ICARDA International Center for Agricultural Research in the Dry Areas

A new approach to mining agricultural gene banks – to speed the pace of research innovation for food security

'FIGS' - the Focused Identification of Germplasm Strategy

Contents

Recent Search Requests received by the FIGS team

FIGS Search Request	Crop	Type	Scientific Crop Name	Accessions Identified
Resistance to Stem rust	Wheat	landraces	Triticum aestivum	500
Drought tolerance	Wheat	landraces	Triticum aestivum	700
Drought tolerance			Triticum turgidum	400
Heat tolerance	Wheat	landraces	Triticum aestivum	150
Heat tolerance			Triticum turgidum	150
Organic/Low input	Wheat	landraces	Triticum aestivum	50
	Wheat	landraces	Triticum turgidum	50
		primitive	Triticum spelta	10
		primitive	Triticum diccoccum	10
		primitive	Triticum monococcum	10
		primitive	Triticum polonicum	5
		primitive	Triticum turanicum	5
		primitive	Triticum vavilovii	5
		primitive	Triticum timopheevi	5
Resistance to Russian Wheat Aphid	Wheat			500
Resistance to Cereal leaf beetle	Wheat	landraces	Triticum aestivum	?
Resistance to Cereal leaf beetle			Triticum turgidum	?
Resistance to Cereal leaf beetle	Barley		Horedum	100
Resistance to Cereal leaf miner	Wheat	landraces	Triticum aestivum	50
Resistance to Cereal leaf miner			Triticum turgidum	50
Resistance to Cereal leaf miner			Horedum	50
Resistance to Stem gall midge	Barley	landraces	Horedum	250
Resistance to stem saw fly	Wheat	landraces	Triticum aestivum	50
Resistance to stem saw fly	Wheat		Triticum turgidum	50
Resistance to stem saw fly	Barley		Horedum	?
Resistance to Chickpea leaf miner	Chickpea	landraces	Cicer	100
Resistance to Chickpea pod borer	Chickpea	landraces	Cicer	100
Resistance to Sitona weevil	Lentil	landraces	Lens	100
Resistance to Bruchids	faba bean	landraces		50

'FIGS': A more precise approach to mining agricultural gene banks

This report presents the possibilities of 'FIGS', a new technique for searching agricultural genebanks, that helps crop breeders and their managers achieve faster and better targeted pinpointing of improved crops for the future. This approach helps genebank managers, crop breeders, development agencies and donors to improve the effectiveness of crop improvement programs.

There are 1700 agricultural gene banks in the world that hold the plant genetic material that crop breeders and agricultural research centers need to breed new varieties of food crops that will ensure food security for future generations.

Agricultural research centers and national breeding programs create new varieties of food crops that fight climate change with heat, cold and drought resistance, or provide resistance to pests and disease that damage crops an lower their yields. The challenge for these professionals is that the genebank searching processes available to breeders today – to identify the best traits of resistance and higher performance that can be bred into new food crop varieties – are largely hit-and-miss.

This report introduces 'FIGS' - the first scientific approach to agricultural gene bank mining, and a scientifically-proven tool that helps breeding programs identify useful traits in plant genetics .

Known as the *Focused Identification of Germplasm Strategy*, FIGS was developed by a group of leading plant genetics scientists led by ICARDA – the International Center for Agricultural Research in the Dry Areas – with the Vavilov Institute (Russia), the Nordgen genebank (Nordic Region) and the Australian Winter Cereals Collection. Over the past five years FIGS has been tested and refined.

In several hundred searchers delivered to date, FIGS has demonstrated that it can identify specific traits for breeders rapidly and precisely. In some cases it has identified traits that researchers have been looking for, unsuccessfully, for a number of years. The results of this research and testing are summarized in several papers in international scientific journals. (*see reading list in annex*).

At its core is a powerful algorithm that matches plant traits with geographic and agro-climatic information about where the samples were collected. This allow very rapid searching of thousands of plant samples conserved in genebanks to pinpoint a number of high potential types that can meet the breeder's strategy.

This report provides examples and evidence to show how the FIGS approaches can improve the effectiveness of breeding for national breeding programs and international research centers. It speeds the work of scientists looking for specific plant traits. In doing this, it helps improve the quality of crop improvement programs and, over the coming decade, can contribute significantly to enhanced food security in the world's low income countries.

1. A call for support, funding, future development and use. What FIGS can do for you

The world needs accelerated routes to future foods

Crop genes hold the secret to unlocking better yield and better nutrition from the farm crops of the future.

In the past 10 years, the demand for food has gone up because of population growth and economic development–as people get richer, they tend to eat more meat, which indirectly raises demand for grain. Supply growth- higher yields, better performing crops, agronomy, farming skills, the supply of land - has not kept up, leading to higher prices. Meanwhile, the threat of climate change is becoming clearer with preliminary studies showing that rising global temperatures alone could reduce the productivity of the world's main crops by over 25 percent. Climate change will also increase the number of droughts and floods that can wipe out an entire season of crops.

One of the simplest insurance strategies to pursue to help combat this risk is to breed better varieties that yield more food and to fight off the myriad threats that farmers and their crops face.

But we are in a hurry. Never before has the world's environment - under man-made climate change - been shifting so fast. And never before has the planet seen so many hungry human mouths to feed - Nine billion at 2050 and counting.

Previous simulations on crop improvement show that the benefits of using improved crop varieties can be substantial provided that the traits of interest are identified early. Useful traits include tolerance to heat, drought, salinity and resistance to major pests and crop diseases.

This is an introduction to a seemingly complex subject. But in reality, the approach mimics natural phenomena as it explores the trait-environment co-evolutionary processes. In effect, FIGS applies to plant genetic resources (stored collections) the same selection pressure exerted on plants by evolution.

