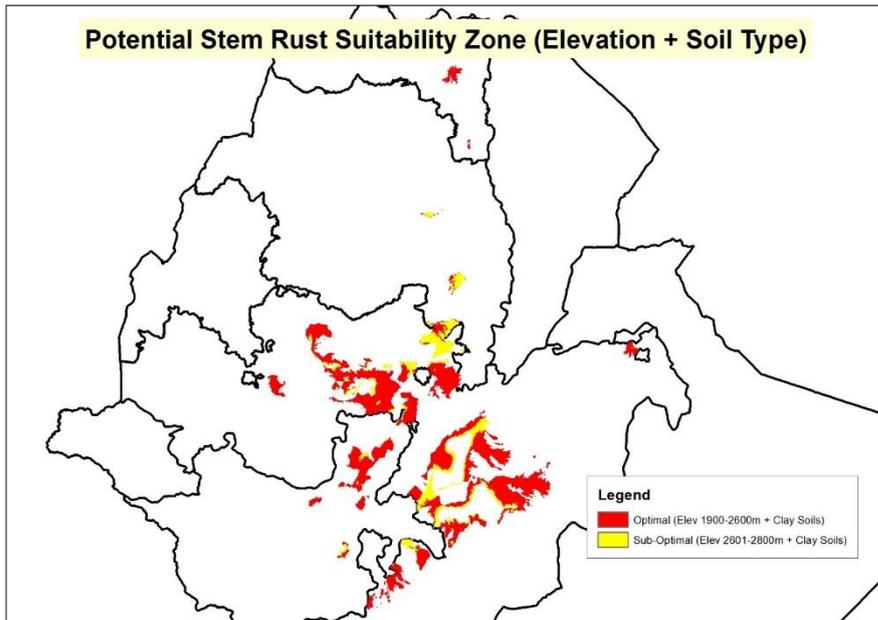
Development of Rust Risk Maps

Based on the survey data, it has been possible to identify where rusts are occurring and extract secondary data on suitability i.e., elevation, soil and climatic factors, to enable risk mapping to be undertaken for stem and yellow rust. This enabled high rust risk areas to be identified and used in combination with other data layers to develop vulnerability maps.

Stem Rust Risk Map

Stem rust risk maps were initially developed in response to the Digalu epidemic in 2013 (Olivera et al., 2015), but have proven robust to identify areas of greatest risk. The risk maps were developed based on hot spots for stem rust infection, derived from survey data using geo-statistical methods and the Gettis-Ord statistic, coupled with optimal elevation zones and soil characteristics. Optimal suitability (high risk) for stem rust was considered to be elevation between 1900-2600m and clay soils (with high moisture retention, so providing moisture for disease development). Sub-optimal suitability (moderate risk) was considered to be elevation between 2601-2800m and clay soils. Fig. 3 shows the stem rust risk map.

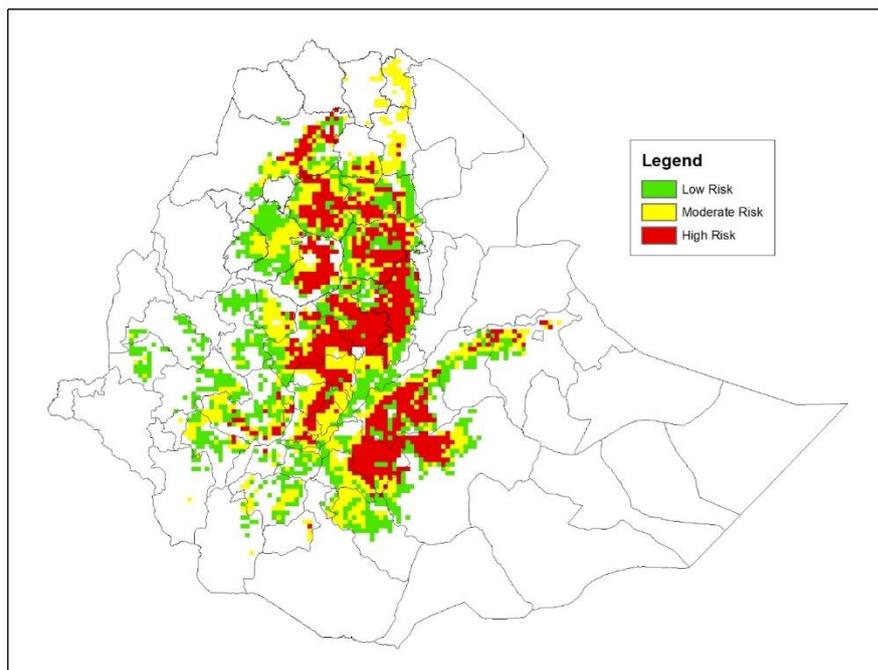
Fig. 3: Stem rust risk map. Optimal suitability indicates high risk and sub-optimal suitability indicates moderate risk.



