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Searching for climate change related traits in plant genetic resources collections using Focused Identification of Germplasm Strategy (FIGS)

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Abstract. Prospects to assess and explore largely untapped plant genetic resources (PGR) collections to search for climate change related traits, such as drought and heat tolerance, as well as pest and disease resistance, are possible through new approaches such as the focused identification of germplasm strategy (FIGS). FIGS approach is based on the paradigm that any germplasm is likely to reflect the selection pressures of the environment under which it evolved. The approach uses trait and environmental data (climate data including phenology data) to develop *a priori* information based on the quantification of the trait-environment relationship. If a dependency between the trait and the environment is detected, the *a priori* information is then used to define subsets of accessions with a high probability of containing the sought after traits. The subsets of accessions are then used for *a posteriori* evaluation. Recent research comparing *a priori* and *a posteriori* information supports the assertion that FIGS can be used as an effective tool to search for traits of resistance to pests and diseases as well as traits to adapt to climate change. This paper presents and discusses some of the recent results where FIGS was used to develop subsets with high probability of finding desirable traits, such as resistance to stripe (yellow) rust, in durum wheat. It also addresses ways in which current FIGS based models could be further enhanced by working the ways in which the environmental data is presented to the models, thereby improving the detection of traits associated with climate change adaptation.

Keywords. Genetic resources – FIGS – Accessions – Pests – Diseases – Resistance – Climate change.

Recherche pour des caractères liés au changement climatique dans des collections de ressources phytogénétiques en utilisant la stratégie d'identification ciblée du matériel génétique (FIGS)

Résumé. L'évaluation et l'utilisation des collections de ressources phytogénétiques largement inexploitées pour rechercher des caractères liés au changement climatique, comme la sécheresse et la tolérance à la chaleur, ainsi que la résistance aux organismes nuisibles et aux maladies, sont aujourd'hui possibles grâce à de nouvelles approches telles la stratégie d'identification ciblée du matériel génétique (FIGS). L'approche FIGS repose sur le paradigme que tout matériel génétique est susceptible de refléter les pressions de sélection de l'environnement dans lequel il a évolué. Cette stratégie utilise des caractères et des données environnementales (données climatiques, y compris les données phénologiques) pour développer une information *a priori* basée sur la quantification de la relation caractère-environnement. Si une dépendance entre le caractère et l'environnement est détectée, l'information *a priori* est alors utilisée pour définir des sous-ensembles d'accessions ayant une forte probabilité de porter les caractères recherchés. Les sous-ensembles d'accessions sont ensuite utilisés pour une évaluation *a posteriori*. Des recherches récentes comparant les informations *a priori* et *a posteriori* permettent d'affirmer que la FIGS peut être utilisée comme un outil efficace pour la recherche de caractères de résistance aux organismes nuisibles et aux maladies tout comme aux caractères d'adaptation au changement climatique. Dans cet article, on présente et on discute des résultats récents de l'application de la FIGS pour développer des sous-ensembles avec une haute probabilité de trouver les caractères recherchés, comme la résistance à la rouille jaune, chez le blé dur. On discute également les possibilités d'améliorer les modèles sur lesquels est basée actuellement la FIGS, en travaillant sur la façon dont les données environnementales sont intégrées dans les modèles, améliorant ainsi la détection des caractères associés à l'adaptation au changement climatique.

