

Damage, diversity and genetic vulnerability:
The role of crop genetic diversity in the
agricultural production system to reduce pest
and disease damage

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Devra I Jarvis, Carlo Fadda, Paola De Santis and Judith Thompson,
Editors

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Financial support for Bioversity's research is provided by more than 150 donors, including governments, private foundations and international organizations. For details of donors and research activities please see Bioversity's Annual Reports, which are available in printed form on request from bioversity-publications@cgiar.org or from Bioversity's Web site (www.bioversityinternational.org).

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Citation:

Jarvis, DI, C Fadda, P De Santis and J Thompson, editors. 2011. Damage, diversity and genetic vulnerability: The role of crop genetic diversity in the agricultural production system to reduce pest and disease damage, Proceedings of an International Symposium 15-17 February, 2011, Rabat, Morocco. Bioversity International, Rome Italy.

ISBN 978-92- 9043-876-2

Bioversity International
Via dei Tre Denari, 472/a
00057 Maccarese
Rome, Italy

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Bioversity International is the operating name of the International Plant Genetic Resources Institute (IPGRI).

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Acknowledgements

The editors would like to thank the governments of China, Ecuador, Morocco and Uganda, the United Nations Environmental Program/Global Environmental Facility (UNEP/GEF), the Swiss Agency for Development and Cooperation, the United National Food and Agriculture Organizations, and Ford Foundation for their generous financial support for this work.

Finally, our most sincere and profound thanks go to many participants whose names and affiliations do not appear in this volume. Many farmers, development workers, educators, researchers, and government officials participated in the many studies presented in this book; it is they who made this work possible.

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Wang	Jun Zhen	<i>The Crop Institute, Yunnan academy of Agricultural Sciences.</i>
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List of Acronyms

ALS	Angular leaf spot
ANT	Anthraxnose
AUDPC	Area Under Disease Progress Curve
BFY	Bean fly
CBD	Convention on Biological Diversity
CBM	Community-based biodiversity management
CBMV	Common Bean Mosaic Virus
CIMMYT	International Center for Wheat and Maize
CRBD	Completely randomized block design
CRRA	Centre Régional de la Recherche Agronomique, ,
CTAB	DNA extraction protocol using Cetyltrimethylammonium Bromide
CYCAS-MED	Crop Yield and Climate Change Impacts: Adaptation Strategies to Desertification Processes in MEDiterranean Areas)
DDV	Diversity Damage and Vulnerability
DEP	Department of Environmental Protection
DFF	Diversity Field Fora
DS	Disease severity
DSF	Diversity Seed Fairs
FAO	Food and Agriculture Organization of the United Nations
FGD	Focus Group Discussion
GI	Geographical indications
GEF	Global Environment Facility
GPS	Global positioning system
GUA	Genotype unit area
HH	Household
ICHORD	Indonesian Centre for Horticultural Research & Development
ICRISAT	
IIHR	Indian Institute of Horticultural Research
INERA	l'institut de l'environnement et de recherches agricoles, Burkina Faso
IER	Institut d'Economie Rurale
INIAP	Instituto Nacional Autónomo de Investigaciones Agropecuarias
INRAN	L'Institut National de la Recherche Agronomique du Niger
INRA	Institut National de la Recherche Agronomique
IPM	Integrated Pest Management
ISSR	Inter-simple sequence repeat
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
IUCN	International Union for Conservation of Nature

LN	Lesion numbers
LS	Lesion size
MAP	Aromatic and medicinal plants
MARDI	Malaysian Agricultural Research & Development Institute
MEP	Ministry of Environmental Protection
MLS	Multilateral System of Access and Benefit Sharing
MoA/SFA	Ministry of Agriculture/ State Forestry Administration, China
NaCRRRI	National Crops Resources Research Institute
NGOs	Non-governmental organizations
NLB	Northern leaf blight
NUS	Neglected and Underutilized Species
PCR	Polymerase chain reaction
PD	Participatory diagnostic
PNHAO	Parc National du Haut-Atlas Oriental
PDA	Potato dextrose agar
PR	Partial resistance
QTL	Quantitative trait loci
RCBD	Randomized complete block design ()
SPSS	Statistical Package for the Social Sciences
SWG	Stochastic Weather Generator
UNEP	United Nations Environment Programme
WDI	Weighted Damage Indices

FOREWORD

Peter Kenmore

Up to 30% of the world's annual harvest continues to be lost to pests and diseases, with developing countries experiencing the greatest devastation. The resulting losses are evolutionary consequence of crops grown in single variety monocultures and the continuing evolution of new races of pest and pathogens that are able to overcome resistance genes introduced by modern breeding. The Irish potato famine of the late 1840s is a dramatic example of the consequences of planting large areas to single, uniform crop cultivars, which led to devastating loss to the rural poor. Small-scale farmers in developing countries, who make up 45-60% of the world's rural dollar-poor, continue to depend on local crop genetic diversity and associated knowledge, in order to survive. For small scale farmers the use of a diversity of traditional crop varieties continues to be part of the disease management strategy in genetically diverse systems.

Most, if not all, known resistance to pests and pathogens in crops used in breeding programmes is derived from local varieties collected from farmers who traditional grow them in genetically diversity systems. Even so, the development of new cultivars grown as monocultures continues to be central to modern agriculture. Breeding programmes exist to develop new varieties and to replace varieties that have "lost" their resistance, but the maintenance cost of the current system is high. Moreover, these resistances may protect for only a few cropping seasons as new pathotypes or pest biotypes emerge. The inherent instability of this system, and thus risk for farmers, has led to a reliance on sequential generations of pesticides and a continuous need to purchase new varieties, usually within a three to five year period. Integrated Production and Pest Management (IPM) is a widely recognized ecosystem approach to crop production and protection. IPM strategies focus primarily on using agronomic management techniques to reduce pesticide use, modifying the environment around predominantly modern cultivars, using biotic control methods. Until recently IPM practices had made limited use of the intra-specific diversity of crop varieties within the farmers' production system to reduce pest and disease damage.

In 2002 a team of international and national partners from China, Ecuador, Morocco and Uganda, Bioversity International, FAO, and faculty from universities in the USA, Australia and Europe come together to discuss ideas on how traditional and modern crop varietal diversity could be used within crop production and pest management strategies to reduce current, and the potential for future, crop damage from pest and diseases. The discussions centred on building an approach to answer the strategic question "What is the probability that a crop population will be overcome by a new mutant pest or disease, or one migrating from a different area?" The premise was that a better understanding of the genetic vulnerability of a farmers' crop population to pest and disease attacks will allow farmers to prepare for, and therefore, to protect their food supply against the probability of future harvest losses. Crops were prioritized by the countries because of their importance for food security, their significance in national breeding programmes, and to ensure representation of different plant breeding systems. Pest and pathogens were selected only

if there was known variation for resistance in the host crop in the countries. Pathogen strains and pest biotypes were also documented to have a high level of diversity, both within a given area and from year to year.

The chapters in this volume are based on results from this research and development partnership which began in 2002, and now includes over 60 national and local government and non-government organizations in the four countries. The partners included agronomists, geneticists, plant breeders, economists, ecologists, pathologists, entomologists, and development organizations linked to FAO's Farmer Field Schools for farmer-to-farmer training in IPM to combine participatory diagnostic information with field observations and experimental trials. The inter-disciplinary teams collect standardized information from farmers on crop varietal diversity, sources of traditional and modern planting materials, and disease management practices that related to crop varietal diversity and implemented (i) field observations of disease incidence for all varieties, traditional and improved, (ii) on-farm and on-station trials and (iii) screen house trials, including, which now have the information and materials to use expand their IPM options to include traditional crop varieties.

A major component of the program was building capacity and leadership abilities of farming communities, Farmer Field Schools, local and national research, education and development agencies and their staff at local and national levels in four countries in the management and access to crop genetic resources to regulate pest and diseases. The program had a strong focus on ensuring gender equity at all levels from farmer training to promoting gender equity in the management teams of the countries.

The chapters include descriptions of the high levels of diversity found within the traditional varieties of a globally agreed set of staple crops for the specific pest and disease systems in the four countries (*maize*: northern leaf blight, Stem borer; *common bean*: ALS, Anthracnose, aphids, bean fly; *faba bean*: aphids, botrytis, bruchids; *banana and plantain*: black sigatoka, fusarium wilt, nematodes, weevils; *rice*: rice blast, rice hopper; *barley*: net blotch, powdery mildew).

The results from this work reveal that traditional crop varietal diversity is an important aspect of farmers' strategies for coping with pests and diseases. Increased diversity in farmers' fields, measured by the number (richness) and spatial distribution (evenness) of local and modern crop varieties was correlated with a decrease in damage levels as the intensity of pest and disease pressure increased. In addition, there was a consistent reduction in variance of damage levels as diversity increased. This gave a clear indication that some of the low-diversity (single variety) farms may have adequate crop yield if they happen to be growing a winning variety that year; if not, or if something in the system changes (markets, climate), then crop damage and yield on these farms is far worse than on more diverse farms. The results support what might be expected on a risk-management argument for diversity use to reduce pest and disease damage.

Cross-site on-farm experiments of traditional varieties with higher resistance to pest and diseases, when grown outside their home sites, have been identified and these potentially resistant varieties have already been taken up by both the local farming communities for their own experimentation and by the national breeders involved in this project for further analysis for use in crop varietal mixtures and crop improvement.

Damage, Diversity and Genetic Vulnerability: the Role of Crop Genetic Diversity in Agricultural Production Systems

Fadda, C.; Jarvis, D.I.; De Santis, P.

INTRODUCTION TO THE PROGRAMME OF WORK

Much of the 30% of the world's annual harvest lost to pests and diseases occurs in developing countries (Oerke et. al, 1994). The resulting economic and food resource costs are, to a significant extent, a consequence of crops growing in monocultures and the continuing evolution of new races of pests and pathogens that are able to overcome resistance genes introduced by modern breeding, creating the phenomenon of boom and bust cycles (Bourke, 1993; Wolfe and Finch, 1997; Singh et al., 2006). Breeding programmes exist to develop new varieties and to replace varieties that have lost their resistance, but the maintenance cost of the current system is high particularly for developing countries (Strange and Scott, 2005); the International Center for Wheat and Maize (CIMMYT) reportedly spent 35% of its budget in 1989 on "maintenance research". The inherent instability and thus risk for farmers leads to a reliance on various generations of pesticides.

The potential negative consequences of planting large areas to single, uniform crop cultivars were recognised as early as the 1930s by agricultural scientists (Marshall 1977). When farmers sow cultivated varieties with uniform resistance to a pest or disease, the crops can become susceptible to attack by pathogens able to overcome the resistance and epidemics can result. Susceptibility of five major commercial cultivars of banana to the fungal disease black sigatoka resulted in Central American countries losing nearly 47% of their banana yield (FAO, 1998). Rice blast epidemics in Korea in the 1970s caused 30-40% yield losses. Cassava mosaic virus causes annual yield losses of up to 40% in some parts of Africa, where many depend on cassava as an important nutritional resource (Otim-Nape and Thresh, 1998).

The agriculture research community has been constantly trying to reduce the incidence of the pests and diseases highlighted above. Integrated Pest Management (IPM) is a widely recognized ecosystem approach to crop production and protection that combines different management strategies and practices to grow healthy crops and minimize the use of pesticides with considerable success. Until recently IPM methods have concentrated on using agronomic techniques to modify the environment around predominantly modern cultures to reduce the need for pesticides, making limited use of the opportunities offered by the effective deployment of the intra-specific diversity of local crop varieties themselves, despite their importance for small-scale farmers and the role they play as a primary source for the new resistant germplasm. Local crop varieties provide about 39% of the resistant germplasm used in the breeding programmes of major crops such as maize, wheat, soybean, sorghum and barley (Duvick 1984).

Local crop genetic diversity, and the indigenous and other knowledge they have acquired to manage this diversity, is one of the few assets available to small-scale farmers in developing countries to meet their livelihood needs. These small-scale farmers in developing countries, who make up 45-60% of the world's rural dollar-poor (Lipton 2006), continue to depend for their survival on local crop genetic diversity and associated knowledge. Loss of genetic choices, reflected as loss of local crops or traditional crop varieties, diminishes farmers' capacities to cope with changes in pest and disease infestations, and leads to yield instability, food insecurity and loss, further exacerbating poverty. (Ostergard et al., 2009; Harlan, 1972; Thurston et al., 1999; Trutmann et al., 1996; Thinlay et al., 2000; Finckh, 2003; Mundt, 1991; de Vallavieille-Pope, 2004).

For small scale farmers the use of a diversity of traditional crop varieties continues to be part of the disease management strategy in genetically diverse systems (Jarvis et al., 2007). In many regions of the world, farmers have local preferences for growing mixtures of traditional and modern varieties, which they understand provides resistance to local pests and diseases and enhances yield stability (Trutmann et al., 1996; Thinlay et al. 2000). The main purpose of "genetic mixtures", or mixtures of varieties of the same crop, for pest and disease management is to slow down pest and pathogen spread. The basic principle that enables varietal mixtures to reduce the severity of disease was stated by Wolfe in 1985: "*Host mixtures may restrict the spread of disease considerably relative to the mean of their components, provided the components differ in their susceptibility.*" This is considered to be the mixture effect.

As people move around the globe with genetic resources, so does resistant and virulent germplasm. Resistance genes evolve in response to new pathogens and pests, as well as there being remnants of resistance from old diseases in other regions (Dinoor and Eshed 1997).

The global importance of this phenomenon led to a team of international and national partners from China, Ecuador, Morocco and Uganda to come together in 2002 to first discuss ideas on how traditional and modern crop varietal diversity could be used to reduce current -- and the potential for future -- crop damage from pest and diseases. Each of the four countries contains areas of important traditional varietal diversity for an agreed set of six target crops: rice (*Oryza sativa*), maize (*Zea mays*), barley (*Hordeum vulgare*), common bean (*Phaseolus vulgaris*), faba bean (*Vicia faba*), banana and plantain (*Musa* spp.) with each country containing different types of resistance to major pests and pathogens in their local crop varieties, maintained in traditional farming systems.

Each of the four countries has at least two of their target crops in common with one of the other countries, thus linking diversity of primary centres of diversity to secondary centres of diversity. Each country has poor small-scale farmers, who depend on the traditional varieties of these crops for their livelihoods.

The set of crops were agreed upon by the national partners so that they would represent different breeding systems (cross-pollinated, partially outcrossing, self-pollinated, clonal), as differences between varieties would be expected to be less prominent in cross-pollinated crops than in self-pollinated ones. Banana and plantain, as a result of their sterility, have followed a clonal crop improvement strategy, with farmers doing most of the selection breeding. Pest and pathogens cover those that are determined by major and minor genes (one gene or a complex of genes provide resistance), seed-borne, soil-borne and air-borne diseases, and pathogens or pests affecting different plant organs (aerial and roots). Furthermore, the life cycles of major pest and disease that affect these crops are well studied. In this way, the host/pest or host/pathogen system within this programme is representative of a much larger set of host/pest or host/pathogen interactions, allowing for scaling up to other similar crops and host/pest systems.

Three years of project implementation based on these premises have resulted in the collection of important information on farmers' knowledge on diversity of crops, diversity of pests and pathogens, resistance of different varieties and seed flows. This information was complemented

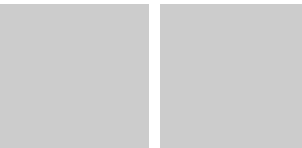
with experiments conducted on-farm, on-station and in glasshouse. In addition, economic data were collected under the damage abatement framework model, i.e. how relevant is diversity to reducing crop damage and under the choice experiment approach to estimating the value farmers give to resistance to pests and diseases and diversity in relation to other important traits.

The answers, or part of the answers, to these questions will come from a symposium divided into eight Sections, which step by step will go towards a more integrated understanding of the data collected during the life of the project. Session 1 focuses on diversity and field resistance, comparing diversity and damage at household levels. Session 2 presents data from on-farm and on-station trials to understand variation in host resistance. We ask the question: How do the traditional varieties that farmers grow differ in their resistance to pests and diseases? Session 3 examines variation in pathogen and pest biotypes. Is there variation in virulence and aggressiveness for the target pests and diseases? Do we find differences in wetter or drier years; have we seen changes overtime as rainfall is becomes less predictable? Session 4 reviews the results of glasshouse experiments to measure genetic vulnerability of the host populations. Can we compare crop populations across sites and say that some populations probably have less diversity than others and that migrations of new pathogens or mutations of existing pathogens will damage the crop?

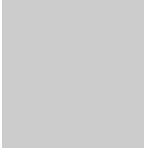
Sessions 5 and 6 examine farmers' management methods and choices in how they use crop varietal diversity to reduce damage from pests and diseases. What is the evidence that farmers are already making decisions about using crop variety diversity specifically to cope with pests and diseases? How does the way farmers obtain their seeds and planting material affect their use of diversity to manage pests and diseases? The last two Sessions, 7 and 8, examine where we are in our understanding of the advantages of using crop genetic diversity to reduce pest and disease damage and genetic vulnerability, and how this information is relevant for informing policy makers to put in place regulations that promote the use of crop genetic diversity as a tool for reducing poverty and enhancing ecosystem resilience.



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 1



Diversity and Field Resistance: Comparing crop varietal diversity (evenness and richness) to damage indices (FGD, Household Surveys and Option 1)

Introduction: Linking Diversity and Field Resistance

Jarvis, DI; De Santis, P.; Colangelo, P.; Murray, T.

INDIVIDUAL INTERVIEW FORM

I. Farm mapping showing spatial distribution of varieties among and within plots.

Interviewer asks: “We would like to understand the distribution of varieties among and within plots”

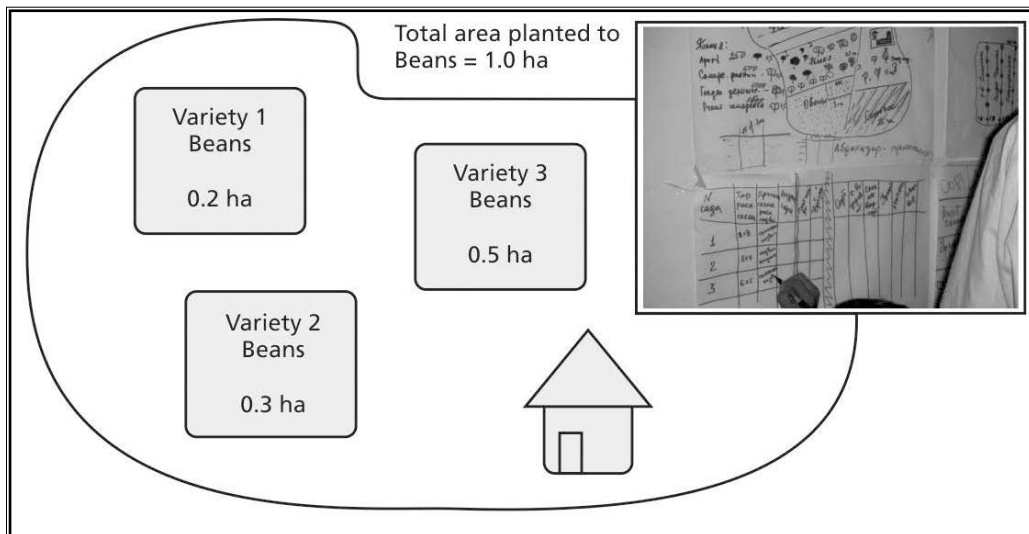
The interviewer then asks the farmer to draw a farm map showing: a) boundaries and area of his/her land, and marking this according to how he/she divides the farm into plots (write the plot name or label if applicable).

The interviewer then asks the farmer to give: a) total area of his/her farm (write this on the top part of the map), and b) area of each plot (write inside each box representing the plot).

Then the interview asked the farmer to identify for each plot/field the crop/s planted for the current season -- labelled by name, symbol and/or divided into sub-plots.

Then for each target crop of the project grown at this site, the interviewer ask the farmer what varieties of each target crop are grown for each plot/sub-plot, and the interviewer+farmer labels the each plot with the names the varieties.

Example of MAP drawn with farmers:



II. Overall guidelines for farmer field disease and pest evaluation

The following describes the steps involved in conducting disease and pest evaluations for on-farm surveys that are attached to the household survey of all 60 farms interviewed per site. The purpose of these procedures is to obtain objective observations of the severity of project diseases and pests for each variety the farmer is growing by collecting the observations in such a way that they are representative of each farm.

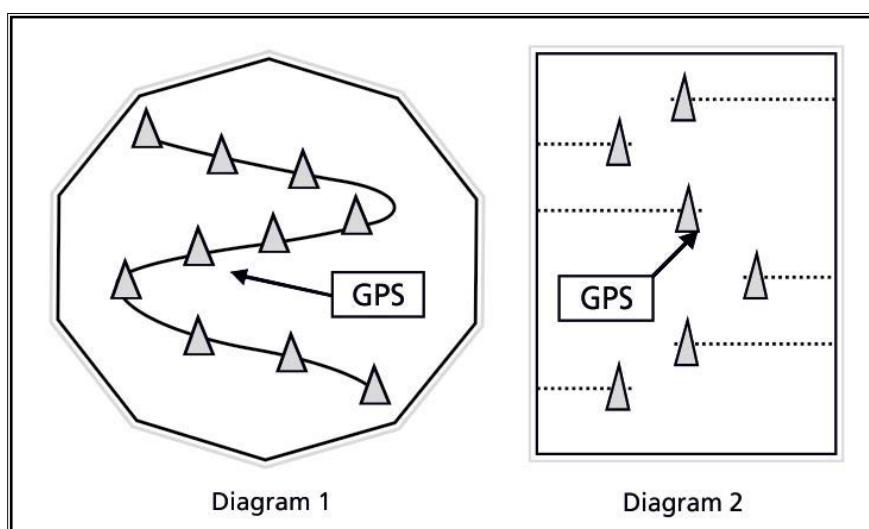
For each variety the farmer grows give a score for each project target disease or pest. The score for each variety will be the average of 30 observations and each score should be for one or more individual plants

Step 1. Take the map of the farmer's field you drew with the farmer during the HH survey for the location of each plot and the varieties grown in each plot.

Step 2. Go to each plot where the target crop is planted and note differences in shape of the plot and changes in elevation across the plot. Draw a larger picture of each plot which you will use to mark disease or pest severity ratings

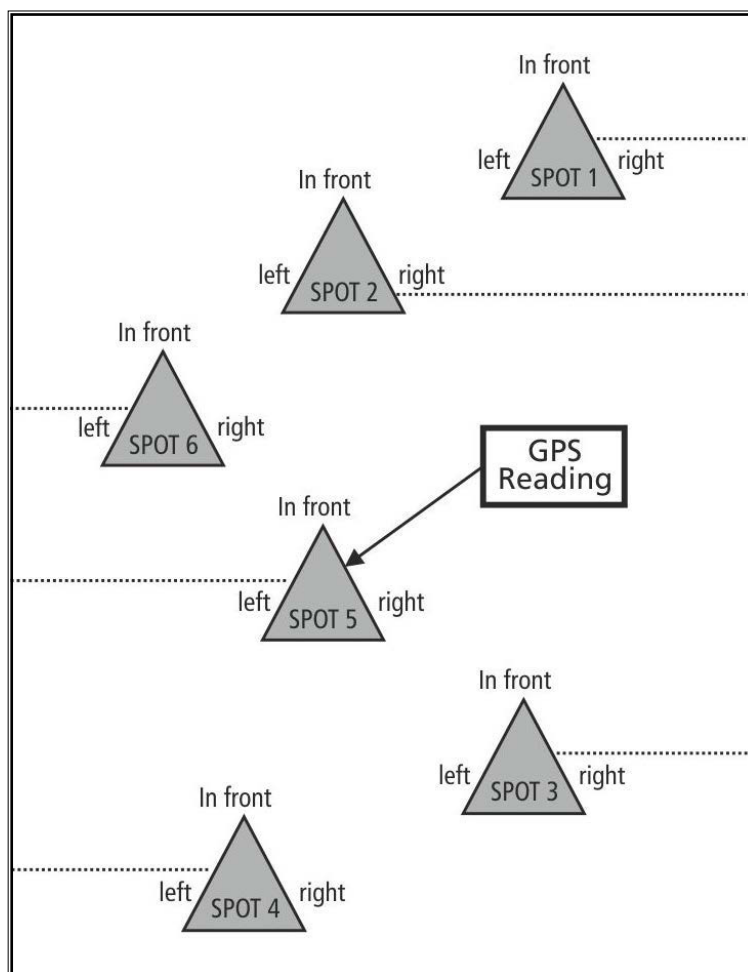
If the variety is growing in several plots, then rate the variety in as many distinct plots as possible. If all plots cannot be rated, then rate as many as possible and select plots that are farther apart or at different elevations on the same farm over plots that are closer to each other. The purpose is to allow you to have a total of 10 spots or 30 observations per variety that cover the variability of the different plots planted to the same variety.

Step 3. Pick a starting point for each plot and walk in a zig-zag path from one end of the plot to the other covering the whole planting of that variety, crossing different rows, avoiding the edge, and from high to low elevation, as shown in the Diagram 1 below. If walking zig-zag through the field will cause too much damage to the crop, walk into the plot at different points along the plot as shown in Diagram 2.



Step 4. Stop at 10 spots along this path (or if the variety is grown in three plots, you may make three stops in one plot, three stops in another plot, and four stops in the third plot). Larger plots will have more steps between each spot and smaller plots will have fewer steps.

Step 5. At each stopping spot make three observations: one to the left, one to the right, and one straight-ahead. Write these observations on your drawing of the plot. Rate one or more plants in each of these areas using the rating scale provided for the target disease or pest. Take a GPS reading when you are in the middle of each plot.



If varieties are grown in a mixture, then each mixture should have 30 observations.

- Use the map you drew with the farmer to locate plots with mixtures.
- The map should have names of the varieties in the mixture; if not, add them to the map.

- Check also with the farmer if the proportions of the different varieties they gave you earlier are correct. You might see differences in a plot that a farmer has said has only one variety (or drawn only one variety on the earlier map), ask the farmer whether the different height of plants or different looking plants within the plot are different varieties. If so ask the farmer to tell you what proportion of the seeds are of each variety, and go back and modify the original plot map in the survey (See Section III below for an example).
- If possible, record the disease or pest rating separately for each variety in the mixture for a total of 30 observations. For example, disease score for short + disease score for tall = 30 total, but you might have 10 of the short and 20 of tall or 15 of short and 15 of tall.

EXAMPLE: Ratings for Disease incidence

Variety Name _____

EXAMPLE:

- 0 No disease
- 1 Low: 10% or below
- 2 Medium: 10-25%;
- 3 High > 25%

Observation	Spot	Disease/Pest Incidence rating				GPS reading <i>(1 only at center of each plot)</i>
		Disease/ Pest 1	Disease/ Pest 2	Disease/ Pest 3	Disease/ Pest 4	
01	Spot 1 - right					
02	Spot 1 - left					
03	Spot 1 -in front					
04	Spot 2 - right					
05	Spot 2 - left					
06	Spot 2 - in front					
...	...					
...					
...					
028	Spot 10 - right					
029	Spot 10 - left					
030	Spot 10 - in front					

III. Combining household interviews with field observation to have a more accurate determination of diversity in farmers' fields.

The case of barley in China of where varieties are grown in mixtures and which may be applicable for common beans, and other varieties grown in mixtures.

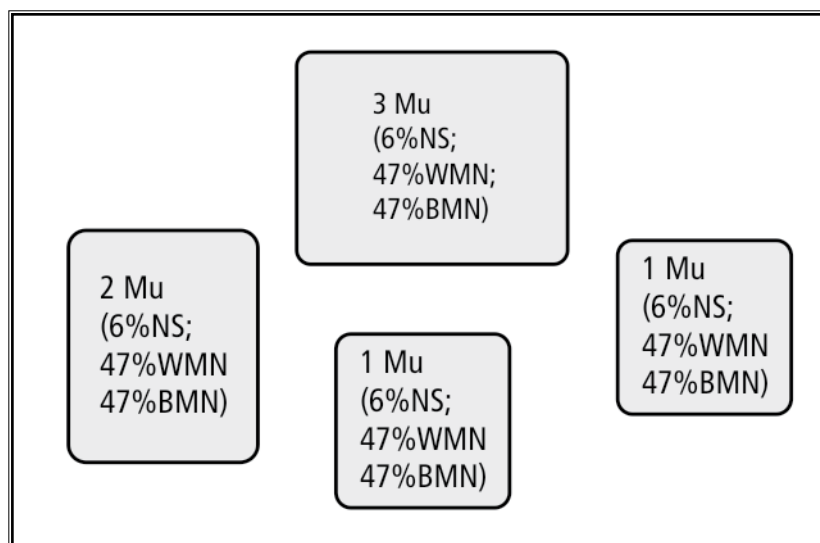
During the FGD farmers brought five different barley varieties to the meeting and described each of them. Yet, during the individual household survey most farmers in the village stated that they were only growing one barley variety, the MaNai variety.

The household survey was followed directly after by field observation for pest and disease incidence (OPTION 1). As the interviewers walked through the farmer plots, they noted from different plant height and morphology that the farmer's plot seemed to have at least more than one variety grown in the Ma Nai variety field.

When the farmer was asked about whether there was more than one variety in her field she said that the MaNai variety always contains some Nai Shu.

The interviewers then asked, whether the Nai Shu variety covered up to 10% of the field and the farmer was very precise in telling the interviewer that there was not 10% of Nai Shu, but only 6 to 7% of Nai Shu in the plot. The farmer then mentioned that in addition to Nai Shu, the variety Ma Nai was really two varieties, White Ma Nai and Black Ma Nai, and that you could only see the difference of the Ma Nai varieties closer to harvest. The farmer also told the interviewers that the Ma Nai contained 50% white MaNai and 50% black MaNai.

When asked if she separated the seeds for planting, she told the interviewer that the seeds of the three varieties were mixed together and used for all her four plots, whose total area was 7 mu (1 mu =1/12 Ha) – see drawing below.



The interviewers also checked to see if the grain seeds were separated for any different uses, but found that they were managed together, and in making the local food of roasted barely they were also eaten together.

The result of the household survey combined with the walk through the farmer's field, and the fact that at the FGD the interviewer had background information on the portfolio of local barely varieties for the community allowed the interviewers to have a much more accurate picture of the barley diversity in the farmer's field.

Thus richness of barley (number of varieties) was three (Nai Shu, White Ma Nai, Black Ma Nai) instead of only one, and evenness calculations could be made based on the mixture of varieties in her four plots as follows: 6 % Nai Shu; 47% White; Ma Nai; 47% Black Ma Nai.

$$\text{RICHNESS} = 3$$

$$\text{EVENNESS} = 1 - [(.06)^2 + (0.47\%)^2 + (0.47)^2] = 0.524$$

Had the interviewer only considered one variety as the farmer first stated without deeper investigation we would have had a Richness of 1 and Evenness of 0 for this farmer.

IV. Calculating damage: Household damage indices

Several years ago the large chemical companies in the US and EU, were trying to standardize and perform a mega-analysis across plots and locations on pest and disease damage which would require a standardized plot information for disease rating. This led to a 0 to 100 scale rating, which up until that point, included incidence (percentage of plants affected or branches, or leaves) and severity. These two pieces of information are then combined to come up with a damage index.

For example, if we have a 0-5 rating scale for severity and a 0-100 scale for incidence, we multiply them together, e.g., we multiply incidence by severity $(30/2)/5$ – so everything is on a 0 to 100 scale.

Second, we have to use the average severity of the affected plants only. For example, 10 plants have severity ratings for individual plants, only three of those plants are affected, therefore incidence = $3/10$, and the average severity scale 0-3 scale (rating 1 on plant 1, 2 on plant 2, and 3 on plant 3) = $(1+2+3)/3 = 2$ the average severity rating for the diseased plants, then multiply $2 \times$ percentage of plants affected $(3/10 = 30\%) = 0.6$. Then 30% (incidence) \times average severity $((1+2+3)/3=2)/$ divided by the total range of the scale (3): $(30\% \times 2)/3 = 20\%$ damage index. These then have to be weighed by the percent area covered for each variety at the household level to arrive at a weighted Household Damage Index.

Relating crop damage levels on-farm to crop varietal diversity measured by richness, evenness and diversity for rice in China and maize in Sichuan (Options 1-2)

Wu Shuo; Yang Xue Hui; Peng Hua Xian.

Name of country and sites

Rice sites are Yuan Yang, Shi Lin and Xi Shuang Ban Na in Yuan Nan, Mei Tan in Gui Zhou, She Hong in Sichuan, P. R. China.

INTRODUCTION

The project was carried out in Yunnan, Gui Zhou and Sichuan from 2008-2010. The three provinces are all in southwest China. The three provinces border each other. They are characterized by mountainous, hilly and flat lands. Agriculture is the main activity and source of income for most farmers. Grain production is mainly for subsistence. Rice, wheat and maize are the important staples, followed by legumes (bean and pea), vegetables, tobacco, tea, sugar cane, etc. Rice is the one of the important crops in the three provinces.

METHODS

1. Household (HH) and Focus Group Discussion (FGD) surveys

There are five rice sites in China. They are Shi Lin, Yuan Yang, Ban Na in Yun Nan Province, Mei Tan in Gui Zhou Province, She Hong in Sichuan Province. There is one maize site in Zhao Jue of Sichuan. Sixty households (HH) were randomly selected for survey from each site. The five FGD groups, including groups of leaders, old men, young men, old women, young women, were selected for the survey in each site. Ten people in each group were surveyed. All of the HH and FGD survey questionnaires were based on expert discussions.

2. Sampling method for panicle blast

A Z-shaped path was used for rapid assessment in rice fields. Thirty observations were made per variety per household, with three hills observed in each of ten locations.

The grading standard of rice blast (panicle blast) in the fields was as follows:

Grade	Severity	Standard
0	0	no symptoms
1	light	disease percentage <10%
2	middle	disease percentage 10%-25%
3	high	disease percentage >25%

3. Sampling method for maize NLB

A Z-shaped path was used for rapid assessment in the field. Thirty observations were made per variety in each household. Three plants were observed per location using four leaves under the female ear/plant.

RESULTS

RICE

1. Households and varieties

Site	Household	Variety (modern / landrace)	Landrace	Modern variety
Yuan Yang	60	28	19	9
Shi Lin	60	20	2	18
Xi Shuang Ban Na	77	20	18	2
Mei Tan	60	23	8	15
She Hong	60	39	8	31
Total	317	130	55	75

2. Rice Pests/Diseases in Five Rice Sites

In total, 44 pests/diseases were identified from five sites. The identified pest/disease varied from site to site. The important pests/diseases are rice blast, rice false smut, rice plant hopper, rice sheath blight and rice stem borer in the five sites. Rice blast and rice plant hopper were named the two most important pests and diseases by both farmers and scientists/technicians.

3. The relation of richness and disease percentage of rice blast (panicle blast)

Figure 1 shows that while richness is for 3 (three varieties), the disease percentage was under 2%, and the crop damage levels on farm was low. With richness of 2 (two varieties), the disease percentage was from 0 ~ 7%. With richness of 1 (only one variety), the disease percentage was from 0 ~ 12%, and the crop damage levels on farm is high. Therefore, the disease percentage

decreases with increasing richness. In effect, crop varietal diversity can decrease damage of the panicle blast.

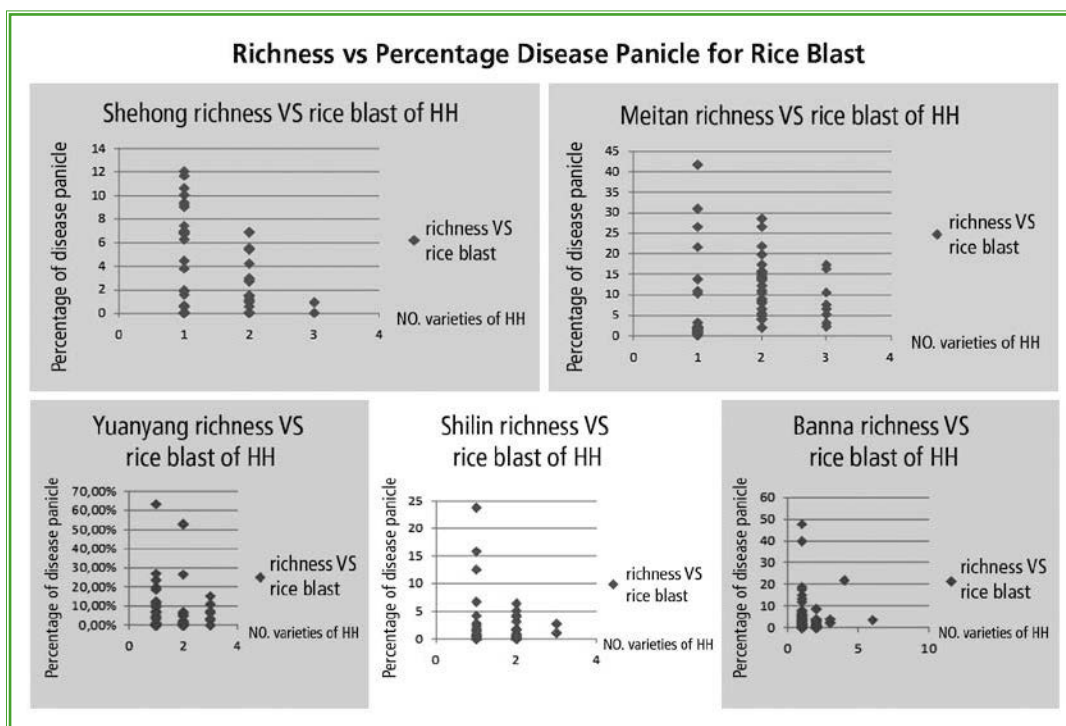


Figure 1 Richness vs percentage of disease panicle for rice blast

4. The relation of evenness (Simpson) and disease percentage of rice blast (panicle blast)

With increasing evenness, rice blast decreased. The result showed that variety evenness must be high to effectively control the occurrence of pest/disease.

MAIZE

1. Households and varieties

In the maize site of Zhao Jue, 60 HH were surveyed and 22 varieties were obtained, consisting of 8 landraces and 14 modern varieties.

2. Rice pests/diseases in the maize Site

In total, 14 pests/diseases were identified in the site. The identified pest/disease varied by year. The normal pests/diseases are maize rust, NLB, smut, maize borer, armyworm and grub.

Maize rust and NLB and maize borer were the most important pests and diseases in the farmers' fields.

3. The relation of richness/evenness (Simpson) and weighted disease index of NLB

With richness of 4 (four varieties), the maximum weighted disease index of NLB is 30 and the crop damage levels on farm is low. With richness of 3 (three varieties), the maximum is 40. With richness of 2 (two varieties), the maximum is 80. Finally, with richness of 1 (only one variety), the maximum is 100% and the crop damage level on-farm is high. In effect, crop varietal diversity can decrease damage of the maize NLB with increasing richness. Under increasing evenness, NLB disease decreased. The result show that when variety evenness is high, it is effective at controlling maize NLB's occurrence.

DISCUSSION

In general, the trial showed that variety richness/evenness is high and very effective in reducing damage from disease. But most of farmers only planted one or two varieties in their fields, especially for rice in She Hong. For maize in Zhao Jue, where many farmers planted 3-4 varieties in the fields, better results were obtained than for rice in She Hong.

ACKNOWLEDGMENTS: Thanks to participating farmers, project partners, Bioversity and UNEP/GEF. We wish to thank UNEP/GEF for its financial support to the project.

Participatory diagnosis of crop genetic diversity to reduce pests and diseases on-farm in common bean in Cotacachi, Ecuador

Pazmiño, J.; Ochoa, J.B.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L) associated with maize is an important component of the agro ecosystems of the highland valleys of Ecuador. Common bean cultivation is additionally characterized by high intraspecific diversity of two main types: allpas (growth habit III) and chakras (growth habit IV). The genetic variation of these common bean types appears associated with the balance of the agro ecosystem avoiding the negative impact of biotic and abiotic stresses.

Pests and diseases are important biotic stresses that can cause serious crop losses. Crop diversity might be a key factor in reducing these losses. Diversity, pests and diseases have been interacting in the agro-ecosystem for millennia, with farmers shaping these interactions. Therefore, farmer knowledge about diversity is important for enabling better understanding of the biological aspects of interactions, but also for identifying strategies for strengthening farmers in conservation initiatives. A Participatory Diagnostic (PD) process was implemented in Cotacachi to study common bean diversity associated with pests and diseases.

PD was designed not only to characterize farmer knowledge and to learn from farmers, but also to identify problems, needs and opportunities that will be addressed in future interventions in the communities.

METHODS

PD was designed to be implemented in two steps, the Focal Group Discussion (FGD) and Individual Interviews (II). For FGDs farmers were asked to bring samples of their crop variability as well as samples of diseases. With these materials a friendly discussion was established among farmers and organizers. During FGDs, facilitators were guided by a list of key questions. To obtain natural and spontaneous answers from farmers, a comfortable, friendly and relaxed atmosphere was created. A bilingual rapporteur speaking Qechua was necessary to have better communication and because some of the participants did not communicate well in Spanish, especially old men.

Eight topics were addressed by the FGDs: 1) landrace diversity at village level; 2) farmers' knowledge of pests and diseases; 3) assessment of resistance of varieties, 4) practices that use intra-specific diversity, 5) seed sources, 6) seed storage and seed cleaning, and 7) practices they recommend or they don't recommend. Additional information considered important and related to the subjects were also addressed.

Individual interviews were organized in farmers' fields to further analyze the information and quantify knowledge obtained in FGDs. Sixty farmers were randomly selected in Cotacachi through a questionnaire developed through FGDs.

RESULTS AND DISCUSSION

The contributions of young and old women on most of the FGDs was very valuable. Their knowledge of variability, pests and diseases, cultural practices and pest management was solid and analytic. This is due to the full involvement of women in farming activities, as men regularly leave the community to work in the city.

Two different types of common bean called allpa and chakra were clearly distinguished in Cotacachi. Within each of these types a remarkable morphological variation exists, suggesting that these types are very variable populations. These populations in addition appear diverse among communities and farms. During FGDs, farmers were partially able to distinguish or identify populations within the mixtures they grow. They only identified the type (allpa or chakra) to which the population belonged, showing little interest in, or perhaps lack of knowledge of, the specific identity. However, during individual interviews and especially in school seed fairs, farmers were able to name every single individual population of the mixture, and even the modern varieties that have been introduced to the mixture. Around 67 different populations (phenotypes) were obtained in these events, but including mixtures from key farmers, the number increased to 104 populations.

The morphological traits regularly used by farmers to describe common bean varieties are: root size, growth habit, leaf size, color of the flower, size and shape of the pod and size of the plant, as well as grain test, earliness and resistance to diseases.

The main reasons given for conserving common bean diversity are mainly family custom (84%), conservation of diversity (35%), grain quality (29%) and grain similarities (24%). Some farmers explicitly mentioned conservation of biodiversity, which appeared to be influenced by conservation initiatives taking place in Cotacachi. Diversity conservation to avoid the negative effect of biotic or abiotic stresses was not mentioned; however, some farmers believed that local varieties adapt better to their environment than introduced varieties, which demand fertilization.

Farmer knowledge of pests and diseases is generally limited and does not regularly differentiate between biotic and abiotic stresses. Any foliar symptom is called "blight" and disease origin is generally associated with the climate, especially rain (43%). Additionally, they believe diseases come from neighbors (33%), pesticides (27%), or animals/man (23%). Plant transmission from diseased to healthy plants (66%) was also mentioned by farmers. Knowledge about disease transmission suggests that farmers are aware of some epidemiological aspects of diseases.

Farmers regularly plant their own seeds and seed flow is not an important aspect of common bean diversity. Farmers often share seeds with relatives, especially from father/mother to son/daughter. Modern varieties have been introduced to the mixture, but their frequency is low. Introduction of the modern varieties "TOA", "cargabello" and "mil uno" is most likely associated with farmer interest in increasing diversity.

After harvesting, 79 % of farmers first select the seed for the next season. Seed selection criteria are mainly healthy seed (77%), large seeds (57%), normal seed color (26%) and uniformity of the seed (23%). The rest of the grain is stored, but since it is for a short time, farmers do not regularly take any pest control measures (90%), but some use ash or store the grain over herbs (10%).

Pest and disease management is associated with cultural practices such as insect traps (85%), weeding (57%), manure application (57%), crop rotation (8%), crop association (2%) and chemical

fertilization (2%). The use of diversity to control pest and diseases was not explicitly mentioned. It might be because the contribution of diversity is not obvious in the field, as disease epidemics are regularly few. The low incidence of disease epidemics might be directly associated with resistance operating in the mixture, while the maintenance of susceptible populations might be due to other associated advantages.

Relating crop damage levels on-farm to crop varietal diversity measured by richness, evenness and diversity for common bean in Uganda

C. Kiwuka; J. W. Mulumba; J. Adokorach; R. Nankya.

INTRODUCTION

Small-scale farmers depend on local genetic diversity to ensure sustainable production systems and meet their livelihood needs. Loss of genetic choices as reflected by loss of traditional crop varieties diminishes farmers' capacities to cope with changes in pest and disease infection that leads to yield instability and loss (UNEP, 2010). The use of variety mixtures, multilines, or different varieties in the same production environment, has been found to reduce disease incidence and increase productivity without the need for pesticides (Hajjar *et al.*, 2007). Mixing crop species and/or varieties can delay the onset of diseases by reducing the spread of disease-carrying spores, and by making environmental conditions less favorable to the spread of certain pathogens (Altieri, 2004). This study was thus set out to assess the amount of common bean (*Phaseolus vulgaris*) diversity managed by farmers in three sites; Rubaya, Kabwohe, and Nakaseke and the level of damage on-farm as estimated from two *P.vulgaris* diseases (anthracnose and angular leaf spot) and one pest (bean fly). Following Jarvis *et al.* 2008, three measures (richness, evenness and divergence) were used to estimate the level of diversity maintained by the farmers in the study sites.

METHODS

Data on on-farm diversity and disease severity was collected through Focus Group Discussions (FGD) and household surveys. This paper is based on household survey data because FGD disease severity measures were full of unrealistic perceptions that limited the data analysis and interpretation. Following Jarvis and Campilan (2006), a total of 180 households and farms (60 households and farms from each study site) were purposely selected and the common bean diversity and disease severity on-farm were assessed by use of direct field observation and key informant interviews guided by structured and semi-structured questionnaires. The name and number of *P.vulgaris* varieties, their area of coverage and disease severity on-farm were recorded for each household.

Disease severity was estimated from 30 different points on a farmer's field by assessing three plants front, left and right. The plants were assessed basing on a scale of 1 for low, 2 for moderate and 3 for high severity. The diseases assessed were angular leaf spot (ALS) and anthracnose (ANT) and the pest was bean fly (BFY). The household and community weighted disease index (WDI) were estimated from the product of the disease index (at the plot level) and the frequency

of each variety present in the plot. The area planted with each variety was estimated by using local area measurements, converted to square meters and hectares. The area growing both modern and traditional varieties was noted to calculate the total area planted with the crop and the proportion of the farm-grown traditional varieties. Average farm richness was calculated as the average number of traditional varieties per household while total community richness was calculated by summing the number of distinct traditional varieties found across villages in the community. Following Magurran (2003), evenness was estimated as a complement of d ($1-D$), where D is the Simpson measure of dominance. Percentage divergence (the partition of diversity between and within farms) was calculated as the difference between community and farm index values divided by the community Simpson index (Jarvis *et al.*, 2008). The relationship between diversity measures and damage indices on-farm were estimated by correlation and regression analyses of richness and disease damage indices.

RESULTS

As presented in Table 1, the mean on-farm richness ranged from 2.42-2.45 while community variety richness ranged from 15 to 27 across sites. Although the mean number of varieties managed within and between communities did not differ significantly, the proportions in which these varieties were grown differed significantly ($0.01=p<0.05$). On-farm evenness was between 0.37 and 0.49 while community evenness was appreciably high, ranging from 0.74 to 0.86. Divergence as a measure of the possibility of any two randomly chosen households within the same community growing different varieties was quite impressive as it ranged from 33% to 56% across sites. The levels of damage on-farm were significantly different within and between communities ($p<0.05$). Table 2 shows that Kabwohe had higher disease damage indices than Rubaya while among the diseases; ALS had higher damage indices than ANT. Table 3 summarizes the relationships among the diversity estimates with the damage indices while Figs. 1-3 display these relationships. There were mostly negative but weak correlations among the diversity estimates and damage indices within and across sites. All the relationships were not statistically significant ($p>0.05$) and only 1% of the variation in all the relationships was explained ($R^2=1$). These relationships were based on data from two sites (Rubaya and Kabwohe) only because disease and pest severity data was not collected efficiently in Nakaseke. This also limited the analysis of the relationship among diversity measures and damage indices at community level.

DISCUSSION

This study was set out to assess the relationship among diversity on-farm and damage levels and the results clearly show that although farmers maintain a substantial amount of *P.vulgaris* diversity, there is probably need for proactive management practices that fully maximize its potential. The weak negative correlations among diversity measures and damage indices portray the hidden potential of the diversity in farmers' fields to control pests and diseases if arranged and managed efficiently. This is in context with Mundt (2002) and Wolfe (1985) in Hajjar *et al.*, 2007, who stated that a principal purpose of the use of genetic mixtures for disease management is to slow the pathogen's spread by slowing the rate and incidence of infection provided the components differ in their susceptibility. Mechanisms involved include: increasing the distance between susceptible cultivars; creating a physical barrier to spore dispersal; decreasing the proportion of susceptible plant tissue; overcoming selection pressure for pathogens to surmount valuable forms of disease resistance; increasing selection in host population for more competitive or more resistant genotypes; increasing competitive interactions among pathogen populations and inducing resistance

in the host for subsequent infection (de Vallavieille-Pope, 2004; Finckh *et al.*, 2000; Garrett and Mundt, 1999; Jarvis *et al.*, 2007a,b). When fully equipped with the resistant varieties from on-farm and on-station studies, there is hope that farmers' field management practices can be improved to optimize the potential of crop genetic diversity in reducing pest and disease damage.