Yellow Rust Risk Map

A similar, but slightly different approach was taken to develop a yellow rust risk map. A combination of rust hot spots and a multi criteria weighted overlay analysis using elevation (SRTM data - <https://cgiarcsi.community/data/srtm-90m-digital-elevation-database-v4-1/>) and precipitation (WorldClim data - <https://www.worldclim.org/>) was used. Elevation criteria were given a 70% weighting with optimal elevation range being: 2200-3100m, moderately suitable elevation 1800-2200m and low suitability elevation being <1800m. Precipitation data were given a 30% weighting, with 800-1400mm considered optimal, >1400mm moderately suitable and <800mm low suitability. The derived yellow rust risk map is given in Fig. 4. Strong correlation was seen with the survey data.

Fig. 4: Yellow Rust Risk Map Ethiopia.



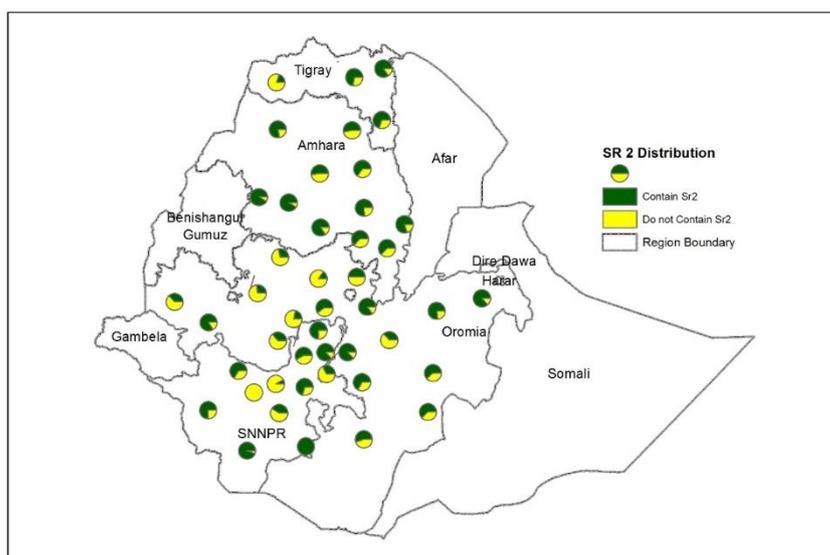
Resistance gene information / infection risk

Reliable molecular markers are now available for several of the important stem rust resistance genes. Currently, molecular marker data are available for the following stem rust resistance genes (and associated genes for other diseases): *Sr2*, *Lr67/Yr46/Sr55/Pm46*, *Lr34/Yr18/Sr57/Pm38*, *Sr24*, *Sr24/Lr24*, *Sr25/Lr19*, *Sr26*, *Sr31*, *Sr35*, *Sr36*, *Lr37/Yr17/Sr38*, *Sr42*, *1RS*. Additional genes such as *SrTmp* can be postulated based on seedling screening with diverse stem rust isolates. In partnership with the USDA-ARS Cereals Disease Laboratory, Minnesota and the USDA-ARS, Raleigh, North Carolina an increasing proportion of the released wheat varieties and advanced breeding lines in Ethiopia have been screened using the stem rust resistance gene markers. In combination, single race screening nurseries for stem rust have been developed in Ethiopia using key stem rust races (Hundie et al., 2019). This increasing resistance gene information can now be linked to the DNA fingerprinting variety information.

Linkage of this marker data to known variety distributions enables an indication of the stem rust resistance gene distribution to be determined. One example of this approach indicates the proportion of varieties with key stem rust resistance genes – with the *Sr2* complex used as an exemplar. Data are based on variety identification using DNA fingerprinting and summaries are presented at the zonal level.