The concepts summarized in this report are based on the hard work and vision of plant genetic scientists who have been collaborating across the world, in many different centres and with many different specialities. They hope that widespread backing for and deployment of FIGS will have a significant on future food production, nutrition, poverty and hunger.

There are currently in excess of seven million potentially agriculturally important accessions held in the world's 1700 gene banks from the Svalbard to Syria.

Join the scientific consultation on using and improving the FIGS tool

The FIGS consultation is an ongoing discussion started by the FIGS core scientific team and open to all researchers interested in using or developing the FOGS tool.

Join the consultation to add ideas and suggest improvements to the FIGS tool, ask a question about using FIGS, benefit from the results of past FIGS searches or interact with the FIGS research team.

http://figs.icarda.org/ConsultationWiki/

World food background

As a source of useful agronomic trait variation, plant genetic resources have the potential to help meet the world's continuously increasing demand for food crops. Plant improvement depends largely on a combination of 50-60,000 trait loci of the plant genome (the pieces and location of data that make up genetic code). The challenge, however, is how to find these "important" alleles as there are over 7 million accessions (seed and plant samples) worldwide stored in genebanks in national and CGIAR international centers. These accessions are assembled in collections as repositories representing hundreds or thousands of years of selection and adaptation to local conditions. Searching these collections for important traits can be a daunting process since most of the accessions in these collections lack evaluation for traits of specific interest for specific environments.

To meet the needs of the anticipated increase in world population, estimated to reach 9.3 billion people by the year 2050 (UN figures) will require a substantial increase of global food production, reckoned to be a 70 percent more increase over 2005/2007 period food production (FAO 2009).

The projected demand for cereals grain alone, as both food and animal feed, is expected to reach three billion tonnes by 2050, an increase of nearly one billion more than today's 2.1 billion tonnes (FAO 2009). This boosted agricultural production depends on two options: better agronomic practices and the application of genetics or plant improvement.

The development of improved varieties is based on an understanding of genetic variation for important agronomic traits, and better deployment of such genetic trait variation within crops. The genetic option or genetic improvement relies mainly on the utilization of novel germplasm. In wheat the contribution of genetic improvement to the overall rate of yield progress is put at 1% a year over the last 30-40 years and even more (up to 2-3%) based on CIMMYT and ICARDA material. It's a contribution that is due to the selection of several genetic traits such as phenological adaptation (short growth duration), the efficient use of water, resistance to biotic stresses (diseases and insects), tolerance to abiotic stresses (such as drought and salinity), and superior grain quality.

As a result of the beneficial interaction between genetic improvement and the positive evolution of modern agronomy (agronomic practices) there has been a steady increase in these yield rates.

The good news is that - as a viable source of useful genetic trait variation, plant genetic resources have the potential to help further meet the continuously increasing demand in food crops. We just need better systems to narrow the likely candidates and better funding to pay for such system developments and wide deployment. And we know that a combination of genetic improvement and better agronomic practices has lead in some regions to substantial increase in yield, even with less water resources.

While there is a multitude of high yielding modern crop varieties in use today, the work of plant breeders is by no means finished. A variety that is successful today can overnight be rendered ineffective by changes in the agro-ecosystem, like changes in virulence spectra of pests...

If the world is to efficiently unlock the potential of plant genetics to feed a hungry world in the future, then new systems of "mining" these genetic resources held in agricultural gene banks need to be developed. Plant breeders are in a hurry to solve problems of rampant pest and disease loss, cold, heat and drought tolerance, salinity tolerance.

The task, as it stands, has been described as looking for a needle in a haystack. Using current methods and funding levels it is impossible to screen all available plant genetic materials to identify seed samples carrying the genetic variation required for new crop breeding improvements and breakthroughs.

This technical barrier to accessing novel genes is a major constraint to increasing crop productivity, to reducing poverty and to ensuring food security, all of which are now even more acutely needed due to climate change and environmental pressures.

FIGS is the '*Focused Identification of Germplasm Strategy*. It uses cutting-edge applied Bayesian mathematics and geographical information data to help plant breeders to more effectively sort through the millions of plant samples conserved in the world's seed gene banks. Put simply, it facilitates the rapid identification of traits that make crop varieties tolerant to drought, excessive heat or cold, and resistant to insect pests and a variety of crop diseases that reduce field yields in low-income and more developed countries.

The plant genetic resource identification approaches presently deployed, range from 'lucky dip' to a 'core collection' concept, which aims to capture as much genetic diversity as possible, using a small subset of 5-10% of a total collection. A core (or reference) collection offers the benefit of easy-to-manage sets of plant genetic material. But many breeders are wary of this approach, as it does not necessarily deliver the material that is most likely to contain the specific traits required by them as they look to improve crop performance.

FIGS has been developed, tested and refined over the past six years by a research team from ICARDA – The International Center for Agricultural Research in the Dry Areas – with partners including the Vavilov Institute (Russia), the Nordgen genebank (Nordic Region) and the Australian Winter Cereals Collection. Its development is continuously supported by GRDC.

The method uses detailed information about the environment from which plant genetic samples were collected to precisely predict where plant traits – such as disease resistance or adaptability to extreme weather conditions – are likely to have evolved. Accessions from these areas have a higher probability to contain the traits and genes of interest. From this calculation are assembled smaller subsets of genetic material that have a high potential to contain the plant traits that breeders need to develop their robust new varieties.

It is now at the validation stage, requiring widespread "road-testing" and implementation funding before it is rolled out to become an accepted and valued tool for gene discovery.