Table 1. Household and community diversity estimates

Site	Mean Household richness	Mean Household evenness	Community richness	Community evenness	Divergence	
Rubaya	LM	2.42	0.39	25	0.86	0.54
	L	1.05	0.28	19	0.86	0.54
	M	1.37	0.21	-	-	-
Kabwohe	LM	2.45	0.37	27	0.84	0.56
	L	1.03	0.86	23	0.74	0.58
	M	1.4	0.51	-	-	-
Nakaseke	2.45	0.49	15	0.74	0.33	

$P > 0.05$ for richness and $P < 0.05$ for evenness

LM (Local and Modern varieties)

L (Local varieties)

M (Modern varieties)

- Missing data

Table 2. Household and community damage estimates

Site	Mean household damage indices		
	ALS	ANT	BFY
Rubaya	18.32	8.69	
Kabwohe	37.96	17.68	4.38
Nakaseke	-	-	-

$P < 0.05$

ALS (Angular leaf spot)

ANT (Anthracnose)

BFY (Bean Fly)

- Missing data

Table 3. Correlation coefficients for diversity measures and damage indices

Sites	Variables		Pearson's correlation, R		
	Dependent(Y)	Independent(X)	(L+M)	L	M
Rubaya	WDI ALS	HH richness	0.03	0.18	-0.07
	WDI ALS	HH evenness	0.01	0.18	-0.12
	WDI ANT	HH richness	-0.08	-0.20	- 0.08
	WDI ANT	HH evenness	-0.06	-0.18	0.05
	WDI BFY	HH richness	-	-	-
	WDI BFY	HH evenness	-	-	-
	Kabwohe	WDI ALS	HH richness	-0.13	-0.10
WDI ALS		HH evenness	-0.01	-0.05	0.02
WDI ANT		HH richness	-0.06	-0.05	-0.05
WDI ANT		HH evenness	-0.14	-0.02	-0.10
WDI BFY		HH richness	0.04	0.04	0.01
WDI BFY		HH evenness	-0.04	0.06	-0.07
Nakaseke	WDI ALS	HH richness	-	-	-
	WDI ALS	HH evenness	-	-	-
	WDI ANT	HH richness	-	-	-
	WDI ANT	HH evenness	-	-	-
	WDI BFY	HH richness	-	-	-
	WDI BFY	HH evenness	-	-	-

P>0.05

WDI (Weighted disease index)

ALS (Angular leaf spot)

ANT (Anthracnose)

BFY (Bean Fly)

HH (Household)

- Missing data

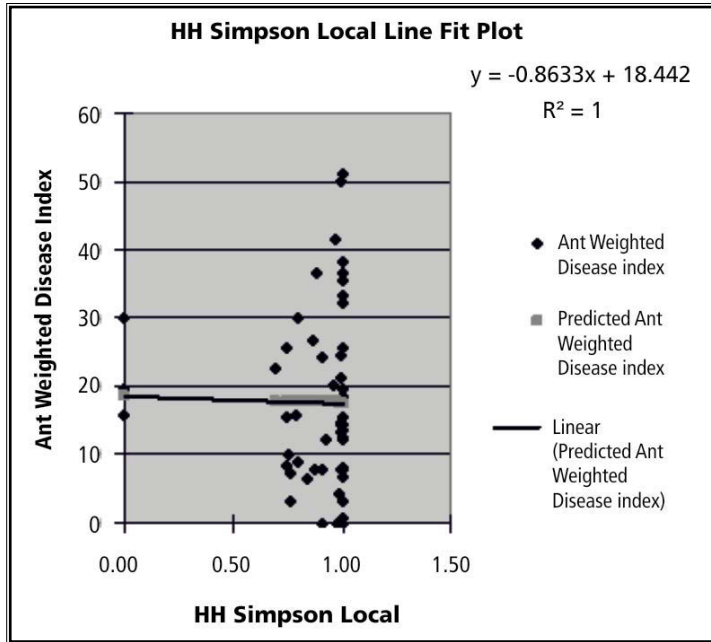


Fig.1 Relationship between evenness and damage levels by Anthracnose in Kabwohe

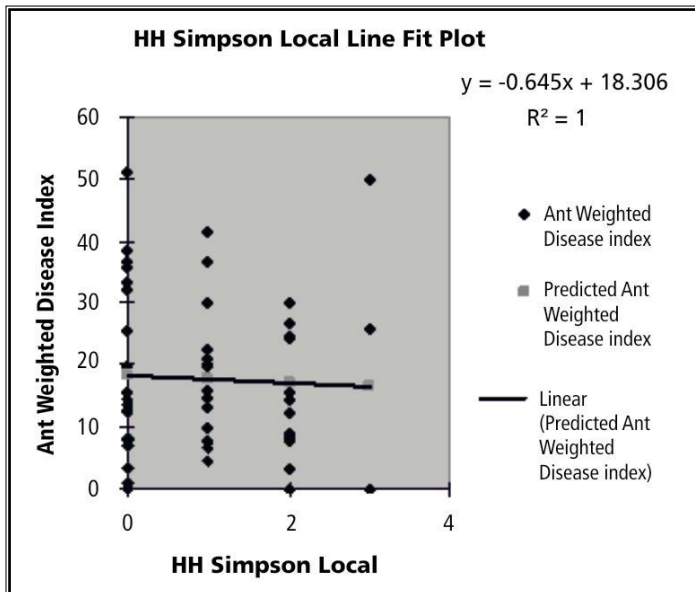


Fig.2 Relationship between richness of traditional varieties and damage levels by Anthracnose in Kabwohe

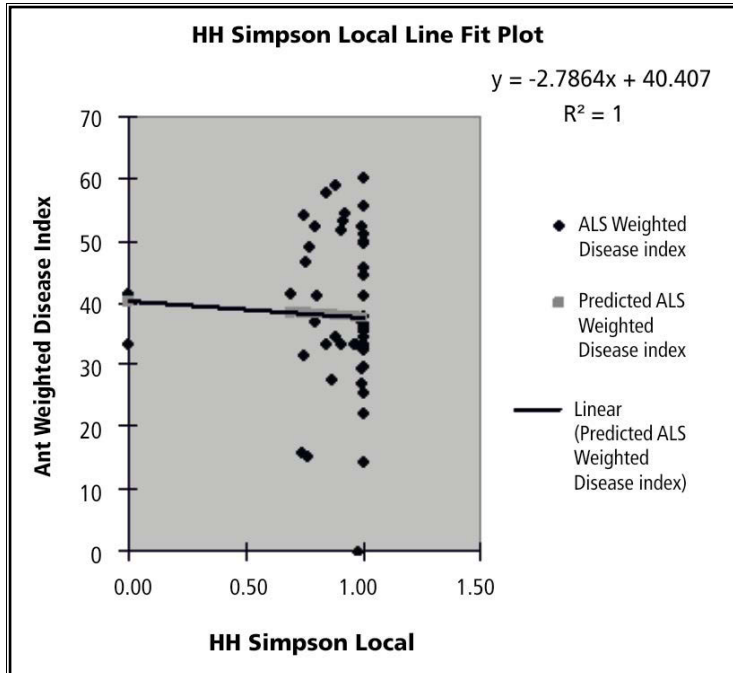


Fig.3 Relationship between evenness of traditional varieties and damage levels from angular leaf spot in Kabwohe

Faba bean and barley local varietal diversity in project sites in Morocco

L. Belqadi; B. Ezzahiri; Taoufiqi S.; M. Sadiki.

INTRODUCTION

Faba bean (*Vicia faba* L.) is the most important grain legume in Morocco, representing 50% of the 500,000 hectares annually planted to grain legumes. Barley covers more area than the other cereals (common and durum wheat). The two crops are complementary because the Moroccan farming systems are based on rotation legumes/cereals, particularly faba bean/barley in the Taounate region. For the two species, the cultivars currently used by the farmers are local populations that have been traditionally selected by farmers under different environmental conditions.

This study is aimed at presenting first the results of field characterization of phenotypic variation of faba bean and barley local accessions in relation to geographic origin in the Taounate region based on a set of traits. The second part of this presentation is focused on farmers' perception for the management of the genetic diversity of faba bean and barley in Taounate. Varietal composition of these crops was assessed in three sites (Ourtzagh, Galaz and Tissa).

MATERIAL AND METHODS

To characterize the phenotypic variation of these two species, an experiment was conducted at M'rissa experimental station in Larache. The plant material was sampled from local varieties of faba bean grown in the Taounate region.

For faba bean, the material was assessed for eight agromorphological traits and yield components. The experimental design is randomized complete block with two replicates. The traits measured are plant height, leaflet size, leaflet shape, pods/plant, grains/population, grain yield/plant, grain weight and grains per pod.

For barley, an experiment was conducted with 110 populations using randomized complete blocks with two replications. The traits measured are the important discriminatory criteria used by farmers: number of grains per ear, weight of 100 grains, number of rows/ear.

To appreciate farmers' perceptions in the management of the genetic diversity of faba bean and barley in Taounate, surveys were conducted with groups of farmers or individual farmers to collect information on their knowledge, practices, problems and needs. In these surveys of 173 farmers, the local varieties were listed, named and described by the farmers. Lists of different varieties of faba bean and barley were established for each site. Diversity indices were calculated to quantify the partition of the diversity in the region and within each site.

RESULTS

For Faba bean, the results of trials using univariate analysis (Table 1) showed the most discriminating traits and also revealed significant differences between local varieties. The hierarchical tree constructed on Euclidean distances revealed the groupings of the 13 varieties in six principal classes.

For barley, the results of the variance analysis of yield components (weight of 100 kernels and the number of rows) demonstrated that there is a significant difference among the populations for those criteria (Table 2). The multivariate analysis using a cluster method allowed the researchers to classify the populations in four different groups.

For faba bean, the data of the surveys conducted in order to understand farmers' perceptions in managing diversity to control pests and diseases demonstrated that the local cultivars are designated by names based on descriptors, which refer to distinctive phenotypic traits (seed color, size and number of seeds per pod). The results showed a comparable trend in the three sites. It is the variety Beldi Rbai which is dominant in the two sites of Ourtzagh and Galaz. The Tissa site has a variety composition different from the two other sites (Figure 1) -- more modern varieties were used. According to farmers, the use of modern varieties increases yield although they are not adapted to the region and are susceptible to diseases. The varietal richness and other indices of diversity were summarized in the graphs. The sites of Ourtzagh and Tissa present more of the diversity than Galaz Site.

For barley, the number of varieties used in the three communities is low. The Beldi variety is preponderant for the three sites. Two modern varieties are used by farmers in the three sites (Figure 2).

DISCUSSION

For both species, local populations contain a large variability for the traits studied. Across all farmers cultivating faba bean and barley currently and over the 10 last years, faba bean has the largest varietal diversity. In terms of faba bean, farmers are satisfied with the performance of the local varieties (Beldi), their resistance to biotic stresses, their adaptation to this region and their low capacity to change the seeds.

For barley, the variety naming system underestimates genetic diversity. The name of the variety indicates a large unit which is highly heterogeneous and expresses a large diversity between populations. Thus it is important to go beyond the actual farmers' naming system for more precise assessment of genetic diversity

Table 1: Results of univariate analysis of means of traits studied in faba bean

Trait (Faba bean)	Source of variation	df	Mean squares	F	Significance
Plant height	Variety	12	572,262	8,572	0,000
Leaflet Size	Variety	12	1,915	4,524	0,000
Leaflet shape	Variety	12	,500	3,370	0,000
No. of pods/plant	Variety	12	374,402	24,765	0,000
Grain yield/plant	Variety	12	663,230	3,220	0,000
Grain weight	Variety	12	0,962	2,304	0,008
Grains /pod	Variety	12	10,424	6,637	0,000

Table 2: Results of univariate analysis of means of traits studied in barley

Trait barley	Variation source	F	Significance
Number of grains/ear	Population	1,355	0,57
	Error		
	Total		
Weight of 100 grains	Population	1,550	0,11
	Error		
	Total		
Two rows	Population	1,413	0,36
	Error		
	Total		
Six rows	Population	1,413	0,36
	Error		
	Total		

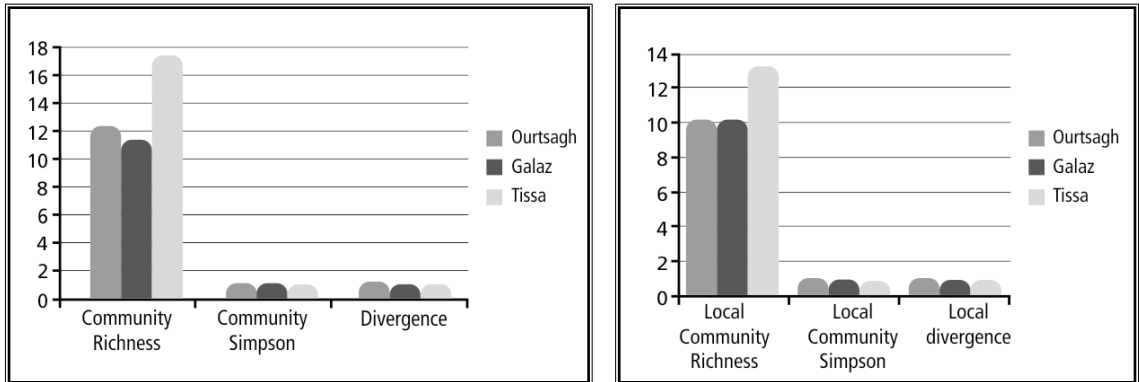


Figure 1: The varietal richness and other indices of diversity in faba bean

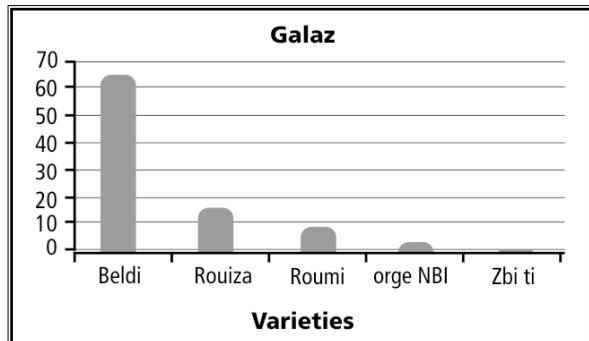
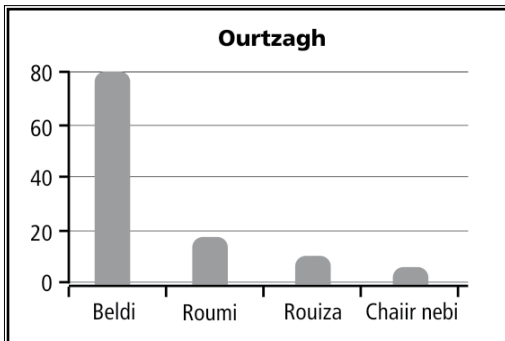
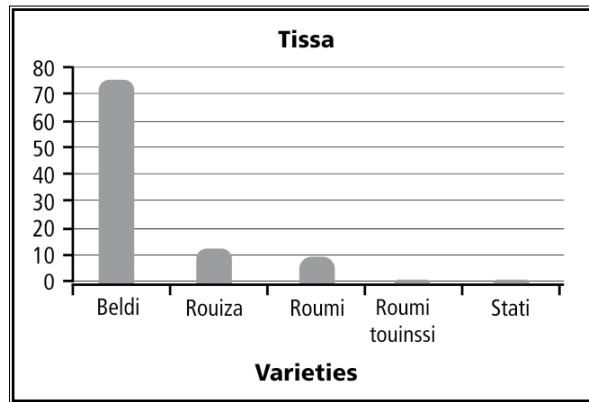


Figure 2: The profile varietal of barley in the three communities

Damage, diversity and genetic vulnerability: the role of crop genetic diversity in agricultural production systems

He Yuhua; Bao Shiyong; Wang Liping; Lv Meiyuan; Yang Feng; Zheng Aiqing; Zhou Picao; Sun Yonghai; Tie Chaoliang.

INTRODUCTION

Yunnan has the largest area of cultivation of faba bean in China, with the area in the range $2 \times 10^5 \sim 3.3 \times 10^5$ ha each year. Over 80% of the area is distributed in the lowland plains, with the remainder in mountainous regions in the west and north of the province. Faba bean is planted after the rice crop is harvested in autumn (October) and is harvested at the end of April. Faba beans are planted by one of two methods: "rice field planting" and "dry land planting". In the plains, where Maichang village is located, faba beans are planted by the first method. After the rice has been harvested, the fields are soft and the soil has a high moisture content, and people are able to press the seeds into fields directly by hand with no need to plough. This is regarded as the best way of planting for faba bean production in China. However, over 70% of the area of Yunnan is mountainous, including Zhongben village, where farmers need to plough the dry land prior to planting faba bean. There are also some rice fields in the mountainous regions where "rice field planting" is used.

Two villages, Maichang and Zhongben, that represented the two major environments and production systems in Yunnan were surveyed to determine the level of diversity of crop species and faba bean varieties in the two systems. Xundian County, where Maichang village is located, lies in the north-east of Yunnan. The rate of education is over 98.5%, the forested area is 41.63%, total cultivable area 3.3×10^4 ha, and faba bean area $4 \sim 5 \times 10^3$ ha. Maichang village is at an elevation of 1750m, annual average temperature 14.5 C, annual precipitation 1100mm, total cultivable area 300 ha and faba bean area over 200 Ha. The major crops in the village are rice, maize and tobacco (summer) and faba bean, wheat and rape (winter). Lucheng town, where Zhongben village is located, lies to the west of Yunnan. The rate of education is over 95%, the forested area is 46.3%, total cultivable area 2212 Ha and faba bean area 1881 ha. Zhongben village is at an elevation of 1800m, annual average temperature 15.7 C, annual precipitation 860mm, total cultivable area 146 ha and faba bean area ~ 100 ha. Maize and rice are the main crops in summer and faba bean is the main crop in winter.

METHODS

FGD: Five groups were identified for the FGD in each village; young males (20~40 years old), young females (20~40 years old), old males (over 50 years old), old females (over 50 years old) and village leaders (all ages and both sex). Each of the five groups was composed of 10 respondents and three investigators and represented the 569 households in Zhongben village and

887 households in Maichang village. Respondents provided faba bean samples at the time of answering the survey. The FGD survey obtained information on the number of faba bean varieties, agronomic characters, pests and diseases in the crops, resistance of the varieties and seed source. There were only seven faba bean varieties in Zhongben village, and ten varieties in Maichang village. It was difficult to find young males to join in the FGD, because most people in this group are employed off-farm. This is a serious problem in villages in Yunnan, especially in the mountainous areas, where farmers find it difficult to make a living in the fields.

HH survey

Prior to undertaking this work, it was necessary to determine how many households plant faba bean in each village per year. Based on this number and according to a sampling rate of 10%, 63 households were selected at random to visit in Zhongben village and 66 households in Maichang village. Each selected household was visited and the survey, which took about 10-20 minutes to complete, obtained more specific information than in the FGD, including the varieties, resistance, pest and disease, fertilizer and pesticides, methods for seed storage, and seeds source. Respondents from Zhongben village reported 24 faba bean varieties, five diseases (rust, chocolate spot, root rot, Fusarium wilt, powdery mildew) and three pests (aphids, leaf-miner, weevil), while in Maichang village there were 14 faba bean varieties, three pests (aphids, leaf-miner, weevil) and four diseases (rust, root rot, Fusarium wilt, chocolate spot). After completing the questionnaire, each farmer's faba bean fields were surveyed for pests and diseases. Each field was surveyed at ten points with three plants sampled at each point to give 30 plants sampled per field. This survey was undertaken in late February when faba beans were at the flowering and early podding stages. Two months later, at harvest time, seeds were collected from the surveyed households and these seeds were sown in the middle of October at Zhongben and Maichang villages to enable comparison between varieties collected at each location. These varieties were sown at each site arranged as four replications, with one row (25 plants) of each variety per replicate. Although some data was collected from the 100 plants per variety, there was very severe drought and frosts in Yunnan from Sep 2009 until Sep 2010 and many plants senesced prematurely during early flowering so yield data was not available.

RESULTS

Overall Estimates of Diversity

Fourteen varieties were surveyed in Maichang village and 24 varieties were surveyed in Zhongben village. Traditional varieties dominated the faba bean crops at both locations with 78.6% of crops sown with traditional varieties in Maichang village and 75% in Zhongben village. The average Simpson index was high at both locations (0.85 and 0.88), but at the farm level, it did not differ significantly for diversity (Simpson index was 0.06 and 0.04). At the community level, there were significant differences in both the number of varieties (see above) and total area (Maichang was 107586 m², Zhongben was 87418 m²). Although Maichang's total area sown to faba beans was much more than Zhongben, there were many more varieties grown at Zhongben.

Relationships between pest, disease index and diversity of varieties

Rust, aphids and weevil were surveyed at the two sites. Farmers were readily able to recognize aphids, rust and chocolate spot and at Zhongben over 84% farmers could detail their characteristics (symptoms, damage) correctly, and over 70% farmers could detail characteristics of aphids

and rust at Maichang. The relationships between pests, diseases and Simpson index in Zhongben site are presented in Figures 1-3. Only aphid damage level shows a decline. Maichang site has the same linearity (R^2) trend, R^2 is rust, aphids and weevil.

DISCUSSION

Overall Diversities

The majority of households at each location grew a single faba bean variety, however two varieties were grown by some households (15.8% at Maichang and 12% at Zhongben). No household grew more than two varieties. The relatively high number of faba bean varieties grown at each village but the low number of farms that grew more than one variety resulted in a higher Simpson index at the community level, but a lower richness and evenness at the farmer level.

Pest, disease index and varieties diversity

Normally, farmers do not control rust with pesticides in Yunnan when they plant faba bean. In the two sites, they control it with plant improved varieties (44%), crop rotation (41%) or spacing density (36%). In Maichang site, these figures are 42%, 48% and 23%. In Zhongben site, these methods cannot control rust very well, because the Rust index is 99.7% in Maichang site, 75% in Zhongben. However, the rust index is lower in Zhongben because of the presence of more varieties than in Maichang site. As to the aphids and weevil, we did not find any varieties for pest resistance in the two sites, although there is a lower pest index (aphids: 51% and 50%, weevil: 40% and 38%). In the Maichang and Zhongben sites, there is a lower pest index, with the use of pesticides (from 927~2450g/ha) given as the main reason. Moreover, Zhongben site has a lower pest and disease index than Maichang site because of the number of varieties.

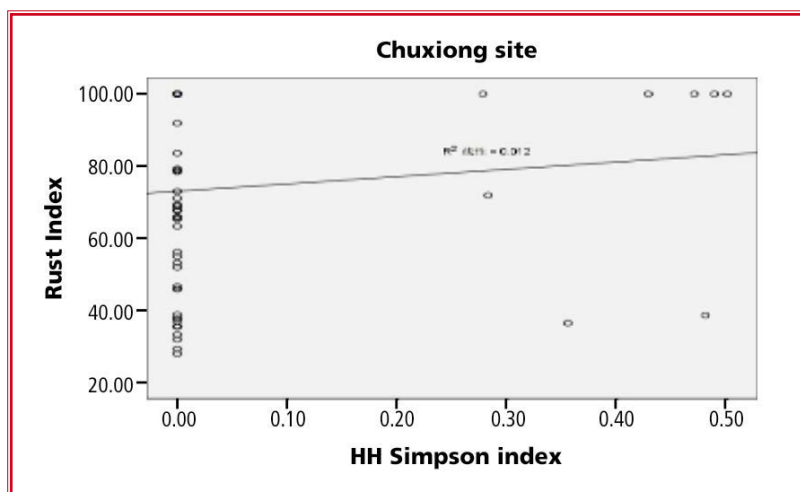


Fig 1 Relationships between rust disease index and HH Simpson index

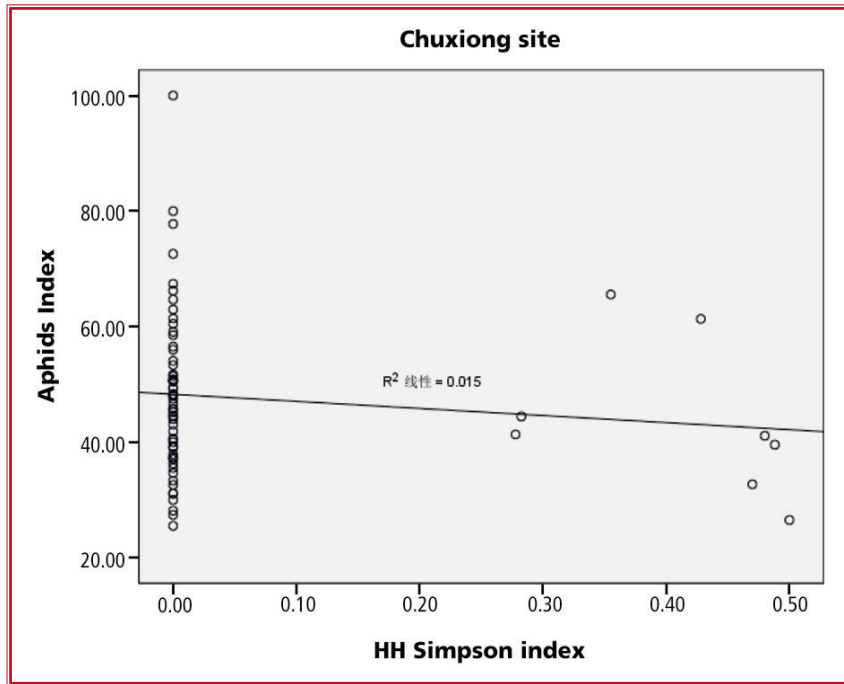


Fig 2 Relationships between aphids index and HH Simpson index

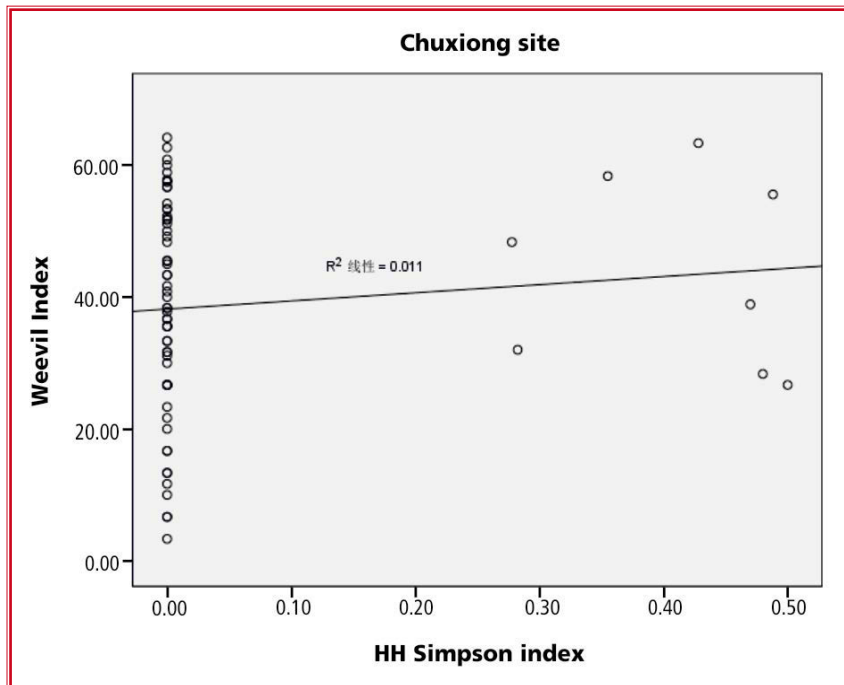


Fig 3 Relationships between weevil index and HH Simpson index

Relating crop damage levels on farm to crop varietal diversity measure by richness, evenness and diversity for banana in Ecuador

Suárez-Capello, C; Agama, J.

INTRODUCTION

Musa cultivars are major agricultural crops for most farms in Ecuador, particularly on the coastal plain and in the Eastern región. Throughout Ecuador, plantain is a basic component of family nutrition *Musa* cultivars are part of any farming system in the lower areas of the country, the coast and the Amazon. It is estimated that Ecuador has approximately 120,000 hectares dedicated to cooking bananas, with more than 45,000 concentrated in the northern coastal regions. The banana industry occupies approximately 200,000 hectares in the southern regions. In terms of total exports, banana cultivars occupy eighth place in the export chain.

MATERIAL AND METHODS

Two sites were selected for investigation of plantain (El Carmen and La Mana), with five farmer group discussions held in each site. In addition, key informants were interviewed and their opinions recorded and 126 farm households were interviewed in household surveys.

The approach used was to prepare a series of tables with the information collected in farmer group discussions, key informant interviews and household surveys. A second level of analysis is in process to determine the response to the questions and hypotheses proposed by the project. Richness and evenness was calculated for locations sampled within sites.

RESULTS

When richness was plotted against evenness, the groupings that resulted showed that there is a link between low levels of evenness and areas with single crops. Data obtained from household surveys for the three identified constraints (black sigatoka, black weevil and nematodes) identified black sigatoka by the numbers of functional leaves, black weevil infestation by the number of galleries and nematode damage by the number of plants on the ground. These were plotted against richness and evenness.

DISCUSSION

Independently of variations between the sites, the effect of diversity in terms of the number of cultivars or richness and distribution evenness seems to have an impact on pest incidence and

disease severity. This opens the possibility of including this factor in a broader IPM strategy and offers opportunities for improving the livelihoods of small farmers

Figure 1 Zones of Concentrated Banana production in Ecuador

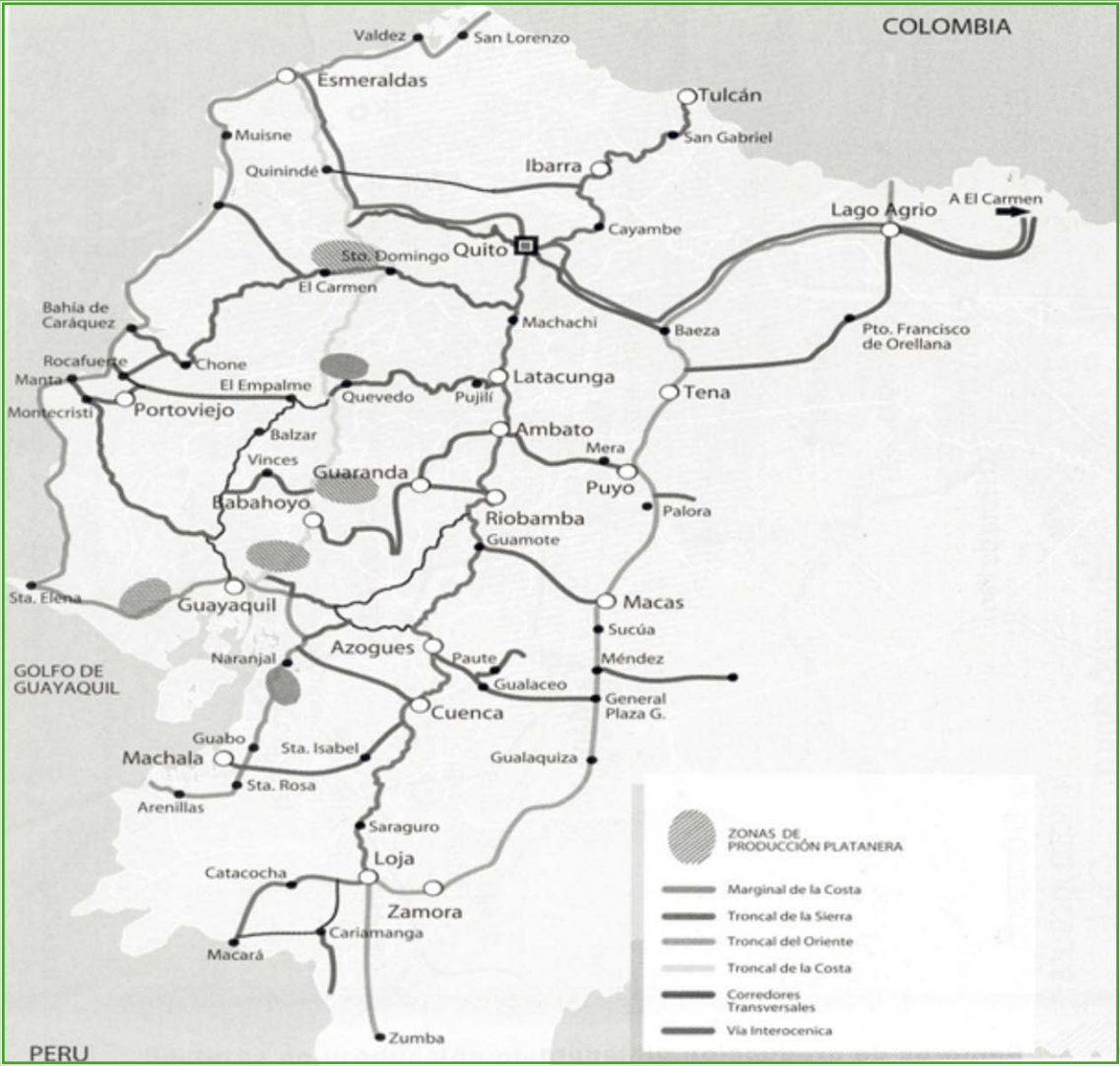


Table 1 Cultivars of Musa in the zones of El Carmen and La Mana (FGD)

Cultivares	El Carmen					La Maná				
	Old Men	Hombres Jóvenes	Mujeres Viejas	Mujeres Jóvenes	Líderes	Hombres Viejos	Hombres Jóvenes	Mujeres Viejas	Mujeres Jóvenes	Líderes
Sto. Domingo							x	x	x	x
Platanillon						x		x		
Orito manzano						x				
Guineo Filipino						x				
Guineo exportación						x	x	x	x	x
Guineo injerto				x						
Guineo 4 filos			x							
Limeño morado			x							
Limeño			x			x	x	x	x	x
Guineo de jardín					x					
Gross Michael (G.M)		x								x
Barraganete	x	x	x	x	x	x	x	x	x	x
Dominico	x	x	x	x	x	x	x	x	x	x
Guineo seda* (G.M)	x	x	x	x	x	x	x	x	x	
Maqueño verde	x	x	x	x	x		x	x		
Maqueño morado	x	x	x	x	x	x	x	x	x	x
Hartón	x	x	x	x	x	x	x	x	x	x
Orito (vocado de reina)	x	x	x	x	x	x	x	x	x	x
Guineo enano (Cavendish)	x	x	x			x				
Barraganete enano	x	x								
Dominico blanco	x	x						x		
Guineo de montaña		x				x				
Total (23)	10	12	11	8	8	13	10	12	9	9

Table 2: The amount and frequency of cultivars in farmers hands in locations of the two sites

Cultivar	Monocultivo		Two Varieties		Three Varieties		Four Varieties		Five Varieties		Six Varieties		% Promedio/ Caso
	Frecuencia	%Promedio	Frecuencia	%Promedio	Frecuencia	%Promedio	Frecuencia	%Promedio	Frecuencia	%Promedio	Frecuencia	%Promedio	
Barragante	3	100	16	98,95	25	93,92	12	98,17	3	98,12	3	72,55	93,62
Orito							1	0,5	2	0,2	3	0,77	0,49
Banano													
Hartón													
Dominico													
Maq Morado													
Guineo Seda													
Barr Enano													
Maq Verde													
Dominico guineo													
Platano Sto Domingo													
Dominico mejorado													
Guineo de jardín													
Guineo Filipino													
FHIA Dominico													
Limeño													

El carmen

Table 3 Evenness as a function of the number of cultivars (richness)/location/site

Zona	Localidad	Richness	evenness	Plot Area musa	Range cultivars
El Carmen	Agua Sucia	4	0,0215	2,08	2 a 4
	La Bramadora	6	0,3318	3,42	2 a 6
	Palmar de las Mercedes	3	0,0133	7,67	1 a 3
	La Medianía	5	0,0311	5,25	4 a 5
	Los Almendros	5	0,0376	2,83	3 a 5
	San Pedro de Suma	4	0,0214	6,5	2 a 4
	San Ramón de Tigrillo	6	0,0237	5,83	2 a 6
La Maná	Comuna Chipe I	6	0,5381	4,25	1 a 6
	Comuna Chipe II	3	0,3116	4,18	2 a 3
	Comuna Chipe III	4	0,6003	5,93	2 a 4
	Estero Hondo	3	0,4115	5	2 a 3
	Guasaganda	4	0,6076	2,6	1 a 4
	Santa Cruz	6	0,7241	8	3 a 6
	San José del Estero	4	0,4070	6,38	1 a 4
	Manguilita	4	0,1515	4,93	1 a 4
	San Gerardo	2	0,0010	7,6	1 a 2
	San Pablo de Maldonado	3	0,0597	7,93	1 a 3
	Selva Alegre	2	0,0995	3	1 a 2

Appart from the oritoarea, cultivars
Are more evenly
Distributed in La Mana

Evenness1=Homogeneity

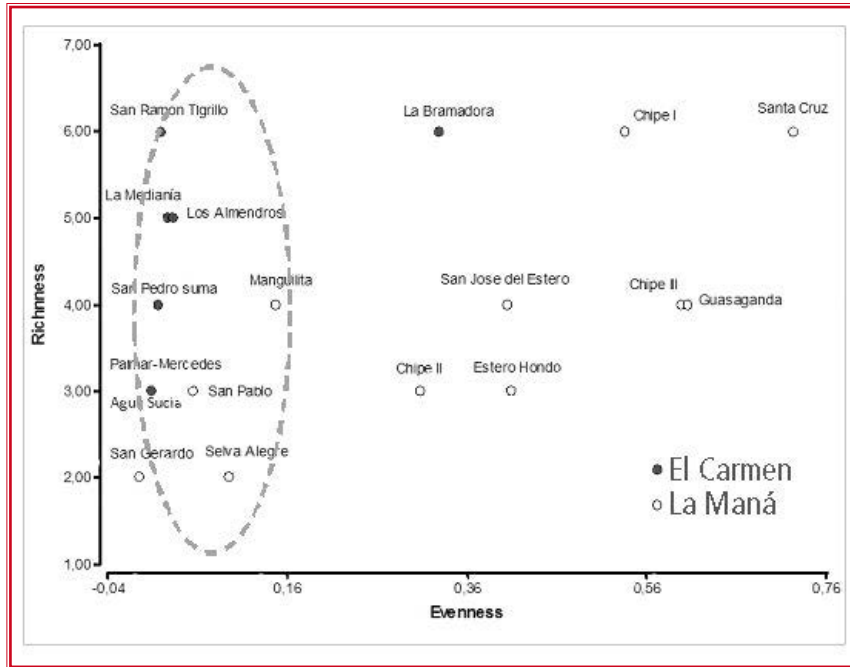


Figure 2 Plotting richness against evenness

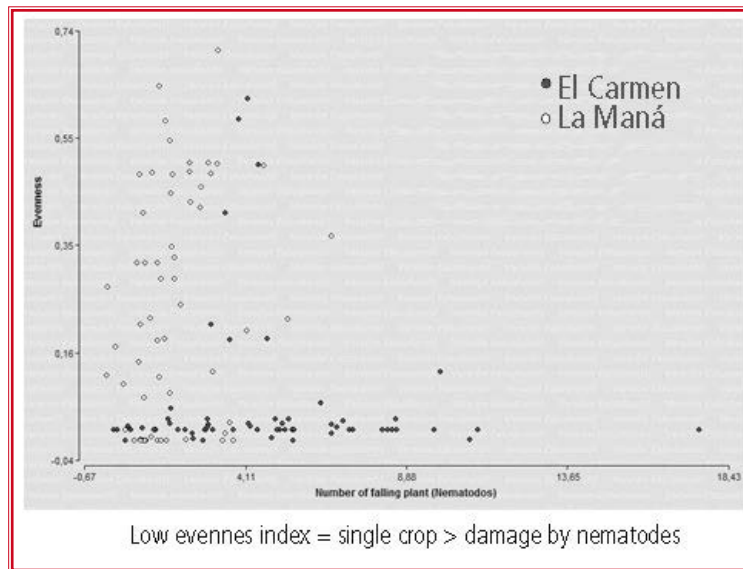


Figure 3: Nematode damage plotted against richness and evenness

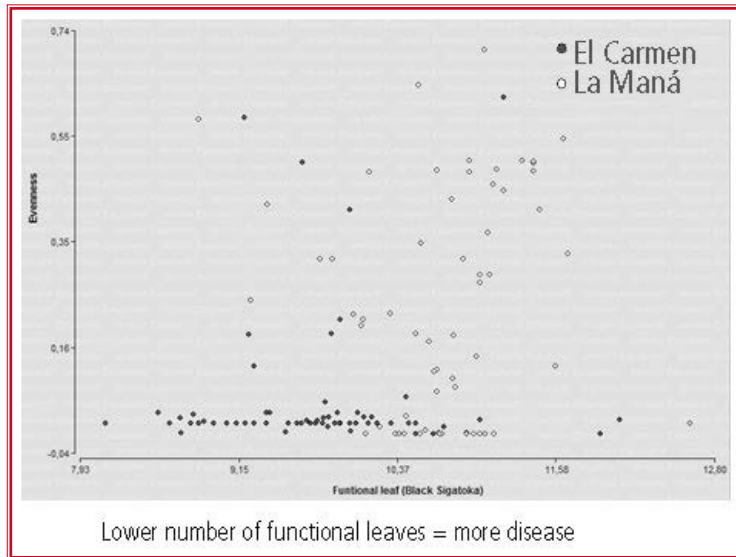


Figure 4: Black sigatoka damage plotted against richness and evenness

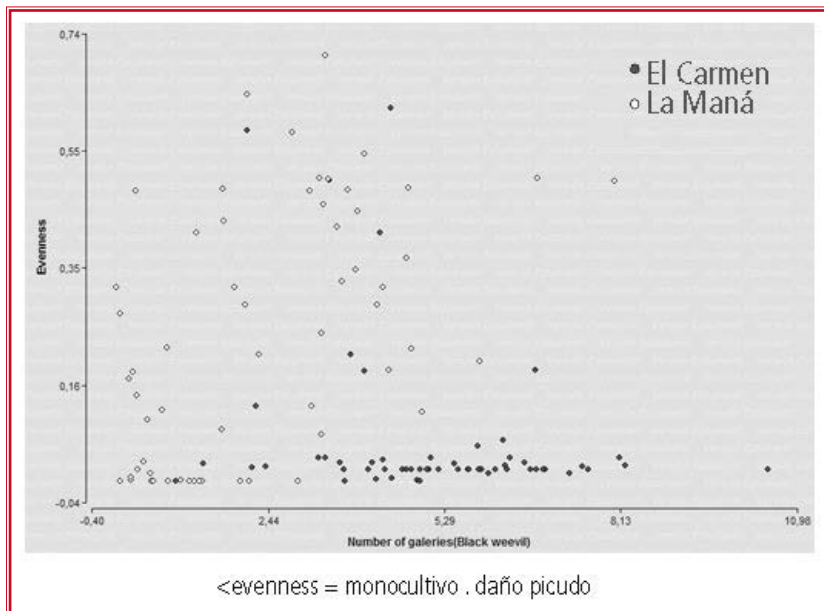
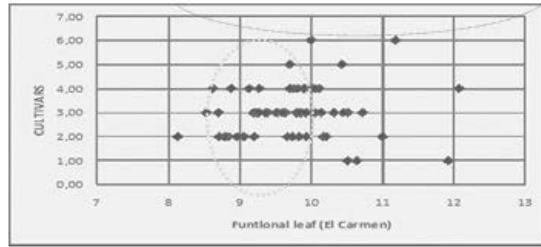


Figure 5: Black weevil damage plotted against richness and evenness

Richness in two sites related to Black Sigatoka damage on Musa cultivars, measure as number functional leaves. INIAP, Ecuador 2011



"Disease incidence in El Carme accounts for Around 1,5 leaves less than in La Maná

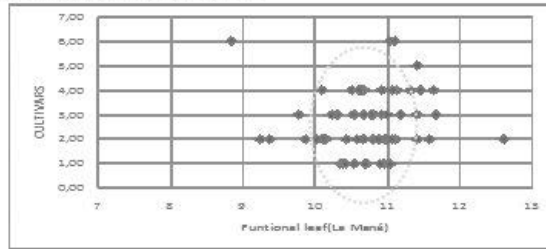


Figure 6: Richness and disease incidence in two sites

Black weevil damage (corn galleries) in two ecuadorian sites in relation to number of cultivars

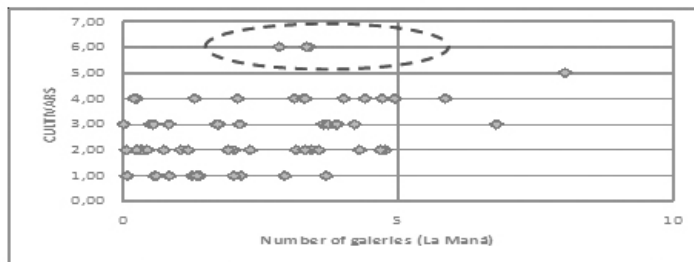
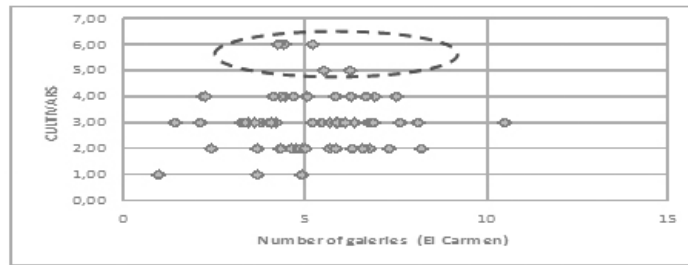


Figure 7: Black weevil damage in two site related to number of cultivars

Number of cultivars (Richness) related to nematode damage as number of falling plants in two sites Ecuador, 2011

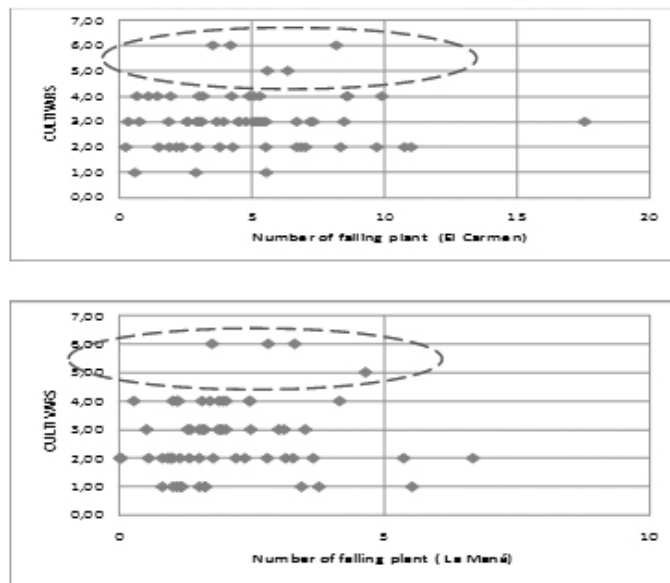


Figure 8: Richness related to nematode damage in two sites

Traditional knowledge of the use of barley genetic diversity to control pests and diseases

Chun-yan Li; Huang Yuan; Yu Guo; Chun-lin Long.

Yunnan Province has a long history of cultivation of barley (*Hordeum vulgare* L.), a very important crop in the grass family. There are abundant local barley varieties in the plateau area of Yunnan, which is considered one of the centers of diversity. Two villages, one in Shangri-la county of northwest Yunnan and one in Songming county of central Yunnan, were selected as our field sites to study both the traditional knowledge of using local barley varieties to control pests and diseases, and the indigenous agricultural management by means of focus group discussion (FGD) and individual interviews. It was shown that Participatory Rural Appraisal is a useful approach for investigating farmers' indigenous knowledge. Farmers can also improve their capacity for using crop diversity to control pests and diseases. Farmers have a rich trove of indigenous knowledge of the use of crop diversity for controlling pests and diseases. It is necessary to enhance the conservation and use of indigenous knowledge of crop diversity's contribution to reducing pests and diseases, because such knowledge is disappearing rapidly.

Key words: barley, focus group discussion, individual interview

INTRODUCTION

Focus group discussion (FGD) is a procedure in which the project staff and partners learn about traditional agricultural knowledge and local crops from local people by talking to them rather than teaching them. Individual interviews are another way to learn about local crops. In contrast to FGD, individual interviews allow the researcher to obtain more information about the informant's whole family. Barley (*Hordeum vulgare*) is the fifth largest cultivated cereal crop in the world. In China, Yunnan Province is the genetic diversity center for barley. Shangri-la and Songming counties have a long history of cultivating barley. Due to the high diversity of barley landraces here, we selected the two counties as two project sites for carrying out FGDs and individual interviews. The two sites are located on the map (Fig 1):

METHODS

Focus group discussions

We selected three villages located in different areas in each county. Shangri la County contained Quwadi, Xianfeng and Reshuitang villages while Songming County contained Dashao, Hongshiyang, and Changlinggan villages. Five groups were organized in each village to carry out FGDs with separate groups of old male farmers, young male farmers, old female farmers, young female

farmers and government leaders. Each group included ten local people. Then we conducted the questionnaire interviews according to the project plans.

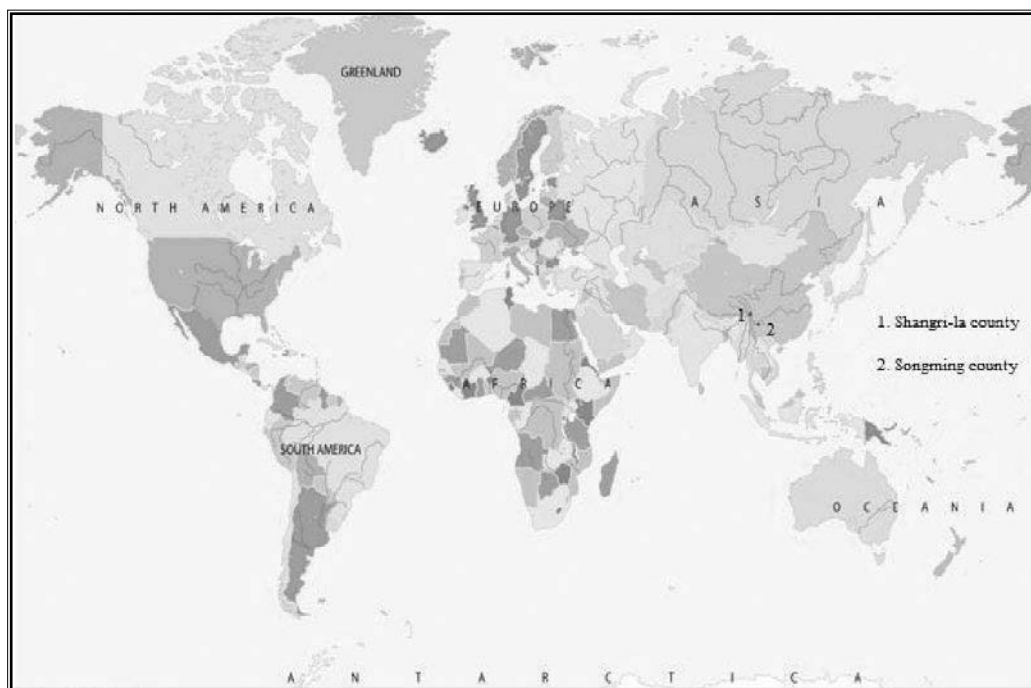


Figure 1 Location of the investigation

Individual interviews

A total of 60 farmers were interviewed in each village. The 60 farmers were selected from all of the farmers in three villages by random sampling until 60 farmers were selected who met the following requirements:

- (1) All of the 60 farmers belonged to different families.
- (2) Half of the farmers were adult male farmers and the other half were adult female farmers.