Sr2 complex: This is an extremely important minor gene (or complex of minor genes) that provides durable adult plant resistance to stem rust. This gene has remained resistant for over 100 years. Although, it must be noted that on its own it does not provide adequate resistance (only partial resistance), so it needs to be combined with other genes to be effective. However, this is an important gene that gives baseline protection against stem rust. Based on variety distribution data, *Sr2* has been deployed widely throughout the main wheat growing areas of Ethiopia (Fig. 5). This is due to its presence in widely adopted varieties such as Kakaba – carrying *Sr2* and likely at least one other minor APR gene. Wide deployment of this durable APR gene is undoubtedly an indicator of success of the wheat breeding programs in Ethiopia, but further work is needed to ensure that more varieties are developed with additional, additive resistance in combination with *Sr2*.

Fig.5. Distribution of *Sr2* gene complex based on DNA Fingerprinting variety distribution



Knowledge on yellow rust resistance genes currently lags behind, although an increasing amount of work is now being done and increased information is now becoming available (Gebreslasie et al., 2020).

Improved knowledge has also been obtained on the pathogen side through the long-term surveillance. A critical component of the surveillance has been collection of samples and undertaking race analysis. Through these activities undertaken at the EIAR Ambo lab, the Global Rust Reference Center, Denmark and the USDA-ARS Cereals Disease Lab it has been possible to identify the key stem and yellow rust races and determine the virulence profile of these races. Annual surveys and sampling permit monitoring of race populations and the detection of new races. Using the resistance gene data, in combination with field trial data and the virulence profiles of the rust races, it has been possible to develop infection risk tables by variety for the key stem and yellow rust races. The infection tables and scoring by variety and race have used the initial criteria given in Table 2.

Table 2: Infection table criteria used to score varieties for specific rust races.

Score	Infection Risk	Reaction	Severity
1	very low	R - RMR	15%
2	low	MR	30%
3	medium	MRMS	40-50%
4	high	S	60-70%
5	Very high	VS	90-100%

This increasing set of information on both the host and the pathogen side is now making it possible to integrate all the available data on variety distribution, rust risk, variety resistance genes and variety infection risk to specific races into a single vulnerability mapping system.

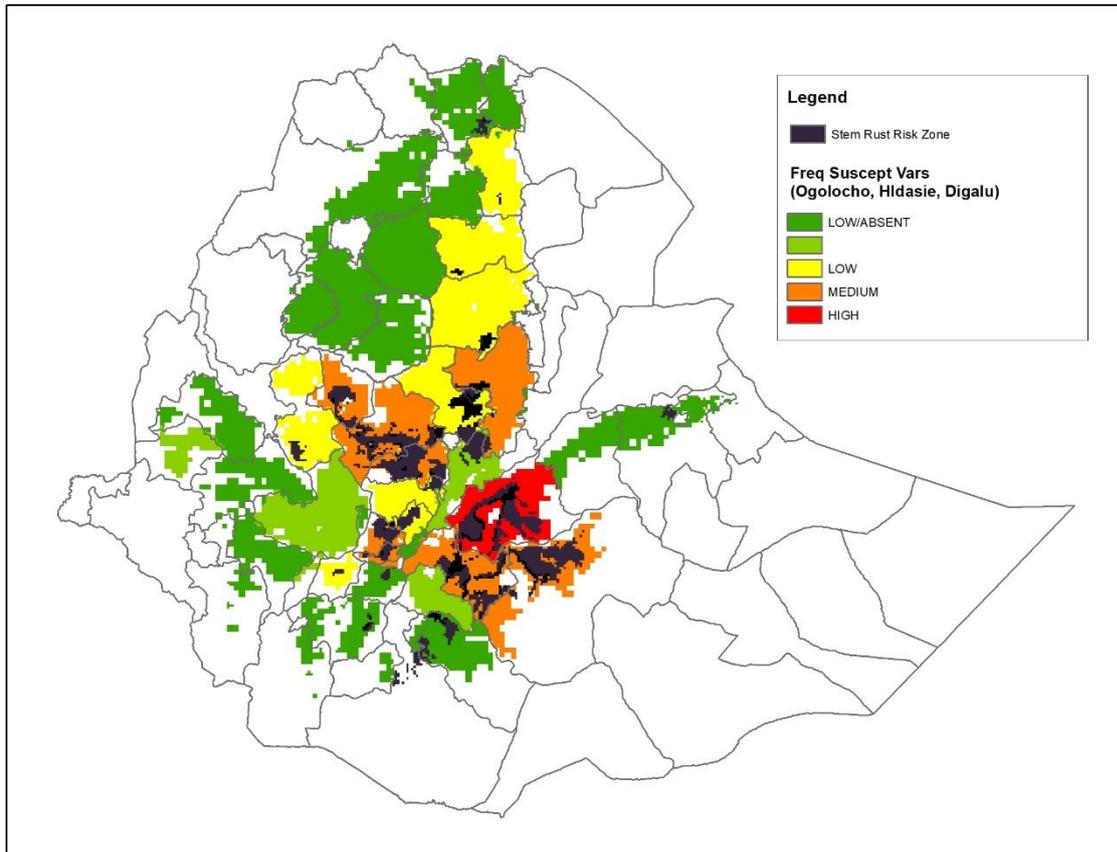
Development of an initial vulnerability mapping tool