New research partnership on plant traits to reduce the risk of climate change

A new partnership that aims to more effectively pinpoint heat and drought tolerant plant traits using FIGS has been started between the CGIAR Research Program on Climate Change, Agriculture, Food Security (CCAFS), the University of Helsinki, ICARDA's FIGS research team, and research partners from Azerbaijan, China, Ethiopia, Finland, India, Thailand, Morocco.

This platform expands the work of FIGS beyond the search for plant traits that address biotic stresses, to look at abiotic stresses, particularly climate change related-traits – namely drought and heat.

One of the platform's recent research activities, led by the University of Helsinki, uses faba bean as a model crop to better pinpoint drought-related traits. This research validates the efficiency of FIGS to identify subsets of germplasm with a high probability of finding climate change related-traits in a plant genetic resources collection.

Study results confirmed that FIGS can assist in the identification of accessions with desirable trait expression and contributed to the proof of concept of the approach. They show that the discrimination between the two subsets (those with sought after traits and those lacking these traits) can be based on physiological traits such as leaflet and canopy temperature and relative water content. These traits can be used for drought-tolerance selection. This study supports the premise that FIGS can be effective at identifying plat resistance to changing climate conditions.

The platform aims to:
1. Develop an on-line support system to support researchers breeding plants for climate change resistance.
2. Further develop and refine the FIGS approach.
3. Generate climate trait sets for plant genetics and agro-biodiversity that relate to climate change and develop new subsets for climate change extremes (heat, cold and drought).
4. Evaluate some of these subsets phenol-typically and geno-typically, and develop a prototype for climate change-related traits.
5. Develop proposals for further consolidation of the platform.

2. FIGS – faster and more focused delivery of tomorrow's crops

The FIGS approach provides breeders with an efficient short cut to a best-bet list of promising accessions. It should be routinely used in the selection of screening genetic resource collections. FIGS has the potential to greatly reduce the resources required to mine genetic resource collections. It saves time and it saves money.

It is a triumph of modern science. Plant breeding has produced substantial crop improvement, not least with respect to crop yields. Modern cultivars sometimes show higher yields than traditional landraces. However, landraces and wild relatives of the cultivated plants still hold many useful traits and properties valuable for further crop improvement. Such properties include disease/pest resistance and durable tolerance to changes of environmental conditions including the effects of climate change.

Many of the old landraces and some of the crop wild relatives are maintained as living collections in genebanks. Unfortunately much of this material lacks the evaluation data required to assist plant breeders to readily find the seed samples most likely to possess the genetic variation they require for future advances. The utilization of such landraces and wild relatives therefore requires large and costly field experiments to systematically screen the germplasm material for the target trait properties.

To help solve this difficulty, A *Focused Identification of Germplasm Strategy* (FIGS) was proposed to exploit the assumed link between the eco-geographic environment (climate), where traditional agricultural crops evolved and were selected, and their possible adaptive trait properties.

The theoretical background for FIGS was introduced almost two decades ago, while more recent results provides the first experimental evidence in support of this approach. Early work by the Russian scientist N.I. Vavilov in the 1930s and the Core Collection sampling approach proposed in 1984 by the Australian scientists O.H. Frankel and A.H.D. Brown provides the theoretical foundations that underpin this new "trait mining" approach.

FIGS uses cutting-edge applied Bayesian mathematics and geographical information data to help gene bank managers to more effectively mine the millions of plant seed samples conserved in the world's agricultural gene banks. It enables the rapid identification of traits that make crop varieties resistant to drought, excessive heat or cold, to insect pests and a variety of crop diseases that reduce farm yields in low-income and developed countries.

FIGS is based on the premise that the environment strongly influences natural selection and consequently the geographic distribution of organisms. FIGS creates ‹best-bet› trait-specific subsets of material by passing accession-level information, especially agro- climatic site information, through a series of filters that increase the chances of finding the adaptive trait of interest.

ICARDA's genebank is particularly responsive to the FIGS approach since it is unique in the CGIAR system in having up to 70% of its seed samples geo-referenced. But for other genebanks the ICARDA GIS unit can also provide a detailed environmental profile for any collection site in the whole of Eurasia.
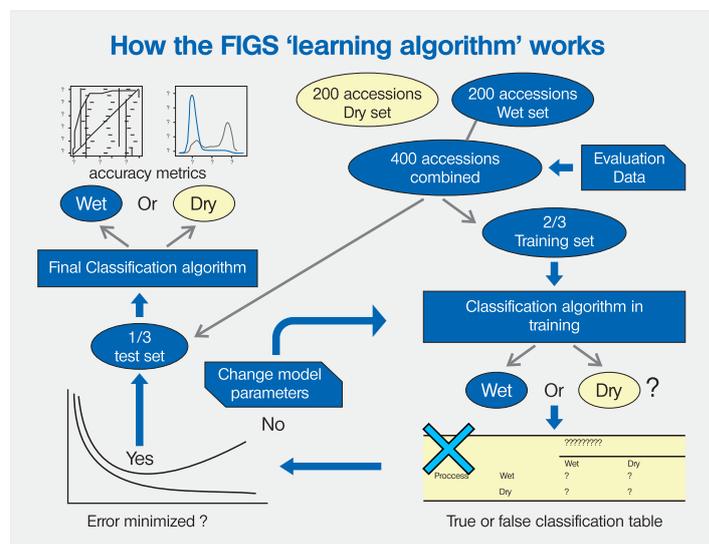
Standard plant genetic resource identification approaches, range from 'lucky dip' to a more calculated 'core collection' concept, which aims to capture as much genetic diversity as possible, using a small subset of perhaps 5%-10% of a total collection. A core collection offers the benefit of easy-to-manage offerings of plant genetic material. But based on the decisions of a gene bank curator, this does not always deliver the material that is most likely to contain the specific traits required by breeders looking to improve crop performance. Experience has shown that, in general, breeders are wary of the core collection approach.