Statistical analysis

The diversity was evaluated by richness, evenness and variation. Household richness was the number of the barley landraces held by a family. Community richness was the number of the barley landraces in a site. Household evenness (H) was calculated by the formula: $H = 1 - \sum p_i^2$, where p_i was the ratio of i th barley landrace acreage to the total barley landraces acreage of a family. Community evenness (E) was calculated by the formula: $E = 1 - \sum p_i^2$, where p_i was the ratio of the i th barley landraces acreage to the total barley landraces acreage of a site.

Divergence (D) was calculated by the formula: $D = (E - H) / E$, where H was the average of the household evenness of a site. It was a possibility that two random families in a site cultivated different landraces.

RESULTS AND DISCUSSION

Diversity evaluation

Richness

The two sites had the same community richness of 3, namely, there were three landraces in both sites (Table 1). The average of family richness in Shangri-la County was 2.117 and ranged from 1 to 3. A total of 27 families (45%) cultivated 3 barley landraces; 13 families (21.67%) cultivated 2 landraces; 20 families (33.3%) cultivated 1 landrace. The average of household richness in Songming County was 1.117 and ranged from 0 to 2. A total of 11 families (18.33%) cultivated two barley landraces; 45 families (75%) cultivated 1 landrace; 4 families (6.67%) cultivated modern cultivars. The Shangri-la County had a higher household richness than Songming County. Local names of varieties are given in Table 5.

Evenness

The community evenness was 0.225 in Shangri-la and 0.565 in Songming. The household evenness, with an average of 0.168 (in Shangri-la) and 0.066 (in Songming), ranged from 0 to 0.625 (in Shangri-la) and 0 to 0.5 (in Songming).

Table 1 Community richness

Project sites	Shangri-la	Songming
Household (HH) average planting area (mu)*	5.47	4.726
Range of HH planting area (mu)	1-13.23	0.9-12.5
Average HH planting area for traditional varieties (mu)	5.354	4.224
Range of HH planting area for traditional varieties (mu)	1-13.23	0-12.5
HH planting ratio of traditional varieties (%)	98.6	88.8
Range of HH planting ratio of traditional varieties (%)	46.12-100	0-100
Community planting ratio of traditional varieties (%)	97.88	89.38
Average HH richness	2.117	1.117
Range of HH richness	1-3	0-2
Community richness	3	3
Average HH evenness	0.168	0.066
Range of HH evenness	0-0.625	0-0.5
Community evenness	0.255	0.565
Divergence	0.34	0.88

Variation

The variation was 0.34 (in Shangri-la) and 0.88 (in Songming), indicated that the possibility that random two families in a site cultivated different landraces was 34% or 88%.

Local knowledge of crop pathology

Descriptions of healthy and unhealthy plants

Farmers judged the merits of a landrace by plant health (Figures 2a and b).

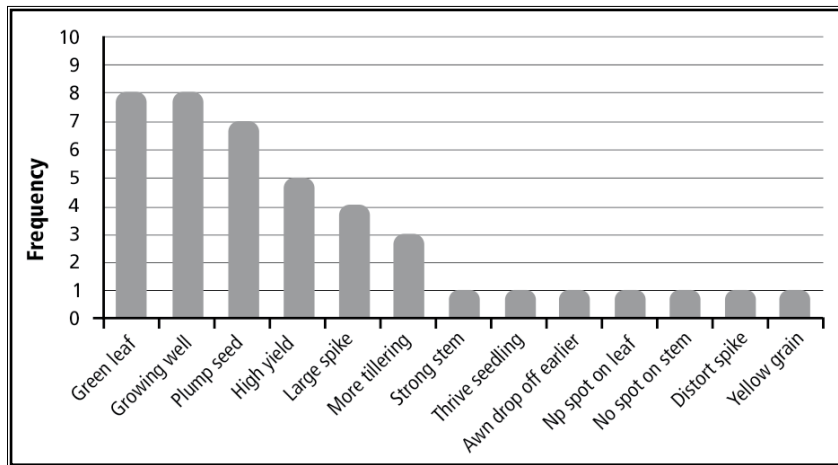


Figure 2a Plant health described by farmers

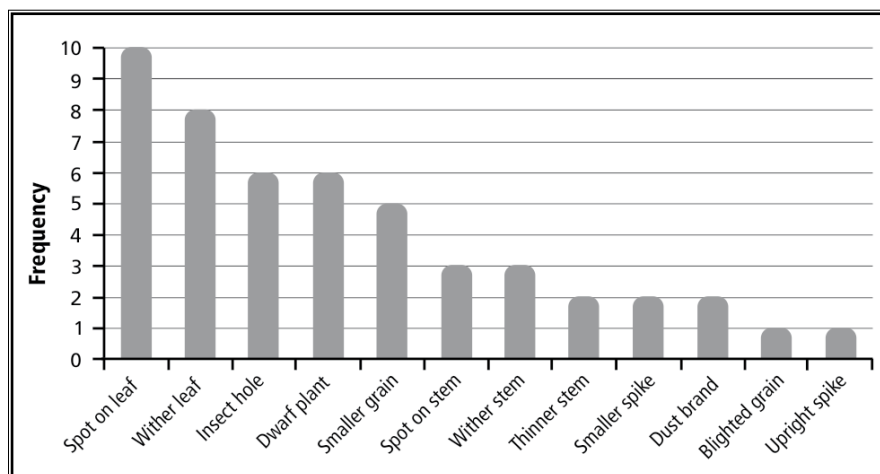


Figure 2b Plant health described by farmers

Descriptions of main pests/diseases

A total of 6 pests/diseases were described by farmers, including rust, smut, aphid, cutworm, yellow dwarf, weevil (Table 2). These occurred in different growing stages (Table 3). The yellow dwarf disease of barley was found only in Shangri-la and the weevil was found only in Songming.

Table 2 Pests/diseases described by farmers

Pest/disease	Descriptions									
rust	the leaves withered, rust on the leaves and stems, dwarf, small spikes, small grains, low yields									
smut	the spikes became black, no grain									
aphid	sucked the juice, yellow leaves and stems, slows growth, shriveled grains									
cutworm	broken roots, plants died									
yellow dwarf	Dwarf, yellow leaves, low tillers, low yields									
weevil	Insect holes in the grains									

Pest/disease	Damage positions					Damage stages				
	leaf	stem	spike	root	grain	seeding	tiller	heading	maturity	grain
rust	x	x				x	x	x		
smut			x					x		
aphid	x	x	x				x	x	x	
cutworm				x		x	x	x	x	
Yellow dwarf	x	x				x	x	x		
weevil					x					x

Table 3 Pest/disease damage

Pest/disease	Damage positions					Damage stages				
	Leaf	stem	spike	root	grain	Seeding	tiller	heading	maturity	grain
Rust								X		
Smut							X	X		
Aphid	X	X	X			X	X	X	X	
Cutworm	X	X	X	X	X	X	X	X	X	X
Yellow dwarf	X	X				X	X	X		
Weevil								X		

Types of damage caused by the pests and diseases

The six kinds of pests and diseases caused different types of damage to barley on a scale of 1 to 5. The lower the number was, the more serious the damage (Tables 4a and b). The yellow dwarf disease was the most serious of all in Shangri-la and in Songming it was the cutworm.

Origins of the pests and diseases

The origins of the common pests and diseases according to the farmers are listed in Figure 3.

Resistance of varieties to pests and diseases

Resistance was evaluated with a score from 1 to 4. 1 = no resistance, 2 = low resistance, 3 = moderate resistance, 4 = high resistance.

Resistance in different growing stages

The 11 cultivars (Table 5) showed different resistance in different growing stages (Table 6).

Table 4a Types of damage caused by pests and diseases

Pest/disease	Types of damage				overall importance of pest/disease
	Yield	Grain size	Feed	Height	
Rust	3	4	3	3	3
Smut	4	1	4	4	4
Aphid	1	2.5	2	2	2
Cutworm	5	5	5	5	5
Weevil	2	2.5	1	1	1

Table 4b Types of damage caused by pests and diseases

Pest/disease	Types of damage				overall importance of pest/disease
	Yield	Grain size	Feed	Height	
Rust	3	4	3	3	3
Smut	4	1	4	4	4
Aphid	1	2.5	2	2	2
Cutworm	5	5	5	5	5
Weevil	2	2.5	1	1	1

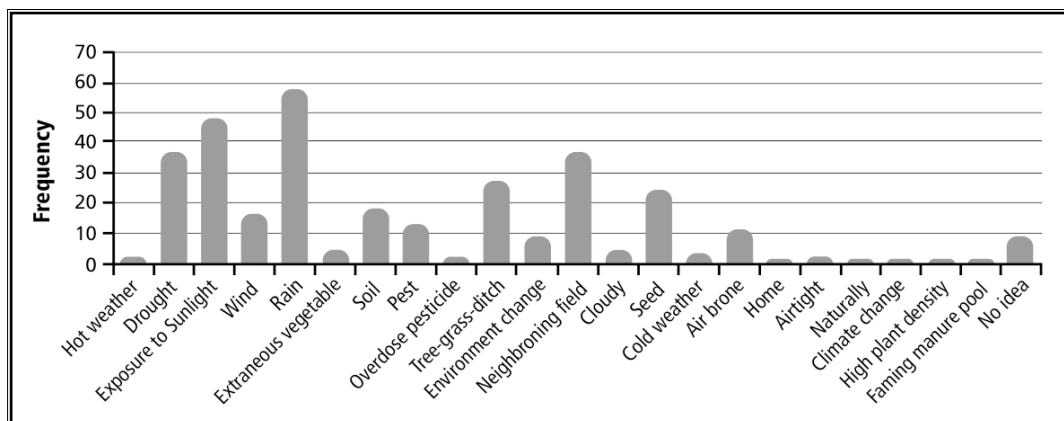


Figure 3 Causes of damage as described by farmers

Table 5 Local names of barley varieties

Code	Local name	Types	Collecting location
1	manai	local	Shangri-la county
2	naige	local	Shangri-la county
3	naina	local	Shangri-la county
4	naishui	modern	Shangri-la county
5	hair barley	local	Songming county
6	rice barley	local	Songming county
7	blossoming barley	local	Songming county
8	high beer barley	modern	Songming county
9	short beer barley	modern	Songming county
10	six-row beer barley	modern	Songming county
11	bare beer barley	modern	Songming county

Table 6 Resistance in different growing stages

Variety	Resistance during growing stages					Overall resistance
	seeding	tiller	heading	maturity	grain	
Manai	3	2	2	3	4	3
Naige	2	2	2	3	4	2
Naina	2	1	2	3	4	2
Naishui	4	4	4	4	4	4

Resistance to different pests and diseases

The 11 cultivars showed different resistance to different pests and diseases (Table 7).

Table 7 Resistance to different pests and diseases

Variety	Resistance during growing stages					Overall resistance
	seeding	tiller	heading	maturity	grain	
Hair barley	3	2	2	3	3	2
Rice barley	3	3	3	4	1	3
Blossoming barley	3	3	2	4	3	3
High beer barley	3	3	3	4	3	3
Short beer barley	3	3	3	4	3	3
Six-row beer barley	4	3	3	4	3	3
Bare beer barley	3	3	3	4	3	3

Changes of resistance in time and space

Most farmers believed that the barley varieties planted in similar environments had similar resistance and the barley in a wet, cold year had higher resistance than in a dry, hot year (Figures 4a and b). Changes in resistance by variety are shown in Tables 8a and 8b.

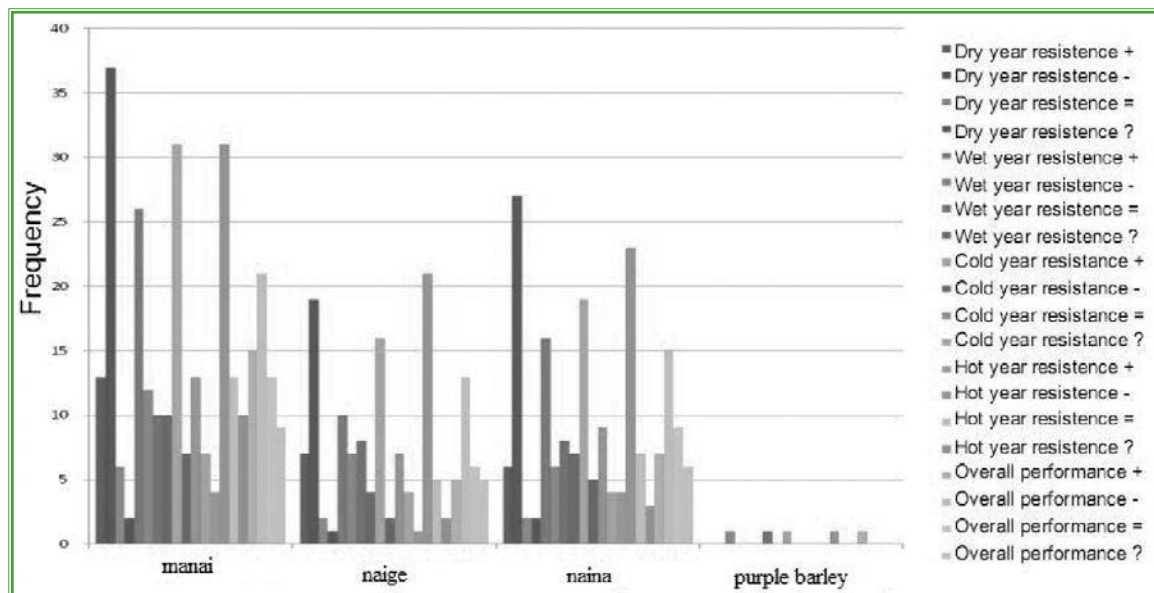


Fig. 4a: Resistance under different climate conditions

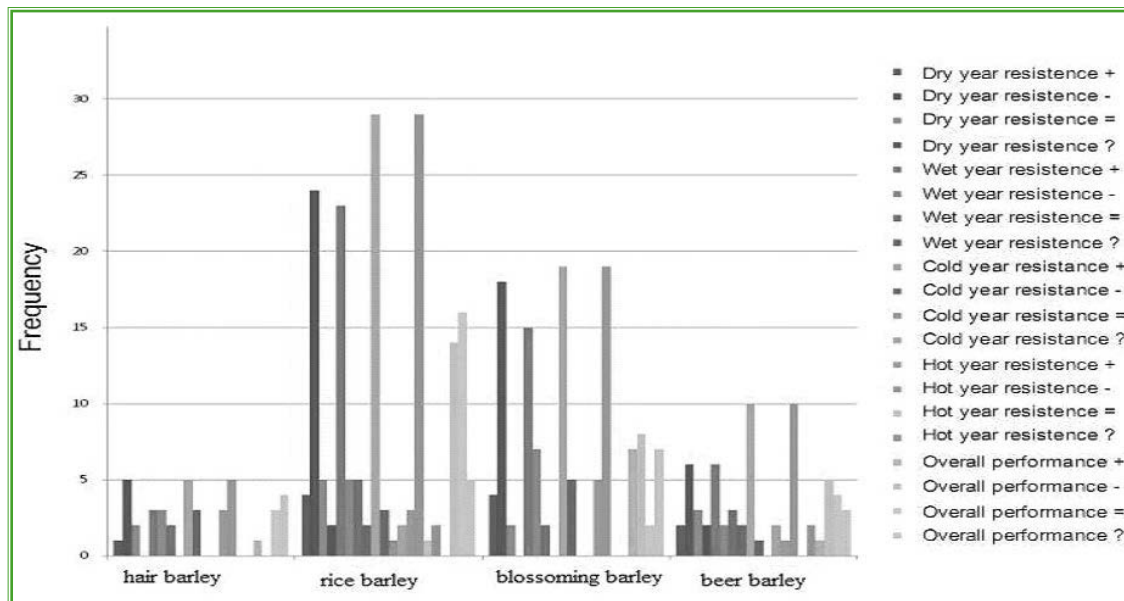


Fig. 4b: Resistance under different climate conditions

Methods for controlling pests and diseases

Farmers had many methods for controlling pests and diseases, including both traditional and modern methods (Fig 5). In Shangri-la there were more farmers who mixed several barley varieties together to plant than in Songming. The Shangri-la County was far away from Kunming, the economic center of Yunnan Province. Due to its remote location, modern agricultural systems had minor effect in Shangri-la, where farmers used more traditional methods than those in Songming. The farmers'

Table 8a Reasons cited for changes in resistance

Variety	Rust	Smut	Aphides	Cutworm	Yellow dwarf	Change in resistance (+/-)	Why?
manai	3	3	2	4	2	-	Planted for a long time and degenerated
naige	2	3	1	4	1	-	Planted for a long time and degenerated
naina	2	3	1	4	1	-	Planted for a long time and degenerated
purple barley	3	3	2	4	2	=	Plant for a short time

Table 8b Reasons cited for changes in resistance

Variety	Rust	Smut	Aphides	Cutworm	Yellow dwarf	Change in resistance (+/-)	Why?
manai	3	3	2	4	2	-	Planted for a long time and degenerated
naige	2	3	1	4	1	-	Planted for a long time and degenerated
naina	2	3	1	4	1	-	Planted for a long time and degenerated
purple barley	3	3	2	4	2	=	Plant for a short time

Seed system

The origins of the seeds included self-supply, exchange and market (Fig 7). The majority of the seed sources were self-supply.

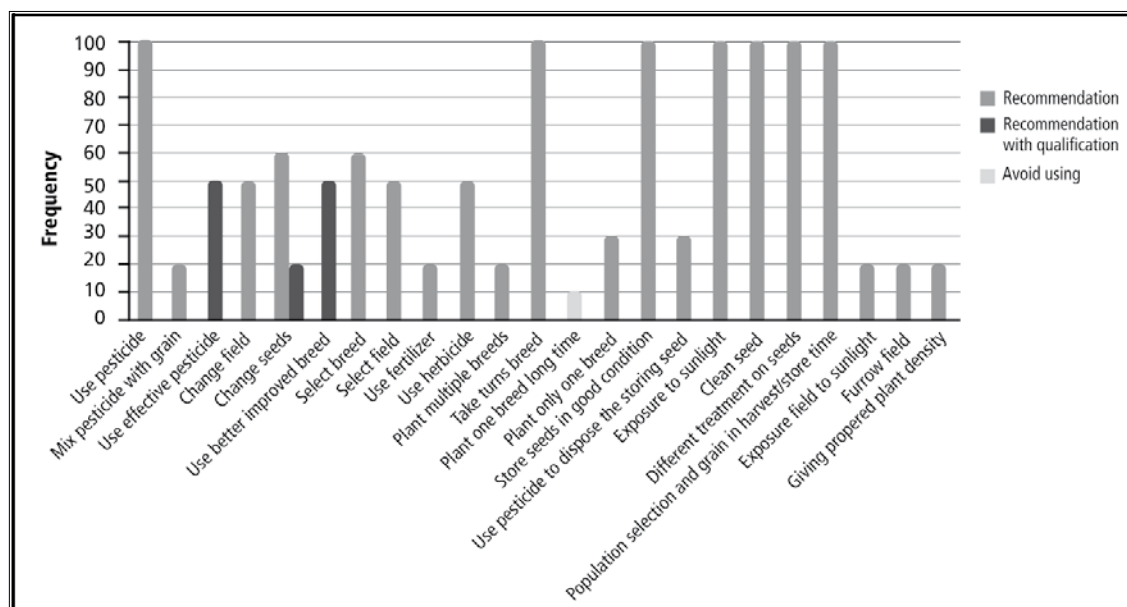


Fig. 5: Recommendations of farmer practices

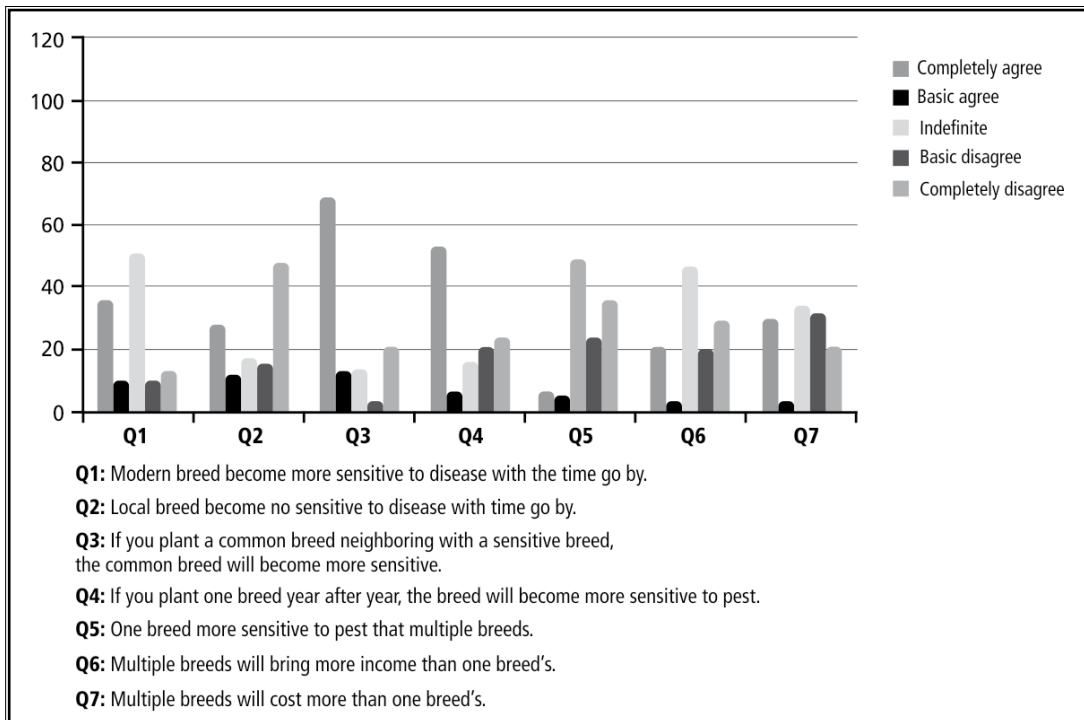


Fig. 6: Farmers' evaluation of use of genetic diversity to control pests and disease

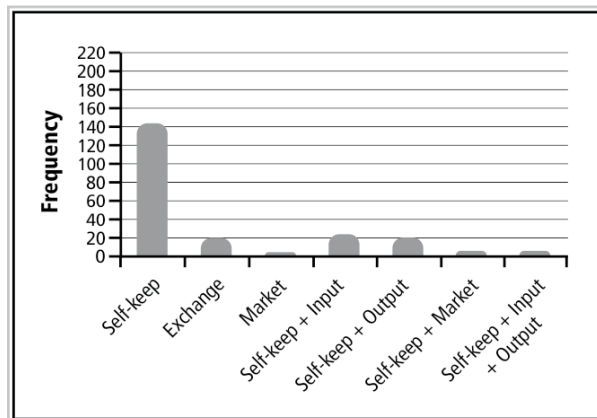


Fig. 7: Seed system

Analysis of the genetic diversity of local barley germplasm (*Hordeum vulgare* L.)

Taoufiqi, S.; Belqadi, L.; Ezzahiri, B.; Sadiki, M.

INTRODUCTION

Local varieties of barley are still widely used by farmers despite the large number of varieties listed. These populations are still maintained by farmers and modified from one generation to another. Gradually, these local varieties acquire characteristics adaptive to biotic and abiotic stresses in their areas of cultivation. These varieties display a wide range of adaptability and have evolved under the pressure of natural selection in their agro-ecological environments, as well as under farmer-induced pressures. This study aims to analyze the local diversity of barley in the region of Taounate in order to contribute to the development of the scientific basis needed to support farmers in managing the genetic diversity of the species.

MATERIAL AND METHODS

A trial was conducted in an experimental station (Mrissa of ORMVA Loukkous) in the region of Larache. The plant material analyzed in this study includes 110 barley populations originating in three different sites (Tissa Ourtzagh, Galaz) located in the region of Taounate. The experiment was carried out with a randomized complete block with two replicates. At harvest, yield components were evaluated based on samples of 20 randomly selected ears of barley in each population. Measured characteristics were the number of grains per ear, the number of rows per ear, and the weight of 100 grains. The statistical method used to analyze the data is descriptive analysis, both univariate and multivariate. Thus, percentages, averages, minimum and maximum values for each character measured were calculated to identify the similarities and dissimilarities between the different characters studied. The yield components were subjected to analysis of variance (ANOVA 1) to a single classification criterion. Populations were grouped by the cluster method using a hierarchical cluster. These tests were performed by SPSS statistical software.

RESULTS AND DISCUSSION

The descriptive analysis revealed significant differences between the 110 populations for all traits studied. Thus, the number of grains per spike, indicating the fertility of the cultivated variety, varies between 7 and 69 with an average of 32.2. The weight of 100 grains, a characteristic which indicates the quality of grains, varies between 4.3 g to 11.4 g with an average of 6.6 g. Character analysis based on the number of rows per ear showed that populations with two rows of spikes represent only 3% of the total populations.

The analysis of variance (Table 1) showed that there is a significant difference between the populations studied for all three measured traits: the number of grains per ear, the weight of 100 grains and the number of rows per ear. We concluded from these results that there is a remarkable genetic variability both between and within local populations of barley.

Cluster analysis has grouped the 110 populations in four main classes (Table 2). This classification helps to separate the populations into homogeneous and heterogeneous groups. However, it does not reveal the variation of intra-population diversity. This hierarchical analysis has also confirmed the presence of genetic variability in populations of barley which agreed well with the phenotypic variability described.

Table 1 Analysis of the variance of yield traits and the number of rows

ANOVA						
Characteristic	Source of variation	Sum of squares	Degree of freedom	Middle of squares	F*	Signification
Number of grains / ear	Population	20815,182	109	190,965	1,355	,057
	Error	15506,000	110	140,964		
	Total	36321,182	219			
Weight of 100 grains	Population	328751629,287	109	3016069,993	1,550	,011
	Error	214056259,144	110	1945965,992		
	Total	542807888,432	219			
Two rows	Population	1,355	109	,012	1,413	,036
	Error	,967	110	,009		
	Total	2,322	219			
Six rows	Population	1,354	109	,012	1,413	,036
	Error	,967	110	,009		
	Total	2,322	219			

Table 2 Size and composition of the four groups obtained by ascending hierarchical classification

Group	Effective	Populations
1	26	51-110-62- 69- 89- 103- 37- 1- 71- 44- 90- 42- 101- 109- 81- 99- 36- 93- 94- 107- 73- 61- 104- 63- 65- 60
2	80	27- 45- 4- 10- 35- 16- 82- 17- 29- 14- 2- 3- 38- 86- 5- 28- 74- 80- 34- 32- 75- 100- 108- 79- 105- 76- 72- 98- 70- 84- 50- 8- 9- 83- 102- 52- 87- 43- 7- 78- 77- 13- 24- 23- 30- 15- 46- 55- 48- 11- 95- 12- 20- 22- 31- 53- 19- 54- 57- 67- 106- 18- 96- 40- 56- 25- 47- 97- 59- 39- 41- 21- 88- 49- 85- 26- 58- 66- 33- 6
3	3	64- 68- 91
4	1	92

Variation in host resistance to chocolate spot within and among traditional cultivars in faba bean maintained by farmers in Morocco

Ezzahiri, B.; Belqadi, L.; Aqtbouz, N.; Touati, N.; Sadiki, M.

INTRODUCTION

Chocolate spot disease caused by the fungus *Botrytis fabae* is the most destructive leaf disease in Morocco. The infection of faba bean by this pathogen is of two types, "aggressive," causing blackening and death of part of the whole plant, and "non-aggressive," causing discrete chocolate-coloured lesions. The pathogen is necrotrophic and infects, colonizes and kills living tissue to obtain energy to grow and multiply.

There are two types of resistance of faba bean to chocolate spot, as there are for other diseases: specific resistance interferes with the disease cycle by totally preventing the emergence of symptoms and/or the production of spores. Partial resistance interferes with one or more of the steps of the cycle, resulting in slowing disease progress and/or reducing pathogen multiplication.

Only varying levels of quantitative resistance have been reported in the Faba-*Botrytis* system. Bouhassan et al. (2004) detected significant differences among genotypes for reactions to the disease in the field. However, no complete resistance was observed. Although differences in the virulence of isolates have been reported (Hutson and Mansfield, 1980), and the existence of races has been proposed (Hanounik and Maliha, 1986), no comprehensive description of races of *B. fabae* has been carried out so far. A set of differential lines should first be established, and then used to evaluate the virulence of a collection of isolates of diverse origin under the same environmental conditions.

In order to determine whether intra-specific diversity with respect to disease resistance exists within the sites in Morocco, farmers' perception and field observations, as well as on-farm, on-station and glasshouse experiments, were used to assess the variability of the resistance of faba bean varieties and populations to chocolate spot.

MATERIAL AND METHODS

Farmers' perception of the resistance of the faba bean varieties to chocolate spot

Data on farmers' perception of the resistance of faba bean varieties to chocolate spot were obtained during HH surveys and ranged in scale from 0 to 3. The most resistant varieties were scored 3.

Disease evaluation in the farmer's field

For the evaluation of the reaction of faba bean varieties to chocolate spot, a visual notation based on a 0-3 scale was utilized. The categories of the scale were 0: absence of disease; 1: few spots on lower leaves; 2: spots up to 50% of leaves; 3: spots on leaves and stems.

On-farm and on-station experiments

A collection of 100 populations of faba bean from the sites was evaluated both on-farm and on-station. On-farm trials located at Galaz, Tissa and Ourtzagh were conducted following the same practices utilized by farmers. In each site, the collected populations were planted in one bloc. Each population was planted in four rows, one meter each. An on-station trial was implemented at M'rissa experimental station located 160 km north of Rabat. The collected populations were planted in one bloc. Each population was planted in four rows, one meter each.

In all trials, the reactions of the plants were scored at pod formation. For each population, 10 plants were scored individually. The reactions of plants to *B. fabae* were scored according to a 1-5 visual scale. The scale is based on a combination of lesion type, lesion frequency and extent of damage, with 1: no symptoms or very small spots; 2: very small and discrete lesions; 3: some coalesced lesions with some defoliation; 4: large coalesced sporulating lesions, 50% defoliation, some plants dead; 5: extensive lesions on leaves, stems and pods, severe defoliation, heavy sporulation, blackening and death of more than 80% of the plants.

Glasshouse experiment

The evaluation of the resistance of the 100 populations of faba bean was conducted in a glasshouse against two isolates of *B. fabae*. These isolates were purified from lesions of the aggressive form of the pathogen. The isolates were grown and increased on Faba Bean Leaf Agar. A water solution of 3.106 spores/ml was obtained and sprayed onto seedlings of faba bean. The inoculated plants were placed in a moist chamber for 24 hours and then moved to a glasshouse. The reactions of the inoculated plants were scored 15 days after inoculation, using the 1-5 scale described above.

Statistical analysis

The data collected in the experiments were analyzed for variance. Mean comparisons and multivariate analysis of the collected data were also conducted using SPSS.

RESULTS AND DISCUSSION

Farmers perception of the resistance of faba bean varieties to chocolate spot

The farmers consider that in general some varieties of faba bean are resistant to chocolate spot, while others are susceptible. However, the farmers' perception of resistant varieties differed from one site to another (Figures 1-3).

According to the varietal composition of each community, farmers classify their landraces depending on the degree of resistance to chocolate spot. In Ourtzagh, farmers found Hmami to be the most resistant. Galaz farmers argue that the two varieties Sbai beldi and Tsai Roumi are the

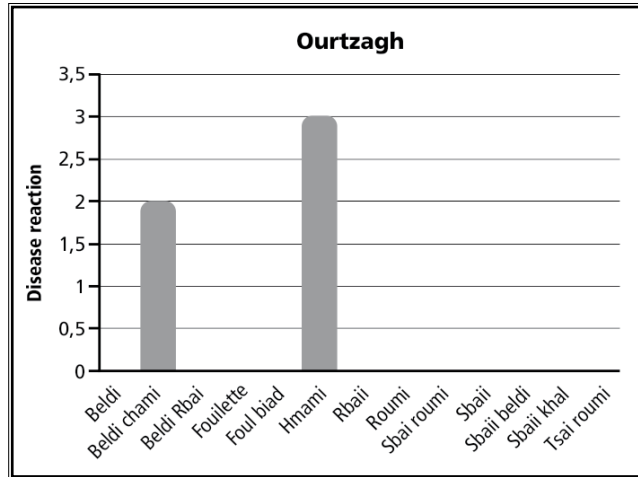


Figure 1 Farmers' perception of the resistance of faba bean varieties to chocolate spot at Ourtzagh site

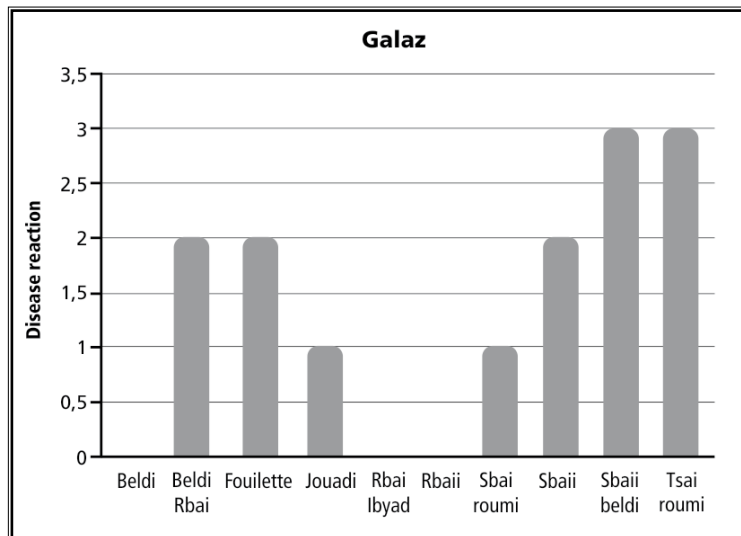


Figure 2 Farmers' perception of the resistance of faba bean varieties to chocolate spot at Galaz site

most resistant. Farmers from Tissa believe that varieties Abriti, Fouilette, Sbair beldi and Hjawii are more resistant than the other varieties.

Disease evaluation in the farmer's field

The information on the assessment of the disease severity for each cultivated variety is presented in figures 4-6. In Ourtzagh site, mixtures (Beldi Rbai-Sbairi, Beldi-Roumi, Beldi rbai-Fouilette) and

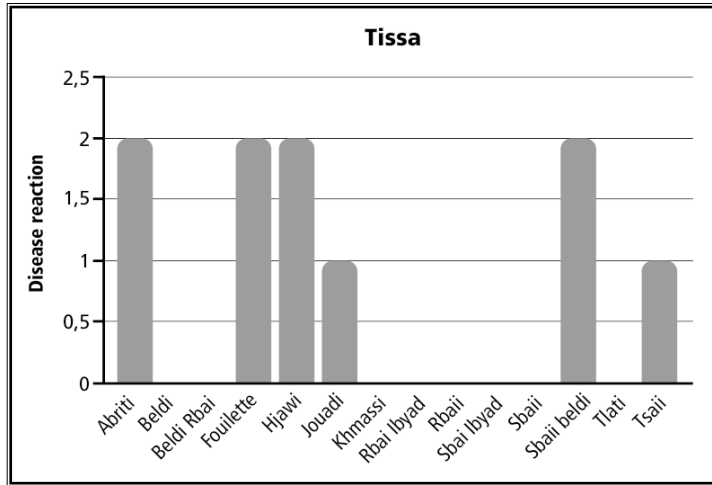


Figure 3 Farmers' perception of the resistance of faba bean varieties to chocolate spot at Tissa site

Beldi rbai and Beldi chami varieties appear to be susceptible to chocolate stains. Sbaii beldi, Rbai and Sbaii varieties appear less often attacked by this disease. While Beldi, Sbaii roumi varieties and mixtures (Beldi-Sbaii, Beldi Rbai-Roumi and Sbaii-Rbaii) have little spots, indicating that these varieties may be resistant to the disease.

In Galaz site, the varieties the most affected by the disease are Rbai Lbyad, Sbaii Beldi and Sbaii Roumi. Varieties Rbai, Sbaii Beldi and mixture (Beldi-Sbaii) are less attacked, while the Beldi variety and mixtures (Beldi-Rbai-Jouadi, Beldi rbai-Sbaii and Sbaii beldi-Jouadi) have the lowest average rating (Figure 5).

The notation at the Tissa site revealed remarkable differences between varieties for their reaction to chocolate spot. Indeed, the varieties Fouillette, Rbaii, Beldi, Abriti and khmassi were

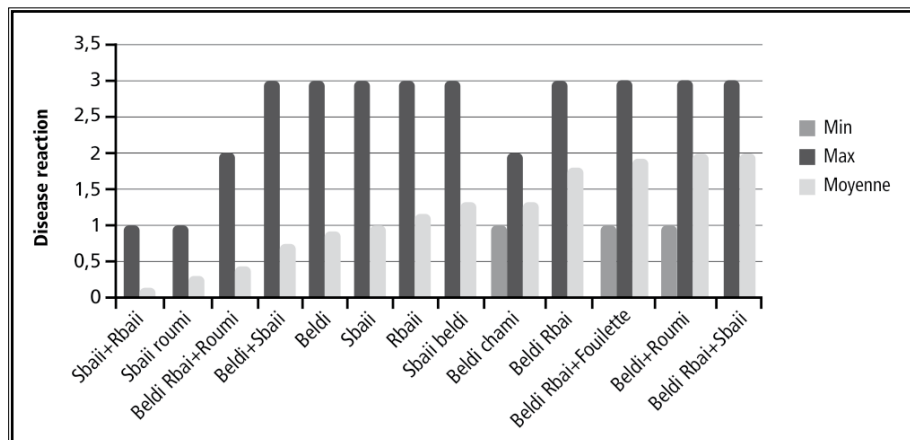


Figure 4 Field scoring of Botrytis in the Ourtzagh community

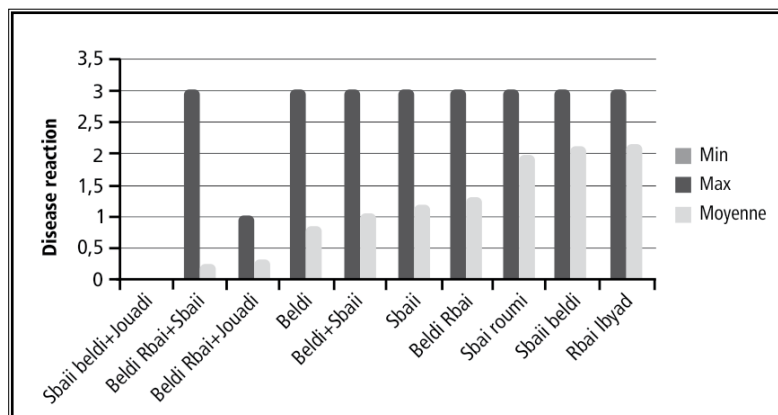


Figure 5 Field scoring of Botrytis in the Galaz site

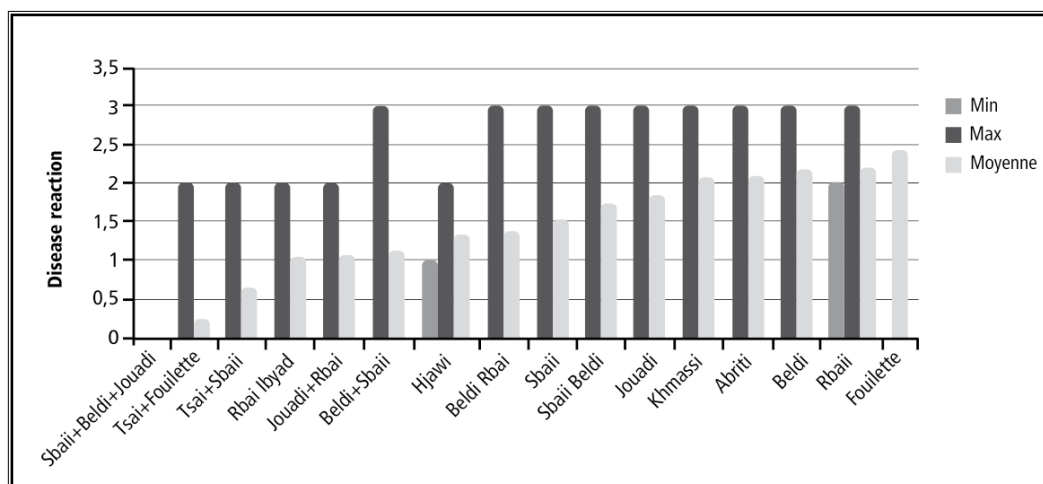


Figure 6 Field scoring of Botrytis in Tissa community

heavily attacked by disease, Jouadi, Sbaili beldi, Sbaili, Beldi rbai and Hjawi varieties were less attacked. Mixed varieties expressed the lowest ratings of disease reaction (Figure 6).

On-farm and on-station evaluation of faba bean populations to chocolate spot

On-farm experiment

Only the results from Tissa site are presented here. The difference in the reaction to chocolate spot between populations of faba bean was highly significant. Also highly significant were differ-

ences obtained between populations according to their origin. The ranking according to a Duncan test (Table 1) indicated that the faba bean populations collected from Tissa and Ourtzagh were similar in their reaction to chocolate spot.

Table 1. Mean comparison of the reactions to chocolate spot of faba bean populations according to their origin (on-farm experiment)

	Site	N	Sous-ensemble pour alpha = 0.05	
			1	2
Duncan	Tissa	819	2,48	
	Ourtzagh	60	2,68	2,68
	Ghafsay	1096	2,72	
	Significance		0,053	0,722

On-station experiment

The disease level was high in the station. Highly significant differences were found between populations of faba bean for their reaction to chocolate spot. Also, highly significant differences were obtained between populations according to their origin: the populations originating from Ghafsay (mean reaction = 4.17) were more susceptible than the populations from Ourtzagh (mean reaction = 3.7) and Tissa (mean reaction = 3.6). According to their reaction to *Botrytis faba*, 17 Ghafsay populations were highly resistant, 38 were moderately resistant, 18 moderately susceptible and 45 were susceptible. In Ourtzagh, according to their reaction to *Botrytis faba*, 12 populations were highly resistant, 29 were moderately resistant, 28 moderately susceptible and 31 were susceptible.

Glasshouse experiment

The evaluation of sources of resistance in faba bean carried out in the laboratory was performed by using two isolates of *Botrytis* from two different regions (Taounate and Larache). The result indicated that the local populations react the same way against both isolates and the majority of populations were susceptible (79 populations) while only 21 were resistant.


The experiments conducted on-farm, on-station and in the glasshouse indicated that a whole range of reactions was observed from susceptibility to resistance. The populations of faba bean reacted differently to chocolate spot according to their origin. These preliminary results suggest the presence of diversity of resistance in faba bean (Bouhassan et al., 2004) and the possible specialization of the pathogen (Hutson and Mansfield 1980).

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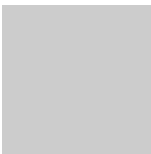
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DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 2



Variation in host resistance within and among traditional cultivars (FGD, HH survey, Options 2, 4)

Variation in host resistance within and among traditional cultivars in Maize maintained by farmers in China

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INTRODUCTION

The community selected for our ongoing GEF project is Xiding Town in Yunnan province, China. The local crops are mainly paddy rice, maize, upland rice and tea. As maize is the target crop of the Project, we wanted to carry out research on variation in host resistance within and among traditional cultivars through anglicizing data from FGDs, HH surveys, Option 2.

METHODS

The 70 households that planted maize (out of a total of 77 households) in Xiding Township were investigated through FGDs. The seven households that planted crops other than maize were examined through household surveys.

The maize varieties sampled for Option 2 consisted of 40 seedlings (clusters) of each maize variety planted (a total of 17 varieties). (Table1). We selected the four households to plant five sets of maize varieties:

- (a) In Bada village (Farmer Shazhe), one set of maize seeds was planted according to local conventional cultivation practices;
- (b) In Bada village, Farmer Qiezuo planted three sets of maize seeds, with the space between lines 80cm, the length between pits from 35cm to 40cm and two to three seeds per pit. A small amount of Terbufos (prevention against *Agrotis ypsilon*) and compound fertilizer (N: P: K= 15:15:15) was used. Local traditional management practices were also used.
- (c) In Man Yan kai village: Farmer Yanenzhang sowed one set of maize seeds following local traditional cultivation and management methods;
- (d) In Manpilaozai village Farmer Yanbujiao sowed one set of maize seeds using local traditional cultivation and management methods.

For the maize varieties under investigation, the morphological and biological traits were documented and damage from diseases and pests of maize in the fields were recorded. The resulting data was analyzed with SPSS software.

RESULTS

The distribution of maize varieties in Xiding included the planting of two or more local maize varieties by 19 households, accounting for 24.68% of the 77 households investigated. Another 32

planted two or more different crops in addition to rice, with the use of an intercropping model in one plot, account for 41.56% of the 77 households investigated. The crops planted included: tea, coix seed, soybean and marijuana. These crops covered 50% of the plot area. The number of years varieties were planted ranged from 1 to 70. Once farmers choose one local variety to plant for particular traits such as good taste, better resistance or wide adaptability, they would not change them.

Twenty households planted the Selileng (Selilemg) variety, equal to 25.97% of the total HHs. Of these, 55% regarded it as high-yielding, with good resistance traits. It was mainly used for forage. Twenty-seven HHs, or 35.06% of the total, planted the Aduxiu variety. The trait most valued by farmers was high yield. Twenty-three HHs (29.87%) planted the Seleleng variety; farmers appreciated its high yield and good resistance. (Modern variety) Eleven HHs (14.29% of the total) planted the modern variety Zajiaozhengda 615; farmers cited its high yield, its use in distilling wine, early maturity, forage. (Modern variety), Nine HHs (11.69% of the total) planted the modern variety Zajiao; the trait most prized by farmers was prematurity. Eight HHs (10.39% of the total) planted the Selebai variety, while the varieties Zhengda 819, Selile and Selibai were planted by only one HH.

Table 1 Maize germplasm resources list in Xingding country

Order	Variety	Origin	Number of planted
1	Bengdimaya	Sichuan	40
2	Yiqu	Sichuan	40
3	Suonuoyiqu	Sichuan	40
4	Baimaya	Sichuan	40
5	Nosuyiqu	Sichuan	40
6	Leibomaya	Sichuan	40
7	Bengdiyiqu	Sichuan	40
8	Suwan1hao	Manyankan	40
9	Selileng	Manpi	40
10	Huangyumi-1	Bada	40
11	Selebai	Manpi	40
12	Huangyumi-2	Mannai	40
13	Aduxiu	Zhuoluo(people)	40
14	Zhenhe1hao	Zhaozixian(people)	40
15	Huidan1hao	Zhaozixian(people)	40
16	Zhengda615	Seed ompany	40
17	Hongyumi	Manpi	40

According to the results of the FGD and the HH survey, the varieties showing medium to high disease resistance are Aduxiu, Seleleng, selileng, Zajiaozhengda 615, Selebai and Zajiaozhengda 819 showed low to moderate resistance, e.g., the damage by pests and disease to Aduxiu (first planted area in Xiding) was low (Fig.1). A total of four kinds of pests were examined: corn leaf blight, a small spot of corn, corn borer and gray leaf spot. In the corn leaf blight survey, six varieties of the disease were on the performance level of 1 to 2. In the maize survey of *Bipolaris maydis*, 6 cultivated varieties of had rating conditions of 1 to 3, while corn borer damage in the survey in general only caused serious pest harm (Level 2 to Level 3) in Selileng.

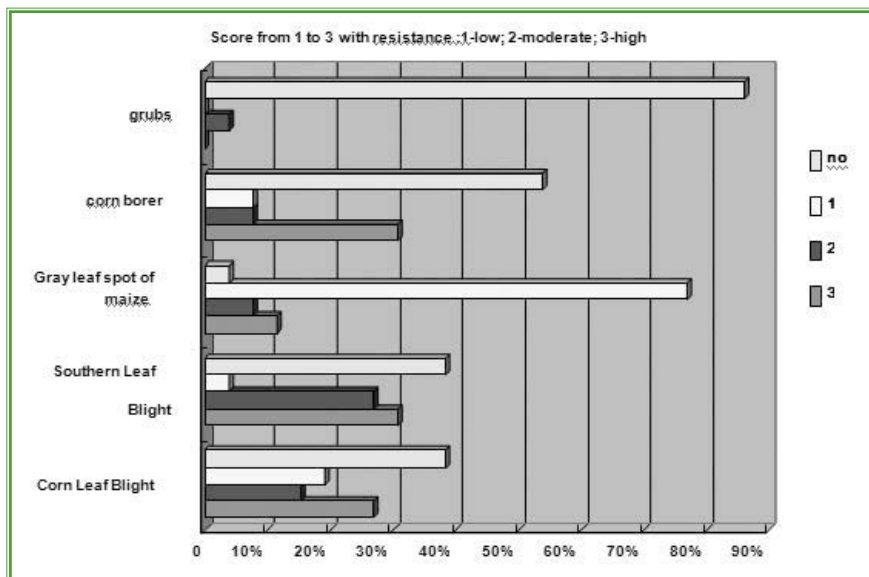


Fig.1 Resistance of Aduxiu to pest and disease (from FGD and HH survey)

In field experiments, 17 varieties showed a low resistance level to *Bipolaris maydis* and corn gray spot, (1 grade, see Table 2). No damage from corn northern leaf blight, corn curvularia leaf spot, common corn rust or corn head smut was seen in the 17 varieties (Table 2). The morphological and biological traits of maize in field experiments showed that Hongyumi from Xiding has highest thousand grain weight, 418.63g. Leibobaimaya from Sichuan province has the highest germination rate, 84.79%. Selileng from Xiding also has a good germination rate, 83.07%(Table 3).