Using the datasets described in the previous sections it has been possible to develop tools that integrate host, pathogen and environment in order to provide an ex-ante assessment of vulnerability to decision makers. This approach has been piloted in Ethiopia, as a result of the availability of variety distribution data derived from DNA fingerprinting.

In 2019 in Ethiopia, the first vulnerability maps were introduced and included in the pre-season planning for stakeholders, including the Ministry of Agriculture. This was done in response to the first detection of an important new Ug99 stem rust race in Ethiopia. Race TTKTT – part of the Ug99 lineage and of concern due to combined virulence against important resistance genes *Sr31*, *SrTmp* and *Sr24* – was initially detected in Kenya in 2014 but was confirmed in samples from Ethiopia in 2018. Given the presence of *Sr24* in several Ethiopia varieties this was seen as a threat to wheat in Ethiopia, so the first vulnerability map was developed and presented to stakeholders.

Based on the virulence profile of race TTKTT and the known resistance genes present in varieties, the following varieties were considered to be at risk: Ogolcho, Milenium, Alidoro, Honqulo, Shorima (possibly having additional resistance?), QulQula, Hulluka, Hoggana, Biqa, Bollo. + Hidasie, Digalu, Wane. Using the DNA fingerprinting data on variety distribution and the stem rust risk zone map, it was possible to create the vulnerability map shown in Fig. 6.