Using such current methods and at current funding levels it is virtually impossible to screen all available plant genetic materials to identify characteristics carrying the genetic variation required for new crop breeding improvements and to deliver major breakthroughs. This is a key constraint to increasing crop productivity, reducing poverty and ensuring food security – all of which are now even more acute under the scenario of climate change.

Caption

There has to be fresh thought given on how to access and unlock the world's agricultural crops genetic treasure chest. To breed new crop varieties with resistance and new characteristics requires access to novel genes that possess the desired trait. These novel genes are buried in plant genetic resource collections like those conserved within the CGIAR's gene banks and in the many national gene banks worldwide. With over 7.2 million genetic resources available, finding candidate samples with just the right desirable trait has been described as looking for a needle in a haystack.

FIGS has been developed, tested and refined over the past six years by a research team from ICARDA – The International Center for Agricultural Research in the Dry Areas – with partners including the Vavilov Institute (Russia), the Nordgen genebank (Nordic Region) and the Australian Winter Cereals Collection. Thanks to the continuous financial support provided by GRDC.

The FIGS approach is starting to catch on amongst gene bank managers and breeders. Demand for FIGS-selected material (from the FIGS team) has come from more than 20 crop research institutes worldwide – in Australia, West Asia, the Middle East, North Africa, Europe and North America. In India, the agricultural research community is planning to use FIGS to speed up its innovation processes for crop development.

So what is the science and mathematics behind FIGS? The method uses detailed information about the environment from which plant genetic samples were collected to precisely predict where plant traits – such as disease resistance or adaptability to extreme weather conditions – are likely to evolve. Accessions from these areas are accepted to have a higher probability to contain the traits and genes of interest. With this information, smaller subsets of genetic material can be assembled that have a high potential to have the plant traits that breeders need to develop their robust new varieties.

Rapid access to desired plant traits

The FIGS approach has proved successful where large scale 'screening exercises' have previously failed to find their target. New genes for resistance to Powdery Mildew, Sunn Pest and Russian Wheat Aphid have been identified in relatively small plant genetic FIGS sets. In a desktop study using the results of a large screening exercise to identify genes conferring resistant to the virulent wheat stem rust strain (Ug99), the FIGS method proved highly efficient at discerning between environments that yield resistant plants and those that do not.

Another encouraging example is the multi-year search by an ICARDA researcher – of thousands of plant types in the ICARDA genebank – for bread wheat types with resistance to the Sunn Pest insect, which causes major economic losses to crops in Central and West Asia and North Africa. Over this period, no resistant accessions (individual samples conserved by a genebank) were identified using classic search approaches. Recently, using a specially targeted FIGS subset of potentially resistant plant materials, the same researcher found Nine accessions with resistance to Sunn Pest at the seedling stage which are now being used in the ICARDA breeding program, and are available to other breeders on request.

Rare and adaptive traits are difficult to capture in the core...

A germplasm collection is often the result of historical events and arbitrary decisions; collecting missions and specific research programs can result in over-representation of certain material whereas other types of material can be under-represented. Core collections try to increase the balance between the types of material in a relatively small selection of accessions.

A team of scientists at the International Center for Agricultural Research in the Dry Areas (ICARDA), the Nordic Genetic Resources Center (NordGen) and Bioversity International, investigated in 2010 the use of modern data mining approaches for FIGS. Results from their study were published in the September-October 2010 issue of Crop Science. The research was also presented as part of the Botany seminar series at Copenhagen University in February 2011.

Two datasets with measurements of crop resistance to fungal diseases were analyzed with this new trait mining (FIGS) approach. The National Plant Germplasm System (NPGS) of the United States Department of Agriculture (USDA) kindly provided the agricultural datasets for this study. The reaction to stem rust infection on wheat was measured during 1988 to 1994, and the reaction to net blotch on barley was measured during 1988 to 2004 by crop scientists in the USA. The results from this study demonstrate that eco-climatic data from the collecting sites where food crops were cultivated can be used to predict and identify important crop traits.

The objective of FIGS is to increase the likelihood of finding a target crop trait in material from germplasm collections. Predictive computer modeling using FIGS will thus reduce the time period required for the development of new improved cultivars, as well as the costs concerning the use of land area for field experiments and human labour. The result will be quicker and more efficient breeding and development of cultivars and commercial crop varieties best suited to challenges of farming tomorrow.

What is a core collection?

There are seven million plant accessions in the world's agricultural gene banks world-wide. But the huge size of some collections can limit accessibility, and hinder the use and management of material to practical breeders and others.

With total collections it is difficult -
- to get an overview of the collection and thus to decide what should be added or could be removed,
- to chose material since there is so much material to chose from,
- to focus; knowing very much about a relatively few accessions can be better than knowing relatively little about very many accessions.
- to find rare traits, particularly when the evaluation of the trait is expensive.

To improve this situation it has become an accepted technique amongst germplasm managers to select a limited set of accessions from the collection that contain as much genetic diversity as possible: known as a core collection. This concept was first introduced in the 1980s. It is defined as 'a limited set of accessions which represents, with a minimum of repetitiveness, the genetic diversity of a crop species and its wild relatives'.

Core collections now claim to reflect the diversity in collections and applications:
- most are created to represent (a part of) an existing collection or (parts of) several existing collections, but some are newly created,
- some represent a complete genus, including wild species, whereas others represent a small part of the genepool,
- some contain as much diversity as possible, but most give higher priority to a certain type of material, reducing the amount of diversity captured.