Discuss:

The reasons given for planting more maize varieties was as follows: 1) Full and reasonably use of the land with improved efficiency and increased revenue: 2) one variety for poultry feed, one for wine production, another as food for the farmers themselves because of the good taste. In poor and remote villages, corn was mainly an upland crop, and local varieties have good resistance and high yields. And through FGDs, HH surveys and field experiments, we discovered that most local varieties display more good resistance than modern varieties to most of the maize diseases and pests, such as corn leaf blight, corn borer and gray leaf spot. Host resistance within

Table 2 Resistance of varieties to pests and diseases in field experiments

	Corn northern leaf blight resistance level	Bipolaris maydis resistance level	Corn curvularia leaf spot resistance level	Common corn rust resistance level	Corn head smut resistance level	Corn borer resistance level	Corn gray spot resistance level
Bengdimaya	0	1	0	0	0	0	1
Yiqu	0	1	0	0	0	0	1
Suonuoyiqu	0	1	0	0	0	0	2
Baimaya	0	1	0	0	0	0	1
Nuosuyiqu	0	1	0	0	0	0	1
Leibomaya	0	1	0	0	0	0	1
Bengdiyiqu	0	1	0	0	0	0	1
Suwan1	0	1	0	0	0	0	1
Selileng	0	1	0	0	0	0	1
Huangyumi-1	0	1	0	0	0	0	1
Selebai	0	1	0	0	0	0	1
Huangyumi-2	0	1	0	0	0	0	1
Aduxiu	0	1	0	0	0	0	1
Zhenhe1	0	1	0	0	0	0	1
Huidan4	0	1	0	0	0	0	1
Zhengda615	0	1	0	0	0	0	1
Hongyumi	0	1	0	0	0	0	1

Note : Score from 1 to 3 with resistance :1-low; 2-moderate; 3-high
0, no damage

and among traditional cultivars was stable; variation in host resistance was not obvious. Some local varieties such as Lebobaimaya from Sichuang province have good adaptability and can be used as new resistant varieties to plant in Yunnan province .We also suggested that local farmers could select more than one local variety to plant in fields in order to keep the maize host plant resistance to pest and disease.

Table 3 The morphological and biological traits of maize in field experiment

Variety	Single grain weight Average (g)	SD	CV	Germination rate Average (%)	SD	CV	Thousand grain weight average (g)	SD	CV
Aduxiu	0.163	0.027	16.57%	78.56	5.856	7.45%	321.36	36.813	11.46%
Baimaya	0.152	0.035	23.29%	82.18	2.501	3.04%	388.83	66.361	17.07%
Bendiyiqu	0.145	0.027	18.37%	82.13	3.167	3.86%	373.09	55.919	14.99%
Hongyumi	0.151	0.034	22.51%	82.57	2.470	2.99%	418.63	46.684	11.15%
Huangyumi-1	0.152	0.028	18.61%	80.55	1.910	2.37%	304.17	45.134	14.84%
Huangyumi-2	0.167	0.069	41.22%	80.16	17.450	21.77%	325.68	30.125	9.25%
Huidan4hao	0.162	0.023	14.04%	80.25	4.115	5.13%	322.53	54.062	16.76%
Leibobaimaya	0.129	0.021	15.92%	84.79	2.645	3.12%	298.28	28.145	9.44%
Nuosuyiqu	0.171	0.024	13.78%	82.65	4.365	5.28%	378.97	38.267	10.10%
Suonuoyiqu	0.149	0.022	14.58%	83.92	4.076	4.86%	362.87	39.983	11.02%
Suwan1hao	0.170	0.022	12.72%	80.15	3.108	3.88%	307.18	37.806	12.31%
Yiqu	0.145	0.023	16.04%	80.75	3.011	3.73%	380.59	85.297	22.41%
Zhengda615	0.148	0.011	7.41%	80.47	2.103	2.61%	283.14	33.277	11.75%
Zhenhe1hao	0.161	0.023	14.37%	83.86	1.879	2.24%	329.23	37.449	11.37%
Selebai	0.069	0.015	21.83%	79.59	3.294	4.14%	192.89	29.227	15.15%
Selileng	0.146	0.023	15.64%	83.07	2.455	2.96%	298.99	37.863	12.66%

Mixture effect of common bean on rust and yield under on-farm and experimental conditions in Ecuador

Espinosa, I.; Ochoa, J.B.

INTRODUCTION

Common bean is an important crop component of traditional agriculture in the highlands of Ecuador. It is cultivated in association with maize in complex mixtures. Cultivation of mixtures has been used in traditional agriculture since the crop was domesticated or introduced for cultivation. Two different common bean types are differentiated in Cotacachi: allpas and chakras. Allpas are early types and belong to the growth habit III, while chakras are late and belong to growth habit IV. Both types of common bean are associated with maize and cultivated in mixtures. Allpas are planted between maize plants while the chakras are planted together and climb on the maize. In Saraguro, the mixturiados, resembling chakras, are regularly late, belong to growth habit IV and are planted together with maize.

Maintenance of the mixtures in the agro ecosystem is mostly an ancient tradition (Pazmiño, J. and Ochoa J. 2011). However, tradition must have resulted in farmer consciousness of the value of diversity to improve productivity of the agro ecosystem. In the field, value of diversity appears to be associated with the agro ecosystem balance avoiding the negative effects of biotic and abiotic stresses.

Rust caused by *Uromyces appendiculatus* (Pers.) is an important disease of commercial common bean cultivation. However, in traditional agriculture, the disease appears less important. Resistance operating in the mixture farmers grow might explain the reduced rust epidemic in the field. On-farm and on-station experiments were conducted to study the contribution of the mixtures to keeping the rust epidemics in the field low.

METHODS

Two planting systems, genotype mixtures and individual populations on small plots, were studied on farms and under experimental conditions. For the on-farm study, six allpa and six chakra mixtures obtained from six farmers from Cotacachi were mixed and planted in a plot of 44 rows of 20 m long with a row spacing of 0.8 m. Two seeds of the mixture were planted together with two seeds of maize variety INIAP-122 every 0.6 m (site). After germination, only one common bean plant per site was allowed to grow. One hundred eighty plants were randomly selected in the plot in which the variables were assessed. In the small plot planting system, each common bean population that was part of the mixture was planted in two-row plots of 4 m long with a row spacing of 0.6 m. Two common bean seeds with two seeds of maize variety INIAP-122 were planted every 0.6 cm. Similarly after germination, only one common bean plant per site was allowed to grow and five plants per population were selected for evaluation.

For the experimental condition study, three balanced mixtures were produced by mixing 10 seeds of eight phenotypic populations of allphas, 14 phenotypic population of chacras and 13 phenotypic populations of mixturiados. A phenotypic population consisted of seeds with a similar color pattern and shape. The allpa balanced mixture was planted in eight-row plots of 6 m long spaced by 0.8 m, and two allpa seeds were planted between maize plants. The chakra and mixturiado balanced mixture were planted in 12 rows of 6 m long spaced by 0.8 cm. Two seeds of these mixtures were planted together with two seeds of maize variety INIAP-101 every 0.6 m (site). For the three types, 40 sites were randomly selected. On these sites only one common bean plant was allowed to grow to assess the variables. In the small plot planting system each common bean population that is part of the mixture was planted in two-row plots of 4 m long with a row spacing of 0.6 m. Two common bean seeds with two seeds of maize variety INIAP-122 were planted every 0.6 m. After germination, four sites were selected and only one common bean plant was allowed to grow for evaluation. A plant of the susceptible variety was planted every 2 m within the mixture and small plots to make the rust epidemic uniform.

Disease severity (DS) of rust in the selected plants was evaluated every two weeks using the Cobb modified scale (James, 1971). The area under disease progress curve (AUDPC) was then calculated using DS data (Shanner, G. and Finney, R.E. 1977). Number of pods per plant, number of seed per pod and the weight of 100 seeds were also evaluated in the selected plants. ANOVA and mean analyses were performed using the INFOSAT statistical program.

RESULTS AND DISCUSSION

In Cotacachi, differences in rust DS were clearly observed between the planting systems, in both allpas and chakra populations, and in all cases the DS on mixtures were lower than in plots. In the allpa population (Table 1), rust DS was significant lower, except for populations 10 and 4, in which the tendency reversed. This apparent inconsistency is most likely due to the genetic variation of some phenotypic populations, which could have overestimated or underestimated the mixture contribution; however, it should not have significantly affected the overall contribution of the mixture. In the allpa mixture the epidemic was 48% lower than in plots. In the chakra mixture the contribution was even more evident, but only for susceptible populations. Populations with DS lower than 10% in plots scored higher DS in the mixture (Table 1). In chacras, the overall contribution of the mixture was 58%.

Differences in DS among and within planting systems in the experimental station trails were also high. Low DS on mixtures compared with plots observed in on-farm experiments was confirmed in controlled-condition trials for the three common bean types (Tables 3, 4 and 5). As in the on-farm experiments, the mixture contribution mostly operated on susceptible populations, while the resistant populations showed higher DS. For the three common bean types, the contribution of the mixture to keep the disease epidemic low was significantly high, especially in chakra and mixturiados, in which the DS was 50% and 25.3% lower respectively than in plots (Table 4 and 5). The mixture contribution to keep the rust epidemic low in chakra and mixturiados demonstrates farmer rationality in using mixtures in Cotacachi and Saraguro.

The mixture also contributed to improvement of yield in on-farm and experimental condition studies, except for allpas. However, yield improvement was not correlated with DS. Correlation analysis of DS and yield was not significant either for plots or for the mixtures. Yield improvement on the mixtures was more associated with drought tolerance improvement than disease reduction. Yield improvement by the mixtures in chacras reached 25.4%. The low yield of allpas in the mixture was most likely due to plant competition with chacras, as the mixtures chacras and allpas were planted together, while in small plots, allpas were grown alone. The overall yield

contribution of the mixtures under experimental conditions was 50 kg/ha, 9 kg/ha and 160 kg/ha for allphas, chakras and mixturiados; which means a yield improvement of 14%, 1.3% and 32.2 %, respectively.

The planting system did not affect seed size and weight, since the weight of 100 seeds was similar in plots and mixtures. However, large differences in weight of 100 seeds exist among and within types (allpa, chakras and mixturiados) and are associated with the diversity of the crop.

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Table 1 Severity and AUDPC of rust, yield per plant, yield per hectare and weight of 100 seeds of allpa populations from Cotacachi evaluated in on-farm conditions in two planting systems: small plots and mixtures. Cotacachi, Imbabura-Ecuador.

Population	DS of rust ¹		AUDPC ²		yield (gr)/plant		yield (kg)/ha		100 seeds weight (gr)	
	Plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	Mixture
10	0.0 a	18.8b	0a	253b	27.1ab	7.4	564.6	153.7	37.8ab	30.3ab
3	4.0ab	1.9a	80a	29a	16.0abc	11.6	333.3	241.2	33ab	36.2ab
3.1	6.7abc	1.2a	133ab	28a	16.4abc	11.2	341.7	233.5	31.2ab	38.3ab
18	6.7abc	4.0a	200abc	60a	5.5c	8.8	114.6	182.7	47.4ab	36.2ab
4	17.0abcde	45.0c	510abc	663c	5.2c	15.2	108.3	316.7	35.0ab	37.9ab
2.2	18.8abcde	6.1ab	238ab	96ab	13.4abc	14.2	279.2	295.0	27.6ab	29.8ab
4.1	45.0cde	5.0a	1425c	38a	5.7c	17.0	118.7	353.1	35.0ab	41.2a
1	56.7de	6.5ab	700abc	99ab	29.0a	14.1	604.2	293.3	37.9ab	33.5ab
Average	19.4	11.1	410.8	158.3	14.8	12.4	308.1	258.7	35.6	35.4

¹Cobb modified scale 0-100

²Calculated using the values of DS

Table 2 Severity and AUDPC of rust, yield per plant, yield per hectare and weight of 100 seeds of chakra populations from Cotacachi evaluated in on-farm conditions in two planting systems: plots and mixtures. Cotacachi, Imbabura-Ecuador.

Populations	DS of rust ¹		AUDPC ²		yield (gr)/plant		yield (kg)/ha		weight of 100 seeds (gr)	
	plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	Mixture
48.1	5.0ab	44.0de	175a-e	919abc	9.8bcd	23.0	204.2	479.2	43.9abc	45.1ab
29	5.0ab	48.5de	175a-e	844abc	21.2abcd	16.0	441.7	333.3	47.1abc	42.7ab
65.1	15.0a-e	6.7ab	525a-g	125abc	9.8bcd	9.2	204.	191.7	46.8abc	45.8ab
29.1	16.2a-g	62.5e	519a-g	1225c	16.4abcd	26.9	341.7	560.4	50.7abc	44.4ab
45	21.7a-j	27.5bcd	438a-i	788abc	22.0abcd	35.2	458.3	733.3	62.2ab	52.8ab
58.1	22.5a-h	5.0ab	700a-i	38a	9.1bcd	13.6	189.6	283.3	46.3abc	52.7ab
64	27.5a-j	44.0de	962a-j	919abc	9.4bcd	18.7	195.8	389.6	44.0abc	46.9ab
25	36.2a-j	2.5a	1028a-j	19a	22.1abcd	16.1	460.4	335.4	43.7abc	46.1ab
28	52.0b-j	8.3abc	1750g-j	188abc	12.0bcd	13.8	250.0	287.5	63.3ab	44.6ab
67	52.0b-j	27.5bcd	1558e-j	619abc	7.1cd	22.4	147.9	466.7	39.3bc	31.4b
33	52.0b-j	44.0de	1364c-j	413abc	3.8cd	21.8	79.2	454.2	39.4bc	44.5ab
46	56.7d-j	10.0abc	1750g-j	112abc	13.2bcd	8.4	275.0	175.0	50.4abc	57.8ab
50	62.5f-j	10.0abc	1619f-j	206abc	8.7bcd	13.3	181.2	277.1	53.1abc	44.2ab
38	68.3g-j	5.0ab	1429c-j	112abc	23.6abcd	11.3	491.7	235.4	49.2abc	41.5ab
21	68.3g-j	33.3cde	2042hij	733abc	14.5bcd	15.1	302.1	314.6	67.3a	47.9ab
22	71.2hij	18.8abcd	1684g-j	431abc	8.9bcd	13.1	185.4	272.9	34.3c	40.5ab
47	71.2hij	44.0de	2144ij	863abc	5.3cd	13.4	110.4	279.2	39.3bc	35.6ab
65	71.2ij	46.8de	1838g-j	1060bc	10.3bcd	12.6	214.6	262.5	55.0abc	56.6ab
50.1	80.0j	6.7ab	1181b-j	100ab	10.4bcd	14.9	216.7	308.3	53.1abc	59.2a
Average	45.0	26.1	1204.3	511.3	12.5	16.8	260.5	349.4	48.9	46.3

¹Cobb modified scale 0-100

²Calculated using the values of DS

Table 3 Severity and AUDPC of rust, weight of 100 seeds, yield per plant and yield per hectare of allpa populations evaluated in experimental conditions in two planting systems: plots and mixtures. Tumbaco – Pichincha- Ecuador. 2010.

Population	DS of rust ¹		AUDPC ²		Weight of 100 seeds (gr)				yield (gr)/plant				Yield (kg)/ha					
	Plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	mixture				
141	5,0	A	26,2	ab	409	b	1937	c	46,4	a	45,0	a	26,0	a	20,4	ab	542	425
3	7,8	Ab	8,4	a	152	a	132	a	44,2	a	57,7	a	8,0	b	15,2	ab	167	317
140	17,5	Abc	15,0	b	413	ab	376	b	40,9	a	48,9	a	7,3	b	14,5	ab	152	301
142	20,0	Abc	32,5	b	1105	c	2865	d	54,4	a	50,7	a	23,9	a	33,0	a	498	388
1	21,3	Abcd	12,4	b	502	ab	272	ab	39,0	a	47,6	a	8,4	b	28,1	ab	175	585
143	31,3	Bcd	30,0	b	541	ab	630	ab	48,0	a	45,0	a	24,2	a	10,8	ab	225	225
6	35,0	Cd	21,0	ab	872	b	262	ab	38,4	a	44,3	a	16,2	ab	10,0	ab	338	209
2.1	37,5	Cd	32,5	b	665	b	445	ab	48,9	a	49,8	a	7,4	b	11,7	ab	154	243
9	53,8	D	28,3	b	684	b	548	ab	47,7	a	48,3	a	9,2	b	8,0	b	191	167
Average	25,5		22,9		594		830		45,3		48,6		14,5		16,9		302	352

¹Cobb modified scale 0-100

²Calculated using the values of DS

Table 4 Severity and AUDPC of rust, weight of 100 seeds, yield per plant and yield per hectare of Chakra populations evaluated in experimental conditions of two planting systems: plots and mixtures. Tumbaco – Pichincha- Ecuador. 2010

Populations	DS of Rust ¹		AUDPC ²		weight of 100 seeds (gr)		yield (gr)/plant		yield(Kg)/ha	
	plot	mixture	plot	mixture	plots	mixture	Plots	mixture	plot	mixture
	48	10,5 a	8,0 ab	776 bcd	588 bcd	50,1 a	72,8 a	21,9 abcd	16,8 cd	456
40	11,3 a	8,0 ab	1033 b-f	616 bcde	45,3 a	37,4 a	32,1 abcd	35,0 bcd	669	730
27.1	12,5 abc	9,0 ab	988 bcde	766 cdef	46,0 a	53,1 a	12,2 cd	24,4 cd	254	509
67	13,8 bc	8,0 ab	819 bc	658 cde	44,5 a	52,2 a	53,1 abc	90,0 a	1107	1876
29.1	14,3 bc	9,3 ab	1488 c-h	899 c-g	56,1 a	62,8 a	20,9 abcd	28,1 bcd	436	586
45	16,3 bcd	9,0 ab	2085 f-j	745 cde	75,6 a	58,5 a	65,9 a	14,5 cd	1374	302
29	22,5 bcde	10,0 abc	1218 b-g	943 c-g	45,7 a	49,8 a	61,2 ab	14,0 cd	1276	292
46	26,3 cdef	17,1 abc	2031 f-j	1297 c-g	54,6 a	60,1 a	43,9 abcd	41,0 bc	915	355
29.2	30,8 ef	18,3 abc	2063 e-i	1555 defg	43,7 a	55,2 a	10,8 cd	21,5 cd	225	448
28	40 efg	25,0 bc	2546 hijk	1947 fg	93,2 a	48,3 a	46,1 abcd	57,9 b	961	1207
65	47,5 gh	31,4 c	3683 kl	2219 g	63,9 a	68,3 a	14,0 cd	16,1 cd	292	336
53	67,5 h	60,0 d	3419 jkl	3842 h	50,0 a	73,1 a	17,9 bcd	38,8 bcd	373	309
21	70 h	5,0 a	3059 ijkl	332 abc	37,5 a	39,9 a	14,6 cd	23,9 cd	304	498
50	78,8 i	8,0 a	1107 bc	672 b	54,8 ab	79,6 b	28,3 ab	27,1 b	590	565
Average	33,6	16,8	1940	1220	60,7	57,9	30,4	32,1	659	668

¹Cobb modified scale 0-100

²Calculated using the values of DS

Table 5 Severity and AUDPC of rust, weight of 100 seeds, yield per plant and yield per hectare of mixturiado populations evaluated in experimental conditions of two planting systems: plots and mixtures. Tumbaco – Pichincha- Ecuador. 2010

Populations	DS of rust ¹		AUDPC ²		Weight of 100 seeds (gr)		yield(gr)/plant		yield(Kg)/ha									
	plot	mixture	plot	mixture	plot	mixture	plot	mixture	plot	mixture								
92	6,5	a	17,5	a	635	b	1514	b	47,0	ab	45,6	a	5,2	b	18,9	b	108	394
74.1	9,33	a	11,5	a	1307	bc	988	b	52,0	b	43,5	a	23,7	ab	23,6	b	494	492
125	15	ab	12,5	a	1426	bc	1067	b	82,3	c	74,4	b	6,6	b	50,0	a	138	1042
84	15,8	bc	16,0	a	2143	bcde	1396	b	49,2	ab	41,0	a	3,0	b	28,3	b	63	590
74	17,5	bc	6,8	a	2331	cde	182	a	39,9	ab	39,6	a	9,9	b	9,1	b	206	190
74.2	18,33	bcde	8,0	ab	1108	b-f	196	abc	44,0	a	46,5	a	7,0	cd	7,3	d	146	152
106	21,3	cde	8,0	ab	663	b	686	cde	64,0	a	43,8	a	22,4	abcd	7,0	d	467	146
144	22,5	cde	12,9	abc	1227	b-g	248	ab	50,0	a	51,2	a	36,5	abcd	37,2	bcd	761	775
105	25	d	20,0	abc	1395	b-g	1639	efg	52,8	a	48,5	a	25,3	abcd	19,4	cd	527	404
108	25	de	17,5	abc	1662	e-i	145	defg	37,4	a	37,6	a	11,6	cd	22,9	cd	242	477
80	26,3	def	10,0	abc	2334	ghij	112	a	48,6	a	50,7	a	43,2	abcd	25,2	cd	901	525
78	31,7	ef	14,5	abc	1369	b-g	1185	c-g	54,8	a	47,2	a	8,0	cd	23,1	cd	167	482
91	38,8	g	56,0	d	1461	b-g	3623	h	43,6	a	39,6	a	6,7	cd	19,1	cd	140	398
Average	21,7		16,2		1434		999		51,6		46,9		15,3		22,4		337	497

¹Cobb modified scale 0-100

²Calculated using the values of DS

Resistance of maize local cultivars from Cotacachi and Saraguro to *Exserohilum turcicum* in Ecuador

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INTRODUCTION

The agro-ecosystems of the highlands of Ecuador are associated with traditional agriculture in diverse ecological regions. Traditional agriculture is in turn associated with complex cropping systems in which the maize-common bean association is the key component of the system. This association is characterized by high diversity since it has been in place since early plant domestication. Cotacachi and Saraguro are indigenous areas representing the maize-common bean agro-ecosystems in Ecuador, where high diversity of maize is maintained.

Maintenance of maize diversity appears associated with agro-ecosystem stability, since the diversity can reduce the risk of biotic and abiotic stresses. Diseases are important biotic stresses that can cause serious losses. The maintenance of diversity might historically have been a key strategy for reducing crop losses due to plant diseases. Northern leaf blight (NLB) caused by *Exserohilum turcicum* (Pass.) Leonard & Suggs is a frequent disease of maize, especially in temperate areas of Ecuador, and it is a potential threat to other traditional maize areas due to climate change. Although *E. turcicum* is highly pathogenic, no serious losses are found in traditional temperate areas unless highly conducive conditions are present.

The importance of diversity might be associated with plant resistance that is contributing to the reduction of the negative impact of crop diseases. Major and minor resistance genes have been identified for *E. turcicum* (Welz, H.G. and Geiger, H.H. 2000). These two types of resistance are most likely operating in an inter-related manner and strengthening each other in traditional agriculture in Ecuador.

To study the availability of resistance to *E. turcicum* in Cotacachi and Saraguro local cultivars, a complementary analysis of on-farm and experimental conditions in Cotacachi and Saraguro was carried out.

METHODS

Field and greenhouse complementary experiments were carried out to allow better understanding of the resistance of maize local cultivars from Cotacachi and Saraguro to *E. turcicum*. Two on-farm field experiments under natural infection were conducted in Cotacachi-Imbabura and Saraguro-Loja and under artificial inoculation in Tandapi-Pichincha. In Cotacachi, the local maize cultivars (Table 1) were evaluated on three farms (replications). Each cultivar was planted in two-row plots 6 m long with row spacing of 0.8 m. In Saraguro, cultivars (Table 2) were evaluated in Llavicocha and Conchabon. These cultivars were planted in two-row plots 5 m long with row spacing of 0.8 m. A row of the variety INIAP-101 susceptible to *E. turcicum* was intercalated

between cultivars to create a uniform epidemic. In Tandapi, a representative collection of Cotacachi and Saraguro cultivars were evaluated (Table 3). The cultivars were planted in two-row plots 5 m long with row spacing of 1 m. The variety INIAP-101 was also intercalated between varieties and the race 123 of *E. turcicum* was inoculated on the variety INIAP-101. A spore suspension of 1×10^4 /ml was sprayed over the INIAP-101 plants two months after planting. This experiment was replicated and the varieties in the second replication were distributed randomly. In all experiments, lesion numbers (LN) per plant and the disease severity (DS) (James, W.C 1971) were evaluated every 14 days in 10 plants taken randomly since the epidemic initiated. The area under disease progress curve was calculated using the DS data (Shaner, G.. and Finney R.E. 1977). The lesion size (LS) was evaluated at silk stage in 10 lesions taken randomly in the same plants. Data from field studies were subjected to ANOVA and the mean analysis was calculated using Duncan and Tukey tests.

RESULTS AND DISCUSSION

The NLB epidemic was higher in Saraguro than in Cotacachi, due to warmer temperatures and high humidity. Differences in LN, LS and DS were clearly observed among regions and among cultivars (Table 1 and 2). Despite the low disease pressure in Cotacachi, differences of resistance among regions and cultivars were observed. Cultivar Morocho amarillo showed the lowest values of LN, LS and DS and the highest levels of resistance of the cultivars evaluated. Cultivar Morocho amarillo carries a new source of major gene resistance, which was easily identified in greenhouse studies (Cathme M. - Ochoa J.B, 2011). The remaining Cotacachi cultivars, although showing low values of LN, LS and DS, do not carry good levels of resistance, since the values are similar to the highly susceptible variety INIAP-101.

Most cultivars from Saraguro showed low values of LN, LS and DS. The low disease values of Saraguro cultivars result from the association of mixed expression of major resistance genes and quantitative resistance. However, quantitative resistance appears to be more important than major genes in Saraguro cultivars, since the frequency of major genes within Saraguro and Cotacachi cultivars is similar (Cathme and Ochoa. 2011). Resistance in commercial varieties varied from fairly high in INIAP-180 to very low INIAP-101 because INIAP-180 was derived from a local population of Killu sara, while INIAP-101 is an introduced variety.

In Saraguro, the NLB disease pressure was high and leads not only to differentiation in resistance among cultivars, but also to differences in pathogenicity. The plant pathogen interaction between Blanco tusilla and Mezcladito with the pathogen population of Llavecocha and Conchabon suggests differences in pathogen population among sites. Despite plant/pathogen interactions, fair levels of resistance to pathogen populations of both sites were noted. Cultivars Zhima criollo tusa roja, Blanco diente de caballo, Morocho mater, Blanco tusilla, Blanco mezcla, and Blanco criollo showed relatively low LN, LS and DS when compared with INIAP-101 (Table 2). However, high levels of resistance that could be associated with major genes were not present and the resistance appears a mixed contribution of major genes and quantitative resistance (Cathme and Ochoa. 2011). The rest of Saraguro cultivars also appear to carry some levels of resistance if compared with INIAP-101.

The resistance to NLB in natural infections in on-farm experiments was further analyzed under artificial inoculations in Tandapi-Pichincha. The differences in resistance among cultivars within sites and among sites observed in on-farm experiments were confirmed in controlled-condition studies. The high resistance of Morocho amarillo observed in Cotacachi was confirmed in this study. Field resistance of Morocho amarillo was associated with a low infection frequency and small lesion size, which was confirmed in seedling experiments (Cathme and Ochoa. 2011). Re-

Table 1 Lesion number, lesion size and disease severity of NLB of local cultivars from Cotacachi and Saraguro evaluated in CumbasConde-Cotacachi

	NLB lesion number ¹		NLB lesion size (cm) ²		NLB disease severity ³	
Cotacachi cultivars						
Morochoamarillo	3,6		7,1		7,7	
Yurasara	5,2		9,6		14,2	
Morochosblanco	5,3		9,1		14,0	
Yana sara	5,7		9,7		12,3	
Tzapasara	5,8		10,3		14,4	
Killusara	6,1		11,2		15,0	
Sangre Cristo	7,3		10,8		15,1	
Chulpi	7,8		10,4		16,7	
Average						
Saraguro cultivars						
ZhimaCriollo	2,3	a	6,8	abc	9,6	bcd
Cauqueño	2,8	ab	8,7	cd	9,0	abcd
Zhima 1	3,0	abc	7,8	abcd	7,3	abc
Perla	3,1	abcd	8,9	cd	10,7	d
Blanco dientecaballo	3,3	abcd	8,1	bcd	9,4	bcd
ZhimaAmarillo	3,4	bcd	8,1	bcd	10,5	d
Tushilla	3,9	cd	9,3	d	10,4	d
Blanco zhima	4,1	d	8,9	cd	9,1	abcd
Average						
	3,2		7,9		8,9	
INIAP varieties						
INIAP-180	3,8	a	8,6	a	12,7	
INIAP-192	5,1	a	9,2	ab	12,5	
INIAP-122	5,2	a	10,3	bc	13,7	
INIAP-124	5,3	a	9,5	ab	14,1	
INIAP-102	6,4	a	11,0	c	13,4	
INIAP-101	10,8	b	9,7	abc	18,1	
Average						
	6,1		9,7		14,1	

1. Evaluated at silk stage in 10 plants taken randomly

2. Evaluated at silk stage in 5 lesions of 10 plants taken randomly

3. Evaluated at maturity stage using the Cobb modified scale

Table 2 Number of lesions, lesion size and disease severity of NLB of local cultivars from Saraguro evaluated in Llavecocha and Conchabon - Saraguro, 2010

	NLB lesion number ¹		NLB Lesion size ²		NLB severity ³	
	Llavecocha	Conchabon	Llavecocha	Conchabon	Llavecocha	Conchabon
Shima criollo tuza roja	5,6a	3,8a	17,0 a-h	19,0 a-b	22,1 a-c	11,8 a-b
Maíz blanco diente caballo	7,2ab	7,8 a-b	21,5 f-h	23,9 b	14,0 a	19,1 a-d
Morocho mater	7,4ab	9,1 a-c	22,5 h	24,8 b	23,2 a-c	19,3 a-d
Ligerito	8,0ab	12,4 a-c	16,0 a-g	21,3 b	33,5b-d	22,9 a-d
Blanco tusilla	8,4ab	19,9 a-d	17,6 a-h	22,7 b	23,3 a-c	29,4 c-e
Blanco mezcla	10,1ab	9,3 a-c	13,4 a-c	19,8b	23,8 a-c	19,6 a-d
Shima blanco	10,6ab	12,6 a-c	21,0 e-h	23,9b	23,3 a-c	19,8 a-d
Blanco criollo	10,8ab	5,7 a	18,1 b-h	21,8b	19,0 a-b	14,8 a-c
Shima del Cerro	11,6ab	8,8 a-c	16,9 a-h	21,1b	28,5 a-d	20,0 a-d
Rocano criollo	11,8ab	13,5 a-c	15,4 a-e	21,0b	28,4 a-d	22,4 a-d
Shima amarillo	12,2ab	13,2 a-c	17,2 a-h	23,0b	26,2 a-d	23,4 a-d
Zapón mater	12,5ab	5,9 a	20,7 e-h	22,8b	29,7 b-d	17,5 a-d
Blanco	13,1ab	7,5 a-b	20,2 d-h	23,7b	30,6 b-d	18,7 a-d
Blanco zapon	14,0ab	22,9 b-d	17,2 a-h	21,4b	39,7 d	30,9 d-e
Shima	14,3ab	10,4 a-c	21,5 f-h	17,8 a-b	27,3 a-d	21,3 a-d
Morocho criollo	14,9ab	25,3 c-d	20,5 d-h	20,3b	27,7 a-d	29,3 c-e
Tusilla	15,2ab	14,9 a-c	14,7 a-d	23,9b	34,8 c-d	21,9 a-d
Amarillo criollo	16,1ab	9,1 a-c	15,1 a-e	22,4b	31,2b-d	18,8 a-d
Mezcladito	16,4ab	3,5 a	11,8 a	18,7 a-b	36,1c-d	16,1 a-d
Diente caballo	16,9ab	6,6 a-b	11,7 a	20,6b	35,3c-d	21,5 a-d
Blanco comadre	17,1ab	15,5 a-d	18,3 b-h	22,3b	35,4c.d	23,7 a-d
Chauqueño	17,3ab	3,4 a	14,2 a-c	9,9 a	33,0b-d	8,6 a
Shima negro	17,5ab	11,0 a-c	16,3 a-g	22,4b	34,4c-d	21,8 a-d
Floreado mater	17,5ab	13,3 a-c	21,6 g-h	23,7b	28,9	20,0 a-d
Guarami blanco	18,7ab	14,4 a-c	13,8 a-c	23,3b	33,0	25,7 b-d
Shima blanco	19,0ab	8,6 a-c	19,1 c-h	22,8b	36,9	20,2 a-d
Blanco criollo	20,4ab	10,8 a-c	17,1 a-h	21,5b	32,7	19,5 a-d
Blanco	21,3ab	8,6 a-c	12,8 a-b	22,8b	32,2	18,2 a-d
INIAP 101	21,8ab	32,1 d	12,7 a-b	18,3 a-b	90,0	41,2 e
Zapon amarilla	22,6ab	6,9 a-b	18,9 c-h	24,2b	35,5	20,0 a-d
Mezcladito	22,7ab	5,8 a	20,9 e-h	24,8b	28,7	17,4 a-d
Criollo shima	23,4ab	15,6 a-d	20,5 d-h	22,7b	35,6	24,4 b-d

Table 2: continues next page

Table 2: continued

	NLB lesion number ¹		NLB Lesion size ²		NLB severity ³	
	Llavecocha	Conchabon	Llavecocha	Conchabon	Llavecocha	Conchabon
Tzapa	20,8	17,0 a	18,5 a	25,2 a	34,4	27,0 a
Sangre de Cristo	22,9	27,8 a	18,5 a	22,4	35,4	32,1 a

1. Evaluated at silk stage in 10 plants taken randomly
2. Evaluated at silk stage in 5 lesions of 10 plants taken randomly
3. Evaluated at maturity stage using the Cobb modified scale

Table 3. Severity, number of lesions, lesion size and AUDPC of Northern Leaf Blight in a core collection of maize from Cotacachi and Saraguro evaluated to race 123 inTandapi-Pichincha. 2011

Cultivars	Disease Severity (%) ¹		Number of lesions ²		Lesion Size (cm) ³		AUDPC ⁴		
Cotacachi cultivars									
Morochoamarillo	1,5	a	0,7	a	2,4	a	23,9	A	
Yana sara	10,5	b	7,5	a	8,5	b	219,5	B	
Chulpi	28,7	c	21,2	b	11,5	bc	573,5	Bcd	
Killusara	30,7	c	23,0	b	11,8	bc	594,4	Bcd	
Yurasara	35,0	c	21,5	b	14,7	c	585,8	Bc	
Morocho blanco	37,2	c	27,3	b	12,7	bc	729,4	Cd	
Tzapasara	45,0	c	30,0	b	13,4	bc	924,4	D	
Average	26,9		18,7		10,7		521,6		
Saraguro cultivars									
Zhimacriollo	4,1	a	3,5	a	7,9	A	105,7	Ab	
Amarillo zapón	4,2	a	2,0	a	8,1	A	95,8	A	
Floreado	4,5	ab	3,2	a	9,9	ab	80,6	Ab	
Tusilla	5,2	ab	2,4	a	11,2	ab	107,8	Abc	
Blanco cristal	12,7	bc	11,2	ab	20,3	bc	238,9	Bcd	
Zhimaamarillo	20,0	c	18,9	b	24,4	c	354,9	Cd	
Diente de caballo	20,3	c	19,8	b	25,6	c	415,5	D	
Morocho del cerro	23,4	c	19,4	b	27,4	c	491,7	D	
Blanco zhima	24,0	c	16,7	b	26,2	c	419,9	D	
Average	13,2		10,8		17,9		256,7		
Iniap 101	92,5		-		-		1855,0		

1. Evaluated at maturity stage using the Cobb modified scale
2. Evaluated at silk stage in 10 plants taken randomly
3. Evaluated at silk stage in 5 lesions of 10 plants taken randomly
4. Area Under Disease Progress Curve

sistance of Morocho amarillo at seedling stage was also characterized by a long incubation period if lesions developed; however this resistance is mostly associated with immunity (Cathme et al 2011). The field resistance of Yana sara from Cotacachi and Zhima criollo, Amarillo zapón, Floreado and Tusilla from Saraguro is clearly associated with few lesions and medium LS (Table 4). The resistance in these cultivars appears of partial nature since most of the population on these cultivars showed intermediate to susceptible reaction types at seedling stage (Cathme and Ochoa. 2011). This also suggests that it is difficult to discern partial resistance at seedling stage.

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Screening of Ugandan farmers' bean varieties for resistance to angular leafspot caused by PHAEOSARIOPSIS GRISEOLA

Olango, N.; Paparu, P.; Mulumba, J.W.

INTRODUCTION

In East Africa, angular leaf spot (ALS) disease caused by *Phaeoisariopsis griseola* is among the most important biotic constraints to common bean production (Wortman *et al.*, 1998). ALS causes losses ranging from reduced yield resulting from reduced photosynthetic area to reduced seed quality and marketability. In Uganda losses are further aggravated by the fact that the majority of farmers do not use fungicides on beans, partly because farmers think that the additional yield obtained may not offset the associated input costs (Kisakye and Ugen-Adrogu, 1990).

Although using varieties resistant to ALS is the most realistic management approach, farmers still plant susceptible varieties because of certain good qualities they usually possess. Unfortunately, breeding of varieties with all farmer-preferred attributes in addition to disease resistance is extremely difficult. Therefore, in order for farmers to maintain their susceptible but desired varieties and reduce the effect of diseases, alternative control options need to be explored. One such option is the use of varietal mixtures (Mundt, 2002; Chakraborty *et al.*, 1995). This study was therefore designed to identify resistant and susceptible varieties for use in varietal mixture trials, aimed at reducing damage caused by ALS disease.

METHODOLOGY

Forty three farmer bean varieties (10 climbers and 33 bushes) were used. Varietal ALS disease severity was evaluated in the screenhouse and in on-station trials. Not all varieties were represented in both trials due to seed shortages. For the screenhouse trial, each variety was planted in a bucket and replicated three times. The buckets were then laid out in a completely randomized design. At 21 days post-planting, they were inoculated with mixture of *P. griseola* isolates collected from bean fields in Nakaseke, Kabwohe and Kabaale districts. The inoculated plants were placed in a humid chamber for four days, after which they were removed. Disease evaluations were done at 10, 12, 14, 17, and 21 days after inoculation (Mahuku *et al.*, 2004), using the 0-5 scale (Ingliš *et al.*, 1988), whereby 0= no disease symptoms, 1= 1-10 % leaflet area with lesions, 2= 11-25% leaflet area with lesions, 3= 26-50% leaflet area with lesions and limited chlorosis, 4= over 50% lesions and extensive chlorosis and 5= complete defoliation.

The on-station field trial was laid out in completely randomized block design (CRBD) with three replications. Within each block, climbing varieties were planted together separate from the bush varieties to avoid any microclimatic effect of the climbers on bush varieties. The varieties were planted in 6m rows 1m apart with an inter-plant spacing of 10cm for the bush type and

20cm for climbers respectively. The experiment relied completely on the natural field inoculum for disease development.

Disease development and progress was assessed using disease symptoms on the first trifoliolate leaf. Six plants from each row were selected at 1m intervals and assessed for disease incidence and severity at the three key bean developmental stages namely: at flowering (R6), pod initiation (R7) and pod filling (R8) stages. Disease incidence was first recorded as 0 or 1; whereby 0 = no disease and 1= disease present. The same plants were assessed for ALS disease severity using the 1-5 scale described by Inglis *et al.* (1988). Disease incidence and severity data were both subjected to analysis of variance.

RESULTS

Screenhouse disease evaluation

The results show that there is a significant difference ($P > 0.001$) between bean varieties in their reactions to ALS with Mexico 54 (the resistant check) showing no reaction at all. The other varieties which showed low severity of ALS included: Shemenoha, Katosire, NABE 10c, Kishoga, Ngwinorale (NABE 8c), Kankuryemabarukye, Kankuryemabarukye purple, Brown Nico, NABE 13 and NABE 14 (Shemenoha having the least severity). Most of the varieties screened, however, had very high disease scores with up to 15 varieties ranging from Kasirira to Kankuryemabarukye army green (see fig. 1) having the maximum disease severity score of 5.

On station field disease evaluation

We observed that all varieties screened were infected with ALS, including the resistant check. However, there was a significant difference ($P > 0.001$) among varieties in their disease severity levels. Naka small red showed the least disease severity levels with a score of 1. The other varieties which showed low reaction to ALS with a mean severity score of between 1.1 and 1.4 included Rushare II, NABE 10c, Mexico 54, NABE 13, Kahura, Kayinja, Akeru short, Kasirira, Shemenoha, Nambale short and Kahura short.

DISCUSSION

In both screenhouse and field experiments the disease was present, however screen house infection levels were higher (0-5 in screen house compared to 1-3 in the field). This may be attributed to the fact that artificial inoculation was used in the screenhouse and also conditions of inoculation were specifically suitable for ALS disease development. However, in the field the experiment relied completely on the field inoculum and the environmental conditions may have been unsuitable for disease development and progress. Furthermore, the field used was fairly new having been used only once to grow beans in the previous season; it thus had low levels of inoculum. A few varieties, namely Mexico 54, Shemenoha, NABE 10c and NABE 13, showed low disease severity levels both in the field and in the screenhouse. Of these Shemenoha is an indigenous variety while the rest are improved. The fact that none of the above varieties showed complete resistance both in the field and on-station demonstrates the difficulty in selecting for complete resistance to the disease. This was also corroborated by Allen *et al.*, 1998. We speculate that the difference in reaction could have been due to differences in pathogen pathotypes between isolates used in the screenhouse and those that were present in the field. We however could not confirm the foregoing as we did not conduct pathogenecity tests on the isolates. These

results, however, are not conclusive because more data is currently being analysed for the repeat of the greenhouse experiment, and a repeat of the on-station experiment is planned for this season (March-July 2011).

Figure 1 Greenhouse mean severities of ALS disease on farmer varieties as assessed on day 21 after inoculation

S/no	Variety	Severity	S/no	Variety	Severity
1	Mexico 54	0.0	26	kabwejagule	4.6
2	Nshemenoha	0.2	27	Kanyobwa short	4.6
3	katosire	0.8	28	Mahega long	4.7
4	NABE 10c	1	29	Yellow short	4.7
5	Kishoga	2.1	30	Karolina	4.8
6	Ngwinorale	2.3	31	Kaki short	4.8
7	Kankuryembarukye	2.3	32	shemererwa	4.9
8	Kankuryembarukye purple	2.3	33	Kachwekano	4.9
9	Brown niko	2.6	34	Kasirira	5.0
10	NABE 13	2.8	35	Manyigumulimi	5.0
11	NABE 14	2.8	36	Naka beauty	5.0
12	Kanyobwa long	3.0	37	Naka brown dotted	5.0
13	Bukanja	3.2	38	Naka small red	5.0
14	Mamesha	3.3	39	Nambaale long	5.0
15	Rushare purple	3.4	40	Nambaale short	5.0
16	Kayinja	3.7	41	Rushare	5.0
17	Bwiseri	3.8	42	Shemererowa	5.0
18	Nakawunde	4.0	43	Sugar 31 red	5.0
19	akeru long	4.0	44	Gantagasize	5.0
20	Nakyewogola	4.2	45	Kadugala	5.0
21	Kihura	4.3	46	Kahura short	5.0
22	Akeru short	4.3	47	Kakulungu	5.0
23	Kakururwe	4.3	48	Kankuryembarukye army green	5.0
24	Yellow long	4.6		LSD	1.455
25	Musoke's beans	4.6		%cv	23.1

Figure2 Field mean severities of ALS disease on farmer varieties as assessed at pod filling

S/no	Variety	Mean severity	S/no	Variety	Mean severity
1	Naka small red	1.0	23	Rushare purple	1.6
2	Rushare II	1.1	24	Kankuryembarukye Army green	1.6
3	NABE 10c	1.1	25	Nambaale long	1.6
4	Mexico 54	1.2	26	Kihura	1.7
5	NABE 13	1.2	27	Karolina	1.8
6	Kahura	1.2	28	Yellow short	1.8
7	Kayinja	1.2	29	Kanyobwa long	1.9
8	Akeru Short	1.2	30	Kankuryembarukye purple	1.9
9	Kasirira	1.2	31	Nakawunde lajja	1.9
10	Shemenoha	1.2	32	Mahega	1.9
11	Nambaale short	1.4	33	Shemeshenowa	1.9
12	Kahura short	1.4	34	Brown Nico II	2.0
13	Kadugala	1.4	35	Kaki short	2.0
14	Mamesha	1.4	36	Naka brown dotted	2.1
15	Yellow long	1.5	37	Kanyobwa short	2.2
16	Katosire	1.5	38	Sugar 31 red	2.3
17	Nakyewogola	1.5	39	Gantagasize	2.3
18	Akeru long	1.6	40	Naka beauty	2.4
19	Kishoga	1.6	41	Kankuryembarukye	2.4
20	Bwiseri	1.6	42	Kachwekano	2.6
21	Mahega short	1.6	43	Kakulungu	3.1
22	Manyigumulimi	1.6		LSD	0.5
				%CV	47

Variation in host resistance in the traditional rice varieties maintained by farmers

Yang Xuehu; Yuan Jie; Jiang Jian; Liu Xia; He Haiyong; Chen Xiaojun; Wu Shiping.

INTRODUCTION

Meitan is an agricultural county in Guizhou Province, China. Rice is the major food crop, and rice blast often causes serious yield losses each year. To understand the utility of local crop diversity in reducing disease damage, we measured resistance under farmers' conditions in expanded trials/plots on farmers' fields and through participatory assessment and field analysis.

MATERIALS AND METHODS

Materials

Traditional rice varieties were collected from Yunnan, Guizhou and Sichuan Provinces in China, including two locally susceptible and resistant varieties as check.

Methods

(1) Option 2—On farm trials

Three villages in the Meitan project site were selected with one farmer per village. Three replicates per variety were used, with each replicate grown on a different farmer's field. Each farmer was from a different village. The plot size for each variety was 2 m² with 30 individuals. Ten panicles were surveyed at maturity.

(2) Option 4—Experimental station trials – disease nursery

The plot size per variety was 2.7m². Planting spacing was 30cm×15cm. Agronomic practices were according to local agricultural practices for managing fields. For plot array see Figure 2. For standard of surveying see GB/T 15970-1995 (China).

RESULTS AND CONCLUSIONS

Of the 63 varieties in the on-farm trials, three did not flower, 13 showed resistance to panicle blast with an average percentage of 21.67%, and others were susceptible (see Table 1 and Figure 3). For a variety with resistance from HR to HS, resistance to panicle blast among the 30 individuals varied. For example, Chujing-27 was highly resistance to panicle blast, but also had susceptible

individuals (see Figure 4). Clearly, there were variation of resistance to panicle blast among and within traditional rice varieties. In the experimental station trials, the result of the disease nursery showed that 38, 14 and 6 varieties had HR, R and MR to leaf blast with percentages of 65.51%, 24.14% and 10.34% respectively (see Figures 5, 6).

For panicle blast, no varieties displayed better resistance. Only 11 of the 51 varieties were medium susceptible, with the percentage of 21.57%. And these varieties were also resistant to leaf blast. All these traditional varieties had better resistance to leaf blast than that to panicle blast. Through the surveys and analysis of the data on farmer trials and experimental stations, we found that diversity in resistance with respect to rice blast exists in the traditional varieties maintained by farmers, not only among varieties, but also within varieties.



Figure 1 Traditional rice varieties demonstration on farmer's field

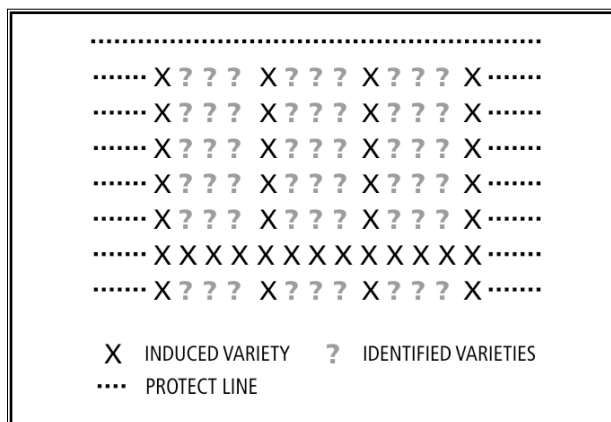


Figure 2 Plot Arra

ACKNOWLEDGEMENTS

We thank participating farmers, project partners, Bioversity and UNEP/GEF

Table 1: Varieties with better resistance

HR	3	Qiena, Zhangmeleng-1, Chujing-27
R	1	Modelong-1
MR	9	Chengnuo-88 Nuoyou-9 Baiyangnuo Qiejiaba Qiege Chujing-24 Bendipinzhong Dulong-1 Xiangnuo

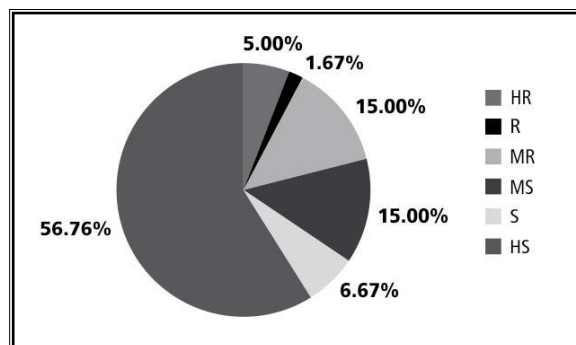


Figure 3: Percentage of resistance ranking

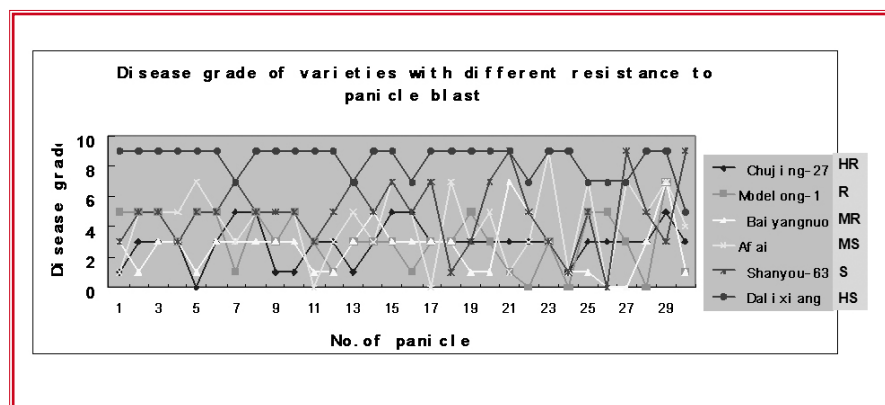


Figure 4 Disease grade of varieties with different resistance assessment

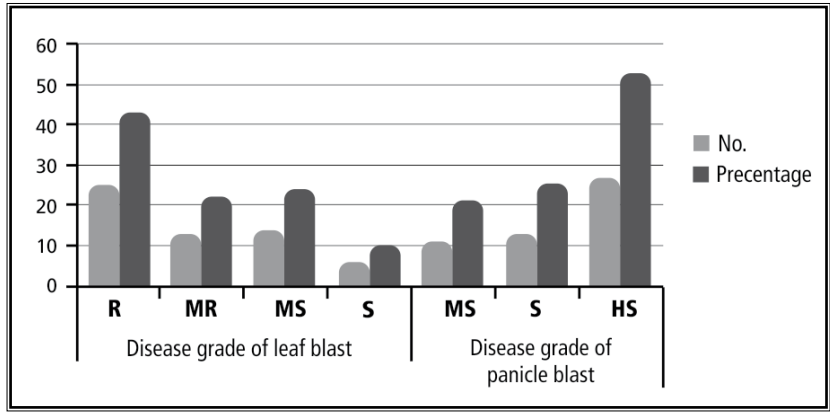


Figure 5 Result of resistance identification in field disease nursery

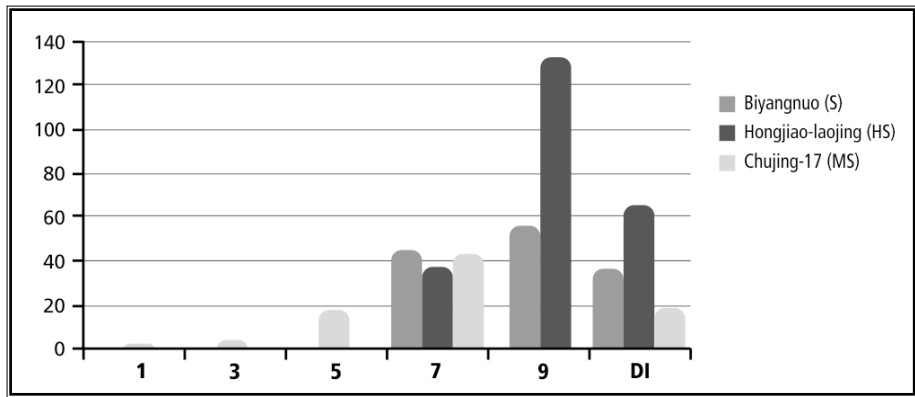


Figure 6 Variation of resistance to panicle blast within varieties

Variation in host resistance to chocolate spot within and among traditional cultivars in faba bean maintained by farmers in Morocco

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INTRODUCTION

Chocolate spot disease caused by the fungus *Botrytis fabae* is the most destructive leaf disease in Morocco. The infection of faba bean by this pathogen is of two types, "aggressive," causing blackening and death of part of the whole plant, and "non-aggressive," causing discrete chocolate-coloured lesions. The pathogen is necrotrophic and infects, colonizes and kills living tissue to obtain energy to grow and multiply.