Fig. 6: Ethiopia vulnerability map for stem rust race TTKTT

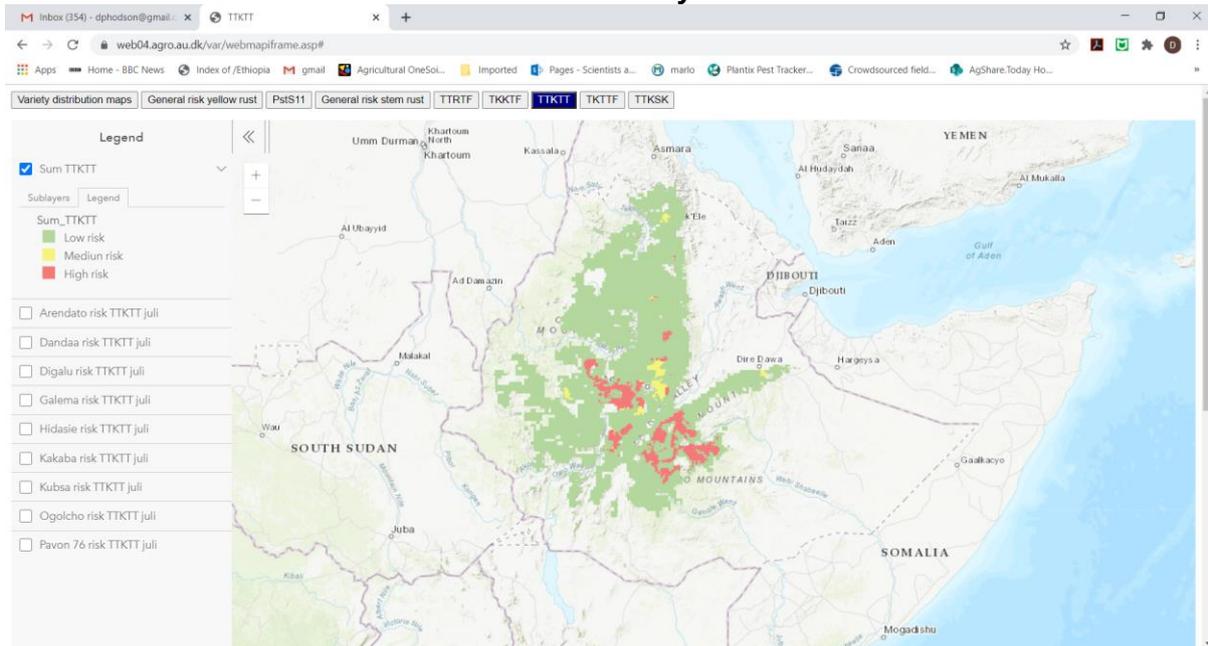


From this map it was possible to visually identify the zones considered to be at highest risk if race TTKTT were to increase and spread i.e, those areas with high proportions of susceptible varieties being grown in high risk areas for stem rust. In order of likely risk these zones were considered to be: Arsi, Bale, West Arsi, South-West Shewa, West Shewa, Hadiya, KT, Horo Guduru, (Selti), (North Shewa). Having this information pre-season contributed to help prioritize scouting and control activities.

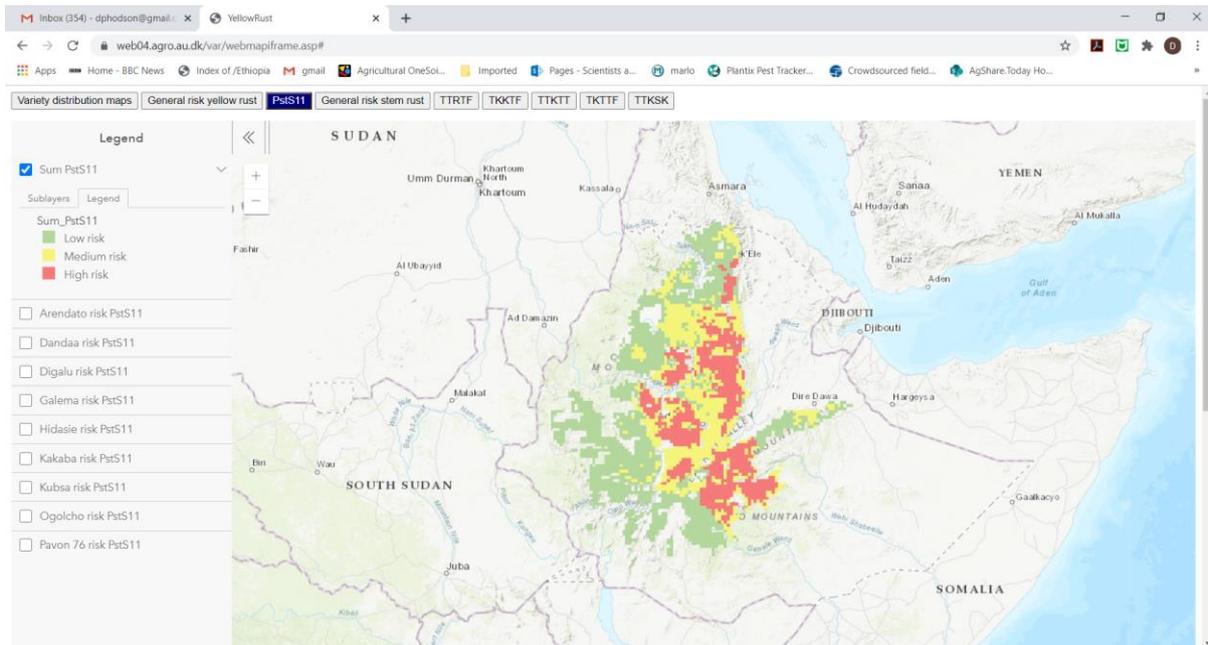
Subsequently the vulnerability mapping approach has been developed further, through a small pilot project involving Cornell University, Aarhus University, Denmark and CIMMYT as part of the Delivering Genetic Gains in Wheat (DGGW) project funded by BMGF & DFID. In this pilot, an interactive web-based mapping application has been developed that allows users to explore vulnerability maps for key stem rust races. Selection of specific race and variety combinations is possible, along with overall vulnerability based on composite variety distribution data. The tool automatically weights and integrates the different input layers to produce a final vulnerability map for any selected combination of rust race and varieties. Expansion to include yellow rust in Ethiopia has now been included. A screen shot of the web-based vulnerability mapping tool is given in Fig. 7. Development work on this tool is ongoing with a first release planned for September 2020.