I – Introduction

Prospects to assess and explore largely untapped plant genetic resources (PGR) collections for agronomically important traits, particularly those linked to climate change-adaptation, are possible through new approaches such as the Focused Identification of Germplasm Strategy (FIGS). Climate change, which is the result of greenhouse gas (GHG) emissions, is causing the atmosphere to heat up (Mendelsohn & Dinar 2009). Crops such as wheat are reported to be more vulnerable to heat stress than drought (Semenov & Shewry 2011). High temperatures during the reproductive phase can reduce the number of kernels per spike, which is an important component of yield (Semenov & Shewry 2011). Both heat and drought stresses are expected to increase in their frequency and intensity in dry areas (IPCC 2012) such as central North America, Northern Africa, Central Asia, West Asia and Western Australia. Although the global climate models (GCMs) differ substantially, they all tend to indicate significant temperature increases in these areas (Girvetz *et al.* 2009). Further, this increase in temperature as a result of GHG emissions is expected to increase depending on emissions scenarios and the extent of mitigation implemented measures to curb their effects (Howden *et al.* 2007, Mendelsohn and Dinar 2009).

Plant genetic resources have contributed enormously towards increased yield in crops (Hoisington 1999) and are a ready source of trait's variation (Qualset 1975). For example, a wheat landrace from Turkey that was conserved in a genebank in 1948 was later discovered, (in the 1980s) to carry genes that are resistant to a range of fungal diseases, and are still in use in current breeding programs (Atalan-Helicke 2012, FAO). However, searching for such traits can be a daunting and costly process given that PGR consists of large collections and populations maintained *in situ* or *on-farm* that are also more prone to yield climate change related traits but yet to be sampled and collected. What is required therefore is an efficient method to select material from these genetic resources so that the probability of finding and locating the required variation is maximized while reducing the number of accessions evaluated and the overall cost implications (Gollin *et al.* 2000). The FIGS approach represents one such method.

The FIGS approach is based on the paradigm that adaptive traits exhibited by germplasm are likely to reflect the selection pressures of the environment from which the germplasm was originally sampled (Mackay and Street, 2004). For example, if a plant population is exposed over a significant period of time to weather conditions that are favourable to consistently high pathogen populations then it is likely that a selection pressure will be imposed on the plant population for the emergence of resistance genes. Paillard *et al.* (2000) found this to be the case for the evolution of powdery mildew resistance in wheat and barley landraces. Thus if a dependency between a given trait and environmental parameters can be defined then the relationship can be used to predict the likelihood of finding a desired trait in a given environment (Mackay and Street 2004, Bari *et al.* 2012, Endresen *et al.* 2012). In this context information about the environmental origins of accessions are used to define trait specific subsets of germplasm with a higher probability of containing the sought-after traits.

This paper presents and discusses how FIGS has been applied to the search for resistance to stripe (yellow) rust in durum wheat. In previous FIGS studies predictive models were applied to historic climate data to search for traits of interest. In this study the models were tested with future climate change scenarios. However, adjustments may be required in the models for change climate scenarios as well as improvement by working ways in which environmental data is presented to the models to improve the search for traits to cope with climate change adaptation. The modelling process is considering separating the induced-shift climate change variation from the overall variation for better prediction.

II – Methodology

1. Data

This study was based on a field evaluation of durum wheat accessions for response to a naturally occurring yellow rust infection at ICARDA during the 2011/2012 season. The environmental data consisted of long-term climate monthly average data for the sites from which the accessions were originally sampled. The study also consists of projected climatic data extracted from three future climate scenarios based on the Canadian Climate Centre (CCC) global circulation model (Boer *et al.* 2000).

All the climate variables were extracted from a grid cell of 1 square km (Table 1) as monthly data (De Pauw 2008). Monthly data are coarse grained and thus more prone to be out of phase in relation to critical stages of crop development (Coops *et al.* 2001), which would be further amplified by climate change effects. Thus the study also used daily data which were derived from the monthly values using models proposed by Epstein (1991) (Hofstra *et al.* 2008).

To better capture the climate change induced-shifts the predictive models were applied to climatic conditions within the growing period. Thus data averages for stages in a crops development where compared to long term climatic averages expressed as monthly values alone. Thus in the modelling process the noise created by differences in phenology between sites and climate change induced-shifts would be eliminated facilitating higher resolutions to detect environment – trait linkages.