There are two types of resistance of faba bean to chocolate spot, as there are for other diseases: specific resistance interferes with the disease cycle by totally preventing the emergence of symptoms and/or the production of spores. Partial resistance interferes with one or more of the steps of the cycle, resulting in slowing disease progress and/or reducing pathogen multiplication.

Only varying levels of quantitative resistance have been reported in the Faba-*Botrytis* system. Bouhassan et al. (2004) detected significant differences among genotypes for reactions to the disease in the field. However, no complete resistance was observed. Although differences in the virulence of isolates have been reported (Hutson and Mansfield, 1980), and the existence of races has been proposed (Hanounik and Maliha, 1986), no comprehensive description of races of *B. fabae* has been carried out so far. A set of differential lines should first be established, and then used to evaluate the virulence of a collection of isolates of diverse origin under the same environmental conditions.

In order to determine whether intra-specific diversity with respect to disease resistance exists within the sites in Morocco, farmers' perception and field observations, as well as on-farm, on-station and glasshouse experiments, were used to assess the variability of the resistance of faba bean varieties and populations to chocolate spot.

MATERIAL AND METHODS

Farmers' perception of the resistance of the faba bean varieties to chocolate spot

Data on farmers' perception of the resistance of faba bean varieties to chocolate spot were obtained during HH surveys and ranged in scale from 0 to 3. The most resistant varieties were scored 3.

Disease evaluation in the farmer's field

For the evaluation of the reaction of faba bean varieties to chocolate spot, a visual notation based on a 0-3 scale was utilized. The categories of the scale were 0: absence of disease; 1: few spots on lower leaves; 2: spots up to 50% of leaves; 3: spots on leaves and stems.

On-farm and on-station experiments

A collection of 100 populations of faba bean from the sites was evaluated both on-farm and on-station. On-farm trials located at Galaz, Tissa and Ourtzagh were conducted following the same practices utilized by farmers. In each site, the collected populations were planted in one bloc. Each population was planted in four rows, one meter each. An on-station trial was implemented at M'rissa experimental station located 160 km north of Rabat. The collected populations were planted in one bloc. Each population was planted in four rows, one meter each.

In all trials, the reactions of the plants were scored at pod formation. For each population, 10 plants were scored individually. The reactions of plants to *B. fabae* were scored according to a 1-5 visual scale. The scale is based on a combination of lesion type, lesion frequency and extent of damage, with 1: no symptoms or very small spots; 2: very small and discrete lesions; 3: some coalesced lesions with some defoliation; 4: large coalesced sporulating lesions, 50% defoliation, some plants dead; 5: extensive lesions on leaves, stems and pods, severe defoliation, heavy sporulation, blackening and death of more than 80% of the plants.

Glasshouse experiment

The evaluation of the resistance of the 100 populations of faba bean was conducted in a glasshouse against two isolates of *B. fabae*. These isolates were purified from lesions of the aggressive form of the pathogen. The isolates were grown and increased on Faba Bean Leaf Agar. A water solution of 3.106 spores/ml was obtained and sprayed onto seedlings of faba bean. The inoculated plants were placed in a moist chamber for 24 hours and then moved to a glasshouse. The reactions of the inoculated plants were scored 15 days after inoculation, using the 1-5 scale described above.

Statistical analysis

The data collected in the experiments were analyzed for variance. Mean comparisons and multivariate analysis of the collected data were also conducted using SPSS.

RESULTS AND DISCUSSION

Farmers perception of the resistance of faba bean varieties to chocolate spot

The farmers consider that in general some varieties of faba bean are resistant to chocolate spot, while others are susceptible. However, the farmers' perception of resistant varieties differed from one site to another (Figures 1-3).

According to the varietal composition of each community, farmers classify their landraces depending on the degree of resistance to chocolate spot. In Ourtzagh, farmers found Hmami to be the most resistant. Galaz farmers argue that the two varieties Sbai beldi and Tsai Roumi are the

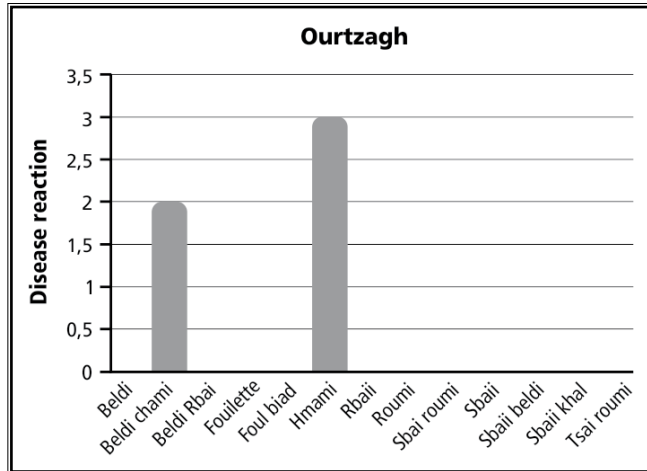


Figure 1. Farmers' perception of the resistance of faba bean varieties to chocolate spot at Ourtzagh site

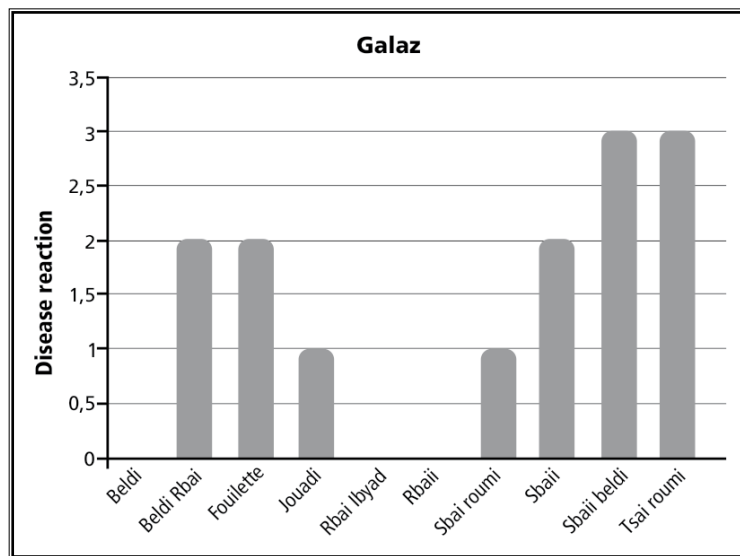


Figure 2. Farmers' perception of the resistance of faba bean varieties to chocolate spot at Galaz site

most resistant. Farmers from Tissa believe that varieties Abriti, Fouillette, Sbai beldi and Hjawi are more resistant than the other varieties.

Disease evaluation in the farmer's field

The information on the assessment of the disease severity for each cultivated variety is presented in figures 4-6. In Ourtzagh site, mixtures (Beldi Rbai-Sbaii, Beldi-Roumi, Beldi rbai-Foui-

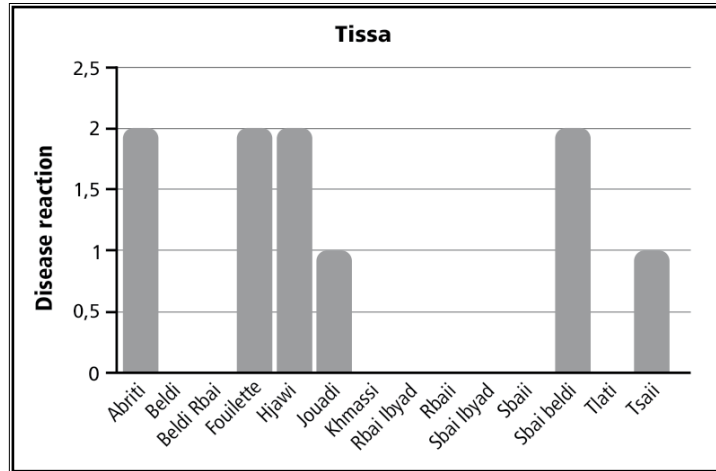


Figure 3. Farmers' perception of the resistance of faba bean varieties to chocolate spot at Tissa site

lette) and Beldi rbai and Beldi chami varieties appear to be susceptible to chocolate stains. Sbairi beldi, Rbairi and Sbairi varieties appear less often attacked by this disease. While Beldi, Sbairi roumi varieties and mixtures (Beldi-Sbairi, Beldi Rbai-Roumi and Sbairi-Rbairi) have little spots, indicating that these varieties may be resistant to the disease.

In Galaz site, the varieties the most affected by the disease are Rbai lbyad, Sbairi Beldi and Sbairi Roumi. Varieties Rbai, Sbairi Beldi and mixture (Beldi-Sbairi) are less attacked, while the Beldi variety and mixtures (Beldi-Rbai-Jouadi, Beldi rbai-Sbairi and Sbairi beldi-Jouadi) have the lowest average rating (Figure 5).

The notation at the Tissa site revealed remarkable differences between varieties for their reaction to chocolate spot. Indeed, the varieties Fouillette, Rbairi, Beldi, Abriti and khmassi were heavily attacked by disease, Jouadi, Sbairi beldi, Sbairi, Beldi rbai and Hjawwi varieties were less attacked. Mixed varieties expressed the lowest ratings of disease reaction (Figure 6).

On-farm and on-station evaluation of faba bean populations to chocolate spot

On-farm experiment

Only the results from Tissa site are presented here. The difference in the reaction to chocolate spot between populations of faba bean was highly significant. Also highly significant were differences obtained between populations according to their origin. The ranking according to a Duncan test (Table 1) indicated that the faba bean populations collected from Tissa and Ourtzagh were similar in their reaction to chocolate spot.

On-station experiment

The disease level was high in the station. Highly significant differences were found between populations of faba bean for their reaction to chocolate spot. Also, highly significant differences were obtained between populations according to their origin: the populations originating from

Ghafsay (mean reaction = 4.17) were more susceptible than the populations from Ourtzagh (mean reaction = 3.7) and Tissa (mean reaction = 3.6). According to their reaction to *Botrytis faba*, 17 Ghafsay populations were highly resistant, 38 were moderately resistant, 18 moderately susceptible and 45 were susceptible. In Ourtzagh, according to their reaction to *Botrytis faba*, 12 populations were highly resistant, 29 were moderately resistant, 28 moderately susceptible and 31 were susceptible.

Glasshouse experiment

The evaluation of sources of resistance in faba bean carried out in the laboratory was performed by using two isolates of *Botrytis* from two different regions (Taounate and Larache). The result

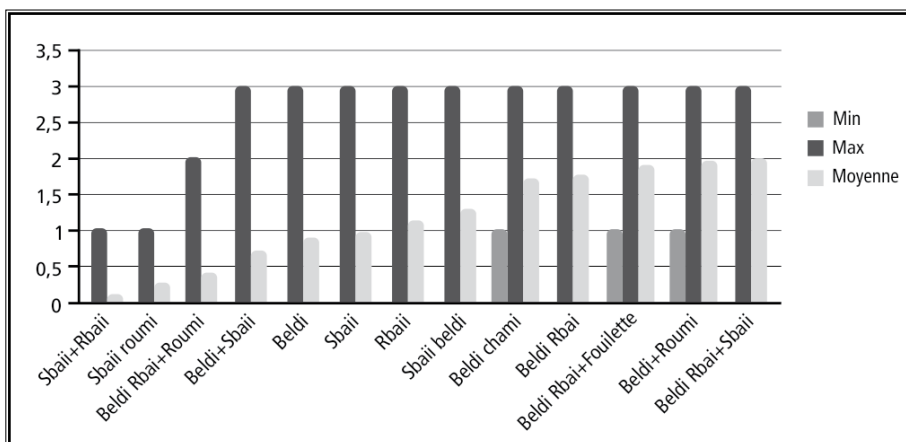


Figure 4. Field scoring of Botrytis in the Ourtzagh community

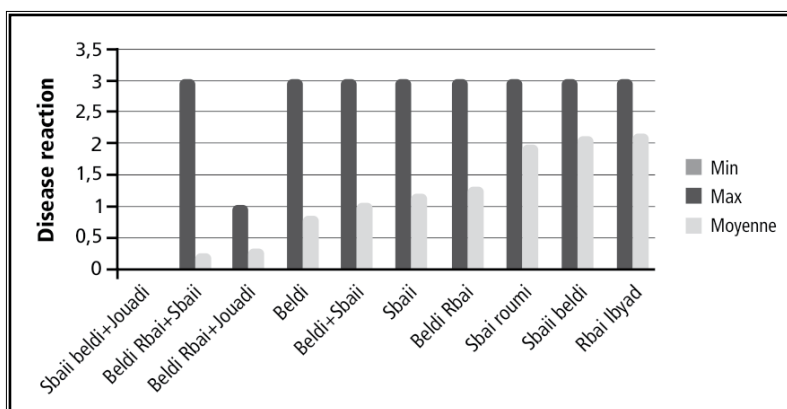


Figure 5. Field scoring of Botrytis in the Galaz site

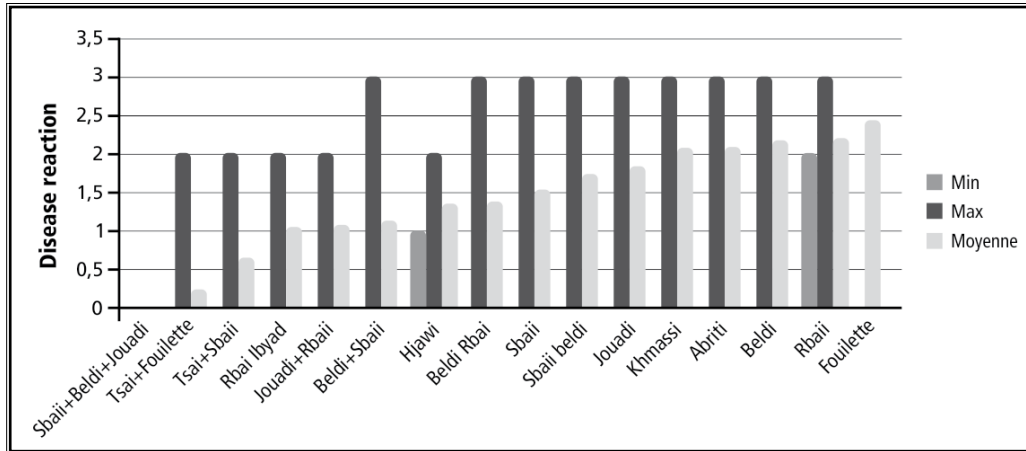


Figure 6. Field scoring of Botrytis in Tissa community

Table 1. Mean comparison of the reactions to chocolate spot of faba bean populations according to their origin (on-farm experiment)

	Site	N	Sous-ensemble pour alpha = 0.05	
			1	2
Duncan	Tissa	819	2,48	
	Ourtzagh	60	2,68	2,68
	Ghafsay	1096		2,72
	Significance		0,053	0,722

indicated that the local populations react the same way against both isolates and the majority of populations were susceptible (79 populations) while only 21 were resistant.

The experiments conducted on-farm, on-station and in the glasshouse indicated that a whole range of reactions was observed from susceptibility to resistance. The populations of faba bean reacted differently to chocolate spot according to their origin. These preliminary results suggest the presence of diversity of resistance in faba bean (Bouhassan et al., 2004) and the possible specialization of the pathogen (Hutson and Mansfield 1980).

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Variation in host Resistance within and among traditional cultivars in banana in the traditional varieties maintained by farmers in Ecuador

Suárez-Capello, C.; Agama, J.; Vera, D.; Cabanilla, M.

Introduction

The epidemic of Black Sigatoka disease that broke out in Ecuador around 1990 affected initially the large plantain area of El Carmen in the northern part of the coastal plain and then spread south into the commercial banana area, using as a bridge all the *Musa* cultivars that constitute part of any farming system in the region. The banana farmers soon incorporated in their management practices the intensive use of fungicides to cope with the disease. This, however, has proven inadequate for the northern coastal plain due to several factors. The type of farmer (smallholder, resourceless) and the production systems (nearly subsistence, low input) could be nominated as the main ones. Studies conducted to deal with the devastating disease reveal other constraints endemic to the crop: Black weevil, caused by ***Cosmopolites sordidus*** and nematodes (***Meloydogine*** sp, associated with poor or absent cultural practices, render the crop very susceptible to the disease. Eventually, traditional and alternative strategies were pursued by organizations of technical assistance to reduce the impact of those pests. Crop sanitation, cultural and biological control and management practices were used to set in place a holistic approach, tailored to meet the needs of the small farmer. Additionally, building farmers' capacities in basic IPM principles produces good results, doubling and tripling yields to a more sustainable level. However, the identified constraints, i.e., Black Sigatoka, black weevils and nematodes are still causing losses in the range of 50 to 70% and other alternatives are needed.

The possibility of integrating intraspecific diversity to the above-mentioned strategy introduced by the project "Conservation and Use of Crop Genetic Diversity to Control Pests and Disease in Support of Sustainable Agriculture" opens an interesting approach for the farmers and the region.

METHODS

At the onset of the project, cultivar diversity on farms was identified, direct and secondary information from other activities in the region was identified, data on cultivar performance and their pests were collected through farmer group discussions and a household survey was carried out on 126 farms in two sites (62 in El Carmen and 64 in La Mana). A database was prepared using an SPSS program and then first analyses were performed with MS Excel data sheets.

Resistance response of cultivars to black sigatoka, corm borer and nematodes (*Meloydogine* and *Radopholus* spp) was evaluate through experiments in the lab and shadehouse using standard

procedures. In each case 10 to 12 cultivars were evaluated. Ten plants/cultivars with four repetitions were used under a randomized block design; they were kept in a shade house with regular irrigation to observe damage development.

RESULTS

Data analysis is *still* in progress due to the lack of local expertise *and experiments are also pending* due to the requirement of 10 to 14 months for the cultivars in use to complete *their* cycle; however, a clear picture is emerging showing zones *with a* tendency to single crop systems as areas where a single cultivar *predominates* (Barraganete (AAB) and Orito (AA) in El Carmen and La Mana) respectively. *These cultivars* present larger concentrations of nematodes (Figure 3), Black weevil (Figure 1) and Black Sigatoka (Figure 2) damage respectively.

All AAA and AA cultivars showed (Figure 4) moderate resistance to *Meloidogyne* as opposed to *R. similis*, which found similar resistance only for Gross Michael (AAA) and Orito (AA); cultivars Williams and Guineo de jardín, though belonging to the same genome as Gross Michael, showed high susceptibility for this nematode. All plantain cultivars (AAB) performed as susceptible or highly susceptible to both nematodes.

A similar situation was found for cultivars evaluated against black sigatoka where symptom development in a six-stage scale and time of development of the disease in days from inoculation grouped cultivars, independently of the evaluation procedure, into three categories of resistance: the Orito (AA) and Limeño (AAB) showed resistance; one AAA (Maqueño Verde) and all the AAB tested showed moderate resistance and the rest of the AAA performing as susceptible (see poster and figure 6).

As for black weevil, the experiment was set up in a highly infested field, leaving corms of all cultivars exposed to weevil attack before planting as a more reliable method. Results to date

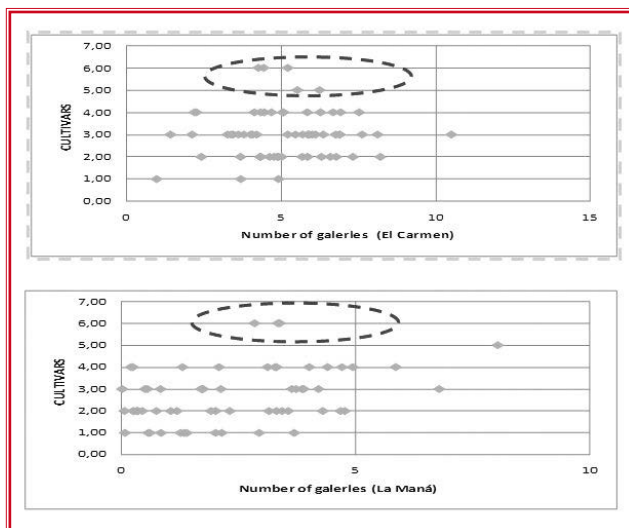


Figure 1 Black weevil damage (corm galleries) in two Ecuadorian sites in relation to number of *Musa* cultivars Pichilingue, Ecuador, 2011

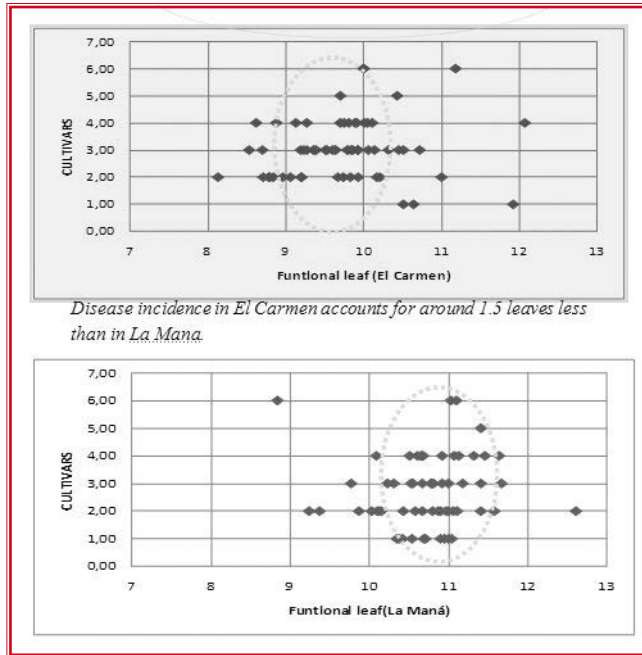


Figure 2: Richness in two sites related to black sigatoka damage level on Musa cultivars, measure as number of functional leaves. INIAP, Ecuador 2011

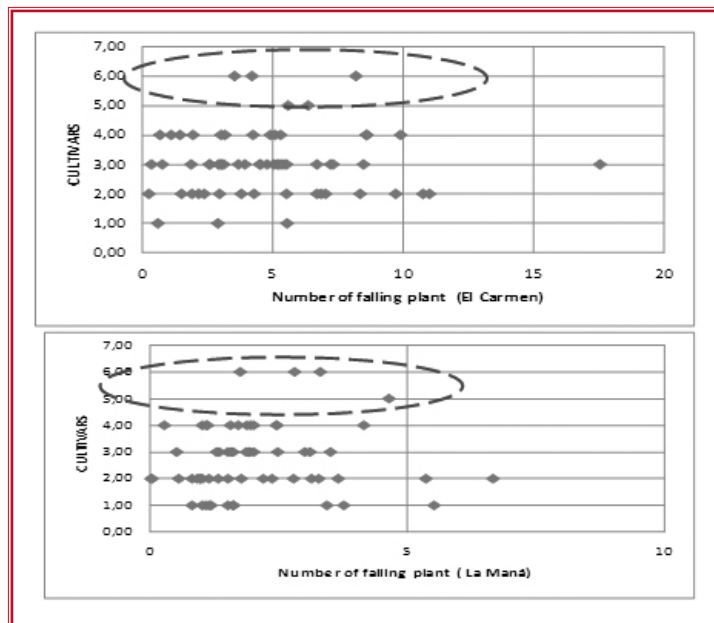


Figure 3: Number of cultivars (richness) related to nematode damage as number of fallen plants in two sites Ecuador, 2011

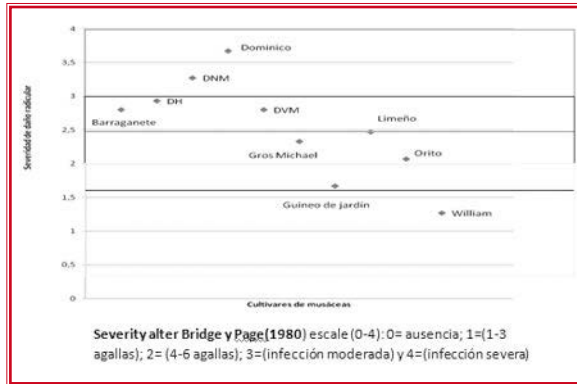


Figure 4 Population of nematodes (*Meloydogine* sp) in 100 grams of roots of 10 *Musa* cultivars 16 weeks after inoculation. EET-Pichilingue 2010.

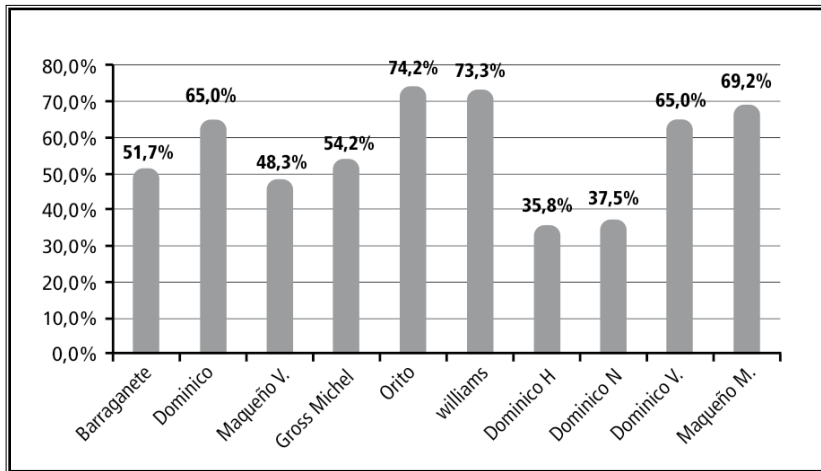


Figure 5 Percentage survival of ten *Musa* cultivars after black weevil, with corns submitted to attack before planting. San Agustín-El Carmen, Ecuador, 2011

(seven months from planting) show a clear preference of the insect for cultivars Dominico hartón barraganete and Dominico negro (AAB), with 76% and 65% mortality respectively. On the other hand, Orito, Williams and Maqueño morado presented resistance with only around 25% mortality or correspondingly 75% survival under the same circumstances.

DISCUSSION

Cultivars under analysis with the best response against the three constraints seems to corroborate those findings, as shown by the HH survey analysis, i.e that a mixture of cultivars may

contribute to both controlling the main pests of the crops and to improving the livelihoods of farmers who could enhance its commercial possibilities (El Carmen case) with other cultivars demanded by local and international markets, and widen their sustainability as in the case of La Mana, where more commercial varieties can be introduced while simultaneously conserving the local ones. We can not envisage a conventional breeding program with *Musa* due to well-known difficulties, but certainly it looks possible to design cropping systems in the interest of farmers using only the available varieties. Crop diversity is showing the way to a lower impact of pests, which reduces the intensity of the problem, allowing farmers to put other IPM practices into place to improve yield with minimum or no pesticide usage.

Figure 6 Black sigatoka stages of development in time (TDE - days) for twelve *Musa* cultivars artificially inoculated with the fungus. INIAP, 2011

Cultivars	TDE	Category
Orito (AA)	75,5	Resistance
Limeño (AAB)	71,25	
Maqueño Verde (AAA)	59,38	Moderately resistant
Dominico Negro (AAB)	58,38	
Dominico Hartón (AAB)	57,38	
Dominico (AAB0)	57,25	
Barraganete (AAB)	55,75	
Dominico gigante (AAB)	55,38	
Guineo de jardín (AAA)	49,75	Susceptible
Filipino (AAA)	49,25	
Gros Michel (AAA)	48,88	
Williams (AAA)	48,88	
X±(0.4881)		
	X	57,25
	S	8,53

TDD- Time of disease Development

Farmers' perception of host resistance to black sigatoka within banana cultivars maintained by farmers in Uganda

Lwandasa, H.; Kubiriba, J.; Mulumba, J.W

INTRODUCTION

Black sigatoka disease, caused by *Mycosphaerella fijiensis*, is the second most devastating disease of banana and plantain. It is spread through air-borne conidia and ascospores. After disposition, the conidia penetrate the stomata and undergo several phases (biotrophic and necrotrophic phase), resulting in abundant cell death that turns the leaves fully necrotic (Rodriguez-Garcia *et al.*, 2010). The disease decreases photosynthesis, reduces fruit size and induces early maturation in susceptible banana cultivars and thus leads to yield reductions that may exceed 50% (Rodriguez-Garcia *et al.*, 2010). Currently recommended control methods for black sigatoka include the use of fungicides, which are limited to developed countries. Their effects on the environment are cause for concern, quarantine restrictions are difficult to enforce, so that cultivar resistance has been mentioned as the preferable option. Wild *Musa* species, especially *M.acuminata* ssp., have been reported to have resistant genes which can be used for breeding. However, the process is slow and expensive (Stover 1969). Banana cultivar diversity has been suggested as a likely option for control of black sigatoka, especially for smallholders who cannot afford to purchase chemicals. Therefore baseline data was collected to assess farmers' knowledge of host resistance of different banana cultivars to black sigatoka.

METHODS

Farmer's knowledge of the variation of resistance among traditional banana varieties was collected through household surveys conducted in three sites (Nakaseke, Kabawohe, and Bunyaruguru). A stratified sampling technique was used to select a random sample of sixty farmers from four villages per site based on the presence of bananas on farms, and the willingness of the farmers to participate. Selected farmers were interviewed individually and responses were noted. The questionnaire consisted of structured, semi-structured and unstructured questions and subsequently the data was entered into designed data sheets. Farmers were also trained to score sigatoka incidence by recording the number of green leaves and the total number of functional leaves per plant. Processed data was analyzed by using descriptive statistics to score scale responses, frequency distributions and mean comparisons.

RESULTS

It was found that farmers grew their bananas in random varietal arrangements predominated by Nakitembe /Entaragaza and Enyeru in Nakaseke/Kabwohe and Bunyaruguru respectively. In

these mixtures, there was a variation in host resistance to black sigatoka within and among farms as reported by the farmers (Table 1). Farmers' responses on host resistance to black sigatoka in Kabawohe and Nakaseke were generally low as compared to Bunyaruguru. In Kabawohe, farmers consider Embire, Enjagaata, Entaragaza, Enyeru, Enzirabushera, Kibuzi and Mbwazirime as highly resistant, Bogoya and Kabaragara as moderately resistant and the rest of the traditional cultivars as highly susceptible to Sigatoka. In Nakaseke they only consider Nakabululu as highly resistant, Kisansa as moderately resistant and the others as highly susceptible. In Bunyaruguru all cultivars were ranked as highly susceptible. In general, eight traditional cultivars are considered to be highly resistant, three as moderate and 32 as highly susceptible.

DISCUSSION

In this study results show a variation in host resistance to black sigatoka in some local varieties from Kabawohe while those in Bunyaruguru and Nakaseke do not. Since similar varieties were generally found in these different sites and in similar random varietal arrangement, it is likely that the low occurrence of the disease in Kabwohe may probably due to some other environmental factor. According to Tushemereirwe, (1996) sigatoka incidence reduces with higher altitudes where temperature and humidity are low, hence affecting spore production, survival and germination. In this study, Kabwohe is at a higher altitude (1469m) compared to Bunyaruguru and Nakaseke at (1150m) and (1133m) respectively. It is therefore likely that the observed difference is attributed to difference in altitude. However there are other factors reported to affect incidence of sigatoka, including enhanced plant nutrition and pruning (Tushemereirwe 1996). Unfortunately these factors were not investigated in the study could also partly explain the observed differences. It is recommended that they are also investigated.

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Table 1 Farmers' rating of resistance status of different cultivars to Black sigatoka

Variety	Kabwohe			Nakaseke			Bunyaruguru		
	n	% Response	% rating Highly Resistant	n	% Response	% rating Highly Resistant	n	% Response	% rating Highly Resistant
Kawanda	10	0	0
Embire	32	3	100
Enyeru	56	4	100	.	.	.	19	37	14
Mujuba	24	0	0
Kibuzi	39	5	100	10	20	0	16	63	0
Mushankara	15	0	0
Enzirabushera	10	10	100
Bogoya	41	5	50	.	.	.	20	70	14
Entaragaza	56	4	100	39	8	0	46	54	20
Kabaragara	38	5	50
Enjagaata	37	5	100	.	.	.	22	59	15
Mbwazirime	25	4	100	21	19	0	12	58	14
Kisansa	.	.	.	12	17	50	.	.	.
Lusumba	.	.	.	27	0	0	.	.	.
Mayovu	.	.	.	21	19	50	.	.	.
Mpologoma	.	.	.	21	20	40	.	.	.
Musakala	.	.	.	19	11	0	.	.	.
Muvubo	.	.	.	11	0	0	.	.	.
Nakabululu	.	.	.	12	17	100	.	.	.
Nakinyika	.	.	.	13	46	17	.	.	.
Nakyatengu	.	.	.	12	14	0	.	.	.
Nambi	.	.	.	10	0	0	.	.	.
Namwezi	.	.	.	14	29	0	.	.	.
Ekigonza	22	50	9
Endyabwari	27	27	0
Enzirabahima	29	45	15
Kabwengye	19	35	0
Kahinja	20	24	0
Mujuba	22	27	33
Muziba	11	91	0
Rweru	10	70	0

_ Refers to (No data)

0 refers to (No response)

N=Number of farms with a particular cultivar

R=percentage (%) of farmers who responded out of (N)

RH=% of farmers who scared a cultivar as highly resistant.

Farmers' perception of host resistance to banana weevil within banana cultivars maintained in Uganda

Lwandasa, H.; Nankinga, J.C.; Nankya, R.; Adokorach, J.; Mulumba, J.W.; De Santis P.; Fadda C.; Jarvis, D.I.

INTRODUCTION

Banana is an herbaceous perennial crop consisting of an underground corm, roots and a shoot. In Uganda there are different varieties of bananas distributed in different agro ecological zones and cultivated for different uses. Bananas are among the most important food crops in the economy of the country and a staple food with sources of vitamins A, C and B6 (Karamura *et. al* 2008). Despite its importance, banana productivity in the country has declined from 30-40 tons/ha to 4-15 tons/ha obtained under research conditions (Karamura *et.,al* 2008). Banana weevil, *Cosmopolites sordidus* (Germar), has been reported as a major pest that has caused yield and crop disappearance from traditional growing areas country-wide (Gold *et. al* 1997, Karamura *et.,al* 2008). For more than a decade, researchers in Uganda have been searching for effective control methods for the banana weevil. However, available research results suggest that no single control strategy is likely to provide complete control for the banana weevil (Gold *et. al* 1997). Currently, available control methods include cultural and chemical means, which is labor-intensive and expensive (Gold *et al.*, 1993). Banana cultivar diversity has been suggested as a likely option for control of weevil, especially for smallholders who cannot afford to purchase chemicals. Therefore a search for baseline information was conducted to assess farmers' knowledge of variability in host resistance to banana weevil within different banana cultivars.

METHODS

Farmers' knowledge of the variation of host resistance among banana cultivars maintained by farmers was collected through household surveys conducted in three sites (Nakaseke, Kaba-wohe, and Bunyaruguru). A stratified sampling technique was used to select a random sample of sixty farmers from four villages per site based on the presence of bananas on farms, and the willingness of the farmers to participate. Selected farmers were interviewed individually and responses were noted. The questionnaire consisted of structured, semi-structured and unstructured questions; the resulting data was entered onto specially designed data sheets. Farmers were also trained to assess corm damage by counting the number of tunnels on cross-sectioned corms of the harvested plants. Processed data was analyzed through descriptive statistics to score scale responses, frequency distributions and mean comparisons.

RESULTS

It was found that farmers grew their bananas in random varietal arrangements predominated by Nakitembe /Entaragaza and Enyeru in Nakaseke/Kabwohe and Bunyaruguru respectively (Table 2). In these mixtures, there was less variation in host resistance to banana weevil within and among farms as reported by the farmers (Table 1). Farmers' responses on host resistance to banana weevil were generally high in all sites. In Kabwohe, farmers consider only Kawanda as highly resistant, Embire as moderately resistant and the rest of the traditional cultivars as highly susceptible to banana weevil. In Nakaseke they only considered Nakinyika as highly resistant, Mpologoma as moderately resistant and the others as highly susceptible. In Bunyaruguru all cultivars were ranked as highly susceptible. Generally, two traditional cultivars are considered by farmers to be highly resistant, two as moderate and the rest as highly susceptible. Further analysis of the corm damage showed a higher value in Bunyanruguru (11 tunnels per corm), followed by Kabwohe (7 tunnels per corm) and least in Nakaseke (3 tunnels per corm).

DISCUSSION

In this study farmers have reported variation in host resistance to banana weevil in some local varieties from Kabwohe and Nakaseke while in Bunyaruguru farmers considered all their bananas as susceptible to banana weevil. Kiggundu *et al* (2003) reported that all local banana cultivars are susceptible to banana weevil with little variation, while some hybrids like Km5 FIAH 17 and kayinja (local) are viewed as highly resistant. It has been observed that farmers generally do not have such hybrids. Those that possess a few probably do not pay much attention to them. The differences in host resistance in different banana cultivars and corm damage across study sites observed by farmers may be attributed to some other factor like sanitation management, which varies among farmers and across sites. Masanza *et al* (2004) observed variation in sanitation levels among farmers and also observed that farms with good sanitation management had low weevil population and corm damage. Unfortunately, while this factor could also partly explain the observed differences, it was not investigated in the study. And low corm damage in Nakaseke is a result of insufficient data collected. The on- going research in the established on-station trial will further confirm the results, although further research is recommended.

Table 2: Farmers' rating of resistance status of different cultivars to banana weevil

SITE VARIETY	Kabwohe			Nakaseke			Bunyaruguru		
	N	R	% RH	N	R	% RH	N	R	% RH
Kawanda	10	90	67	-	-	-	-	-	-
Embire	32	81	46	-	-	-	-	-	-
Enyeru	56	84	26	-	-	-	19	79	20
Mujuba	24	79	16	-	-	-	-	-	-
Kibuzi	39	85	15	10	80	0	-	-	-
Mushankara	15	100	13	19	74	7	-	-	-

Table 2. continued

SITE VARIETY	Kabwohe			Nakaseke			Bunyaruguru		
	N	R	% RH	N	R	% RH	N	R	% RH
Enzirabushera	10	100	10	-	-	-	29	76	0
Bogoya	41	85	9	-	-	-	20	85	0
Entaragaza	56	84	6	39	74	14	46	78	8
Kabaragara	38	84	6	-	-	-	-	-	-
Enjagaata	37	86	0	-	-	-	22	86	5
Mbwazirime	25	88	0	21	67	21	12	92	0
Kisansa	12	-	-	12	83	10	-	-	-
Lusumba	27	-	-	27	67	6	-	-	-
Mayovu	21	-	-	21	67	29	-	-	-
Mpologoma	21	-	-	21	81	41	-	-	-
Muvubo	11	-	-	11	73	0	-	-	-
Nakabululu	12	-	-	12	67	25	-	-	-
Nakinyika	13	-	-	13	69	56	-	-	-
Nakyatengu	12	-	-	12	58	0	-	-	-
Nambi	10	-	-	10	50	0	-	-	-
Namwezi	14	-	-	14	64	22	-	-	-
Endyabwari	27	-	-	-	-	-	27	74	5
Ekigonza	22	-	-	-	-	-	22	73	19

Notes

_ Refers to (No data).

0 refers to (No response).

N=Number of farms with a particular cultivar.

R=percentage (%) of farmers who responded out of (N).

RH=% of farmers who scared a cultivar as highly resistant.

Table 3: Cultivar abundance, average corm damage by banana weevil across sites.

Varietal Mixture	Average No. of tunnels		
	Bunyaruguru	Nakaseke	Kabwohe
Random	11	3	7
Most frequent Cv	Entaragaza (6)	Nakitembe(58)	Entaragaza (57)
Most abundant Cv	Enyeru (523)	Nakitembe(1467)	Entaragaza (38753)

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Farmers' perception of banana nematode pests and cultivar resistance and preliminary observations on the occurrence of banana nematode species at three sites in Uganda

Nabulya, G.; Namaganda, J.M.; Mulumba, J.W.

INTRODUCTION

Bananas (*Musa* spp.) are a basic staple food crop (Stover and Simmonds, 1993) and are ranked as the most important food crop in Uganda where more than 7 million people depend on it for their daily meals (Tushemereirwe *et al.*, 2003). Bananas and their products are sold for income and bring in a gross income of \$154 per year per family (Ngambeki and Rubaihayo, 1996).

Banana production and yields in Uganda have been declining since the 1970s. Previously, banana plantations lasted over 50 years, but now they start to deteriorate after only four years (Karamura, 1993). Plant parasitic nematodes have been identified among the major factors responsible for the decline in banana production (Gold *et al.*, 1993; Kashaija *et al.*, 1994). Average annual yield loss due to nematodes is estimated at about 20% worldwide (Sasser and Freckman, 1987).

Cultural methods such as crop rotation and nematicides can be used to control nematodes (Gowen and Queneherve, 1990), but crop rotation is impracticable in areas where bananas are grown continuously, while use of nematicides in plantations exposes agricultural workers without good skills to health risks. Nematicides are also highly toxic to animals and harmful to the environment. Since there is evidence that nematode resistance and tolerance sources are present in the *Musa* gene pool (Pinochet 1996), host pest resistance would be the best option for nematode control in bananas. However, no cultivar has been found to be totally immune to nematode invasion although nematode populations vary in different banana cultivars Davide and Marasigan (1985). There is need, therefore, to investigate the potential of this varietal variation in tolerance and the effect of varietal mixtures in controlling banana nematodes.

MATERIALS AND METHODS

Farmer's knowledge about banana pests and diseases, and cultivar resistance, was assessed during a household survey. Sixty households were selected from each of the three project sites, namely, Nakaseke in central Uganda, and Kabwohe and Bunyaruguru in southwestern Uganda. The sixty households were derived from a selection of 15 households from each of the four selected villages per site. The information was collected using a semi-structured questionnaire. Rating for resistance by farmers was done on a scale of 1-3 where 1= slightly resistant and 3= highly resistant.

Occurrence of the different nematode species was established from banana roots that were collected from the three sites for use as inoculum in a greenhouse experiment to assess resistance/

tolerance of different banana cultivars to nematodes. Three gunny bags of roots were collected from harvested corms wherever they were found on farms within the site, regardless of whether the farm was one of the selected 60 or not. The sampling was so done because a large volume of roots was required, and since it was destructive sampling, only harvested corms were used. As a good management practice, many farms do not retain harvested corms, so it was necessary to collect roots even from farms other than the selected ones. A sample of the roots was examined for nematode damage before uprooting the whole corm. The roots were then removed from the corm and taken to the laboratory for nematode extraction, identification and population density estimation. The roots were chopped, mixed thoroughly, and 10 subsamples of 5g each were drawn for nematode extraction, using a modification of the Baermann-funnel maceration-filtration technique (Hooper, 1986).

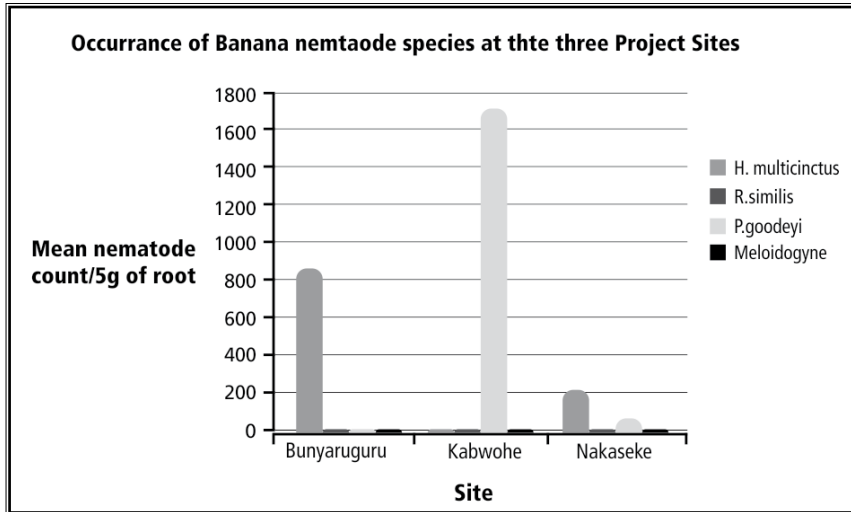
Samples for root necrosis assessment were collected in Bunyaruguru and Kabwohe from 2-10 recently flowered banana plants per cultivar per farm from four selected farms per site. The number of sampled plants varied greatly because only a few recently flowered plants of the same cultivar were available on some farms while others had as many as 10 or even more. The sampled cultivars include Kibuzi, Nakitembe, Enyeru, Mbwarzirume, Musakala and Enzirabahima. Banana roots were collected from a 20 x 20 x 20 cm cube dug close to the plant base, kept in clear polythene bags, labeled and taken to the laboratory for percent root necrosis. Five roots were picked randomly from each sample, trimmed to a length of about 10 cm and split longitudinally to expose the root cortex and stele. One half of each root was examined for necrosis, thus each of the five-root pieces represented 20% of the total. Percent of root necrosis was scored by estimating the proportion of necrotic cortical tissue (reddish-purple lesions) on each half root. The percentages for each of the five root pieces were added to obtain the total percent root necrosis (Bridge and Gowen, 1993). Since the number of observations per farm varied, a weighted average percent root necrosis was calculated. This was done by weighting the cultivar means by the number of observations on each farm. http://en.wikipedia.org/wiki/Weighted_mean (last modified on 20 December 2010 at 15:22).

RESULTS

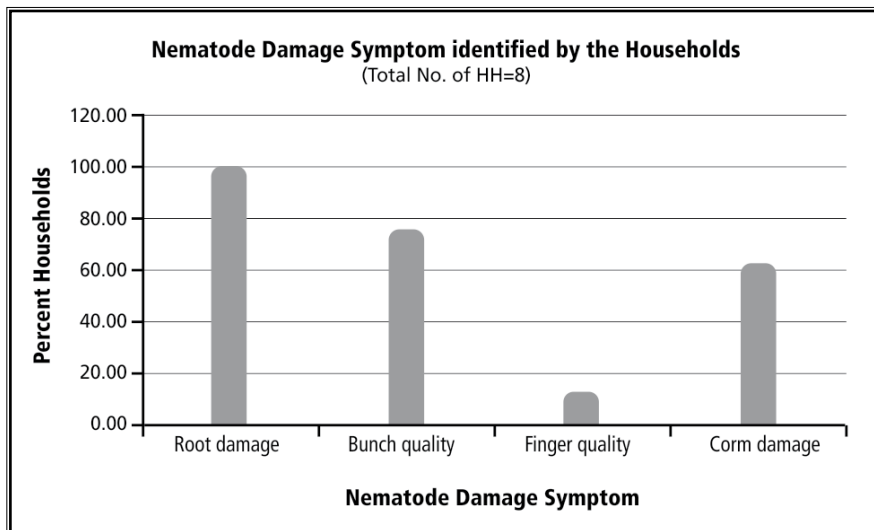
Whereas banana bacterial wilt (BBW) and weevils are easily recognized by the majority of farmers, nematode infestation is not easily detected (Graph 1). None of the households in Bunyaruguru and Kabwohe identified nematodes as a problem in their banana plots. In Nakaseke however, 13.3% of the households mentioned nematodes as a problem. All the households that identified nematodes as a problem were able to associate them with root damage while 75% and 62.5% of the households associated nematodes with bunch quality and corm damage respectively (Graph 2).

In Nakaseke, only four households were able to rate banana cultivars for resistance to nematodes. Cultivars believed to be resistant include the local cooking banana varieties Nakinnyika, Mayovu, Mbwarzirume, Kisansa, Lusumba, Katwalo, Nakyatengu, Nakitembe and Namwezi. The introduced FHIA hybrid, FHIA 17 was also mentioned. The average rating and weighted value is given in Table 1.

Examination of banana root samples collected from the three project sites revealed that the spiral nematode *Helicotylenchus multicinctus* (Cobb) Golden was the predominant species in Bunyaruguru and Nakaseke while the lesion nematode *Pratylenchus goodeyi* Sher & Allen was the predominant one in Kabwohe. *P.goodeyi* was present at the three sites, with the highest population density in Kabwohe and negligible numbers in Bunyaruguru. The burrowing nematode, *Radopholus similis* (Cobb) Thorne, was not present at any of the sites while the rootknot nematode

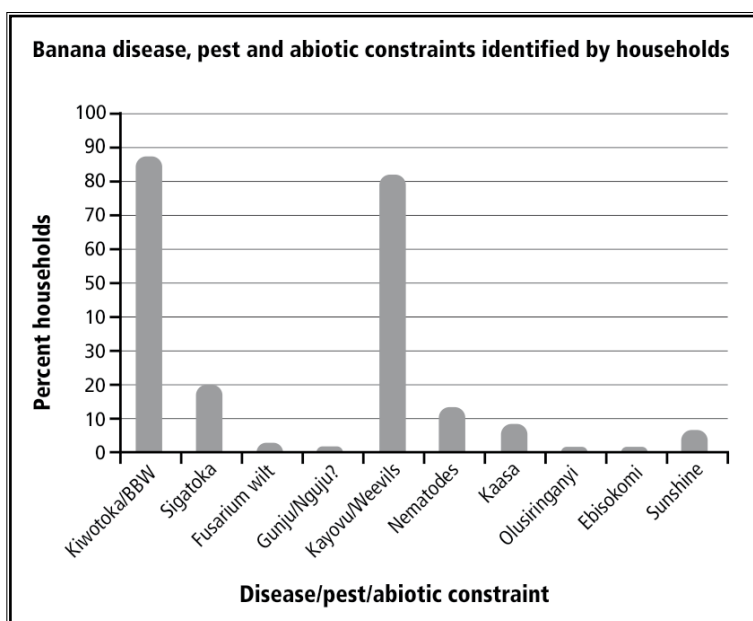


Graph 1: Banana disease and pest problems identified by the households in Nakaseke



Graph 2: Damage symptoms associated with nematodes by households in Nakaseke.