Fig. 7: Web-based vulnerability mapping tool interface screenshots

A. Stem rust race TTKTT overall vulnerability



B. Yellow rust race PstS11 overall vulnerability



Conclusion

Wheat rusts, notably stem and yellow rust, are the main biotic constraints to wheat production in Ethiopia. Their ability to cause devastating losses, high mobility and constant evolution make them a priority for both surveillance and breeding programs. Linking data from these existing efforts to the results obtained from DNA fingerprinting is providing added value. Accurate varietal identification and distribution mapping, based on DNA fingerprinting,

is permitting new insights into breeding impact, crop vulnerability and also aiding preparedness.

Accurate varietal distributions are giving information on where susceptible varieties are located in relation to areas with high rust risk. This information can then assist the prioritization of areas for varietal replacement, awareness raising on the need for effective control of rusts and guide fungicide deployment strategies.

Similarly, knowledge on the likely distribution of rusts resistance genes can give insights on the impact of breeding programs in the deployment of useful resistance, but also flag areas of emerging genetic vulnerability.

Through the integration of increasing amounts of data relating to host, pathogen and environment it has been possible to develop wheat rust vulnerability mapping decision support tools. An initial web-based interactive mapping tool has been developed by Aarhus University, Cornell University and CIMMYT that can provide ex ante vulnerability assessment to key races of stem and yellow rust in Ethiopia. This is seen as a valuable contribution to assist with decision making around rust control, either in the short-term through fungicide planning or in the longer-term through variety deployment and targeting strategies.

Despite progress, several limitations and challenges still exist. DNA fingerprinting has provided a critical and accurate snapshot of variety distribution in Ethiopia in 2016/17, but varietal turnover means that such data will become outdated and inaccurate over time. As a result there will be a need to ensure that variety distribution data is continually updated on an appropriate time scale. For wheat in Ethiopia a repeat timeline of 3-5 years would be considered appropriate. Another limitation exists around the knowledge of rust resistance genes present in different varieties and also the virulence profiles of different rust races. Although knowledge has increased tremendously and more reliable molecular markers have been developed there are still many gaps and many unknown genes are present in varieties. Similarly, only a limited number of genes are used in pathogenicity testing. Both these factors can have a big impact on how varieties actually perform in the field when exposed to a new race of the pathogen, making advance prediction prone to errors. The single race nursery approach developed in Ethiopia has given valuable information on field performance against specific rust races, but can only be undertaken once a specific race has become established in the country. Regional screening nurseries, such as that established for stem rust at Njoro, Kenya play a vital role in understanding variety field performance against new races that may be absent in other countries and have the potential for future migration e.g., as was case for race TTKTT highlighted in this report. However, similar screening sites are not present in other important locations or regions. Based on observed migration patterns and pathogen surveillance for stem rust. Screening East African germplasm in the Caucus region (e.g., Georgia) might provide valuable early warning of field reactions to important new races.

Overall, the approach highlighted in this report has shown that with increasing availability of different datasets it is now becoming possible to develop vulnerability mapping decision support tools for wheat rusts. These tools are likely to improve in the future as better data inputs become available and so provide opportunities for enhanced rust control. This represents a value addition and applied use of the data generated from DNA Fingerprinting.

Refs

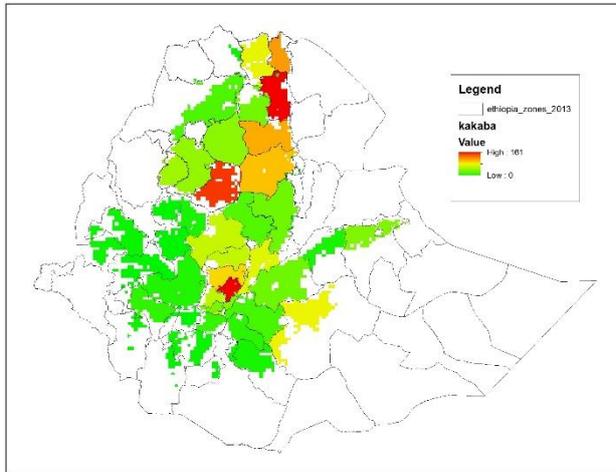
1. Gebreslasie Z.S.,Huang S., Zhan G., Badebo A., Zeng Q., Wu J., Wang Q., Liu S., Huang L., Wang X., Kang. Z., Han D. (2020). Stripe rust resistance genes in a set of Ethiopian bread wheat cultivars and breeding lines. *Euphytica* (2020) 216:17