To estimate the crop development phases a day-degree accumulation model was used from an estimated onset date for each site. The onset date was estimated using a method which determines when neither moisture nor temperature would limit plant growth. The method is based on a modification of a model developed by the Food and Agriculture Organization of the United Nations (FAO 1978, De Pauw 1982).

Table 1. The environment variables used in the study.

Variable Type	Variable Name	Variable Description	Unit	Number
Climatic	<i>Tmin</i>	Monthly minimum temperature	°C	12
	<i>tmax</i>	Monthly maximum temperature	°C	12
	<i>prec</i>	Monthly precipitation	mm	12
	<i>tmind</i>	Daily minimum temperature	°C	365
	<i>tmaxd</i>	Daily maximum temperature	°C	365
	<i>precd</i>	Daily precipitation	mm	365
Phenology	<i>Onset</i>	Date of sowing	day	1

All variables were standardized to a mean of zero and a standard deviation of 1. After the transformation the data was standardized and a comparison made between the transformed and non-transformed data. This data pre-processing was systematically and automatically carried out through the different models.

2. Modelling

In previous models the predictions were limited to past climate data while here the modelling was also carried out on projected future scenarios. The stripe (yellow) rust disease evaluation scores of the growing season 2011/2012 were presented to the models to detect the trait by collection site environment dependency, if it exists. The models were then run on all the durum

collection data held at ICARDA using current climate set of data as well as 2 other sets of future climate data/maps reflecting two emission scenarios: *a* and *b* scenarios. The *b* scenario projects a doubling of CO₂ relative to its preindustrial level (Franklin *et al.* 2013).

The modelling procedure was based on running two models using the current climate variables and then re-run the models using CC variables. The models used are SVM (Support Vector Machine) and RF (Random Forest). RF is a clustering algorithm developed to act like an ensemble classifier where the best splitters are randomly selected at each node among subset predictors ((Breiman 2001; Liaw and Wiener 2002). It is a procedure used in gene selection and classification of microarray data and genome-wide association studies for complex human diseases (Díaz-Urriarte and Alvarez de Andrés 2006; Lunetta *et al.* 2004). Support Vector Machines (SVM), on the other hand, maps input data to a more high-dimensional space that would lead to a better separation of data into respective classes by isolating those inputs which fall nearby the data boundaries (Cortes and Vapnik 1995; Principe *et al.* 2000). The mapping of input data to high-dimensional space is carried out through processes called kernel functions such as radial basis function (RBF) which is the kernel function used in this study for the SVM model. SVM models have been found to distinguish optimally between groups with minimum loss of information (Guo *et al.* 2004; Karatzoglou *et al.* 2006).

The predicted probabilities were then used to delimit areas where the conditions are conducive to occur. After defining the appropriate variograms, the maps were generated using kriging techniques (Cressie 1993). To create maps the R module was applied to irregularly spaced data (Figure 2) where the correlation between sites is (assumed) to be an exponential function of the distance.

III – Results

The results show the presence of relationship between the current or past climate data and the resistance to stripe rust. Both Receiver Operating Characteristics (ROC) values as well as Kappa values are all highly above acceptable values of 0.5 and 0.4 respectively. The ROC plots illustrate also that the curve for the two models were well above the diagonal line, which is expected when the model is different from random. The vertical trend towards the left-hand side is also an indication that the models classified the resistant accessions more correctly with fewer false positive errors (Fawcett 2006). The histograms (right side) illustrate further the extent of separation between the two trait states, resistant on one hand and tolerant on the other, with limited overlapping between the two states. The models were also able to correctly classify sites that yield either resistant or susceptible genotypes with a high correct classification when compared to the previous studies (Table 2). The accuracy of prediction as well as kappa increase reaching up to 0.83 and 0.70 respectively as we move from monthly data to aligned daily data based on onset data (Table 4).