Meloidogyne sp. was present only in Bunyaruguru, and in negligible numbers (Graph 3). Weighted average percent root necrosis is given in Table 2. Apart from Mbwarzirume, the banana cultivars have higher percent root necrosis in Kabwohe than in Bunyaruguru.



Graph 3: Occurrence of banana parasitic nematodes in Bunyaruguru, Kabwohe and Nakaseke

Table 1: Ratings of banana cultivars believed to be resistant to nematodes by the farmers in Nakaseke, and their weighted values

Nematode Resistant Cultivar	No. of Households (n)	Average rating (r)
Mayovu	2	2.5
Kisansa	2	1.5
Nakinnyika	3	2
Lusumba	1	3
Katwalo	1	3
Nakyatengu	1	3
Nakitembe	1	3
Namwezi	1	2
Mbwazirume	2	2.5
FHIA 17	1	3

Table 2: Weighted average percent root necrosis for banana cultivars in Bunyaruguru and Kabwohe

Cultivar	Weighted average percent root necrosis	
	Bunyaruguru	Kabwohe
Nakitembe	1.5	9.3
Enyeru	1.6	13.8
Enzirabahima	4.7	-
Kibuzi	1.7	15.5
Mbwazirume	9.5	7.5
Musakala	-	8

DISCUSSION

Although the farmers in Bunyaruguru and Kabwohe did not recognize banana nematodes as a problem, the results of the occurrence studies show that plant parasitic nematodes do occur in the area, while percent root necrosis assessment results reveal that those nematode species do cause damage to the banana roots. In addition, earlier studies recorded the presence of banana nematodes in both Bunyaruguru and Bushenyi. (Gold *et al.*, 1993; Kshaija *et al.*, 1994). In Nakaseke, all the households that recognized nematodes as a problem were able to associate them with root damage. This is an indication that they actually had some knowledge about nematodes. From the number of households in Nakaseke that rated banana cultivars for resistance to nematodes, it is evident that farmers' knowledge in this area is limited.

Although the weighted average percent root necrosis appears to be higher for some cultivars than others and in Kabwohe more than in Bunyaruguru, it cannot be deduced from these results that those with less root damage are more resistant than others. Banana plants on the different farms have obviously been exposed to different population levels of nematodes, depending on the source of planting materials and history of the plot. There is need to carry out controlled cultivar evaluation experiments before conclusions can be made. Once the more nematode resistant/tolerant cultivars are identified, there is need to further evaluate them in various mixture arrangements for their potential in controlling banana nematodes.

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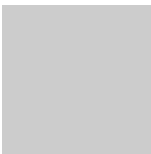
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DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



POSTER
SESSION-A



(A-1) Diversity and Field Resistance
(A-2) Variation in Host Resistance

Understanding of farmers' perception of local faba bean reaction to chocolate spot disease due to *Botrytis fabae* Sard

Touati, N.; Belqadi, L.; Ezzahiri, B.; Sadiki, M.

INTRODUCTION

In the region of Taounate, the faba bean crop is subjected to various stresses affecting the level of yield and yield stability. Several forms of pest control are practiced by farmers. However some of these methods are ineffective and harmful to the environment. To avoid these effects, the use of resistance to diseases such as chocolate spot disease caused by *Botrytis fabae* Sard remains the most effective. Indeed, the selection of local cultivars gradually increased the frequency of favorable genes and associations for the specific varietal type. This strategy can thus improve the resistance of these cultivars and be effective in changing performance. The research conducted as part of this investigation has given an important role to farmers, to better use their breeding capacity, to valorize their skills and local varieties. The study has two major objectives: to understand farmers' perception in the use of local genetic diversity in controlling diseases (especially chocolate spot) and the assessment of local populations of faba bean for their reaction to chocolate spot.

MATERIAL AND METHODS

The first part of this study, concerning the assessment of the importance of chocolate spot, consisted of conducting surveys of 179 farmers in the three sites Ourtzagh, Galaz and Tissa in Taounate province. These surveys were conducted to valorize the local knowledge of farmers and to get an idea of their perceptions in the use of genetic diversity in controlling pests and diseases. The second part of the study analyzed, through an experiment at M'rissa experimental station, the reaction of 184 local faba bean collected from farmers in the region of Taounate. The experimental design adopted in this trial is a randomized complete block with two replications. Local populations were evaluated for their reaction to chocolate spot disease and for different types of agro-morphological traits. The disease severity was scored visually on a 0-3 scale (0: absent, 1: few, 2: moderate, 3: high) during plant maturity stage. The statistical analysis used for analyzing collected data included univariate and multivariate analysis. These tests were made to provide a general description of populations and to assess the genetic variations of populations for their reaction to chocolate spot. Hierarchical cluster analysis and two-step were used to group populations that react the same way towards the chocolate spot disease in the same class. The SPSS (Statistical Package for the Social Sciences) was used for carrying out the various statistical analyses.

RESULTS AND DISCUSSION

The investigations have identified local knowledge in terms of farm management of biotic stresses such as chocolate spot disease. Indeed, farmers are aware of the seriousness of this disease and the importance of local varietal richness (Figures 1, 2 and 3). The analysis of perception shows that the farmers use, directly or indirectly, local genetic diversity to control pests and diseases. This management can occur on two scales:

- Space management: since they recognize that there are differences between plots (Table 1), farmers practice crop rotation with cereals (barley or wheat);
- Time management: farmers found that local varieties do not become attacked if they are cultivated for many years (Figure 4).

The experimental station results indicated that the agro-morphological traits examined showed the existence of very highly significant differences among the 13 local cultivars (Figure 5). Indeed, these traits are related to the number of seeds per pod, the number of pods per plant and seed weight per plant. The notations of the reaction of local materials to chocolate spot disease showed small differences between varieties in contrast to the differences noted in the farmers' fields in the region of Taounate. This result suggests the existence of resistant or tolerant sources of faba bean to *Botrytis fabae* in the local varieties.

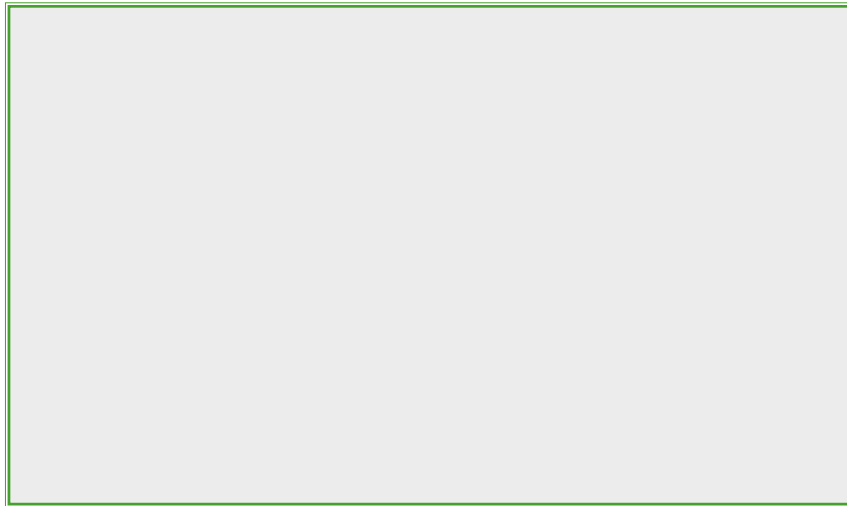


Figure 1 Farmers' perception of local faba bean reaction to chocolate spot disease in Ourtzagh



Figure 2 Farmers' perception of local faba bean reaction to chocolate spot disease in Tissa

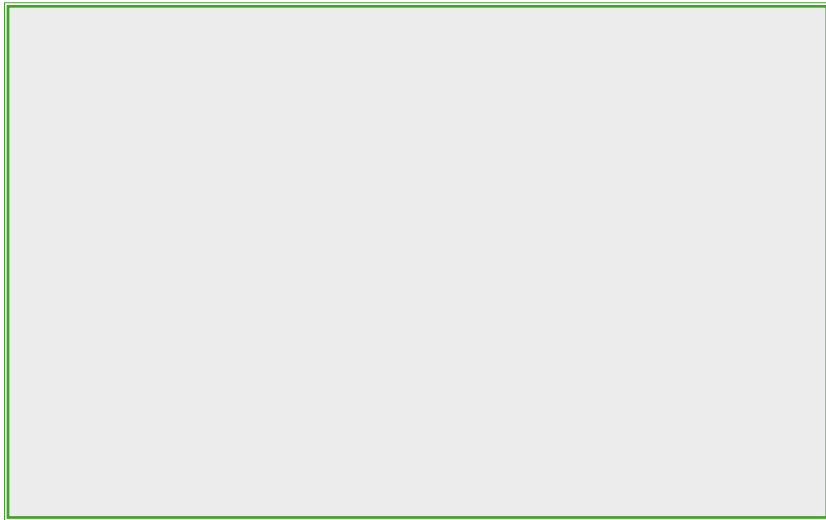


Figure 3 Farmers' perception of local faba bean reaction to chocolate spot disease in Galaz

Table 1: Percentage of farmers believing that there are differences of attacks by Botrytis between plots

Differences of attacks by the disease between plots	Number of farmers (%)		
	Ourtzagh	Galaz	Tissa
1 (Yes)	30	49	28
2 (No)	70	51	72
Total	100	100	100

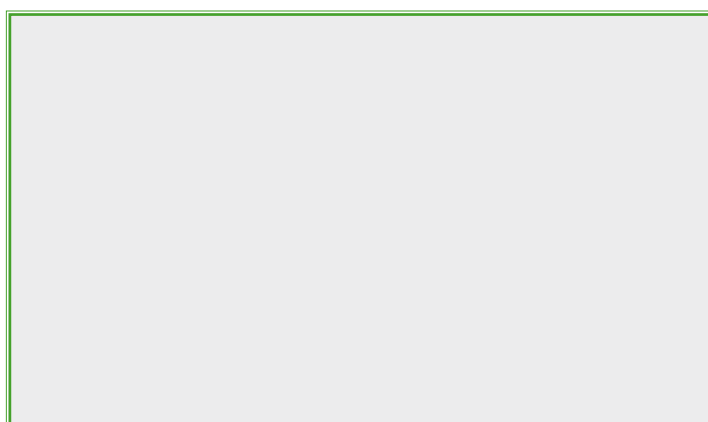


Figure 4 Percentage of farmers believing that local varieties do not become diseased every year

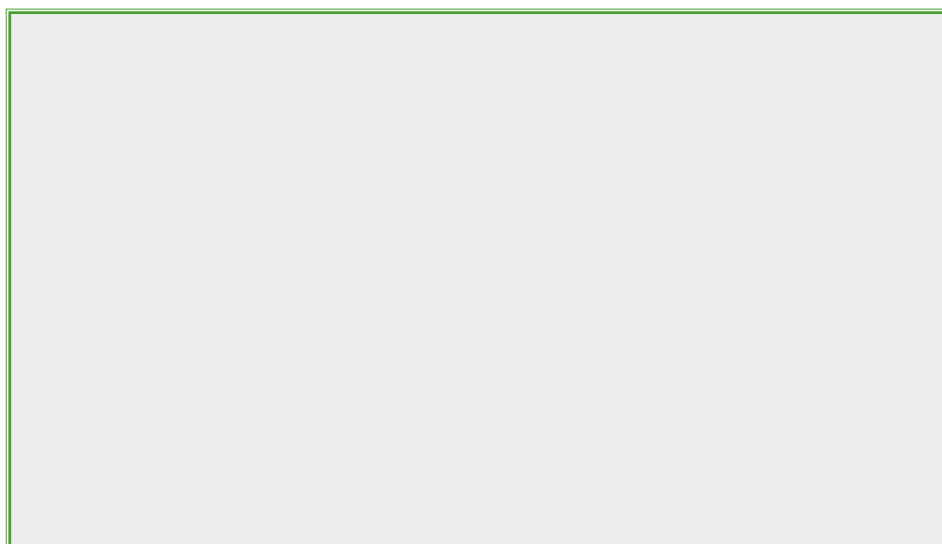


Figure 5 Dendrogram of classification profiles of the 13 local varieties based on distances calculated on agro-morphological traits, yield components and scoring of botrytis

The role of diversity of maize in the control of disease and pests in China

Yang Yayun, Zhao Zixian, He Chenxing, Yu Tengqiong, Huang Qingmei, Xu Furong, Dai Luyuan

INTRODUCTION

Xiding, the selected study site for the UNEP-GEF-sponsored project “Conservation and Use of Crop Genetic Diversity to Control Pests and Diseases in Support of Sustainable Agriculture”, is in Menghai county of Xishuangbanla Dai Autonomous Prefecture, Yunnan Province, China. Farmers traditionally plant maize in this site, so that it was established as a target crop of the project. The project researched variation in host resistance, diversity and field resistance, genetic choices and the value of maize in order to explore the role of diversity of maize in the control of disease and pest and examine the development of sustainable agriculture.

METHODS

To examine the variation in maize host resistance, 70 households that planted maize out of 77 HH in Xiding Township were investigated in focus group discussions (FGDs). The seven HH that planted other crops instead of maize were examined in HH surveys. The primary knowledge about maize resistance to pests and disease were determined from FGDs and HH surveys, followed by field experiments to explore the variation in host resistance. Maize variety samples for Options2 were, in total, 17 varieties planted (including 11 varieties from other sites) and 40 seedlings (clusters) of each maize material. We selected the four households to plant five sets of maize varieties. Results showing the genetic diversity management choices by farmers were obtained through quantifying the answers for the questions designed in FGDs and HH surveys. The morphological and biological traits of maize and surveyed damage by diseases and pests of maize in the fields were recorded and the data analyzed with SPSS software.

RESULTS

Five local maize varieties (Selileng, Selebai, Seleleng, Aduxiu and Selile) as well as three modern varieties (Zajiao, Zhengda 615 and zhangda 819) were planted for variation in host resistance. Aduxiu was planted by 38.57% of HHs, making it the most popular variety in Xiding County (Fig.1). The community Simpson index is 0.775. Community richness is 15, divergence is 0.956. These varieties have been planted over a range of time, from 3 years to 70 years. According to FGD and HH surveys, the varieties showing medium to high disease resistance are Aduxiu, Seleleng, Selileng and Zajiaozhengda 615, while Selebai and Zajiaozhengda 819 showed low to moderate resistance. Seleleng resistance to grubs, corn borer, gray leaf spot of maize, southern leaf blight,

corn leaf blight was moderate (Fig. 2). A total of four kinds of pests (corn leaf blight, a small spot of corn, corn borer, gray leaf spot) were noted. In a survey of corn leaf blight, six varieties of the disease were on the performance level of 1-2. In the survey of maize, six varieties of diseases due to *Bipolaris maydis*, were noted with conditions rated from 1 to 3. Corn borer damage in the survey was seen, in general, to cause serious pest harm (level 2 to level 3) only in Selileng.

Of households, 96.1% think that diseases and pests were reduced through changing crop allocation among varieties. Reducing weeds, keeping the land rich, increasing production, full use of various soil nutrients, and the fact that 18.18% of households opened up new fields, all help to improve production, soil nutrients and income. Since the variety was first grown by farmers, the overall resistance of maize varieties after dry, wet, cold and hot years was still equal to the original one. In dry years, the resistance of Aduxiu variety (the largest area planted, data not shown) was increased. On the contrary, resistance was decreased with respect to the original one in wet years. In cold years, the resistance of Aduxiu was equal to the original one, but in hot years resistance was increased. Resistance of local maize varieties was little affected by variance of temperature and weather, in contrast to the modern variety.

Appraising the resistance of varieties in field experiments, it was shown that the resistance level of 17 varieties to *Bipolaris maydis* and corn gray spot was low (Grade 1) (Table 2). There was no damage from corn northern leaf blight, corn curvalaria leaf spot, common corn rust or corn head smut in the 17 varieties (Table 1)

Full use was made by farmers of genetic choices. In spatial arrangements of maize, the attitude of farmers was to state the same disease damage as in neighbors' fields -- 87.14% of households said "yes" to the same disease level as neighbors, 75.71% thought there were no differences in planted crop damage (or disease/pest attacks) in different plots. One hundred percent of seed sources were from a household's own seeds. Modern varieties were grown for 4-20 years, local varieties were planted 1-70 years. Of the total households, 24.29% selected healthy populations with few pests/diseases by field, 55.71% selected the seeds for the following year through spike selection and 78.85% and 27.12% of households selected plants for seeds in drying and maturity stages respectively. In terms of post-harvest methods for selecting seeds, 87.14% of households dry seed to prevent pests (the seed-drying methods were different) 70% used specific storage locations (warehouses), 26 households (37.14%) sun-dried the seeds and 13 households (18.57%) dried them naturally. Some farmers put the seeds in warehouses and bamboo containers for drying, while 21.43% treated seeds with pesticides. With regard to criteria for choosing high quality seed, 67.14% selected large seeds and 62.86% selected seeds with normal color.

DISCUSSION

Local rice (8 varieties) was rich. Many varieties have been planted for 20-70 years, and all these seeds were from farmers' own saved seed, allowing them to manage the varieties and prevent them from pests and disease. From the survey results, it is seen that farmers often choose the healthy plants and seeds to plant and conserve, and selected seeds in maturity and drying state. Males of the households played an important role in managing varieties. Half of the households were aware of the role of genetic diversity management in controlling the diseases and pests of rice -- they have conserved and kept planting local varieties for a long time. And through FGDs, HH surveys and field experiments, we discovered that these local varieties have moderate to high resistance to most maize diseases and pests, such as corn leaf blight, corn borer and gray leaf spot. Host resistance within and among traditional cultivars was stable. Variation in host resistance was not obvious. The role of diversity of maize in the control of diseases and pests needs further research and the extension of IPM strategies to more places.



Figure1 The maize varieties planted by HHs in Xiding

Comparative analysis of farmers' perception of genetic diversity management of faba bean (*VICIA FABEA* L.) and barley (*HORDEUM VULGARE* L.)

Taoufiqi, s.; Belqadi, S.; Ezzahiri, B.; Sadiki, M.

INTRODUCTION

Faba bean (*Vicia faba* L.) and barley (*Hordeum vulgare* L.) are two traditional crops exploited in the cereals/legumes production system and produced in various areas of Morocco. Thus, the local varieties used by farmers are very important as a reserve of genetic diversity for many characteristics, in particular their reactions to diseases and pests. The farmers, acting directly in the management of this diversity, share a local knowledge which was always very developed in Moroccan rural environments. This knowledge has been exploited by collecting data and information on farmers' perceptions and their approaches to farm management of local diversity in relation to its use for disease control.

This work was conducted as part of a research program on the use of crop genetic diversity to reduce the effect of diseases and pests on-farm. The study focused on maintaining *in situ* genetic diversity of faba bean and barley at the three sites of Ourtzagh, Galaz and Tissa located in the province of Taounate in Morocco.

MATERIAL AND METHODS

To compare the perceptions of farmers in the management of the diversity of faba bean and barley, surveys were conducted in the region of Taounate, an important step in facilitating the management and exploitation of diversity. Indeed, understanding of farmers' perceptions of diversity and its management on-farm is needed to elucidate the effect of socioeconomic and environmental factors on the structure of this diversity and its spatial and temporal evolution. This work involved four points covered from a prepared questionnaire to carry these individual investigations:

- Spatial distribution of varieties in one plot;
- Changing crops over time;
- Methods of controlling pests and diseases;
- Selection of genetic material for the next season.

RESULTS AND DISCUSSION

For the special distribution of varieties, the results of investigations have clearly revealed that the mixture of varieties is more common for faba bean than for barley in the three study sites (Figure 1). Concerning the change of crops over time, the main reason for the change is to increase the yield (Figure 2). The survey results showed that farmers are well aware of methods for control of diseases and pests in both crops (Table 1). The selection of genetic material is more practiced and valued in faba bean than in barley (Table 2).

Thus, in general, we can conclude that the main reason for the conservation and management of genetic resources of faba bean and barley by farmers is to improve production. Therefore, improved earnings from local cultivars are the key to supporting farmers in continuing to maintain genetic diversity *in situ* within and between varieties. The adoption of a set of agronomic techniques economically acceptable to farmers such as crop rotation, tillage and use of minimal inputs, led to both increased performance and improved farmers' income as well as protection of the environment. These techniques aim to control weeds, plant pests and diseases and to carry out the rational application of fertilizer and ensure improved quality of seeds planted.

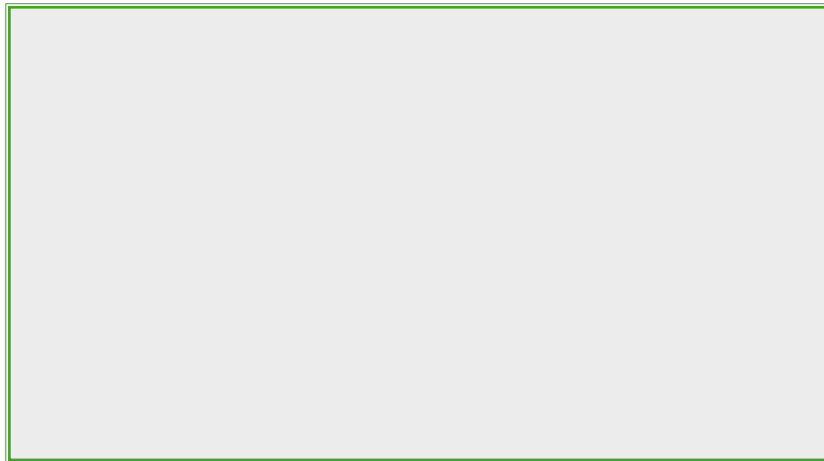


Figure 1 Distribution of farmers according to the reasons advanced to explain the choices of arrangements of varieties on the same plot
a. Faba bean



Figure 1 Distribution of farmers according to the reasons advanced to explain the choices of arrangements of varieties on the same plot
b. Barley

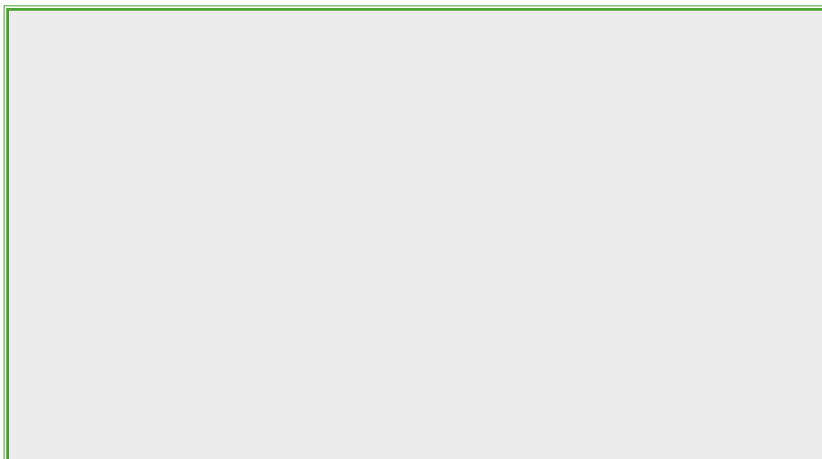


Figure 2 Reasons adopted by farmers to justify the change of varieties over time
a. Faba bean

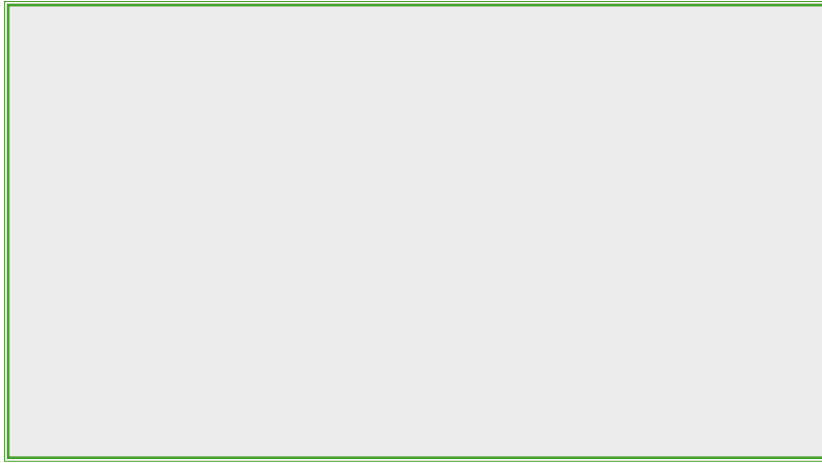


Figure 2 Reasons adopted by farmers to justify the change of varieties over time
b. Barley

Table 1 Methods of controlling pests and diseases

		Percentage of farmers (%)		
		Ourtzagh	Galaz	Tissa
Application of pesticides and fertilizers	Faba bean	84	95	85
	Barley	73	93	68
Use of improved varieties	Faba bean	5	5	3
	Barley	5	3	5
Potting mix on the same parcel	Faba bean	5	4	3
	Barley	4	3	3
Crop rotation	Faba bean	100	100	98
	Barley	100	100	95
Removal of other species of field	Faba bean	43	64	37
	Barley	31	52	31

Table 2 Percentage of farmers adopting different practices to determine which seeds are planted the following year

Different practices to determine what will be planted faba bean seeds the following year		Pourcentage des agriculteurs (%)				
		Ourtzagh	Galaz	Tissa		
Selection of Parcel	No seed selection practices at plot	Faba bean	80	73	58	
		Barley	60	78	68	
	Choosing the best plot in order to collect the seed	Faba bean	2	11	8	
		Barley	4	12	12	
	Choosing a particular part within the plot	Faba bean	3	2	10	
		Barley	4	3	1	
	Planting a specific parcel	Faba bean	13	5	0	
		Barley	-	-	-	
Plant selection	No selection of plant	Faba bean	80	80	78	
		Barley	100	93	100	
	Remove unwanted plants types of Parcel	Faba bean	13	19	3	
		Barley	-	-	-	
	Seed treatment	No seed treatment	Faba bean	77	76	63
			Barley	56	67	39
Seed treatment with pesticides		Faba bean	13	5	10	
		Barley	13	18	22	
Selection criteria	Seed treatment with products other than pesticides	Faba bean	22	13	30	
		Barley	40	32	34	
	Overall selection in the choice of seeds	Faba bean	68	80	42	
		Barley	100	87	97	
	Selection of big seeds	Faba bean	63	64	47	
		Barley	-	-	-	

Relating crop damage levels on-farm to crop varietal diversity measured by richness, evenness and diversity for rice in China

Qu Wen-Lin; Cao Feng-Juan; Lu Chun-Ming; Wang Yun-Yue.

INTRODUCTION

Rice is the major food crop, and rice blast often causes serious yield losses each year. Richness and evenness are two key notions of biological diversity that could reflect the local status of biological diversity. To understand the relationship between the diversity of local rice varieties and yield loss caused by rice blast, the richness, evenness and blast damage in five rice sites were surveyed. The five rice sites included three located in Yunnan Province, one in Guizhou Province and one in Sichuan Province. Traditional knowledge of using rice variety diversity to control pests and diseases was surveyed.

METHODS

- *In situ* observation and quantification of rice blast infestation level in farmers' fields at five rice sites.
- 60 households (HH) were randomly selected from each site and surveyed.
- The occurrence of rice blast in the 60 HH's fields at each site were surveyed, using a Z-shaped path for rapid assessment. Thirty observations per variety per household were made, including 10 plots, three observations per plot.
- For the rice blast standards used in the surveys, see GB/T 15970-1995 (China).
- An evaluation was made of rice varieties' disease resistance.
- The richness and evenness in every site was calculated to gain an understanding of the relationship between varietal richness, evenness and rice blast pressure.

RESULTS

A total of 122 rice varieties were collected from five rice sites. Of these, 55 were local varieties and 67 were modern varieties (see Table1). Rice varieties were collected from five rice sites with different panicle blast resistance ability, varying from HR to HS in five sites at the HH levels. (See Table2.)

The relationship between varietal richness and incidence of rice blast in household level at five sites was examined. The results showed an increase of HH richness, and a decrease in the occurrence of rice blast. (See Figures 1-5.) The relationship between varietal evenness and incidence of rice blast in household level at five sites was determined. The results indicated that with the increase of HH evenness, the occurrence of rice blast was reduced (see Figures 6-10).

On the community level, 21 to 34 rice varieties were found at different sites in the five communities compared. The relationship between varietal richness/evenness and rice blast showed that, with increase richness/evenness, the rice blast is reduced. (See Figures 11, 12.)

CONCLUSION

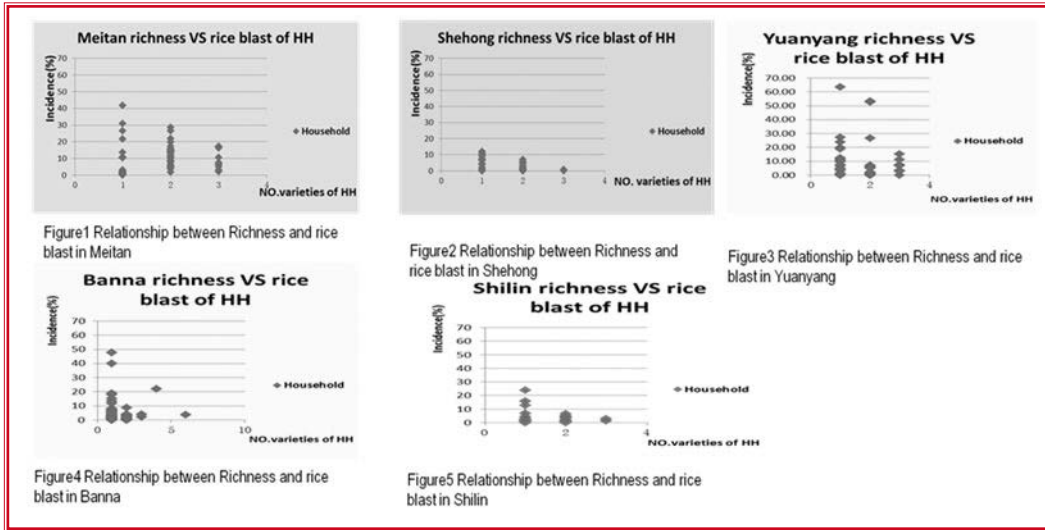
- The use of rice variety genetic diversity in farmers' fields provides an approach to disease control, pesticide reduction, crop damage reduction and production stability.
- The use of intraspecific genetic diversity in farmers' fields contributes to the larger IPM strategies.
- Rice landrace varieties provide a key resistance resource and other good trait material that improves rice breeding.

Table 1 Rice varieties collected from five rice sites

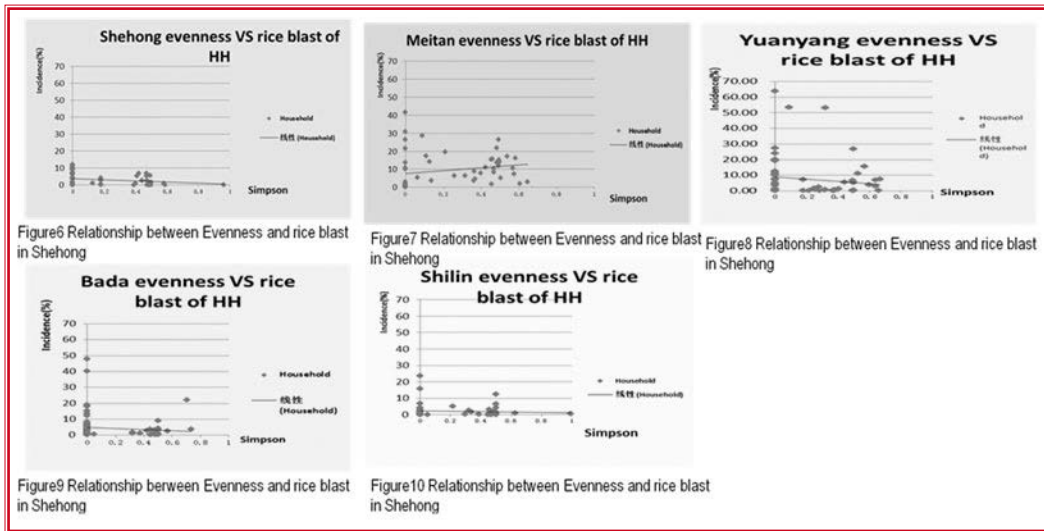
Modern/Local varieties	Project rice sites				
	Bada/ Yunnan	yuanyang/ Yunnan	Shilin/ Yunnan	Shehong/ Sichuang	meitan/ Guizhou
Modern varieties	2	3	19	28	15
Local varieties	20	20	2	6	7
total	22	23	21	34	22

Table 2 Rice blast resistance of rice varieties in five sites

Resistance/ Susceptible	Project rice sites				
	Bada / Yunnan	Yuanyang / Yunnan	Shilin / Yunnan	Shehong / Sichuan	Meitan / Guizhou
No.of HR	10	4	10	18	1
No.of R	8	8	9	12	8
No.of MR	3	3	1	2	4
No.of MS	1	5	1	2	6
No.of S	0	2	0	0	3
No.of HS	0	1	0	0	0



The relationship between varietal evenness and incidence of rice blast in household level at five sites. The results indicated that with the increase of HH evenness, the occurrence of rice blast was reduced. (see Figure 6-10)



Relating crop damage levels on-farm to crop varietal diversity measured by richness, evenness and diversity for barley in China

Wu Shuo; Wang Yun-Yue; Qu Wen-lin; Lu Chun-Ming.

INTRODUCTION

Shangri-la County is located in northwestern Yunnan Province, southwestern China, where naked barley (*Hordeum vulgare* L. var. nudum hook. f.) is an important staple crop for local people. Songming County is located in the center of Yunnan Province where barley (*Hordeum vulgare*) is a major economic crop. Barley net blotch and powder mildew are prevalent diseases and limiting factors in barley production in both Shangri-la and Songming Counties. Barley landrace variety diversity maintained by local farmers contributes to sustainable production and farmers' livelihoods.

METHODS

1. Both Shangri-la and Songming Counties were selected as project sites.
2. 60 households (HH) were randomly selected from each site for surveys. At the same time, *in situ* observations and quantifications were made of both barley net blotch and powder mildew disease infestation levels in farmers fields.
3. Rapid disease assessment was carried out, using a Z-shaped path to determine 10 spots, with three observations per spot -- a total of 30 observations per variety per household.
4. Disease damage on a scale of 0 to 4 was calculated and recorded.
5. Loss = [(flag leaf)*2/3+ (second leaf)/2]/2
6. $DI = \frac{\sum(\text{series} * \text{leaves}) * 100}{\text{supreme grade} * \text{total leaves}}$.

RESULTS

1. A total of 12 barley varieties were planted in farmers' fields in both Counties -- four varieties from Shangri-la County and eight varieties from Songming County.
2. On the household level in both Songming and Shangri-la sites, barley net blotch and powder mildew occurred more seriously in monoculture than when two or three varieties were mixed in fields.

3. On the community level, barley net blotch and powder mildew were more serious in the Shangri-la site (lower varietal richness) than the Songming site (higher varietal richness).

CONCLUSION

1. The results indicated that barley variety diversity in farmers' fields contribute to control of barley net blotch and powder mildew diseases.
2. The results showed that higher barley varietal richness and evenness in farmers' fields result in increased reduction of disease damage.

Resistant Appraisal of Maize Varieties to *Setosphaeria turcica* in Zhaojue, China

Liu Bo Wei; Xu Fu Rong; Wang Jun Zhen; Xi Ya Dong; Fen Kui; Wang Shi Zhong; Peng Hua Xian.

INTRODUCTION

Zhaojue is an agricultural county in Sichuan, China. Maize is the major food crop and forage, and northern leaf blight (*Setosphaeria turcica*) often causes serious yield loss. To understand the utility of local crop diversity in reducing disease damage, we measured resistance under farmers' conditions in expanded trials/plots in farmers' fields and in greenhouses and through participatory assessment and field analysis. The hypothesis examined was that diversity with respect to pest and disease resistance exists in the traditional varieties maintained by farmers.

MATERIAL AND METHODS

Strains collected

The strains were isolated from maize leaves infected by *S. turcica*. They were mixed strains and inoculated in the greenhouse for resistant appraisal of maize varieties/landraces.

Variety/landrace collected

Nineteen varieties (landraces and modern) were tested in the greenhouse/field. There are seven landraces from Zhaojue in Sichuan and six landraces from Menghai in Yunnan. Others are modern varieties from Zhaojue. During the investigation, Variety MO17 was identified as a resistant variety and HuoBai as a susceptible variety.

Appraisal of resistance in the greenhouse

For each tested variety, 30 plants were planted. While the maize plants grew 4~5 leaves, inoculation with pathogen sorghum was carried out. After 10 days of inoculation, the disease index of maize plant was investigated.

Appraisal of resistance in the fields

Each tested landrace/modern was randomly arranged in the field. Each variety was planted in an area of 6m² with 30 plants, replicated three times. No inoculation with sorghum pathogen was

carried out. After 20-25 days of natural occurrence of *S. turcica* in the fields, the disease index of the maize plant was investigated.

RESULTS AND DISCUSSION

The results in the greenhouse study showed that resistance level was low. Many varieties (landraces and modern) were susceptible to *S. turcica* and a few varieties were resistant to *S. turcica* in the greenhouse. Few resistant varieties were noted and there were no landraces or modern varieties that could be identified as highly resistant. Resistant varieties account for 7.69% and susceptible one 92.31% of the total in the greenhouse. In the field, most of the varieties (landraces and modern) were tolerant to *S. turcica* and a few varieties were susceptible to *S. turcica*. Resistant varieties account for 92.31% and susceptible ones for 7.69% in the field.

There were thus no differences in resistance between landraces and modern varieties in the appraisal.

Table 1 Disease classification standard of resistant varieties in greenhouses (unit = plant)

Grade	spot number	spot length
0	No symptom	
1	1-2	
3	3-5	0.5-1 cm
5	6-8	1.1-2 cm
7	9-12	2.1-3 cm
9	12 above	3 cm above

Table 2 Disease classification standard of variety resistance in fields (unit: plant)

Grade	Area of leaf spot above ear, accounting for area of all leaf above ear (%)	Area of leaf spot under ear, accounting for area of all leaf under ear (%)
0	No symptom	No symptom
1	No symptom	< 5%
3	< 5%	6-10%
5	6-10%	11-30%
7	11-30%	31-70%
9	>30%	>70%

Table 3 Evaluation of resistance for landraces/modern varieties to *S. turcica* in the greenhouses/fields

Disease index	Resistance
< 5	High resistance (HR)
5.1-15	Resistance (R)
15.1-30	Middle resistance (MR)
30.1-50	Susceptibility (S)
> 50	High susceptibility (HS)

Table 4 The resistance results of the maize varieties in the greenhouses/fields

Variety	Source	Germplasm	Resistance/susceptibility type	
			Greenhouse	field
Suonuoyiqu	Zhaojue	Landrace	S	MR
Nuosuyiqu	Zhaojue	Landrace	HS	MR
Yiqu	Zhaojue	Landrace	S	MR
Baimaya	Zhaojue	Landrace	S	MR
Bendibaimaya	Zhaojue	Landrace	S	MR
Leibobaimaya	Zhaojue	Landrace	S	MR
Bendiyiqu	Zhaojue	Landrace	S	MR
Bada	Menghai	Landrace	MR	MR
Manpi(selebai)	Menghai	Landrace	S	MR
Aduxing	Menghai	Landrace	S	MR
Manpi (selileng)	Menghai	Landrace	S	MR
Suwan 1	Menghai	Landrace	S	S
Manmai	Menghai	Landrace	HS	MR
Chuandan 15	Zhaojue	Modern	S	R
Nongda 3138	Zhaojue	Modern	S	MR
17 Danjiao	Zhaojue	Modern	S	MR
Liangdan 3	Zhaojue	Modern	S	MR
Zhongdan 2	Zhaojue	Modern	S	HS
Liangdan 4	Zhaojue	Modern	S	S
Huobai (check)	Crop Institute, SAAS	Landrace	HS	HS
Mo17 (check)	Crop Institute, SAAS	USA Inbred line	R	MR

Agronomic and sanitary performance of Musa cultivars in two locations in Coastal Ecuador: La Mana, Cotopaxi and El Carmen, Manabí

Agama, J.; Cedeño, G.; Paez, P.; Suarez-Capello, C.

INTRODUCTION

In Ecuador, mixed crops are a very common feature among small farmers, and occupy approximately 80 percent of the cropping area in the country. Cocoa/coffee and plantain are systems covering more than 250,000 ha and, although in the hands of medium and small farmers, generate annual incomes of more than two million dollars. However, there is no awareness of the possibility of using them as part of an IPM strategy to lower the impact of exclusive pest and diseases, although farmers do have the perception that they depend on crop (genetic) diversity, both inter- and intra-specific, in their production systems for their subsistence. The interaction between components of this agroecosystem and local knowledge about them is considered a rich source of solutions for dealing with many of the production and sanitary constraints they face. With this background in mind, this project was set up in close collaboration between the National Institute of Agricultural Research of INIAP and Bioversity International. The project aims *“to develop and promote tools and methods to apply existing knowledge about use of crop genetic diversity to manage pest and disease pressures. It will exploit the natural resistance that results from the co-evolution of pest and host species, provide farmers with low-input options for pest and disease management, and reduce the use of pesticides and support maintenance of crop diversity”*. At the onset of the project, cultivar diversity on farms was identified and planting material taken to the research station for reproduction; secondary and direct information about the sites, the cultivars and their pests and pathogens were collected through farmer field discussion and individual surveys improved the knowledge of what is available and what the intensity of the problems faced by farmers is. Following this, several studies were undertaken to gain a better knowledge of the reaction of these cultivars to the three main constraints of the crop: Black sigatoka, Black weevil and nematodes. These studies were presented in posters at this symposium; the objective of the work presented here is to evaluate the agronomic and sanitary performance of twelve cultivars under a range of climatic and soil conditions from La Mana and El Carmen sites in order to have a basis for developing diversity-rich strategies for better sustainability of producers' economy and management of Black Sigatoka disease, Black weevil and nematode pest.

METHODOLOGY

Four experimental plots, two in each site, were planted within orchards of collaborative farmers between March and April 2010. Twenty-five plants of each cultivar were planted in small

plots (3 x 3 m) using the most common cultivar of each area as control and borders in the experiment. Plots were planted in a complete randomized design with three repetitions. They are being managed using the principles of integrated pest control, with no pesticide use except herbicides during the wettest part of the year. Variables being registered are height of plants, diameter of pseudostem, number of new shoots (choupons) and leaves, time to flowering and harvest; incidence of pest and diseases.

PRELIMINARY RESULTS

Agronomic data from both sites up to December 2010, that is 8 and 9 months after planting, are shown in Table 1. Preliminary analysis shows differences in development between sites. Some cultivars did not become established (appeared with no data in the table and figure): cultivars “Dominico gigante” and “Maqueño verde” could not adapt to La Mana site, while the same happened with Limeño in El Carmen. Figure 1 shows Sigatoka incidence in La Mana, which confirms evaluations under lab conditions, showing cultivars Limeño and Orito as resistant, reaching just stages 2 and 4 of the disease, while the others have already reached stage 6. It seems evident that development depends on local climate, which has to be considered in intraespecific planting trials.

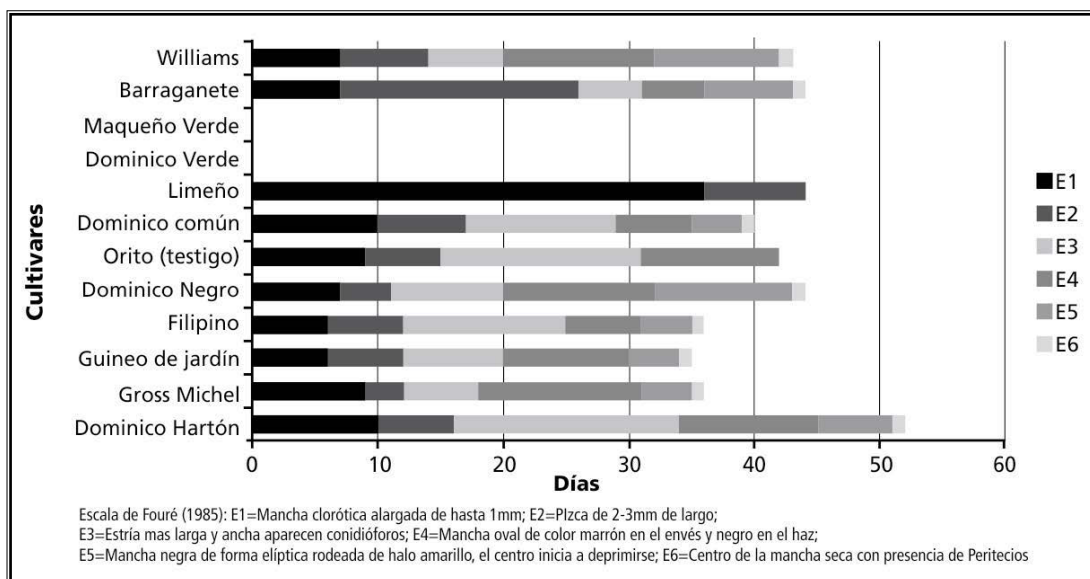


Figure 1 Development of Black sigatoka (*Micosphaerella fijiensis*) in ten *Musa* cultivars under climatic conditions of La Maná site. EET-Pichilingue, 2010

Analysis of faba bean (*Vicia faba* L.) genetic diversity on-farm for resistance to chocolate spot disease due to *Botrytis fabae* Sard

Aqtbouz, N.; Belqadi, L.; Ezzahiri, B.; Sadiki, M.

INTRODUCTION

Faba bean is the major grain legume in Morocco. It is, however, characterized by low and unstable yields. This deficiency in production is partly explained by the harsh climate and partly by biotic stresses, in particular susceptibility to some diseases such as chocolate spot caused by *Botrytis fabae* Sard. Chocolate spot is one of the most devastating fungus diseases in the faba bean crop (*Vicia faba* L.) in Morocco. The selection of genotypes with resistance to *Botrytis* is a sustainable approach to controlling this disease in local production systems. The objective of the present study is to assess the genetic diversity of local faba bean varieties collected in the Taounate region and identify sources of resistance or tolerance to the disease. This study was conducted in the province of Taounate, one of the principal production areas in Morocco.

MATERIAL AND METHODS

The methodology used in this research is based on two approaches. The first is a field evaluation of 100 local populations collected from farmers in the region of Taounate with regard to their reaction to chocolate spot. Disease symptoms were scored visually by using a 5-class visual scale (1: Highly resistant, 2: Resistant; 3: Moderately resistant; 4: Sensitive, 5: Highly sensitive).

The second approach is the evaluation of the reaction of local genotypes in the laboratory by using artificial inoculation of plants with two *Botrytis fabae* isolates collected in two regions (Larache and Taounate). The reaction of the various populations is evaluated after three notations made 10, 15 and 20 days after inoculation, using the same scale as in the field evaluation.

The statistical analysis used for analyzing collected data included univariate and multivariate analysis. These tests were made to compare populations, strains and dates and to assess the genetic variations of populations for their reaction to *Botrytis*. Hierarchical Cluster Analysis and Two-step were used to group populations that react similarly to this disease in the same class. The SPSS (Statistical Package for the Social Sciences) was used for the various statistical analyses.

RESULTS AND DISCUSSION

The field results showed that the germplasm tested contains a wide genetic variability (Figures 1 and 2). Also, the local populations reacted in the same way in both trials in Taounate and Larache. This result suggests that the resistance is stable in space. Moreover, the ranking of populations according to their geographical origins (Tables 1 and 2) showed that both locations, Tissa

and Ourtzagh, contain resistant varieties and can be regarded as the site of sources of resistance to chocolate spot disease.

The laboratory results showed that the majority of populations tested were highly susceptible to the chocolate spot disease (79% of the population) while only 21 populations were resistant (ratings 1-3) (Figure 3). Regarding the progress of the disease in time, it was found that the scoring in the third week after inoculation is the most appropriate for a proper classification of local populations according to their response to infection (Figure 4). Concerning the study of two isolates of the fungus used in the test laboratory, the results showed that the local populations reacted the same way against both isolates of *B. fabae* (Table 3).

In conclusion, this study has shown that the tested germplasm contains a wide genetic variability among local populations of faba bean and secondly it allowed the identification of some sources of resistance/tolerance to *Botrytis*, which could be confirmed and exploited in breeding programs.

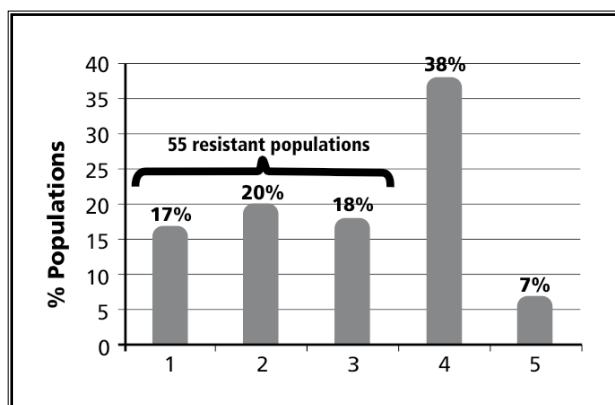


Figure 1 Classification of 100 populations based on average scoring of chocolate spot disease at M'rissa Experimental Station

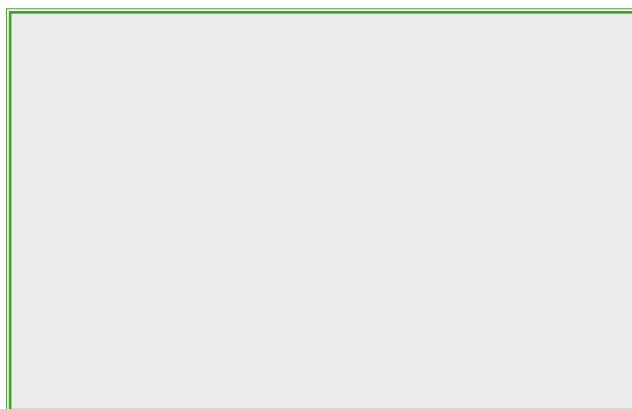


Figure 2 Classification of 100 populations based on average scoring of chocolate spot on farm at Tissa

Table 1 Test Duncan ranking averages of three sites of origin of the populations tested at the experimental station M'rissa

	Common code	N	Subset for alpha = 0.05	
			1	2
Duncan ^{a,b}	3 (Tissa)	803	3,60	
	1 (Ourtzagh)	981	3,71	
	2 (Ghafsay)	60		4,17
	Significance		0,346	1,000

Group averages of homogeneous subsets are displayed.

a. Use the sample size of the harmonic mean = 158.467.

b. The number of groups are not equal. The harmonic mean number of groups is used. The levels of Type I errors are not guaranteed.