2. Hundie, B., B.Girma, Z.Tadesse E. Edae, P. Olivera, E.H.Abera, W.D. Bulbula, B. Abeyo, A. Badebo, G. Cisar, G. Brown-Guedira, S. Gale, Y. Jin and M.N. Rouse. 2019. Characterization of Ethiopian Wheat Germplasm for Resistance to Four *Puccinia graminis* f. sp. *tritici* Races Facilitated by Single-Race Nurseries. *Plant Disease* 103:2359-2366
3. Olivera, P., M. Newcomb, L.J. Szabo, M. Rouse, J. Johnson, S. Gale, D.G. Luster, D. Hodson, J.A. Cox, L. Burgin, M. Hort, C.A. Gilligan, M. Patpour, A.F. Justesen, M.S. Hovmøller, G. Woldeab, E. Hailu, B. Hundie, K. Tadesse, M. Pumphrey, R.P. Singh, and Y. Jin. 2015. Phenotypic and Genotypic Characterization of Race TKTTF of *Puccinia graminis* f. sp. *tritici* that Caused a Wheat Stem Rust Epidemic in Southern Ethiopia in 2013–14. *Phytopathology* 105(7) 917-928.

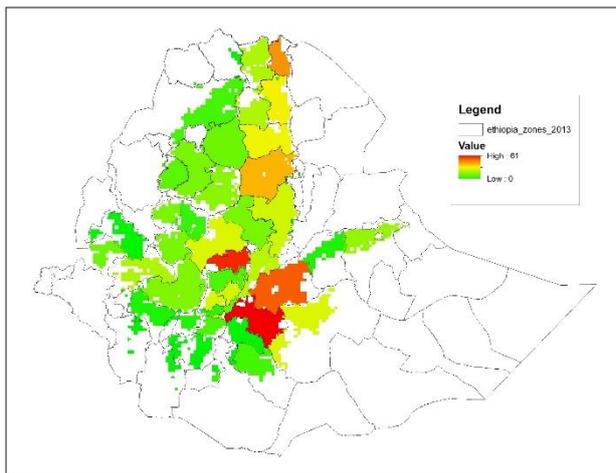
Appendix 1: Variety zonal abundance maps