Snapshot of FIGS – Questions and Answers

How to distill the essence of FIGS – after all it is an apparently complex subject?

The method uses detailed information about the environment from which plant genetic samples were collected to precisely predict where plant traits – such as disease resistance or adaptability to extreme weather conditions – are likely to evolve. Accessions from these areas have a higher probability to contain the traits and genes of interest. From this we assemble smaller subsets of genetic material that have a high potential to have the plant traits that breeders need to develop their robust new varieties.

What's wrong with current, commonly used methods?

Using current methods and funding levels it is virtually impossible to screen all available plant genetic materials to identify characteristics carrying the genetic variation required for new crop breeding improvements and breakthroughs. Most of the other methods are not focused on targeted traits, rather on large diversity base. This is a major constraint to increasing crop productivity, reducing poverty and ensuring food security.

How big is the challenge?

To breed new crop varieties with resistance and new characteristics requires access to novel genes that possess the desired trait. These novel genes are buried in plant genetic resource collections like those conserved within the CGIAR genebanks and the many national genebanks worldwide. With over 7 million genetic resources available, finding candidate samples with the desirable trait is a bit like looking for a needle in a haystack.

How to characterize the FIGS appeal?

It's a technique that formalizes what a good genebank manager/curator might do intuitively. FIGS represents the first real conduit between breeders and the genebank world. I have to say that breeders are very enthusiastic.

Why is it an advance on core collections?

Core collections are too generalized. In a way they are counter intuitive – they try to maximize generalized measures of diversity in as few a number of accessions as possible. Breeders need specific traits. We have analyzed requests by breeders for germplasm from the ICARDA genebank. About 90 per cent of them are for diseases or other specific traits. In developing FIGS we are asserting that core collections don't necessarily capture the "rare genes" required by breeders.

How confident can we be that FIGS is a breakthrough?

FIGS is a "no-brainer" – it is a targeted revolution for crop genetics.

Where are we now in its development?

We are at the proofing stage, but currently swamped by requests from breeders for FIGS use and data.

What does the future hold for FIGS? What can FIGS do for the future?

A computer program that will walk a potential user through the process of using FIGS is being developed. It will also be linked to GeneSys, the global portal on crop genetic resources.

3. How FIGS works – the mathematics behind the magic...

The FIGS approach explores the relation between a crop type's trait and its environmental using environmental variables that are generated through geographical information systems.

The mathematical conceptual framework of FIGS is based on the paradigm that the trait as response variable (Y) depends on the environment (X), where X = $(x_1,...,x_n)$ are covariates. Models are developed to quantify this hypothesized trait-environment dependency. The quantification process leads to the generation of a priori information, which in turn is used in the prediction of accessions that would carry the desired trait. The FIGS approach explores the trait-environmental relationship using the environmental variables that are generated through geographical information systems.

The performance of the models is measured using the metric parameters derived from a confusion-matrix table and the Area Under the Curve (AUC) of the Receiver Operating Characteristics (ROC). The models used are mostly learning based techniques, where the models were trained on previously scored/evaluated genebank accessions. The unknown accessions are tested against the trained test for their placement in their respective group.

The high accuracy of the models is an indication of the presence of the trait environment relationship. This information is used in the prediction of accessions that could carry the trait more than the random.

In Figure 1, the ROC curve shows whether there is a relationship between the trait and the environment, which is then translated in the distribution of the trait state curves being well separated and thus predictable (with however some false positive that is equal to α)

Different methods can be used and ROC is a way to detect the best performing mathematical models which can be used in the prediction of which accessions have a higher probability of containing the desired traits. The mathematical models are developed as algorithms under R language and Matlab (The Mathworks) platforms. These FIGS related algorithms are being deployed for use and re-use by researchers. The aim is to build FIGS modeling routines in R language that would include the full range of modeling techniques ranging from linear (PCA, PLS, SIMCA, LDA) to non-linear approaches (NN, SVM, RF).

FIGS involves both the development of a theoretical framework as well as applied mathematics and statistics that will require a medium that will allow FIGS to evolve conceptually as well as practically and to incorporate other work that is of relevance to FIGS.

R language has been used as a platform for FIGS and will be the most convenient medium for packaging FIGS software to conduct research and to communicate the results to the world plant genetics community.
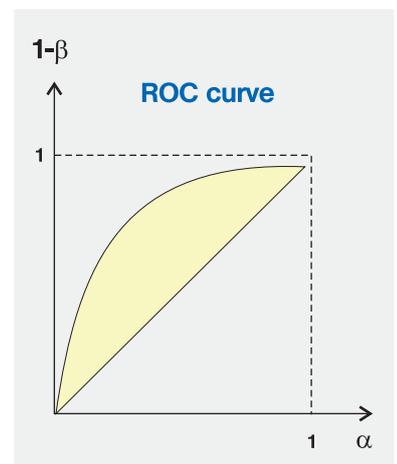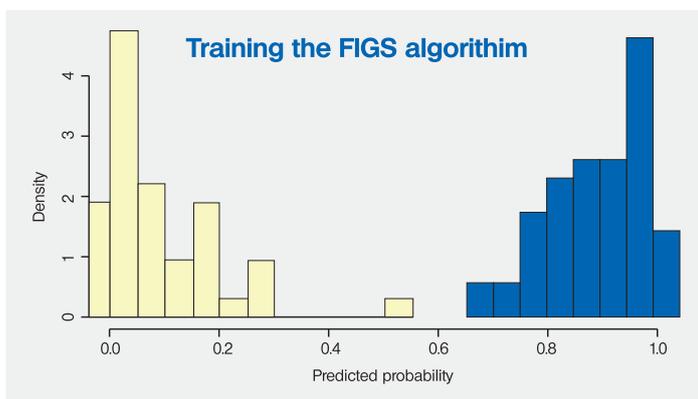

A Receiver Operating Characteristics (ROC) curve shows the relationship between a plant's trait and the environment where it was collected.