Table 2. Accuracy and agreement parameters of daily two fit functions to generate daily data.

fit function	Stat	AUC	OR	SE	SU	CC	Kappa
Spline	mean	0.80	0.32	0.68	0.92	0.87	0.61
	upper CI	0.81	0.35	0.70	0.93	0.87	0.63
	lower CI	0.79	0.30	0.65	0.91	0.86	0.59
Loess	mean	0.79	0.34	0.66	0.92	0.86	0.59
	upper CI	0.80	0.37	0.68	0.92	0.86	0.60
	lower CI	0.78	0.32	0.63	0.91	0.85	0.57

Table 3. Accuracy and agreement parameters of daily data (spline fit function) and monthly data.

Data type		AUC	OR	SE	SU	CC	Kappa
daily data	Mean	0.80	0.33	0.67	0.93	0.87	0.62
	Upper CI	0.81	0.34	0.69	0.93	0.87	0.63
	Lower CI	0.79	0.31	0.66	0.92	0.87	0.61
monthly data	Mean	0.79	0.31	0.69	0.90	0.85	0.58
	Upper CI	0.80	0.33	0.71	0.90	0.86	0.60
	Lower CI	0.78	0.29	0.67	0.89	0.84	0.56

Table 4. Accuracy and agreement parameters of aligned data.

Data type		AUC	OR	SE	SU	CC	Kappa
monthly	Max	0.81	0.28	0.72	0.90	0.86	0.61
daily data	Max	0.82	0.30	0.70	0.93	0.88	0.64
aligned daily data	Max	0.83	0.28	0.72	0.95	0.90	0.70

The presence of the existence of the dependency between climate data and the trait of resistance to stripe rust was used as a *priori* information for the prediction of stripe resistance in independent data. The results are shown in the maps for different CC scenarios. In terms of areas that might yield stem rust variation, Ethiopia was highest followed by India and Turkey. This is also similar to the results that have been reported on the regions that might yield resistance (Singh *et al.* 2006).

IV – Discussion

Recent findings on a study conducted to search for climate change traits such as traits of tolerance of drought where a comparison was made between a *priori* and a *posteriori* information supports the assertion that FIGS can be used as an effective tool to search for traits of adaptation to climate change (Khazaei *et al.* 2013). Similar comparison was also made recently for stripe rust resistance in durum wheat confirming also that FIGS is tool with potential to not only find the sought after traits but on a limited number of accessions (Bari *et al. in press*).

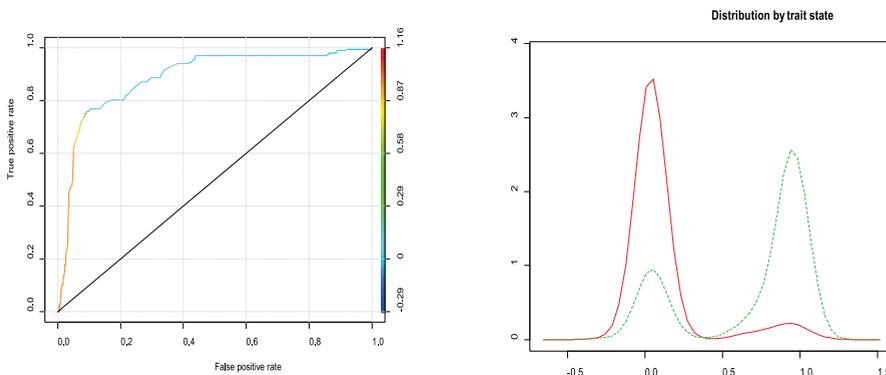


Figure 1. ROC plots for the RF and SVM models applied to the training set of accessions evaluated for Yr disease in 2011/2012 growing season at ICARDA (Left hand side). The ROC curve to the left of the diagonal plot is the true positive rate versus false positive rate. Density plots for prediction of resistance and susceptibility for the RF and SVM models (Right hand side).

[Green line indicates the probability density distribution for resistance and red line indicates susceptibility]

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