Note: Scales on maps on maps differ and show relative abundance for each variety

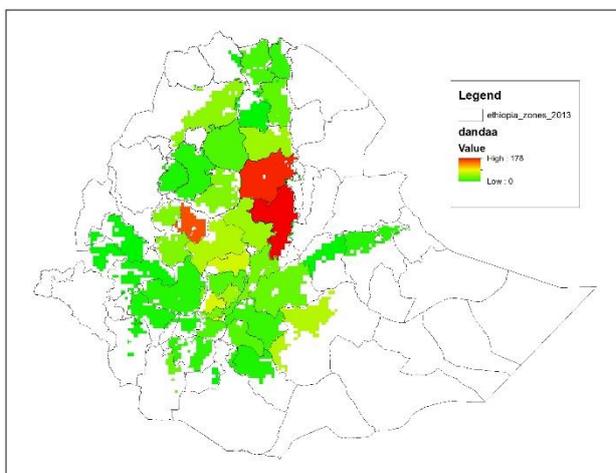
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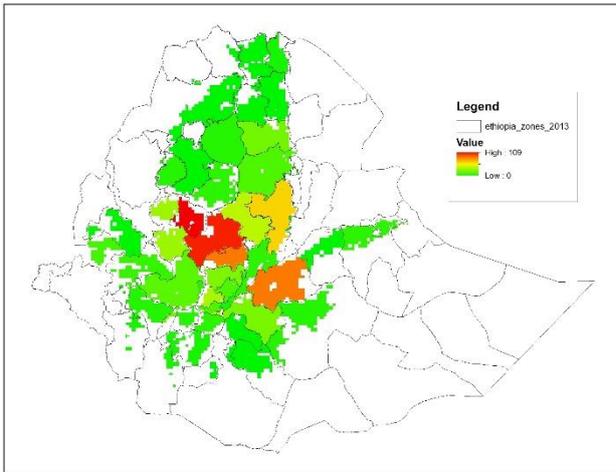
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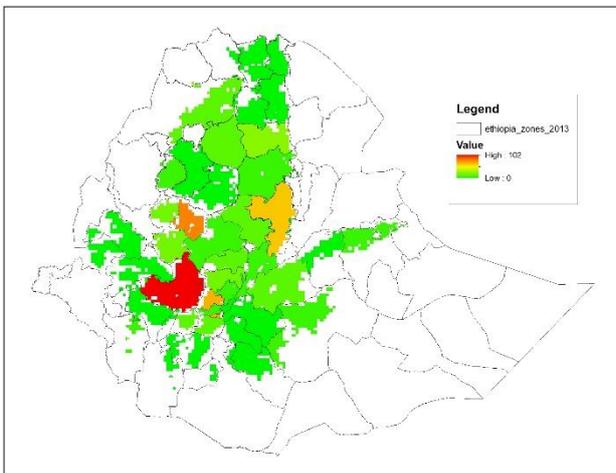
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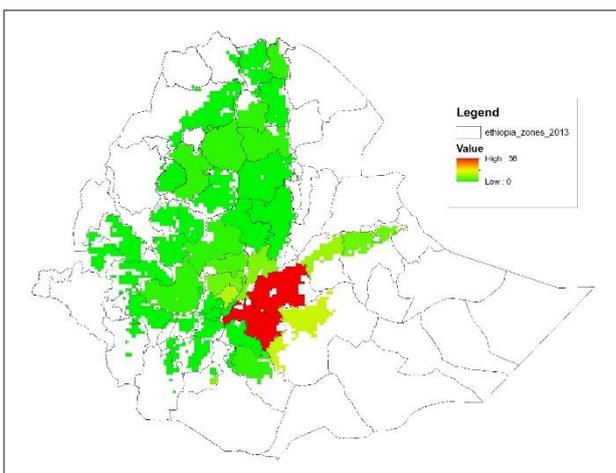
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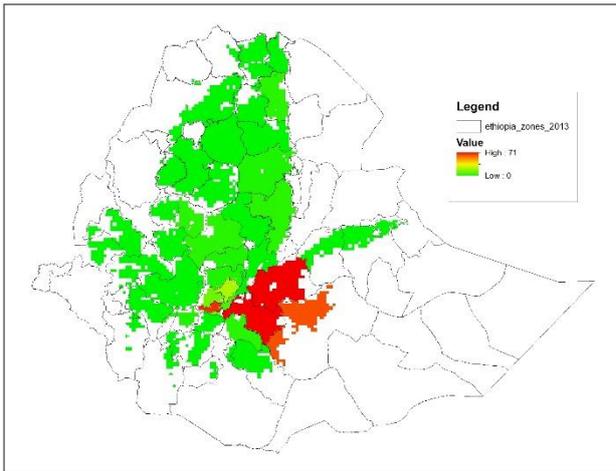
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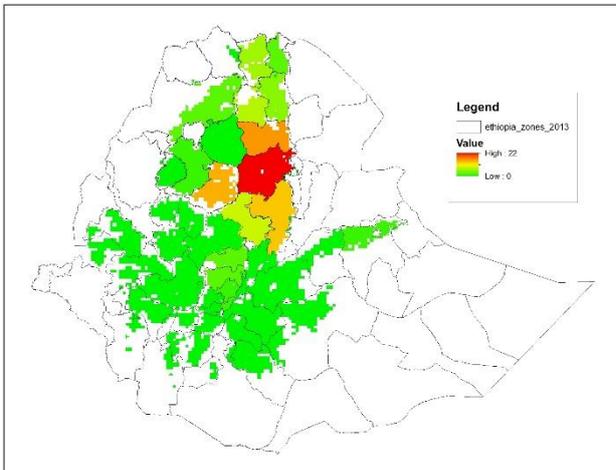
6. Pavon 76



7. Ogolcho



8. Arendato



9. Hidassie