4. FIGS IN USE - CASE STUDIES

4.1. FIGS as a strategy to detect wheat stem rust resistance, linked to environmental variables

The appearance virulent new crop diseases is a typical recurring scenario in agricultural production that can lead to severe yield losses, across countries and entire regions. Stem rust (also known as Black Rust) caused by the fungi *Puccinia graminis* f. sp. *tritici*, has re-emerged as major threat to world wheat following the appearance of new virulent races. Ug99, a particularly aggressive strain of stem rust, was first found in Uganda in 1999 and has since increased the vulnerability of the global wheat yields.

UG99 has taken its toll on wheat production in Sub-Saharan East Africa, Yemen and Iran and now threatens crops in Central Asia and the Caucasus and South Asia; an area that accounts for nearly 40% of global wheat production. Because of its virulence and potential to spread, Ug99 has attracted both public and research community attention worldwide and global efforts to track and monitor its expansion are underway to counter its potential impact.

Plants usually react to virulent strains through the so-called R (resistance) genes group. In the case of wheat, there are about 45 to 50 genes, known as Sr genes, which are thought to confer resistance to different races of stem rust.

Using novel disease resistance genes found in plant genetic resources collections in agricultural genebanks, can help protect wheat crops from attacks by UG99. The genetic resources in these genebanks contain crop landraces and wild relatives that have potential sources for pest and disease resistance critical for the stability and sustainability of global wheat production.

Training the FIGS algorithm. This figure illustrates the ability of the FIGS prediction algorithms to correctly classify the evaluated genebank plant accessions as being from a wet or dry environment based on their trait expression. In this process the algorithms are first 'trained' with the trait data and set membership of a subset of the accessions. The 'trained' models then assign a probability to the remaining accessions – of if they were selected from a dry environment or not. The bars are cumulative frequencies for a given probability. The green cross-hatched bars with the low probabilities are accessions from wet environments and the orange bars with high probabilities are for accessions from the dry environments.

These traits however are rare and may not be captured in representative or fixed genetic resources collections such as core collections. The need to rationalize and streamline the search for rare and adaptive traits has led genebank mangers to develop alternative approaches including the creation of specific or thematic genetic resource collections.

By using the FIGS 'eco-geographical' data of a dataset of plant genetic material with resistance to a specific trait, such as resistance to diseases or pests, researchers were able to successfully identify a number of novel genes in the dataset from environmentally similar sites.

For stem rust resistance, modeling used geographical information system (GIS) approaches detected a relationship between geographical areas and incidence of resistance to stem rust. Some of the traits that have been found to carry strong climatic signals in wild species are being used to model the impact of climate changes.

The FIGS trait-based approach allows breeders to have targeted strategy to select potentially useful genetic materials for crop improvement. It was conceived to provide indirect evaluation of plant genetic materials in genebanks – targeting specific traits using environmental parameters. The approach is based on the hypothesis that the genetic material is likely to reflect the selection pressures of the environment from which it was originally sampled. The FIGS approach addresses the lack of available evaluation data as well as the temporal (the moment when the accession is evaluated) issue of evaluation.

The objective of this FIGS-Ug99research was to detect whether there is a link between stem rust resistance and climate. The results of which will be used to develop a subset of plant genetic material with an increased probability of finding new resistance to stem rust; and to develop algorithms to use in future applications of FIGS for 'trait mining' of large genebank collections.

Overall, the results of this work give indications that the trait distribution of resistance to stem rust is confined to certain environments or areas, whereas the susceptible types appear to be limited to other areas with some degree of overlapping of the two classes. The FIGS team also says that the results point to a number of issues to consider for improving the predictive performance of their models.

4.2. Getting the best from bread wheat landraces

Wheat is the world's most important food crop. In the developing world it is the second most important crop after rice. Demand for wheat currently outstrips the world's ability to produce it – an ability that is also constantly under threat from new diseases, rampant pests and a changing climate.

The Grains Research and Development Corporation (GRDC) of Australia funded a four-year project looking at the targeted exploitation of the N. I. Vavilov Institute of Plant Industry, ICARDA and Australian bread wheat landrace germplasm for the benefit of wheat breeding programs. The project involves a collaborative effort between the famous Vavilov Institute of St Petersburg, Russia, the Australian Winter Cereals Collection hosted by the Department of Primary Industries in NSW, Australia and ICARDA.

While the idea behind FIGS encompasses all crop types held in all genebanks, this project focuses only on bread wheat landraces held in three genebanks to help develop prototype systems.

Each of the above institutes house sizable collections of bread wheat landraces. They are special collections because they are from very diverse environments and feature accessions that were collected early in the 20th Century and, as such, are unique in that many of them could no longer be found in the field due to displacement by modern varieties.

In this project a database containing information about the wheat genotypes and where they came from was compiled. Using historic collection mission reports, the geographic coordinates were captured thus allowing a connection to be built between derived agro-climatic and other parameters

at collection sites. The idea is to build up detailed environmental profiles of the habitats within which a given genotype evolved with subsets designed to capture variation for resistance/tolerance to the following traits - drought, salinity, powdery mildew and Russian wheat aphids.

A core set was developed, using methodologies based on geographic locations of collection sites, to use as a check when screening the FIGS sets. The hypothesis being that researchers are more likely to find trait specific variation in the FIGS sets than in the core set.