Table 2 Test Duncan ranking averages of three sites of origin of the populations tested on farm at Tissa

	Common code	N	Subset for alpha = 0.05	
			1	2
Duncan ^{a,b}	3 (Tissa)	819	2,48	
	1 (Ourtzagh)	60	2,68	2,68
	2 (Ghafsay)	1096		2,72
	Significance		0,053	0,722

Group averages of homogeneous subsets are displayed.

a. Use the sample size of the harmonic mean = 159.574.

b. The number of groups are not equal. The harmonic mean number of groups is used. The levels of Type I errors are not guaranteed.

Table 3 Analysis of variance of dates conducted in the laboratory for two isolates of B. fabae

	Sum of squares	ddl	Mean squares	F	Significance
Inter-strain	0,620	1	0,620	0,562	0,453
Intra-groups	6614,002	5996	1,103		
Total	6614,622	5997			

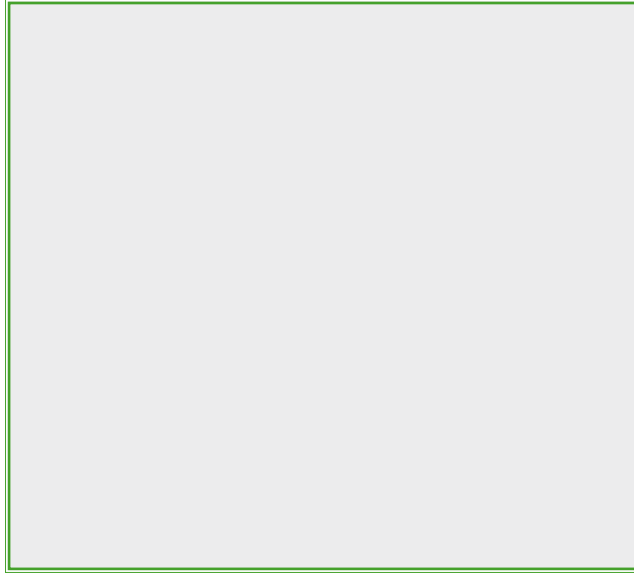


Figure 3 Distribution of local populations of faba bean tested in the laboratory on five classes of resistance

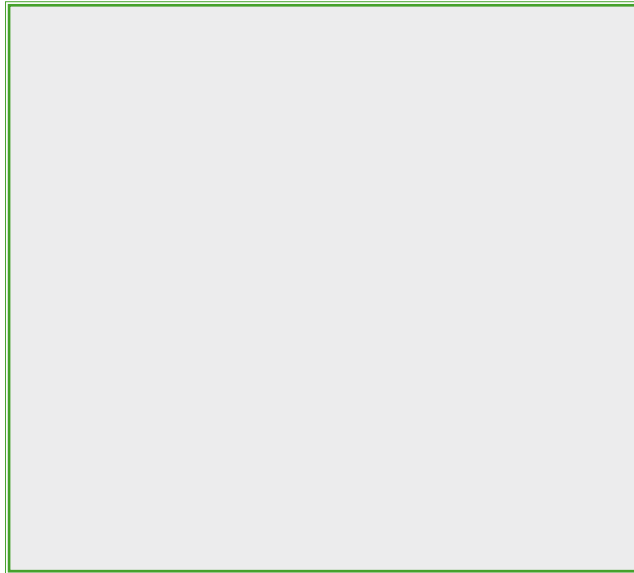


Figure 4 Distribution of indices of the disease during the three ratings

Response of Twelve *Musa* spp Cultivars to Inoculation with *Mycosphaerella fijiensis* Morelet

Cedeño, G.; Castro, B., Vera, D.; Suárez-Capello, C.

INTRODUCTION

Black Sigatoka (*Mycosphaerella fijiensis* Morelet) is the most destructive foliar disease on *Musa* spp, causing more than 50% yield losses on commercial cultivars, especially plantains and necessitating high investment in chemicals as the main pest and disease control method for banana plantations. Producing countries dedicate much effort to developing options for increasing yield and maintaining ecosystem health while reducing costs. One option being explored recently is to incorporate in the general integrated crop management strategy the use of cultivar mixtures to reduce the impact of inoculum production and dispersal. The present research focused on determining the behavior of twelve cultivars of *Musa* spp against the disease under artificial inoculation. Additionally, a complementary study is being conducted to elucidate differences within the fungal population in the area

METHODS

The first study comprises two experiments to evaluate cultivars "Orito" (AA), "Limeño", "Barganete", "Dominico", "Dominico-Hartón", "Dominico gigante", "Dominico negro" (AAB) and "Gros Michel", "Guineo de jardín", "Filipino", "Maqueño verde" y "Williams" (AAA). For the first group, the leaf disk inoculation technique was used. In the Plant Pathology Laboratory at Pichilingue, several bioassays were required in order to keep leaf fragments alive enough time to evaluate disease development. Leaf fragments (2 cm² in size) of each cultivar, kept in semiliquid water agar media (0.2%BactoAgar/L), were inoculated with a conidiospore suspension extracted from leaves collected in the field. After inoculation they were maintained in an incubation chamber with constant fluorescent light until controls produced necrosis of the fragments. Resistance response was confirmed in a second trial, inoculating (1 ml with $1,5 \times 10^5$ cfu/mL) 10-week-old *in vitro* plants of same cultivars. Ten plants/cultivars were used; they were kept in a shade house with regular irrigation to observe disease development. In both trials, incidence and disease development using standard procedures were measured. They were set as a completely randomized design; the Scott & Knott test applied for mean comparison for $p=0,05$.

To evaluate *M. fijiensis* variability, 120 monosporic isolates, 60 each from the sites of El Carmen and La Mana, were collected and procedures for pathogenicity and culture morphology are being developed: Pieces of infected leaves were taken to the Plant Pathology Lab of the Pichilingue Research Station from INIAP, spore discharge on water agar led to single spore isolation on V8 Agar and from here to PDA where observations were made. Morphological criteria of the culture, such

as colony diameter, color and aspect of the cultures, type, size and amount of spores production are being used to characterize each one.

RESULTS

Cultivars showed the same behavior, regardless of inoculum (conidia and mycelium) and type of substrate (fragments of leaves and plantlets) inoculated. According to the mean and the standard deviation of the TSD variable, considering the interval $\bar{X} \pm S$ (0.4881), Orito (AA) and Limeño (AAB) cultivars were considered resistant; Maqueño verde (AAA), Dominico-Hartón (AAB), Dominico (AAB), Dominico negro (AAB), Dominico gigante (AAB) and Barraganate (AAB) perform as moderately resistant and finally the banana cultivars: Guineo de jardín (AAA), Filipino (AAA), Gros Michel (AAA) and Williams (AAA), were shown to be susceptible to black Sigatoka, as can be observed in Table 1.

Bioassays with leaf fragments of 2cm² taken from cultivars William (AAA) and Barraganete (AAB) inoculated with an ascospore suspension of *M. fijiensis* allowed a complete evolution of the disease in 50 days. In order to make a pathogenic evaluation of the isolates, a method for keeping the leaf pieces functional was developed by submerging the leaf fragments into two solutions of citric acid (1g/l) and gibberelic acid (1 ml/l) in water five minutes each and then placed over a layer of PDA. This methodology will be used to test the pathogenicity of the 120 isolates by the leaf disk method. Preliminary results show variation between and within sites considering colony growth and color, with more variability in La Maná site where there are more cultivars and environmental diversity.

DISCUSSION

Cultivars were grouped, independently of the evaluation procedure, into three categories (resistant, moderately resistant and susceptible), as shown in the table. One interesting feature to note is that the Maqueño verde is the only AAA type that groups with AAB group, showing moderate resistance, while the other cultivars of the same genome behave as susceptible. One important concern among La Mana farmers is to keep their crops as organic as possible. Study results have shown that this possibility is feasible through experimentation with their cultivars, redesigning cultivation patterns, for example, using those with lower incidence of phytosanitary problems as barriers for the commercial ones. As for El Carmen, where farmers are more familiar with IPM principles, these findings reveal the advantages of introducing *Musa* diversity in the general IPM strategy, both to reduce pest impact and to help farmers to get away from dependence on very few cultivars while making the best of their considerable experience in dealing with this type of crop.

Table 1 Time of disease development (TDE) from inoculation with *Mycosphaerella fijensis*, for twelve Musa cultivars

Cultivares	TDE	Categoría
Orito (AA) Limeño (AAB)	75,50 71,25	Resistentes
Maqueño verde (AAA) Dominico negro (AAB) Dominico Hartón (AAB) Dominico (AAB) Barraganete (AAB) Dominico gigante (AAB)	59,38 58,38 57,38 57,25 55,75 55,38	Medianamente resistentes
Guineo de jardín (AAA) Filipino (AAA) Gros Michel (AAA) Williams	49,75 49,25 48,88 48,88	Suceptibles
X±S (0.4881)	X S	
	57,25 8,53	

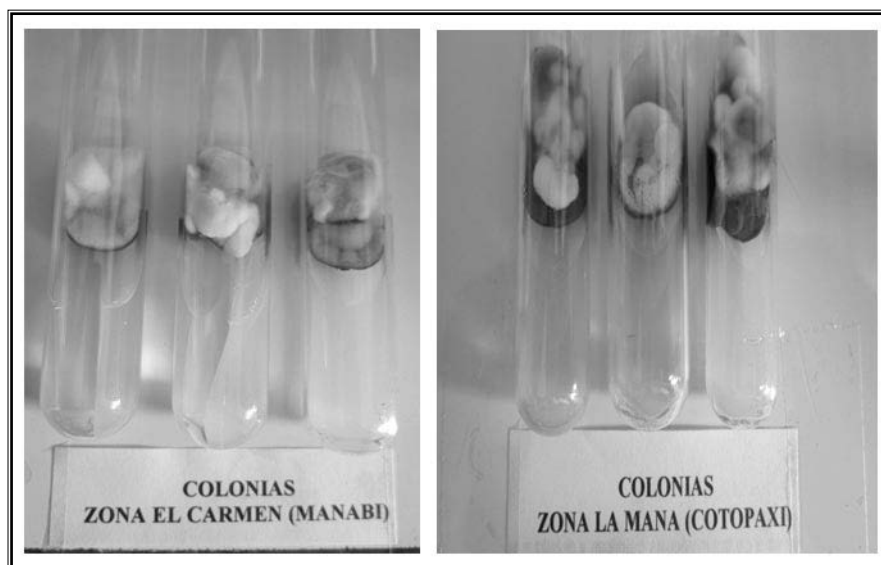


Figure 1 *M. fijensis* cultures showing different colony morphology between two sites, Ecuador.

Analysis of local barley (*Hordeum vulgare* L.) genetic diversity for resistance to net blotch disease due to *Pyrenophora teres* f.sp. *teres*

Chentoufi, L.; Belqadi, L.; Ezzahiri, B.; Sadiki, M.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the most cultivated cereal in Morocco. It covers every year 43 % of the total cereal area. This crop is important in animal feed and a part of human food. Its yield is low, barely exceeding 15 quintals/ha. This is due to many factors such as drought, the use of traditional techniques and the low productivity of varieties and their susceptibility to diseases. Net blotch, caused by the fungus *Pyrenophora teres* f. sp. *teres*, is one of the major diseases of this crop worldwide. The search for sources of resistance to this disease represents the most effective tool against this fungus. In this sense, the present study was conducted in Taounate province, where barley is grown under a traditional system of cultivation and farmers usually produce their own seeds. The present work aims to assess the genetic variability of a local collection of barley for its reaction to the blotch disease and to identify sources of resistance to Net blotch.

MATERIAL AND METHODS

The plant material used in this study consists of 100 local barley populations collected from farmers in three communities: Tissa, Ourtzagh and Galaz. The reaction of these populations to four strains of *Pyrenophora teres* f. sp. *teres* (of which three are from region of Taounate and the other in the region of Larache) was evaluated. These strains were maintained in a culture medium containing V8.

Inoculation of plants was conducted under controlled conditions of humidity, temperature and light. The reaction of the population to different isolates was assessed on two dates (10 and 15 days after inoculation) using a scale from 1 to 5 classes (Class 1 represents the most resistant strains, whereas class 5 includes most susceptible one).

The statistical methods used in the data analysis include descriptive statistics to obtain a general description of the populations. The analysis of variance with one criterion of classification was calculated to compare populations and strains studied and verify the genetic variability of this material. The characters showing significant variability were classified according to a test of Duncan. Among the multivariate analysis used in this analysis include the Two-Step Classification which can show the linear combinations of characters and grouping homogeneous populations in the same class. Software Excel and SPSS (Statistical Package for the Social Sciences) were used for these different tests.

RESULTS AND DISCUSSION

The results of the analysis of plant material have revealed that the germplasm collected in the region of Taounate contains a wide variability with regard to its response to net blotch disease (Figure 1), and the infection of the fungus culture evolves in a remarkable way over the time (Table 1). Multivariate analysis brought together local populations in five uniform classes. The class 1 which contains populations with high disease resistance comprises 28 populations including 23 from the community of Ourtzagh (Figure 2). Moreover, the results of the analysis of strains used in the inoculation showed the existence of a very highly significant difference between them (Table 2). They also revealed that the difference between the strain from the region of Larache and the other three from the region of Taounate is significant (Table 3). Overall, the data suggest that local populations of barley analyzed in this study contain a significant genetic variability *vis-à-vis* the net blotch disease and considerable sources of resistance may exist in Ourtzagh.

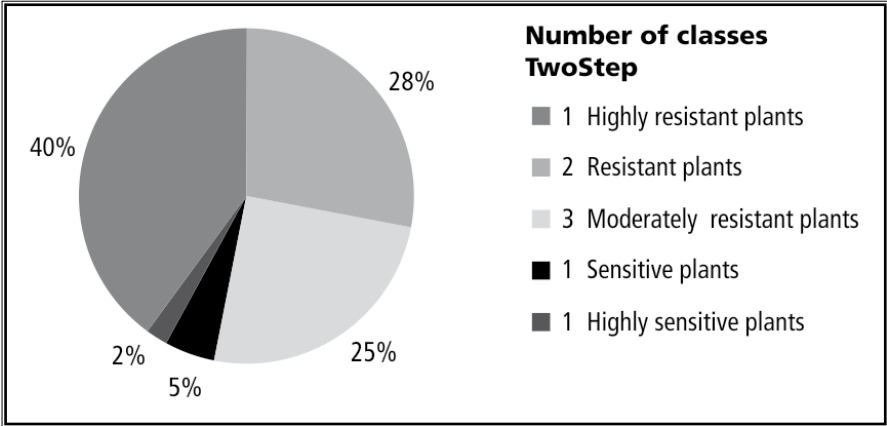


Figure 1 Assigning the importance of the five classes listed by date and by strain

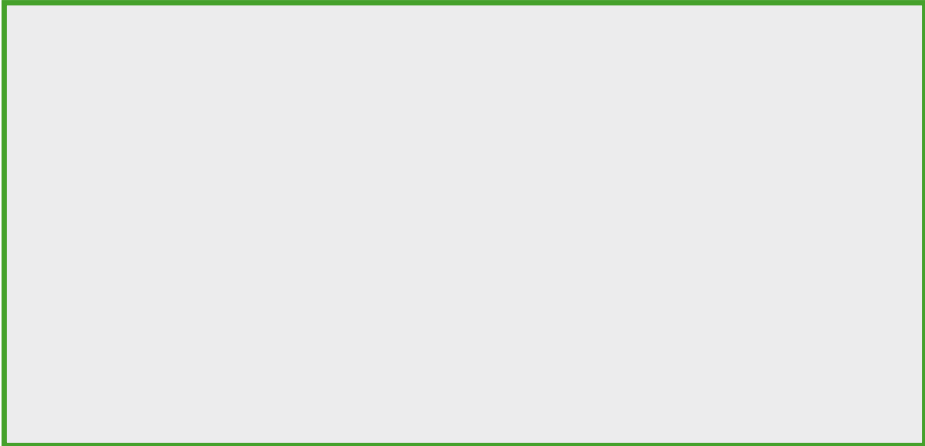


Figure 2 Percentage of resistant populations according to their geographical origin

Table 1 Analysis of variance for comparing dates

	Sum of squares	ddl	Average of squares	F	Significance
Inter-groups	1429,411	1	1429,411	2720,327	,000
Intra-groups	3936,794	7176	549		
Total	5429,205	7177			

Table 2 Ranking of the four strains by Duncan's test

	N	Subset for alpha = 0.05				
		1	2	3	4	
Duncan ^{a,b}	4	1836	1,81			
	1	1764		2,45		
	3	1828			2,52	
	2	1750				2,65
	Signification		1,000	1,000	1,000	1,000

Group averages of homogeneous subsets are displayed.

a. Use the sample size of the harmonic mean = 1793.698

b. The number of groups is not equal. The harmonic average number of groups is used. The level of Type I errors are not guaranteed

Table 3 Descriptive statistics of the four strains

Provenance of strains	Strains	N	Average	Standard deviation	Confidence interval 95% to the average		Min	Max
					Lower bound	Upper bound		
Taounate	1	1764	2,45	,823	2,41	2,48	1	5
	2	1750	2,65	,852	2,61	2,69	1	5
	3	1828	2,52	,819	2,48	2,56	1	5
Larache	4	1836	1,81	,728	1,77	1,84	1	4
	Total	7178	2,35	,870	2,33	2,37	1	5

Comparison of susceptibility of ten *Musa* cultivars to the attack of *Radpholus similis* and *Meloidogyne* spp.

Lopez, J.

Nematodes are one of the main constraints affecting banana and plantain in Ecuador. Root knot nematodes, *Meloidogyne* spp, are the endoparasitic round worms that are the most widespread in the plantain area of El Carmen in Ecuador. They cause the formation of root galls and produce yellowing, stunting and poor yield in the host. *R. similis* is a migratory ectoparasite which cause root necrosis, yellowing and poor yield. Although it predominates in the banana producing region, it has been moved to the plantain area where it is spreading quite fast thanks to its high rate of reproduction, although it is still a localized problem. Although it does not kill plants, it is the main cause of lodging and yield lost. Two experiments were conducted to evaluate the sensibility of ten *Musa* cultivars -- Orito (AA), Gross Mitchael, Williams (AAA); Barraganete, Dominico, Dominico Harton, Dominico Negro, Dominico Gigante (AAB) -- against *Meloidogyne* spp or *R. similis*. *In vitro* plants were placed in large plastic bags (30 x 30") containing sterile top soil. Five weeks alter planting, they were inoculated with the corresponding nematode population and observed for 16 weeks until they were harvested to assess the damage on roots and the population of the nematode. *Meloydogine* spp treatments consisted of inoculations with 100 ml of a suspension of 500 juveniles and eggs extracted from highly infested soil collected on a farm in El Carmen. For *R. similis*, 100-gram pieces of infested root and corms coming from the same source were used, ensuring around 5000 nematodes/100 g of infected tissue, and were buried in two holes in each part of the plant, 10cm from the stem and 10 cm deep. Plants were kept under observation for 16 weeks after inoculation, when they were harvested to evaluate root damage and the population of nematodes per cultivar. All AAA and AA cultivars showed moderate resistance to *Meloidogyne* as opposed to *R. similis*, for which similar resistance was found only for Gross Michael (AAA) and Orito (AA); cultivars Williams and Guineo de jardín, although belonging to the same genome of Gross Michael, showed high susceptibility for this nematode. All plantain cultivars (AAB) performed as either susceptible or highly susceptible to both nematodes.

Comparison of susceptibility of ten *Musa* cultivars to the attack of *Cosmopolitis sordidus* in Ecuador

Velez, M.

This research aims to evaluate the susceptibility of ten *Musa* cultivars (Maqueño morado, Maqueño verde, Barraganete, Dominico, Dominico Negro, Dominico Hartón, Dominico verde (AAB); Gross Michell, Williams (AAA) and Orito (AA)) to the attack of *C. sordidus*. Corms of each cultivar were peeled, cleaned and left in groups for 24 hours within a plantation with high infestation of weevils. Then they were planted in a block within the same plantation. The farm is located in El Carmen site and was selected because it exceeds the accepted critical level of insect infestation (8 to 16 adults weevil/trap). Ten plants each of ten cultivars were planted in a randomized complete block design (RCBD) with five repetitions. Mortality was recorded monthly, starting three months after planting, any aerial symptom being described as well. Results show that cultivars Dominico Hartón, Barraganete y Dominico negro, are very attracted by the weevils, which cause 75, 70 and 65% incidences of mortality respectively. Cultivars Williams, Orito and Maqueño morado showed only around 25% mortality.

Eleven barley cultivars in Shangri-la and Songming County and their phenotype analyses

Chun-yan Li; Huang Yuan; Yu Guo; Chun-lin Long.

ABSTRACT

Shangri-la and Songming Counties in Yunnan Province have a long history of cultivating barley. There were altogether 11 barley cultivars in the two sites. Three repeat experiments to plant the 11 cultivars were carried out in each site and barley phenotype diversity was analyzed. This research showed that there is abundant morphological mutation among the barley varieties collected from two field sites by analyzing average (A), standard deviation (SD) and coefficient of variation (CV) of 19 main morphological characters. CV of grain color and awn length are all over 50%. These two characters are important for indicating barley's morphological features and can be a significant index reflecting morphological diversity.

Key words: barley, phenotype diversity

INTRODUCTION

Barley (*Hordeum vulgare*) is the fifth largest cultivated cereal crop in the world. In China, Yunnan Province is the genetic diversity center for barley. Shangri-la and Songming Counties in Yunnan Province have a long history of cultivating barley .

Phenotype analysis is a basic method of analyzing plant genetic diversity and has been successfully used to characterize barley genetic diversity. Sharma et al. (1994) found a vast variation in morphology between and within landrace populations of Nepalese barley germplasm. In addition, differences in agronomic performance and disease resistance were detected (Baniya et al. 1997) in these landrace populations of Nepal. Witcombe and Murphy (1986) assessed the morphological variation of Himalayan barleys.

In order to gain more information on the genetic resources of barley in Shangri-la and Songming Counties and to estimate the genetic diversity, we analyzed average (A), standard deviation (SD) and coefficient of variation (CV) of 19 main morphological characters.

MATERIALS AND METHODS

1.Plant materials

A total of 11 barley cultivars were selected from the two investigation sites (Table 1, Fig 1, Fig 2, Fig 3, Fig 4). The barley cultivars which had the names of high beer barley and short beer barley in table 1 were the cultivar "two-row beer barley," which was shown in Figures 3 and 4. The two cultivars had same spikes and grains in phenotype .The only difference between them was the height.

2. Statistical analysis

The field experiments were carried out on a plot of land in each village. Three repeat experiments were carried out in each site. The 11 cultivars, which were randomly located on each plot of land, were grown in a rectangle of 1m×3m each. A total of 19 morphological traits were measured and a quantitative analysis was performed (table 2). The average, standard deviation, maximum, minimum, sample range (R) and coefficient of variation (SV) were calculated with Excel and SPSS software.

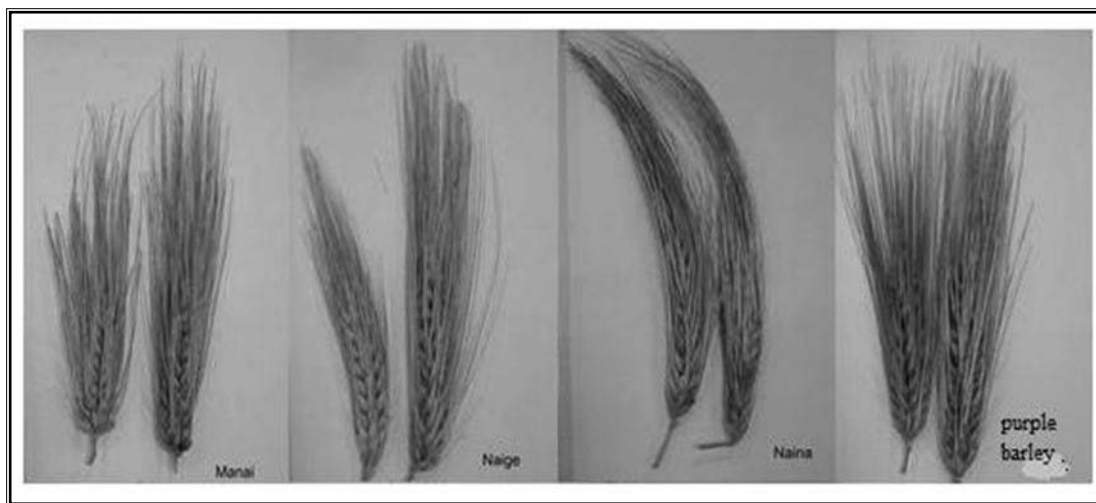


Figure 1 Spikes of four barley cultivars in Shangri-la

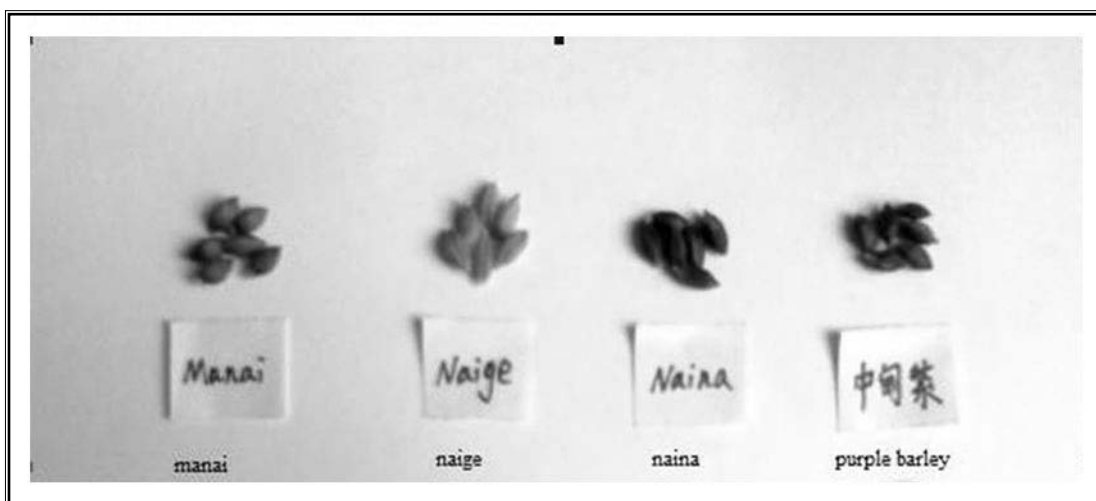


Figure 2 The grains of 4 barley cultivars in Shangri-la

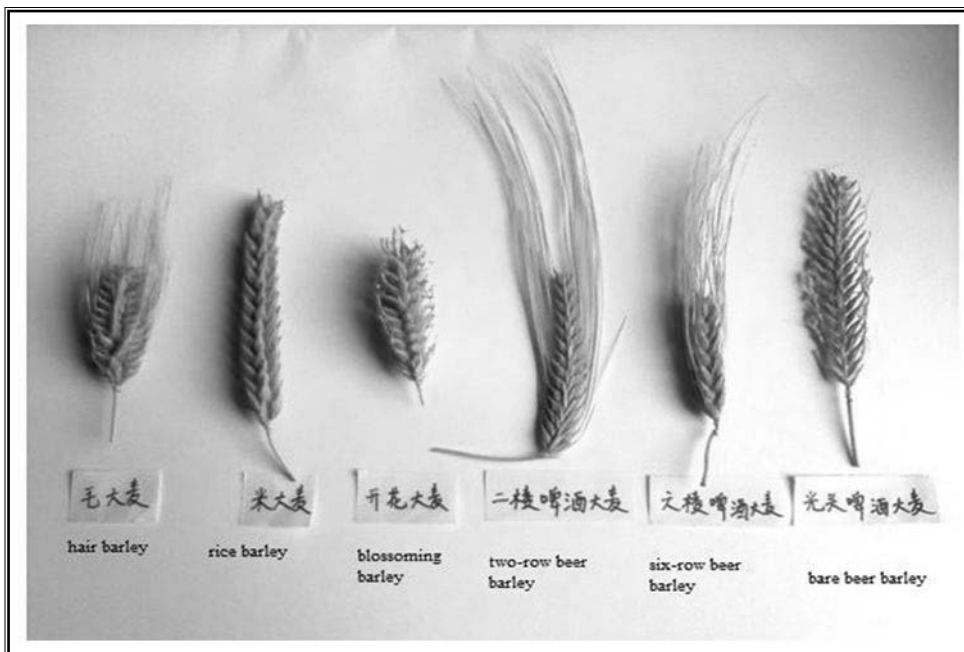


Figure 3 The spikes of 6 barley cultivars in Songming

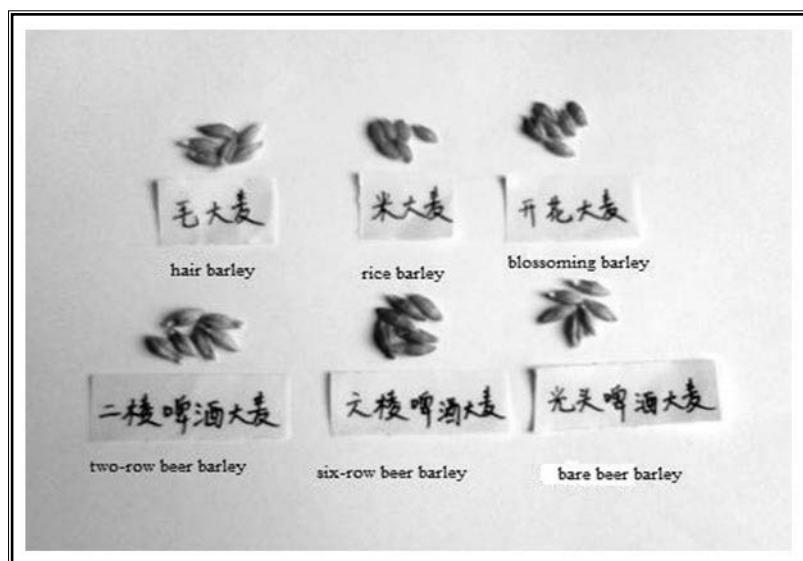


Figure 4 The grains of 6 barley cultivars in Songming

RESULT AND DISCUSSION

The result revealed that the 11 barley cultivars had high phenotype diversity in 19 morphological traits except for the sterile lemma width and awn type (Table 3, Table 4). The value of CV of 19 morphological traits showed that GC> AL> LR> SD> S/FT> N/NB> K/S> AC> HC> RT> SL> PH> GW/S> GL> 1000KW> GT> GW> SLW=S/BA. The mean of CV was 23.84%. GC and AL had the higher CV (beyond 50%), indicating that the two traits were significant characters in the assessment of barley phenotype variations.

A conclusion was based on the phenotype analyses. These showed that the 11 barley cultivars in Shangri-la and Songming, which both had a long history of planting barley, had high diversity. Complementary conservation is imperative for safeguarding these barley recourses.

Table 1 Barley cultivars from two sites

Code	Local name	Types	Collecting location
1	Manai	local	Shangri-la county
2	Naige	local	Shangri-la county
3	Naina	local	Shangri-la county
4	Naishui (purple barley)	local	Shangri-la county
5	Hair barley	local	Songming county
6	Rice barley	local	Songming county
7	Blossoming barley	local	Songming county
8	High beer barley	modern	Songming county
9	Short beer barley	modern	Songming county
10	Six-row beer barley	modern	Songming county
11	Bare beer barley	modern	Songming county

Table 2 Morphological traits (19)

	Traits	Codes	Quantified
1	Plant height	PH	high=1; middle=2; mid-short=3; short=4
2	Spike length	SL	<5cm=1; 5-6cm=2; 6-7cm=3; >7cm=4
3	Rowed type	RT	two-row=1; six-row=2
4	Spike density	SD	thin=1; intensive=2
5	Husk color	HC	yellow=1; purple=2
6	Sterile lemma width	SLW	wide=1; narrow=2
7	Awn length	AL	long=1; short=2; bare=3
8	Sawed or bare awn	S/BA	rough=1; smooth=2
9	Awn color	AC	yellow=1; purple=2
10	Barley and naked barley	B/NB	barley=1; naked barley=2
11	Grain color	GC	yellow=1; brown=2; purple=3; black=4
12	Kernels/spike	K/S	<50=1; 50-60=2; 60-70=3; >70=4
13	1000-kernel weight	1000-KW	<30g=1; 30-40g=2; >40g=3
14	Grain weight/spike	GW/S	<1.6g=1; 1.6-1.8g=2; 1.8-2.0g=3; >2.0g=4
15	Spring and fall type	S/FT	winner sowing=1; spring sowing=2
16	Lodging-resistant	LR	strong=1; middle=2; weak=3
17	Grain length	GL	<0.800cm=1; 0.800-0.900cm=2; 0.900-1.000cm=3; >1.000cm=4
18	Grain width	GW	<0.320cm=1; 0.320-0.350cm=2; 0.350-0.380cm=3; >0.380cm=4
19	Grain thickness	GT	<0.240=1; 0.240-0.260=2; 0.260-0.280=3; >0.280=4

Table 3 The morphological characterization of 11 barley varieties

No	PH (cm)	SL (cm)	RT	SD	HC	SLW	AL	S/BA	AC	B/NB	GC	K/S	1000-KW(g)	GW/S	S/FT	LR	GL (cm)	GW (cm)	GT (cm)
1	94.2	4.8	six	intensive	yellow	narrow	long	rough	yellow	naked	brown	63.2	36.86	1.8	spring	common	0.708	0.389	0.28
2	111.1	7.1	six	thin	yellow	narrow	long	rough	yellow	naked	yellow	71.8	39.18	2.08	spring	low	0.839	0.371	0.28
3	114.7	7	six	thin	yellow	narrow	long	rough	yellow	naked	black	71.6	39.79	2.01	spring	low	0.824	0.369	0.278
4	108.9	7.6	six	thin	purple	narrow	long	rough	purple	naked	purple	70.2	36.94	1.93	spring	common	0.751	0.357	0.268
5	80.3	4.9	six	intensive	yellow	narrow	short	rough	yellow	common	yellow	77.2	35.2	1.91	fall	high	0.839	0.335	0.26
6	84	7.8	six	thin	yellow	narrow	bare	-	-	naked	yellow	75.8	29.55	1.8	fall	high	0.741	0.304	0.226
7	86.9	4.4	six	intensive	yellow	narrow	bare	-	-	common	yellow	64.4	33.5	1.62	fall	high	0.824	0.332	0.254
8	76.9	7.4	two	intensive	yellow	narrow	long	rough	yellow	common	yellow	33.2	42.44	1.36	fall	high	0.988	0.35	0.266
9	64.3	7.6	two	intensive	yellow	narrow	long	rough	yellow	common	yellow	34.1	42.1	1.39	fall	high	0.974	0.348	0.274
10	62.6	4.9	six	intensive	yellow	narrow	long	rough	yellow	common	yellow	54	42.48	1.95	fall	high	1.038	0.359	0.281
11	72.1	5.6	two	intensive	yellow	narrow	bare	-	-	common	yellow	27.2	41.51	1.08	fall	high	0.874	0.357	0.276

Table 4 The frequency of 19 morphological markers differentiation

Traits		Frequency (%)	Traits		Frequency (%)
	high	13.33		<5cm	26.67
	middle	40		5-6cm	20
	mid-short	33.33		6-7cm	13.33
	short	13.33		>7cm	40
	two-row	20		intensive	53.33
	six-row	80		thin	46.67
	yellow	93.33		wide	0
	purple	6.67		narrow	100
	long	73.33		rough	100
	short	6.67	SL	smooth	0
PH	bare	20	SD	yellow	91.67
RT	common	40	SLW	purple	8.33
HC	naked	60	S/BA	yellow	73.33
AL	<50	20	AC	brown	13.33
B/NB	50-60	13.33	GC	purple	6.67
K/S	60-70	26.67	1000-	black	6.67
GW/S	>70	40	KW	<30g	6.67
LR	<1.6g	20	S/FT	30-40g	0.6
GW	1.6-1.8g	20	GL	>40g	33.33
	1.8-2.0g	33.33	GT	fall	53.33
	>2.0g	26.67		spring	46.67
	high	46.67		<0.800cm	46.67
	common	40		0.800-0.900cm	33.33
	low	13.33		0.900-1.000cm	13.33
	<0.320cm	6.67		>1.000cm	6.67
	0.320-0.350cm	33.33		<0.240cm	6.67
	0.350-0.380cm	53.33		0.240-0.260cm	33.33
	>0.380cm	6.67		0.260-0.280cm	53.33
				>0.280cm	6.67

Table 6 The statistical data of 11 barley varieties based on morphological markers

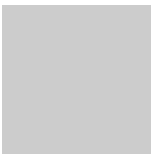
Traits	Mean	Maximum	Minimum	SD	R	CV(%)
PH	89.88	114.7	62.6	16.45	52.1	18.3
SL	6.31	7.8	4.4	1.18	3.4	18.7
RT	1.8	2	1	0.41	1	22.78
SD	1.47	2	1	0.52	1	35.37
HC	1.07	2	1	0.26	1	24.3
SLW	2	2	2	0	0	0
AL	1.47	3	1	0.83	2	56.46
S/BA	1	1	1	0	0	0
AC	1.08	2	1	0.29	1	26.85
B/NB	1.6	2	1	0.51	1	31.88
GC	1.47	4	1	0.92	3	62.59
K/S	60.81	77.2	27.2	16.35	50	26.89
1000-KW	38.67	42.9	29.55	3.76	13.25	9.72
GW/S	1.8	2.14	1.08	0.3	1.06	16.67
S/FT	1.53	2	1	0.52	1	33.99
LR	1.67	3	1	0.72	2	43.11
GL	0.826	1.038	0.708	0.1	0.33	12.11
GW	0.351	0.389	0.304	0.02	0.085	5.7
GT	0.264	0.281	0.226	0.02	0.055	7.58



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 3



Variation in pathogens and pest biotypes
(FGD, HH Survey, Option 3)

Laboratory study of the reaction of *Bruchus rufimanus* on local varieties of *Vicia faba* in Taounate area, Morocco

Chlyeh, G.; Atfaoui, S.; Benboujema, F.; Sadiki, M.

INTRODUCTION

In Morocco, legumes are among the most important crops in terms of socio-economic development. The bean is the most important species in terms of area and production. Nevertheless, this crop has for several decades been characterized by a production level below its potential. This deficiency in production is due partly to abiotic stresses such as drought, salinity and cold as well as biotic stresses. Biotic stresses induce important losses on faba bean crops and occur on two levels: (1) In the field, the losses are predominately due to fungal diseases such as chocolate spot disease (*Botrytis fabae*), rust (*Uromyces fabae*) and anthracnose (*Ascochyta fabae*). In addition, broomrape (*Orobanche crenata*) and aphids (*Aphis fabae*, *A. craccivora* et *Acyrtosiphon pisum*) are major concerns for farmers as they cause important yield losses. (2) In storage, the bean weevil *Bruchus rufimanus* is the major problem for farmers in warehouses. Indeed, the infection starts at the field level by spawning adults on bean pods, but the damage is only levied during storage. This pest behavior, spanning both field and storage stages, complicates the development of methods of control.

The present research analyzes the contribution of local biodiversity to the process of these stresses, with emphasis on beetle pests of *Vicia faba* in three Taounate agro-systems, Ourtzagh, Galaz and Tissa. The main objectives of this study is to evaluate local knowledge and management systems, in addition to analyzing farmers' perceptions concerning faba bean pests and to examining the reaction and interaction of *B. rufimanus* on local varieties of faba bean.

MATERIAL AND METHODS

This study has two components:

1-Individual Surveys

The individual survey assesses the level of knowledge of farmers about varietal resistance. It also reveals whether these farmers use genetic diversity of the bean in existing sites to control pests, and especially the weevil. The survey also reveals the different agricultural practices conducted in post-harvest management. The surveys were conducted among 173 randomly selected farmers in three sites. The timing of the survey coincides with the vetting stage, the beginning of flowering and pod formation, which corresponds with the spawning period of the weevil on the pods. Indeed, adults feed on pollen from flowers of broad beans for the lifting of indurate imagi-

nal diapauses and ovarian maturation. These investigations were supported by observations and direct measurements on plots of faba bean.

2-Laboratory study of the reaction of *B. rufimanus* on local varieties of *Vicia faba*

Germinative capacity of seeds test

Laboratory study shows the importance of damage caused by the beetle to the germinative capacity of seeds. The test was carried out in pots in a greenhouse in a randomized complete block design with three replications. Each pot contained a single seed deposited on five lines. The lines represent the treatments studied on the basis of the degree of damage of *B. rufimanus*

Test for evaluation of resistance to *B. rufimanus* in eight local varieties (fig. 1)

We looked at eight local varieties that are most prevalent in the region. The samples were assembled by farmers surveyed through two collections in 2008 and 2009 at the local storage facility (fig. 2). The several parameters studied for estimating the level of plant resistance to stored grain weevil attacks included the percentage of grains damaged, the number of offspring, the loss in grain weight, development time and the mortality rate. The research results established a classification of eight local varieties studied according to their level of resistance.

RESULTS

Individual investigations reveal the following results:

- Dominance of the variety Sbai in three sites,
- Beldi, Rbaid, Rbaid lbyad varieties are more resistant to biotic stresses,
- Tsai roumi variety is the most resistant to the bean weevil,
- Rbaid Sbai is the most susceptible to weevil,
- There is no practical treatment in storage against the weevil.

The results of the test for resistance to *B. rufimanus* on eight local varieties showed that faba bean seed is slightly influenced by the attacks of the *B. rufimanus* and varieties of small size and black color (V7: Fouila Beldia Lbida ; V8 : Fouilette, and V1 et V5: Sbaï khel) are most resistant to the attacks of the beetle (fig. 3).

CONCLUSIONS

This study showed that there are differences in farmers' beliefs about the causes of the attack of *B. rufimanus* and differences in the preferences of local varieties they use. On the other hand, this study has established a classification of local varieties of the faba bean according to their levels of resistance to *B. rufimanus*

Key words: *Vicia faba* L., *Bruchus rufimanus*, varietal resistance, biodiversity, biotic stress, local variety.

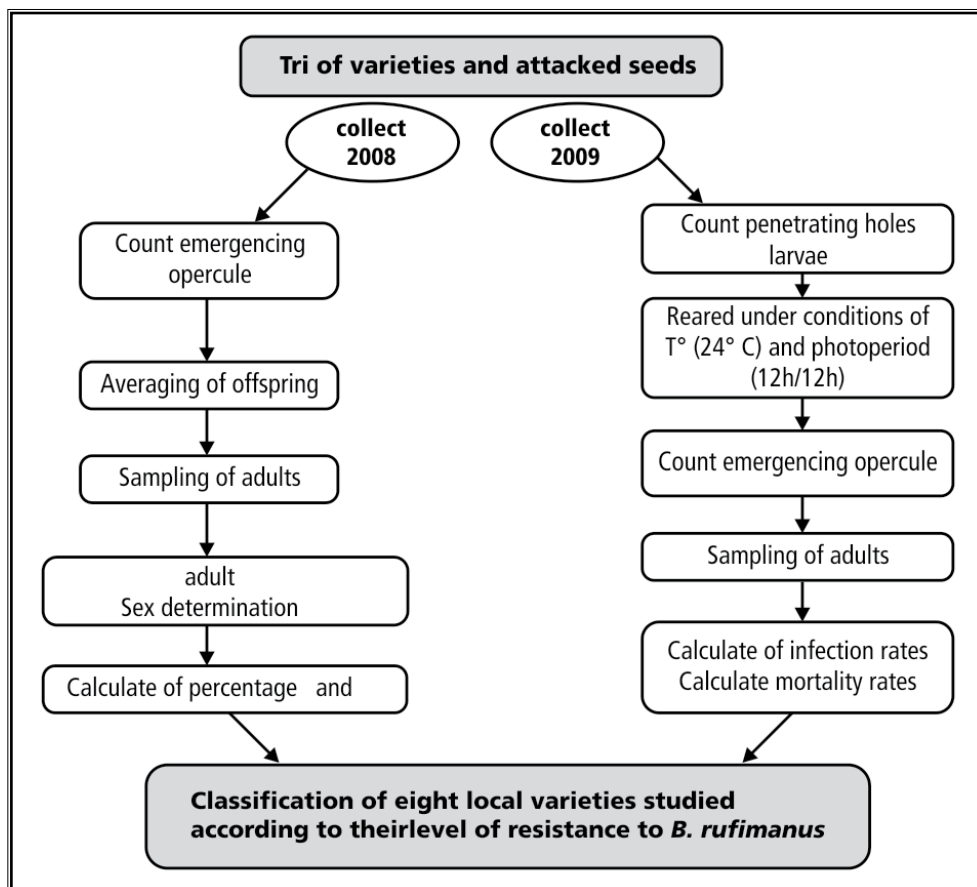


Fig 1: Experimental protocol

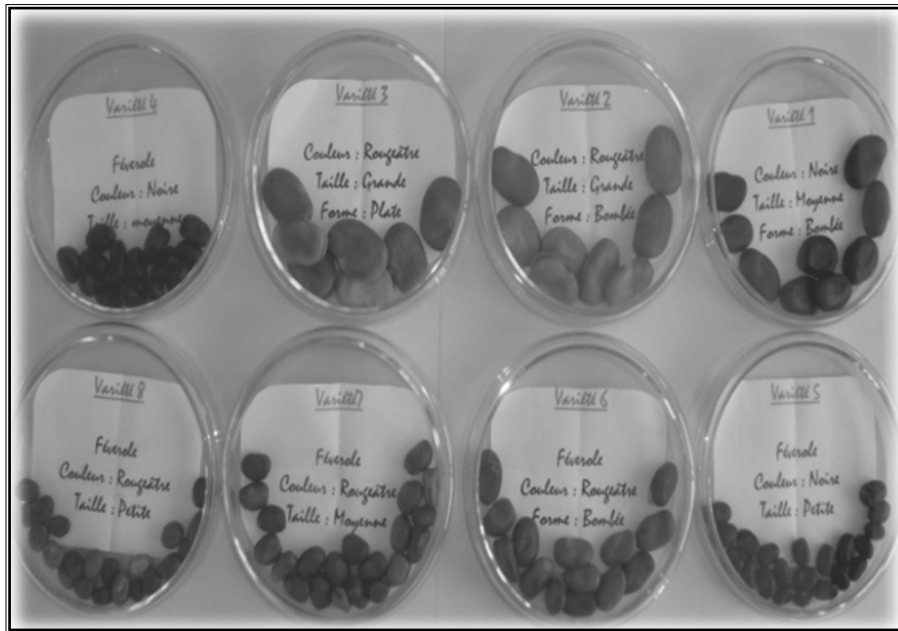


Figure 2: Characteristics of local varieties tested

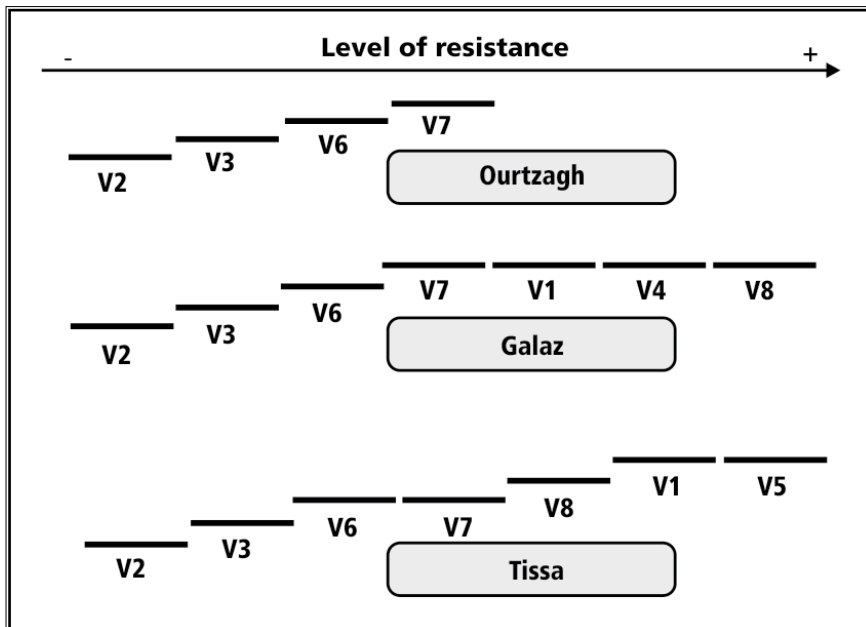


Figure 3: Level of resistance

Variation of *Pyrenophora teres* causing net blotch of barley

Ezzahiri, B.; Belqadi, L.; Chentoufi, L.; Sadiki M.

INTRODUCTION

Net blotch is one of the most important diseases of barley in all major barley-growing regions of the world (Mathre 1982). The casual agent is *Pyrenophora teres* Drechsler (anamorph: *Drechslera teres* [Sacc.] Shoemaker). Two morphologically similar intraspecific *formae speciales* of the net blotch pathogen (producing different symptoms) are known: the net form (*P. teres f. sp. teres*) and the spot form (*P. teres f. sp. maculata*) (Smedegard-Petersen, 1971).

P. teres can overwinter on infested plant residues on barley seed. During the growing season *P. teres* reproduces mainly asexually on barley leaves. Passively liberated haploid conidia are dispersed by wind and rain splashes to surrounding plants and upper leaves mainly within the same field (secondary infection). To complete the life cycle, sexual reproduction occurs on straw debris and leaf fragments. During sexual reproduction *P. teres* is diploid and forms bitunicate asci within perithecia. Two isolates of different mating type are needed for sexual reproduction since *P. teres* is heterothallic and self-sterile. Although the life cycle of *P. teres* is well documented, the importance of different stages of the life cycle for occurrence of net blotch symptoms is still not entirely clear. Virulence studies have revealed the existence of strains with different virulent patterns on selected barley hosts designated as differentials by various authors. Afanasenko et al. (1995) has suggested 11 cultivars as international differentials.

In this paper we summarize the results of a glasshouse experiment that was aimed at the evaluation of the virulence of four isolates of *P. teres f. sp. teres* on 100 populations of barley. These populations were collected from farmers in three communities (Tissa, Ourtzagh and Ghafsay).