The suite of agro-geographic parameters used to describe the collections sites are currently being expanded and further FIGS sets are under development and will be screened when funding permits.

4.3. A new tool in the battle against Sunn Pest

FIGS was applied in the ICARDA genebank to find sources of resistance to Sunn pest (*Eurygaster integriceps*), the major pest of wheat in West and Central Asia and eastern Europe. Sunn Pest can cause 100 per cent losses, but most importantly affects the bread quality even at very low infestation rates . It is reckoned to affect up to 15 million hectares of wheat annually and in excess of US$150 million is spent each year on pesticide treatments in the pest-prone regions.

A FIGS search identified 534 likely accessions. Initial field screening reduced these to 57, and advanced screening resulted in nine candidates with resistance to Sunn pest at the vegetative stage. The resistant varieties developed using the resistance genes found using FIGS form an important part of integrated pest management development, designed to reduce populations of adult insects.
These nine entries are the first wheat sources found with good levels of resistance to Sunn pest at the vegetative stage. They are being used in the ICARDA wheat breeding program to develop wheat varieties resistant to Sunn pest feeding at the vegetative stage.

The 534 accessions identified by the FIGS filtering process were field screened at the ICARDA research station at Tel Hadya during 2007. In the initial evaluation, 10 seeds per hill were planted, in an augmented design, with bread wheat cultivar ‹Cham 6› as a susceptible check every 10 test entries. Plants were covered by mesh screen cages and infested with three adult Sunn pests per hill in mid-March, the time when they usually migrate to wheat fields.

The nine key accessions identified through FIGS are being used in ICARDA wheat breeding programs to develop resistant varieties against overwintered Sunn pest adults, which damage wheat at the vegetative stage (shoot and leaves). Resistance at this stage could be important in reducing overwintered Sunn pest adult populations, as well as nymphal and new generation adult populations, which reduce wheat quality by feeding on spikes (grains). The introduction of wheat varieties carrying resistance at the vegetative stage should be one component of a total integrated pest management program against Sunn pest.

Since all the accessions resistant to Sunn pest came from the same geographical area, either from Afghanistan or from neighboring Tajikistan, it would be advisable to concentrate on these countries when screening other accessions for Sunn pest resistance in the future, and to return for additional sampling.

4.4. FIGS as a strategy to identify climate change adaption traits

Faba bean (*Vicia faba* L.) is an important source of protein in dry areas of developing countries most likely to be impacted by climate change. This has drastic food security implications because faba bean is relatively sensitive to moisture stress when compared to other temperate season grain legumes. So it is imperative that the natural variation for traits related to drought adaptation are identified from the faba bean genepool and used to improve its adaptation to dry conditions.
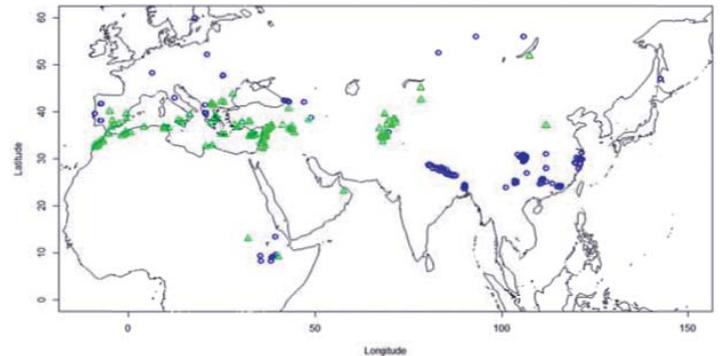
The effectiveness of the FIGS approach to identify Faba bean material containing traits associated with drought tolerance was assessed in a collaboration between the Helsinki University and ICARDA.

The FIGS approach is based on the premise that adaptive traits displayed by an accession will reflect the selection pressures of the environment from which it was originally sampled. To test this premise two subsets of faba bean landraces were selected from environments with contrasting seasonal moisture regimes. The material was grown under controlled conditions and morpho-physiological parameters associated with leaf water status were measured. They included stomatal characteristics, gas exchanges traits, leaf and canopy temperatures, leaf water content and days to flowering. In total 16 traits were measured.

Pinpointing faba bean traits that resist climate change. Faba This map shows the geographic distribution of the collection sites for the faba bean data set from dry environments (green triangle) and from wetter environments (blue circles). Eight climatic variables were used to determine the dryness or wetness of a site.

Three powerful machine learning processes were used to classify the accessions into two groups based on the evaluation data. If the FIGS premise is correct then we would predict that the classification of accessions based on the traits would match the FIGS set membership created by analyzing the collection site climatic data. There was almost a 100% agreement between the FIGS subset membership and the classification based on the traits measured.

The members of the set from dry areas tended to flower earlier, had larger stomata, greater stomatal area, more stomatal area per unit of leaflet, lower transpiration rate and a RLWC than the wet set. The material from the wetter environments had higher transpiration rates and leaf and canopy temperatures.

This investigation illustrates that FIGS is a suitable search strategy for seeking traits for climate change adaptation.

Reading list

Powdery Mildew resistance new gene discovery –

Bhullar, N.K., K. Street, M. Mackay, N. Yahiaoui, and B. Keller (2009) Unlocking wheat genetic resources for the molecular identification of previously undescribed functional alleles at the Pm3 resistance locus. PNAS 106:9519-9524. DOI: 10.1073/pnas.0904152106.

Sunn pest resistance new gene discovery –

El-Bouhssini, M. Street, K. Joubi, A. Ibrahim, Z. Rihawi, F (2009) Sources of wheat resistance to Sunn pest, Eurygaster integriceps Puton, in Syria. Genetic Resources and Crop Evolution 56(8):1065-1069.

Russian Wheat Aphid resistance: new gene discovery –

El-Bouhssini, M., K. Street, A. Amri, M. Mackay, F.C. Ogbonnaya, A. Omran, O. Abdalla, M. Baum, A. Dabbous, and F. Rihawi. 2010. **Sources of resistance in bread wheat to Russian wheat aphid (Diuraphis noxia) in Syria identified using the Focused Identification of Germplasm Strategy (FIGS).** Plant Breeding 30: 96-97.

El Bouhssini, M., Street, K., Amri, A., Mackay, M., Ogbonnaya, F. C., Omran, A., Abdalla, O., Baum, M., Dabbous, A. and Rihawi, F. (2011), **Sources of resistance in bread wheat to Russian wheat aphid (Diuraphis noxia) in Syria identified using the Focused Identification of Germplasm Strategy (FIGS).** Plant Breeding, 130: 96–97. doi: 10.1111/j.1439-0523.2010.01814.x http://onlinelibrary.wiley.com/doi/10.1111/j.1439-0523.2010.01814.x/pdf

Predicting geographic distribution of disease resistance

Endresen, D.T.F., K. Street, M. Mackay, A. Bari and E. De Pauw (2011). **Predictive Association between Biotic Stress Traits and Eco-Geographic Data for Wheat and Barley Landraces.** Crop Science. 51:2036–2055.

Bari, A., K. Street, M. Mackay, D.T.F. Endresen, E. De Pauw, and A. Amri (2012). **Focused Identification of germplasm strategy (FIGS) detects wheat stem rust resistance linked to environmental variables.** Genetic Resources and Crop Evolution 59:1465–1481

Endresen, D.T.F., K. Street, M. Mackay, A. Bari, E. De Pauw, K. Nazari, and A. Yahyaoui (2012). **Sources of Resistance to Stem Rust (Ug99) in Bread Wheat and Durum Wheat Identified Using Focused Identification of Germplasm Strategy (FIGS).** Crop Science [Online first].

Bari, A., A. Amri, K. Street, M. Mackay, E. De Pauw, R. Sanders, K. Nazari, B. Humeid, J. Konopka, and F. Alo. (in press) **Predicting resistance to stripe (yellow) rust in plant genetic resources using Focused Identification of Germplasm Strategy (FIGS).** Cambridge Journal of Agricultural Science, UK.

Searching for climate change related traits – drought –

Hamid Khazaei, Kenneth Street, Abdallah Bari, Micheal Machay, F.L. Stoddard (in press). **The FIGS (Focused Identification of Germplasm Strategy) approach identifies traits related to drought adaptation in Vicia faba genetic resources.** PLOS ONE journal.

Conference presentations

Biodiversity assessment using the FIGS approach for important agronomic/ functional traits. Biodiversity Research Center Symposium, 7-9 December 2011, Montreal. http://qcbs.ca/wp-content/uploads/2011/07/Symposium-booklet.pdf

Mining genetic resource collections for useful traits using Focused Identification of Germplasm Strategy (FIGS) approach. Interdisciplinary Mathematical & Statistical Techniques Conference. 1-4 July 2011, Montreal.

Rational Approach to Identifying and Deploying Novel Trait Expression From Ex Situ Genebank Collections. "Visions for a Sustainable Planet," Oct. 21-24, 2012, Cincinnati, OH. USA.
http://scisoc.confex.com/scisoc/2012am/webprogram/Paper71968.html

Sources of resistance in wheat to sunn pest (Eurygaster integriceps Puton) identified using the focused identification of germplasm strategy (FIGS), XXIV International Congress of Entomology - 2012. http://edunabi.com/~ice2012/sub01_01.html

Mining genebank holdings using the Focused Identification of Gerrnplasm Strategy (FIGS: sources of resistance to Russian wheat aphid, Sunn pest and Hessian fly. The 20th Biennial International Plant Resistance to Insects Workshop - 2012. http://www.hpr2012.umn.edu/PROGRAM.pdf   http://www.hpr2012.umn.edu/

About ICARDA and the CGIAR

Established in 1977, the International Center for Agricultural Research in the Dry Areas (ICARDA) is one of 15 centers supported by the CGIAR. ICARDA's mission is to contribute to the improvement of livelihoods of the resource-poor in dry areas by enhancing food security and alleviating poverty through research and partnerships to achieve sustainable increases in agricultural productivity and income, while ensuring the efficient and more equitable use and conservation of natural resources.

ICARDA has a global mandate for the improvement of barley, lentil and faba bean, and serves the non-tropical dry areas for the improvement of on-farm water use efficiency, rangeland and small-ruminant production. In the Central and West Asia and North Africa (CWANA) region, ICARDA contributes to the improvement of bread and durum wheats, kabuli chickpea, pasture and forage legumes, and associated farming systems. It also works on improved land management, diversification of production systems, and value-added crop and livestock products. Social, economic and policy research is an integral component of ICARDA's research to better target poverty and to enhance the uptake and maximize impact of research outputs.

The Consultative Group on International Agricultural Research (CGIAR) is a strategic alliance of countries, international and regional organizations, and private foundations supporting 15 international agricultural Centers that work with national agricultural research systems and civil society organizations including the private sector. The alliance mobilizes agricultural science to reduce poverty, foster human well being, promote agricultural growth and protect the environment. The CGIAR generates global public goods that are available to all.

The World Bank, the Food and Agriculture Organization of the United Nations (FAO), the United Nations Development Programme (UNDP), and the International Fund for Agricultural Development (IFAD) are cosponsors of the CGIAR. The World Bank provides the CGIAR with a System Office in Washington, DC. A Science Council, with its Secretariat at FAO in Rome, assists the System in the development of its research program.