MATERIAL AND METHODS

Pathogen sampling and isolation

Leaves with net blotch lesions were sampled and put in a paper envelop. The sampling was made from barley fields in the project sites. One sample was collected from an experimental station located near the Atlantic Ocean (250 km west of the project sites). Small pieces (5mm diameter) of infected leaves were cut from each sample. The pieces were put in a solution of ethanol (95%) for 15 seconds and then in a solution of sodium hypochloride for 15 seconds. They were then washed twice in sterile water. The pieces were then placed in a Petri dish moist chamber for three days in a chamber at 21°C with 12 hours of alternating light and darkness. When spores started to form, they are picked off under a binocular microscope with a dry needle and transferred to a V8 juice culture medium (20 gr of Bacto Agar + 200 ml of V8 juice + 10 gr of calcium carbonate + 800 ml of distilled water).

Production of inoculum and spore collection

30 ml of de-ionized water were poured over a plate containing a three-week-old, culture and the spores rubbed off with a wire loop. The conidial and mycelial suspension was filtered through four layers of cheesecloth. The obtained suspension was adjusted to a concentration of 2.10^4 conidia/ml using a hemocytometer slide. A few drops of Tween 20 were added to the spore suspension.

Plant inoculation

Seedlings (2-3 leaves) of 100 barley populations were inoculated by a spore suspension of the purified isolates of *P. teres f. sp. teres*. The spore suspension was sprayed on the plants using a hand atomizer.

Incubation of inoculated plants

Inoculated seedlings are placed in an incubation chamber with saturated atmosphere for 48-72 hours at 18-22°C. The saturated atmosphere was made by creating high relative humidity within the chamber with water pans. At the end of the incubation period, the plants in the seedling containers were left to air dry. The containers with seedlings were transferred to a glasshouse at a temperature of 22C. Disease infection was recorded 14 days after inoculation, using a 1-5 scale: 1 (non symptoms), 2 (small lesions surrounded by a light chlorosis; 3: lesions without netting with chlorosis; 4: netted lesions with little chlorosis; 5: typical net blotch symptoms with chlorosis.

Statistical analysis

The collected data were analyzed for variance. Mean comparisons and multivariate analysis of the collected data were also conducted using SPSS.

RESULTS AND DISCUSSION

The analysis of variance based on the mean reactions of the 100 populations to each isolate of *Pyrenophora teres* indicated that the four isolates were significantly different in their virulence. The four strains were classified using the Duncan test (Table 1). The results of this test showed that the isolate 2 was the relatively the most virulent, with a mean severity of 2.6, while isolate 4 was the less virulent, with a mean severity of 1.8. Isolates 1, 2 and 3 were closer to each other in mean severity. Concerning their origin, isolate 4 was collected from a coastal region near the Atlantic, while isolates 1, 2 and 3 were collected from the sites of the project -- Ain Aicha, Tissa and Galaz.

Differential reactions of host populations to the pathogen isolates

Three groups of host populations were characterized according to their reactions to the four isolates of *Pyrenophora teres* (Table 2):

- Group 1: Populations that reacted similarly to the four isolates.
- Group 2: Populations that reacted differently to isolate 4.

- Group 3: Populations that reacted differently to the four isolates.

Reaction of host populations according to their geographical origin

The plant material utilized in this study was collected mainly from two sites, Ourtzagh and Tissa. Only three populations were collected from Ghafsay. When considering the group of populations that were resistant to the four isolates, it was found that 23 populations were collected from Ourtzagh and five from Tissa (Table 3).

The results obtained in this study with the limited number of isolates indicate that *P. teres* is highly variable. Phenotypic diversity in pathogen populations is commonly analysed by testing the variation in virulence. In many studies, differentiation was recorded based on virulence tests among *P. teres* field populations. This might be due to differences in the barley cultivars grown among regions, which may have exerted different selective pressure on the pathogen (Tekauz 1990). *P. teres* is capable of rapid adaptation, as evidenced by the change in the proportion of the forms of *P. teres* in several geographical regions (Tekauz 1990). Higher diversity was observed within large groups of isolates than within field samples based on AFLP data analysed by Shannon's information index (Peever and Milgroom, 1994). These results are in accordance with short-distance dispersal of *P. teres*. The restricted dispersal among fields could lead to differentiation between them.

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Table 1: Mean virulence of four isolates of *P. teres* f. sp. *teres* on 100 barley populations

	Isolate	N	Sub-group for alpha = 0.05			
			1	2	3	4
Duncan	4	1836	1,81			
	1	1764		2,45		
	3	1828			2,52	
	2	1750				2,65
	Significance			1,000	1,000	1,000

Table 2: Grouping of populations of faba bean according to their reactions to the four isolates of *P. teres*

Group of host populations	Populations
Group 1. Populations that reacted similarly to the 4 isolates	1, 6, 8, 9, 19, 20, 22, 29, 30, 31, 32, 33, 37, 38, 40, 47, 49, 54, 59, 76, 78, 79, 84, 85, 88, 95, 69, 97, 100
Group 2. Populations that reacted differently to the isolate 4.	2, 3, 10, 12, 15, 16, 17, 18, 24, 39, 42, 48, 50, 51, 53, 55, 56, 57, 63, 66, 67, 68, 70, 72, 75, 82, 90, 94, 99
Group 3. Populations that reacted differently to the 4 isolates	4, 5, 7, 11, 13, 14, 21, 23, 25, 26, 27, 28, 34, 35, 36, 41, 43, 44, 45, 46, 52, 58, 60, 61, 62, 64, 65, 69, 71, 73, 74, 77, 80, 81, 83, 86, 87, 91, 92, 93, 98

Table 3: Number of resistant populations of faba bean according to their geographical origin

Site	Populations	Number of populations
Ourtzagh	11, 12, 18, 19, 20, 21, 22, 27, 28, 29, 30, 31, 32, 33, 38, 40, 41, 42, 46, 47, 48, 49	23
Tissa	54, 59, 60, 66, 74	5

Variation in project target pathogens and pest biotypes in rice in China

Chen Bin, Cao Feng-Juan, Chen Hong, Yang Xuehui, Yuan Jie, Peng Hua-Xian, Wang Yun-Yue

INTRODUCTION

The interaction among the host, pests, and the environment is the key factor affecting the occurrence of pests and even the yield loss of the crops. It has been well recognized that an increase in crop variety diversity can improve resistance against pests and diseases.

MATERIALS AND METHODS

Project sites

There were five sites in China: Shilin, Yuanyang, Banna in Yunnan Province, Shehong in Sichuan Province, Meitan in Guizhou Province.

Diversity of rice varieties in project sites

Three households that represented different ecological conditions in the region were selected for the three replications per site. Each household planted a set of target crop varieties (58 rice varieties plus two susceptible and two resistant controls in each local area). For each variety, the planting area was two square meters for rice (1*2m), which included more than 30 individuals.

Diversity of rice blast pathogens and plant hoppers in project sites

The rice blast pathogens were cultured and then DNA was extracted. The primer sequence was based on the sequence of the repetitive element Pot2, an inverted repeat transposon found in *M. grisea*. Similarity matrices were calculated with Dice's coefficient and the SIMQUAL program of NTSYS-pc. Resistance polymorphism of the rice varieties was analyzed by RGA-PCR (Resistance Gene Analog).

Five sites were selected from the rice planting areas in Yunnan, Sichuan and Guizhou province, China. The occurrence of the plant hopper in rice fields in the target sites was investigated using the plant flap method; the occurrence of the plant hopper was evaluated using the rank level according to the density of plant hoppers in paddy fields.

RESULTS

Relationship between richness/evenness and the incidence of diseases and pests in China

The relationship between the Simpson index and the percentage of disease and the rank of planthopper was evaluated in project sites in China. Results showed that the disease decreased with the increase of the community species diversity. Overall, the occurrence of the plant hopper was significantly and negatively related to the Simpson index of the rice varieties in Shilin and Yuanyang (Figure1,2).

Biotypes pests/disease

There were 37 different haplotypes and 27 genetic lineages at 0.85 similar linkage distance level in 212 isolates of blast fungus. One hundred one strains of modern varieties, 19 haplotypes, were divided into 14 genetic lineages of G1, G3, G8, G10, G12, G14, G16, G17, G18, G19, G20, G23, G24 and G27. Among them, G1, G16, G17, G18, G19, G20, G24 and G27 were all from the modern varieties. Ninety nine strains of traditional varieties, 21 haplotypes, were classified as 19 genetic lineages of G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G21, G22, G23, G25 and G26, and there were no obvious genealogical advantages (Figure3).

There were 37 different haplotypes and 27 genetic lineages at 0.85 similar linkage distance level in 212 isolates of blast fungus. Analysis using Resistance Gene Analog (RGA) amplification bands showed the high diversity in inheritance of resistance. Distribution may be related to the planting areas of traditional varieties.

No genetic variation was noted among populations from Yuanyang, Shiling, and also populations within the region, indicating no genetic differentiation. The effect of traditional rice varieties on the biology of plant hopper was evaluated.

CONCLUSION AND DISCUSSION

The blast pathogen population clustering analysis showed that pathogens from the same region with similar genetic structure fall into the same group. Genetic diversity of the blast pathogen population was obviously positively correlated with complexity of variety composition. In other words, greater numbers of genetically diversified varieties would result in more genetic diversity of the blast pathogen population.

Diversity of varieties, including both local and modern, with respect to pests was found in target project sites except for Shehong. There are many traditional varieties in Yuanyang site, and it showed the less occurrence of the plant hopper. The density of the plant hopper infestation was much lower in Shehong, Sichuan Province, even though the diversity of the rice varieties was much lower. Further study is needed to ascertain the reasons for this lower occurrence of plant hoppers under the lower variety diversity.

Pests will decrease with the increase of the diversity of richness and evenness in farmers' fields. Diversity composition and the distribution of varieties can reduce the occurrence of the predominant biotypes of pests, making it a likely strategy in integrated pest management. In this way, pests can be controlled when different varieties with are present in the crop diversity on the community level.

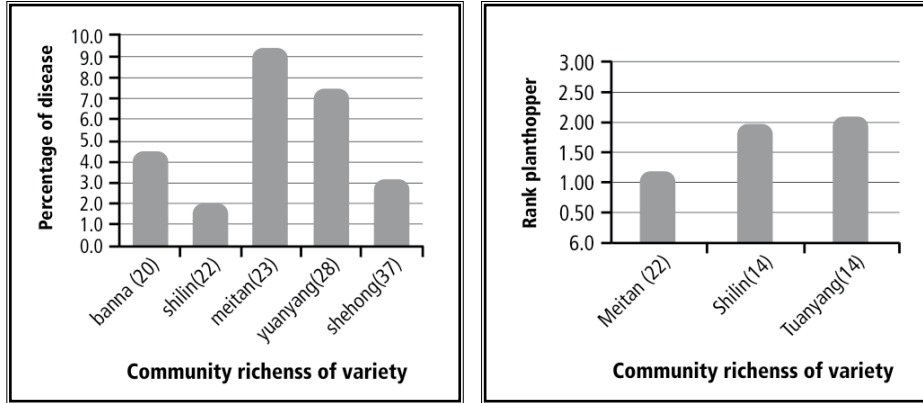


Figure 1: HH Richness vs. HH incidence of rice plant hopper in China

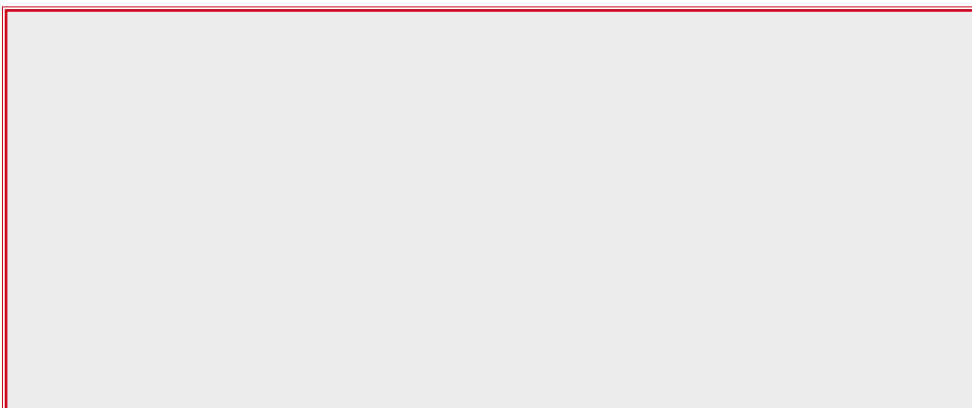
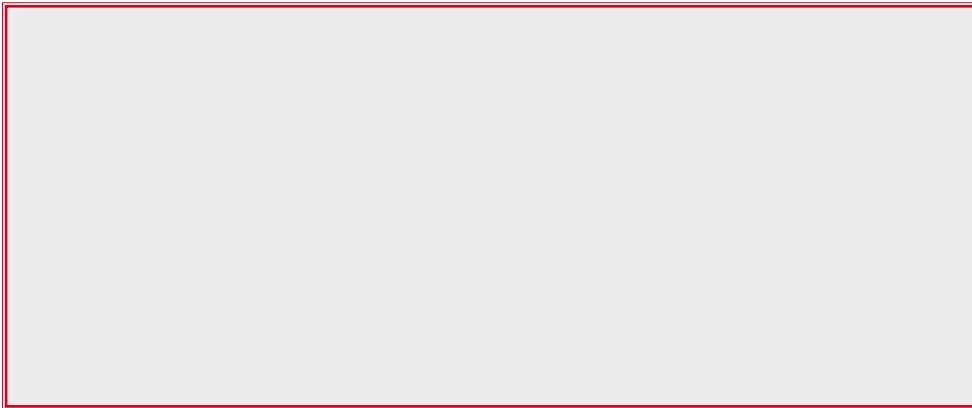


Figure 2: HH Richness vs. HH incidence of rice plant hopper in China

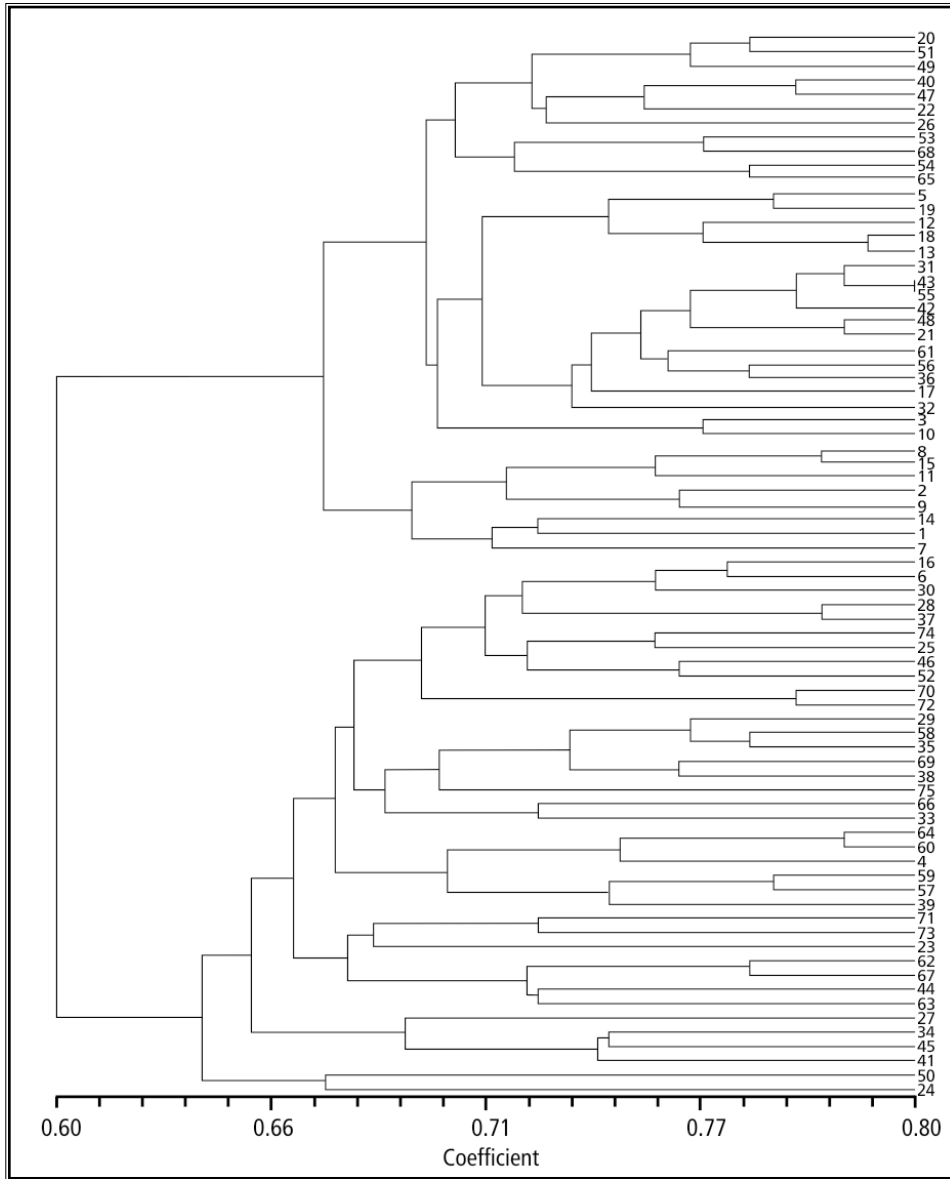


Figure 3: Genetic dendrogram based on polymorphism of RGA

Variation in host resistance to beanfly among traditional common bean cultivars maintained by farmers in Uganda

Ssekandi, W.; Otim, M.; Ugen, M.

INTRODUCTION

The common bean, *Phaseolus vulgaris*, is a vital crop in East and Central Africa, serving as a food and cash crop. Unfortunately, bean yields have consistently remained lower (500 - 700 kg/ha) than the potential yield of 2000 kg/ha, primarily due to insect pests and diseases. Among the insect pests, the bean stem maggot, *Ophiomyia* species, threaten bean production in East and Central Africa. *Ophiomyia phaseoli* Tyron and *O. spencerella* Greathead (Diptera: Agromyzidae) are the two economically important species attacking beans in East Africa (Greathead, 1968), while *O. centrosematis* is rarely recorded. Fly oviposits on the upper surface of the leaf and hatched maggots mine through the leaf petioles and stems. On seedlings, pupation takes place below the epidermis of the stem at or immediately above the ground level. In older plants, pupation takes place at the base of the petiole. Pupation causes cracks, which weaken the plant, and also act as entry points for pathogens. Damage may result in total losses under severe infestation (Abate and Ampofo, 1996), especially under low soil fertility and drought conditions. Farmers use different control methods, including early planting, seed dressing, and the removal of plant remains, ridging, and use of varietal mixtures. In order to optimally use genetic diversity, there is a need to identify the most common bean fly species in the different locations and understand the reaction of the different genotypes (both improved and local landraces) to infestation by these species. This study therefore focussed on evaluating the reaction of different bean genotypes to bean fly infestation and damage.

METHODS

The study involved four on-farm trials at each in Nakaseke, Bushenyi, and Kabale districts, and an on-station set at National Crops Resources Research Institute (NaCRRI), Namulonge during the second season of 2010. On-farm trials were laid in a completely randomized block design. Forty eight varieties were obtained from farmers (mainly landraces) in the three study sites and from NaCCRRI (released varieties). The varieties were sown each in a 6m long row spaced 0.5m apart and 10cm between plants, and left under natural bean fly infestation on-farm. The same varieties were sown on-station in an alpha lattice design. Each variety was sown in four 2m long rows at spacing of 50 cm X 20 cm or 10cm for climbers and bush type, respectively, and replicated three times. Data collection started at 14 days (DAP) and ended at 49 DAP. Data were collected on BSM incidence, plant mortality, larvae and pupal numbers yield. At each sampling, twenty plants were randomly selected per plot and examined for BSM infestation symptoms for estimation of incidence, which was expressed as a percentage of infested plants per plot (on-farm). In addition,

on-station data involved counts of dead plants per plot and recording bean fly pupae and larvae as well as presence of *Fusarium* and *Pythium*. Pupae and larvae were recovered by dissecting dead plants and their number was recorded. Species identification was based on the colour of pupae as described by Greathead (1968). Yield data was taken at physiological maturity when whole plots were harvested, threshed and the seed yield recorded. Data were analysed using a computer software programme GENSTAT Discovery edition.

RESULTS

Two bean fly species were recorded at all the study sites. *Ophiomyia spencerella* was more abundant than *O. phaseoli* in Bushenyi, Kabale and Wakiso (Namulonge-on-station), while the reverse was observed at Nakaseke (Fig. 1). The incidence of plants with BSM damage symptoms was generally lower in Nakaseke compared to the other two locations. The percentage of plants showing symptoms of BSM infestation differed significantly ($p < 0.001$) between varieties; Kaki short, Katosire, Kasirira, Kishoga and Katosire were the least damaged varieties in all the locations. Kaddugala, Kishoga climber, Kanyebwa long, Mahega II, Rushare old, Kihura long and Kahura bush were more damaged in all the three on-farm sites.

In the case of the on-station trial, significant effects ($p < 0.001$) of varieties were obtained for the percentage of dead plants with BSM, *Fusarium* and *Pythium* root rot infestations, numbers of larvae and pupae per plant and seed yield. The percentage of plants with BSM, *Fusarium* and *Pythium* root rot pathogens ranged from 0 – 100% each. The number of pupae per plant ranged from 0 – 16, whilst the larvae ranged from 0 – 6. Among the top ten high-yielding varieties, Kaki short, Nyinagote and Nambale long registered less than 50% of dead with BSM infestation (Table 2). All the lower ten yielding varieties registered more 60% of the dead plants having BSM, but with the highest figures recorded for Akeru short, Ngwinorare and Kankulyembalukye. A simple linear regression of the number of pupae and larvae (independent variables) to mortality (number of dead plants) (dependent variable) showed significant positive relationships for the two variables: pupae – intercept (a) = 1.978, slope (b) = 0.024 ± 0.009 , t-value = 25.89, $p < 0.001$ and coefficient of determination (r^2) = 43.7; larvae - intercept (a) = 1.809, slope (b) = 0.437 ± 0.016 , t-value = 27.38, $p < 0.001$ and coefficient of determination (r^2) = 46.5.

DISCUSSION

Findings from the current study reveal the presence of two bean fly species, an observation that is in agreement with earlier studies. The generally lower BSM damage in Nakaseke compared to the other locations may be in part due to the fact that *Ophiomyia phaseoli* was slightly higher in number than *O. spencerella*. In addition, environmental factors such as temperature, relative humidity and rainfall, are reported to affect bean fly infestation and damage (Talekar and Lee, 1989). The positive relationship between BSM life stages and plant mortality implies factors (climatic or inherent plant factors) that reduce survival and reproduction of BSM will boost management of the pest.

The observation that varieties differ in their reaction to bean fly infestation and damage, ranging from low to high is in agreement with earlier studies. For instance, Ojwang et al (2010) screened 64 bean genotypes and identified seven resistant bean land races. Similarly, Ogetcha et al (2000) identified 13 out of 66 screened varieties to be tolerant to BSM. These, together with our observations, show the presence of resistant landraces currently being grown by farmers, and may in part explain the reasons for varietal mixing. The current study has determined the reaction of some common bean landraces in Uganda to BSM infestation and damage, and will act as a stepping

stone for the choice of varieties for integration into varietal mixture studies. However, further studies are needed to validate these findings before incorporating the varieties for mixture studies. At the same time, the occurrence of BSM and root rot pathogens may call for a holistic approach to the management of the BSM and the root rot pathogens that tend to occur together.

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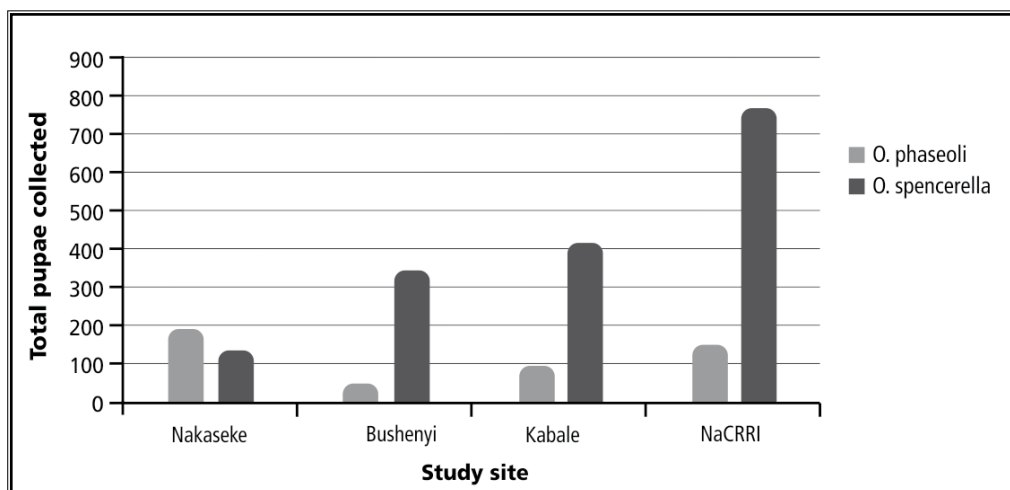


Fig.1 : The incidence of bean fly species at study sites

Table 1: The mean incidence (%) of BSM on ten top and lowest varieties showing symptoms of BSM infestation in the field on-farm in 2010B

Variety	Bushenyi	Kabale	Nakseke	Grand total
Ten top least infested varieties				
Kaki short	12.5	6.75	3	7.4
Kasirira	15.3	11.5	10.8	12.5
Kishoga	18.5	19.8	7	15.1
Katosire	24	17.8	9.8	17.2
Kayinja	29	37.3	27.8	31.3
Shemenoha	33.3	34.5	27.3	31.7
Kachwekano	34.8	37.6	24.3	32.3
Nabe 10C	35.8	37.2	24.3	32.4
Nambale long	38.4	38.1	20.9	32.5
Mexic 54	36.5	36	25.3	32.6
Ten most infested varieties				
Nabe 8C	42	42.8	31.3	38.7
Kanyebwa	42.6	44.5	30.5	39.2
Manyigamulimi	39.3	45.3	36.3	40.3
Kaddugala	42.6	48.3	37.3	42.8
Kishoga climber	48.3	58.3	52.3	53.0
Kanyebwa long	59.8	56.3	48	54.7
Mahega II	56.3	63.5	54.3	58.0
Rushare old	55.5	61.3	58.8	58.5
Kihura long	59	65.3	63.3	62.5
Kahura bush	66	66	64.5	65.5
Grand total	38.4	40.7	30.1	36.4

Table 2: Mean seed yield, BSM life stages per plant, incidence of BSM and pathogen infected plants for top and ten yielding varieties on-station in 2010B

Variety	BSM stages (plant ¹)			Mortality (% dead plants with)		
	Seed yield (g/3m ²)	Pupae	Larvae	BSM*	Fusarium	Pythium
Top ten varieties						
Manyigamulimi	516.7	1.1	0.6	76.7	4.4	5.5
Kaki short	482.0	0.4	0.3	17.9	16.7	11.1
Nabe 10C	467.0	1.4	0.6	64.3	3.1	2.5
Nambale long	453.0	0.3	0.3	42.9	15.5	32.1
Kachwekano	449.3	1.2	0.5	63.3	1.5	1.2
Kabwejagure	385.0	1.8	0.7	74.3	6.5	7.5
Nyinakigote	380.0	0.4	0.6	36.7	4.4	8.9
Yellow long	343.0	1.3	0.9	83.3	2.3	6.4
Nabe 7C	311.7	1.5	0.5	63.6	4.4	3.1
Kanyebwa long	303.3	1.8	0.6	63.8	2.1	2.5
Lower ten varieties						
Nabe 12C	125.7	1.3	0.6	63.5	4.3	1.2
Akeru short	124.0	2.2	0.6	79.7	2.5	2.4
Ngwinorare	122.0	3.2	0.8	81.9	5.4	2.0
Shemenoha	121.3	1.3	0.7	75.0	1.4	2.5
Brown small	112.7	2.2	0.6	78.3	2.1	5.7
Kigome	107.0	1.2	0.4	56.7	1.1	2.8
Kankulyemalukye	104.7	0.8	0.4	79.4	4.3	6.9
Rushare climber	96.7	1.6	0.6	70.8	3.4	4.3
Mamesha climber	92.7	1.6	0.5	69.5	3.8	2.4
Kishoga climber	87.0	1.7	0.9	72.7	2.5	2.6
Grand mean	229.5	1.4	0.6	68.5	4.9	5.5

*Combines pupae and larvae

Pathogenic variability and seedling resistance of maize local cultivars from Cotacachi and Saraguro to *Exserohilum turcicum* in Ecuador

Cathme, M.; Ochoa, J.B.

INTRODUCTION

Maize is an important food crop in the highlands valleys of Ecuador. It is grown in complex agro ecosystems with high genetic diversity. Among other reasons, farmers maintain maize diversity to reduce losses caused biotic and abiotic stresses.

Northern leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard & Suggs is a frequent disease in temperate areas of Ecuador and due to climate change it is a potential threat for maize other traditional areas. Since the Andean region of Ecuador is an important center of maize diversity, plant/pathogen coevolution has been a common phenomenon, in which farmer interventions have been a key component of this co evolution.

The resistance/avirulence gene has been reported for NLB (Welz, H. G and Geiger, H. H. 2000). To analyze the importance and the state of plant/pathogen coevolution in NLB in Ecuador, the diversity of the pathogen in relation to the diversity of resistance in Cotacachi and Saraguro local cultivars was studied.

METHODS

Ten isolates each of *E. turcicum* were collected in Cotacachi and Saraguro regions to study virulence diversity in the greenhouse at Sta Catalina Experimental Station (INIAP) near Quito-Ecuador. The pathogen was isolated and monosporic isolates produced on lactose casein hydrolysate agar (LCA), and the inoculum multiplied on potato dextrose agar (PDA). Monosporic isolates were inoculated on the standardized differential set and races identified as proposed by Leonard K.J (1989). The differential set was composed by lines carrying resistance genes to Ht1, Ht2, Ht3 and HtN and two susceptible lines (Table 1). Plants at the age of 15 days were inoculated with a suspension of 7×10^4 spores/ml. The inoculated plants were incubated for 14 hours at 17-19°C and 90% relative humidity. After incubation, plants were transferred to a growth chamber with a temperature varying from 22°C to 26°C and 70% relative humidity. Disease Severity (DS) was scored 13 days after inoculation using the scale developed by Bigirwa et al. (1993), with some modifications: 0 = no symptoms, 1 = few chlorotic lesions, 2 = some small chlorotic lesions progressing to necrosis. 3 = appreciable number of moderate necrotic lesions and 4 = many big necrotic lesions. The incubation period, the number of lesions and the lesion size were also evaluated in this study. The incubation period was evaluated as the number of days from inoculation to first symptom appearance, the number of lesions was the average of necrotic lesions of five

plants, and the size of the lesion was the average of ten lesions taken randomly in the five plants. NLB races were identified according to the system proposed by Leonard J (1989).

Two isolates representing two distinctive phenotypes of race 123 were used to study the resistance to *E. turcicum* in a representative collection of local maize cultivars from Cotacachi and Saraguro. Plant management, inoculation and the disease evaluation were conducted in a similar manner as that used for virulence studies.

RESULTS AND DISCUSSION

The disease severity alone was not enough to differentiate isolates and to characterize resistance to NLB at seedling stage. The incubation period and the size of the lesion were important parameters that helped identify virulence and resistance in this study. All isolates from Saraguro and Cotacachi carried virulence to Ht1, Ht2 and Ht3, and the isolates belong to race 123 (Table 1). All isolates were avirulent to HtN; however, two phenotypic resistance reactions to the HtN gene were identified: a) long incubation period, the typical resistance reaction observed elsewhere, and b) a mild chlorosis called yellow pinhead (Muiru, 2007). The yellow pinhead reaction type is apparently the first reported for HtN and appears typical of low aggressive isolates of the Ecuadorian pathogen population.

Resistance to NLB was present in most cultivars from Cotacachi and Saraguro. Resistance was mostly associated with DS, a long incubation period and small lesion size. Integrating these parameters, four reaction types were identified: Inm = No symptoms (immunity), R = long incubation period and small lesion size (resistant), I = Intermediate incubation period and small to medium lesion size (Intermediate), S = short incubation period and large lesion size (Susceptible). The first two reaction types (Inm and R) are mostly of major gene nature and have been associated with most of the major genes identified so far (Hooker, A. and Kim, S. 1980). However, the long incubation period and the small lesion size have also been associated with Partial Resistance (Hooker, A. and Kim, S. 1980). The intermediate reaction type (I) could be considered lower levels of susceptibility.

Using the reaction types, resistance in local cultivars was characterized. High variation in reaction types was observed among cultivars, but mostly within cultivars. Most cultivars were mixed populations reacting differentially with the isolates evaluated. Cultivars from Cotacachi varied from very resistant to very susceptible (Table 2). The whole population of cultivar Morochillo was resistant to both isolates; the resistance appears of major gene nature. The remaining cultivars showed variable reaction types within cultivars. In table 2, cultivars from Killu cangil to Puka pintado collectively contained different frequencies of populations with all types of reaction to both isolates; cultivars from Yana sara to Guayaba sara also contained populations with all reactions types except Inm for isolate 2, and the rest of the cultivars showed I and S reaction types for isolate 2, but some cultivars showed Inm and R reaction types for isolate 12. Some cultivars were as susceptible as INIAP-101 for race 2, but a fraction of the population of these cultivars were resistant to race 12 (Table 2).

Cultivars from Saraguro had similar behavior to cultivars from Cotacachi; all cultivars showed variable reaction types within cultivars. In Table 3, cultivars from Dulce del caliente to Zhima Conchabon collectively for both isolates contained different frequencies of populations with all reaction types; cultivars from Blanco zhima to Diente de caballo also contained populations with all reaction types except Inm for isolate 2, and the remaining cultivars contained populations only with I and S reaction types for isolate 2, but some cultivars contained Inm and reaction types for isolate 12.

Resistance/susceptible interactions between cultivars Morochillo and Puka sara with isolate 2 and isolate 12 suggests that the resistant on these cultivars are different. Morochillo is resistant to both races while Puka sara only to race 12 (Table 2). A similar interaction was observed in the Saraguro variety Morocho dulce which was susceptible to isolate 2, but resistant to isolate 12 (Table 3). These interactions are evidence of high variation in resistance of major gene nature in Cotacachi and Saraguro cultivars.

The efficient major gene resistance carried by Morochillo and other possible efficient genes are most likely different from HtN, the only gene from the differentials efficient to the Ecuadorian *E. turcicum* population. HtN comes from the line Méx. 44 belonging to the race Pepitilla from México. (Gevers, 1975).

Due to the high variability in reaction types within cultivars, field severity of a specific cultivars might vary year by year, depending on the population frequency of the infection types involved. For this reason, it will be additionally difficult to discern in these cultivars major and minor gene resistance. However, both resistant types appear to be operating and strengthening each other in the field.

In this study, isolates 2 and 12 belonged to race 123; however, isolate 2 was more virulent than isolate 12, especially on Saraguro cultivars. Therefore, the NLB standard differential set appears incomplete for characterizing virulence for the Ecuadorian NLB population.

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Table 1. Virulence of *Exserohilum turcicum* of 20 isolates from Cotacachi and Saraguro on the NLB differential set composed by four resistance genes (Ht1, Ht2, Ht3 and HtN). Sta. Catalina Experimental Station. INIAP. Quito, Ecuador.

Isolates/origin	Ht1	Ht2	Ht3	HtN	Pa91 ¹	B68 ¹
Cotacachi						
1 Morochos 1	+	+	+	(-)	+	+
2 Morochos 2	+	+	+	(-)	+	+
3 Taitigacho	+	+	+	-	+	+
4 San Antonio Punge	+	+	+	-	+	+
5 Chilcapamba	+	+	+	(-)	+	+
6 Morales chupa	+	+	+	(-)	+	+
7 Antonio Flores	+	+	+	(-)	+	+
8 Topo grande	+	+	+	-	+	+
9 San pablo Lago	+	+	+	(-)	+	+
10 Libertad de Azana	+	+	+	(-)	+	+
Saraguro						
11 Gualaceo	+	+	+	(-)	+	+
12 Gañil	+	+	+	-	+	+
13 Conchabon	+	+	+	-	+	+
14 Conchabon 2	+	+	+	-	+	+
15 Papaya	+	+	+	(-)	+	+
16 Sellin	+	+	+	(-)	+	+
17 Gañil	+	+	+	(-)	+	+
18 Tenta	+	+	+	(-)	+	+
19 Selva alegre	+	+	+	-	+	+
20 Iguachupa	+	+	+	-	+	+

+ = short incubation period and large lesion size

- = absence of symptoms; (-) = long incubation period and small lesion size

¹ Susceptible lines

Table 2. Frequency of NLB reaction types of local cultivars from Cotacachi evaluated at seedling stage at Sta. Catalina Experimental Station. INIAP. Quito, Ecuador, 2010.

	Isolate 2: race 123, HtN (-)				Isolate 12: race 123 HtN -			
	Inm	R	I	S	Inm	R	I	S
Morochillo	60	40	0	0	100	0	0	0
Killu kanguil	44	55	0	0	22	45	0	33
Tabla sara	30	60	10	0	0	33	0	67
Yura chulpi	20	50	30	10	13	25	25	37
Puka kanguil	11	33	44	11	0	14	14	71
Morado sara	20	40	20	20	10	60	10	20
Sangre de Cristo	20	30	40	10	0	50	0	50
Rosado puka	10	20	70	0	11	22	44	22
Puka pintado	12	0	13	75	0	33	0	67
Yana sara	0	30	60	10	0	22	22	55
Tomate sara	0	56	44	0	0	57	29	14
Rosado morado	0	10	60	30	0	0	20	80
Tzapa sara	0	10	10	80	0	13	0	87
Hatum killu sara	0	10	0	90	10	30	20	40
Guayaba sara	0	10	0	90	20	60	0	20
Rosado sara	0	0	50	50	20	60	0	20
Yura sara	0	0	67	33	11	0	33	55
Chulpi puka	0	0	60	40	0	0	10	90
Puka sara	0	0	60	40	67	33	0	0
Mishca	0	0	44	55	0	38	38	24
Hantsi iriticu	0	0	22	78	10	40	40	10
Julin sara	0	0	40	60	25	25	0	50
Killu bola	0	0	30	70	38	25	0	37
Yura rosado sara	0	0	33	67	0	0	0	100
Naupa sara	0	0	0	100	20	10	50	20
Killu chulpi	0	0	30	70	40	40	0	20
Killu chaucha	0	0	0	100	10	20	30	40
Yura chulpi	0	0	0	100	20	0	10	70
Racu killu sara	0	0	0	100	14	0	57	29
INIAP 101	0	0	0	100	0	0	0	100

Inm = Immunity (no symptoms), R = Resistant (long incubation period and small lesion size), I = Intermediate (Intermediate incubation period and small to medium lesion size), S = short incubation period and large lesion size.

Table 3. Frequency of NLB reaction types of local cultivars from Saraguro evaluated at seedling stage at Sta. Catalina Experimental Station. INIAP. Quito, Ecuador, 2010.

Cultivars	isolate 2: race 123, HtN (-)				isolate 12: race 123, HtN -			
	Inm	R	I	S	Inm	R	I	S
Dulce del caliente	50	20	10	20	0	40	25	35
Amarillo tamal	25	50	13	12	0	75	13	12
Blanco morochillo	11	44	22	0	20	20	0	60
Pintado criollo	10	50	10	30	13	75	0	12
Sangre de cuy	13	50	0	37	0	44	12	44
Amarillo cusi	43	29	14	14	14	43	14	28
Morocho	11	11	11	67	11	22	22	0
Amarillo murungo	10	0	20	70	0	0	25	75
Zhima conchabon	11	0	56	33	22	78	0	0
Blanco zhima	0	33	17	50	0	14	57	29
Morocho para humas	0	50	50	0	0	0	13	87
Maiz blanco	0	20	40	40	20	80	0	0
Perla blanca	0	33	50	17	13	38	37	12
Floreado mater	0	14	29	56	0	0	11	89
Diente de caballo	0	10	0	90	0	50	0	50
Zhima cristalino crema	0	0	67	33	0	10	20	70
Zhima pintado	0	0	60	40	0	10	0	90
Chauqueno	0	0	70	30	0	20	10	70
Zhima tocho	0	0	100	0	50	33	0	17
Zhima blanco zapón	0	0	70	30	0	20	10	70
Morocho tusilla	0	0	60	40	13	62	0	25
Sangre	0	0	22	78	0	50	25	25
Blanco pintado	0	0	50	50	13	0	0	87
Cristal tusilla	0	0	56	44	20	0	20	60
Morocho del cerro	0	0	10	90	10	40	40	10
Zhima cuzco	0	0	30	70	0	22	11	67
Amarillo tusilla	0	0	60	40	25	13	0	62
Blanco suave	0	0	13	87	0	83	0	17

Table 3. continued

Cultivars	isolate 2: race 123, HtN (-)				isolate 12: race 123, HtN -			
	Inm	R	I	S	Inm	R	I	S
Rocano amarillo	0	0	44	56	10	10	50	30
Zhima criollo	0	0	17	83	0	30	40	30
Morocho dulce	0	0	11	89	25	75	0	0
Zhima	0	0	30	70	10	40	10	10
Morochillo	0	0	20	40	22	33	0	33
Rojo San Jose	0	0	10	90	0	0	10	90
Aychasara	0	0	11	89	0	0	0	100
Zhima murungo	0	0	10	90	0	0	0	100
Maiz para tostado	0	0	11	89	0	0	0	100
Colorado	0	0	40	60	0	0	0	100
Zhima del caliente	0	0	50	50	0	0	0	100
Zhima grande	0	0	60	40	0	0	0	100
Naves comadre	0	0	78	22	0	0	20	80
Velo de angel	0	0	60	40	0	0	0	100
Amarillo grande	0	0	60	40	0	0	0	100
Joyapu	0	0	63	37	0	0	0	100
Cuzco	0	0	70	30	0	0	0	100
Blanco pequeño	0	0	0	100	0	63	0	25
Blanco picudo	0	0	0	100	14	0	57	29
INIAP-101	0	0	0	100	0	0	0	100

Inm = Immunity (no symptoms), R = Resistant (long incubation period and small lesion size), I = Intermediate (Intermediate incubation period and small to medium lesion size), S = short incubation period and large lesion size.

Pathogenic diversity and resistance of Cotacachi and Saraguro local cultivars on the common bean/rust pathosystem

Vega, L; Ochoa, J.B.

INTRODUCTION

Common bean is an important food crop in the highlands of Ecuador. It is cultivated in monoculture (bush types) for commercial purposes, and in association with maize in complex mixtures (climbing types) for self-consumption. Farmers' practices of planting mixtures in traditional agriculture appear to be associated with the internal balance of the agro ecosystem to avoid the negative impact of biotic and abiotic stresses.

Rust caused by *Uromyces appendiculatus* (Pers.) is an important constraint of common bean commercial cultivation and farmers have often to spray fungicide for disease control. In traditional agriculture, however, the diseases, although present, do not appear to cause serious losses and farmers do not take any control measures except for managing complex mixtures. Genetic resistance operating in the diversity maintained by farmers might explain the reduced disease epidemics farmers experience in their field.

Major gene resistance operating in a gene-for-gene system has been described for *U. appendiculatus* (Stavely, J.R., 1984; Jochua C. *et al* 2008). This type of resistance might be present in the diversity farmers grow and might be important in reducing the epidemic of rust in traditional agriculture. A study to identify pathogen variability and characterize major resistance genes at seedling stage was carried out with a representative collection of *U. appendiculatus* isolates from Cotacachi, and with a representative collection of common bean genotypes belonging to farmers' mixtures from Cotacachi and Saraguro.

METHODS

Virulence studies of 16 isolates of *U. appendiculatus* from Cotacachi were conducted at Sta Catalina Experimental Station of INIAP, near Quito-Ecuador. Single pustule isolates were produced and multiplied in the greenhouse on the susceptible variety Red small garden. Virulence studies were conducted using the rust standard differential set proposed by Jochua *et al* 2008 (Table 2). Five seedlings of each differential were planted in trays 50 cm long, 35 cm wide and 8 cm deep. Seedlings were grown in a greenhouse at 25°C and a relative humidity of 50%. Twelve day-old seedlings were inoculated with 2.5 mg of spores diluted in 30 ml of tap water with tween solvent. The seedlings were transferred for incubation to a growth chamber at 20°C and 90% RH for 16 hours. Plants were then transferred to a growth chamber at 26°C and 60% RH. Rust reaction types were assessed twice at 14 and 18 days after the inoculation using the scale proposed by Stavely 1983 (Table 1). Reaction types ranging from 0 to 3 were classified as resistant and reaction types ranging from 3.4 to 6 were classified as susceptible. Isolates producing susceptible reaction types

were considered to transmit virulence to the resistance gene carried by that specific differential. Race designation was based on the binary notation system for which the varieties of each set (Meso-American and Andean gene pools) have a binary number, and the race is identified by adding the numbers of the differential on which the isolate is virulent (Table 2).

A collection of *allpa* genotypes (Table 3) and *chakra* genotypes (Table 4) from Cotacachi and *mixturiado* genotypes (Table 5) from Saraguro obtained from farmers' mixtures in participatory diagnosis processes were evaluated with regard to isolate 1 (race 45:1) and isolate 9 (race 63:23) (Table 2). Seedling management and the inoculations were conducted in a manner similar to that of the previous study. Rust reaction types were also assessed using the scale of Table 1.

RESULTS AND DISCUSSION

Twelve races out of 16 isolates of *U. appendiculatus* were identified in this study. The high rate of races identified shows the high variability of the pathogen in Cotacachi. Most of the races were unique and the most frequent race (13:1) was identified four times (Table 2). Races varied from very simple (4:1 carrying virulence to genes of Motcal and Ur-7), to very complex (race 63:23 carrying virulence to all genes from South America and to most of the genes from Meso America) (Table 2).

Virulence to all genes from South America and to the genes Ur-3, Ur-5, Ur-7 and the one carried by CNC from Meso America were identified in this study. None of the isolates were virulent to Ur3+ and Ur11. In a previous virulence study in the early 2000s, Ochoa *et. al* 2007 also identified virulence to all South American genes, but only to the gene Ur – 3 from Meso America. Virulence to Ur – 7 and the one carried by CNC from Meso America have new virulence for the common bean rust population in Ecuador. These results show the highly virulent, variable and versatile evolution of the pathogen in Cotacachi, which has also been documented for other regions of the world (Jochua, C.2008).

The highly variable rust population might also be explained by pathogen migration. The pathogen is probably migrating from the lower valleys near Cotacachi, where cultivation of common bean is commercial and modern varieties have been released. Migration can also explain the presence of virulence in Meso American genes, since some commercial varieties and experimental lines with Meso American origin are being cultivated in these valleys.

Resistance studies of local cultivars showed a high variation in resistance. At least two sources of resistance were identified in *allpa* genotypes; however, none of them were efficient with regard to both isolates evaluated (Table 3). Similarly, at least three sources of resistance were identified in *chakras* and at least one is efficient with regard to both isolates. However, the frequency of this relatively efficient resistance is low (Table 4). At least three different sources of resistance were also identified in *mixturiados* and, unlike Cotacachi cultivars, the frequency of resistance in these cultivars is high. The high frequency of resistance in Saraguro cultivars might be due to the lack of virulence of Cotacachi isolates to Saraguro sources of resistance.

Although most of the genotypes are susceptible at seedling stage, especially in Cotacachi, the rust epidemic in the field is not severe, even under conducive conditions; therefore Partial Resistance reported for common bean rust (Hubtu, A and zadoks, J.C. 1995) might be important in keeping the epidemic at low levels in the field.

Most of the sources of resistance identified in this study are not useful for commercial agriculture. However, in mixtures, these sources of major gene resistance together with quantitative resistance, might strengthen each other, contributing to the low disease severity observed in mixtures.

A remarkable result of this study is that the isolate 9 is more virulent than isolate 1 on the standard differential set (Table 2). However, isolate 9 is less virulent than isolate 1 on the three common bean collections evaluated (Tables 3, 4 and 5). Isolate 9 appears to have evolved out of Cotacachi, since it has not developed virulence to Cotacachi resistance genes.

Since isolate 9 is virulent to all South American genes, the resistance found in Cotacachi and Saraguro are new sources of resistance. Furthermore, the resistance/virulence interaction found for the three populations evaluated (Tables 2, 3 and 4) suggests that major gene sources of resistance within and among common bean types are diverse.

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Table 1. Grading scale adopted for *Uromyces appendiculatus* evaluation at seedling stage.

Reaction type ^a	Description	Rust reaction
1	Inmune, no visible symptoms	Resistant
2	Necrotic spots without sporulation	Resistant
2,3	Reaction 2 with few type 3	Resistant
3,2	Reaction 3 with few type 2	Resistant
3	Uredinia < 0.3 mm in diameter	Resistant
3,4	Reaction 3 with few type 4	Susceptible
4,3	Reaction 4 with few type 3	Susceptible
4	Uredinia 0.3 to 0.49 mm in diameter	Susceptible
4,5	Reaction 4 with few type 5	Susceptible
5,4	Reaction 5 with few type 4	Susceptible
5	Uredinia 0.5 to 0.8 mm in diameter	Susceptible
5,6	Reaction 5 with few type 6	Susceptible
6,5	Reaction 6 with few type 5	Susceptible
6	Uredinia 0.8 to 1.2 mm in diameter	Susceptible

^a According to Stavely et al. 1983

Table 2. Reaction types of Cotacachi isolates of rust on the South American and the Mesoamerican differential sets, and race identification, Quito-Ecuador, 2011.

Cultivar or line ^a	Genes	Binary values	Rust isolates ^b																			
			15	14	13	10	6	3	2	4	5	1	16	11	7	12	8	9				
South American gene pool																						
Early Gallatin	Ur-4	1	1	3	4	5	5	5	5	5	5	5	5	5	5,6	5	5	6	6			
RedlandPioneer	Ur-13	2	1	1	1	1	1	1	1	1	1	1	1	2	1	3,4	5	4	6	6		
Montcalm	...	4	4	1	6	4	5	5	5,6	5	5	5	5	5	5,6	6	6	6	6	6		
PC50	Ur-9, Ur-12	8	1	4	5	5	5	5	5	3	5	5	5	6	5,6	6	4	6	5	5		
GGWax	Ur-6	16	1	1	1	1	1	1	1	1	1	2	2+	2+	3	4	5	5	5	5		
PI 260418	...	32	1	1	3	3	3	3	3,4	3	3,4	4	4	4	5	4	5	4	5	4	4	
Meddle American pool																						
GN 1140	Ur-7	1	5	3,4	5	5	5	5,6	5	5,6	3	4,5	3	4,5	3,4	6	5	6	6	6	6	
Aurora	Ur-3	2	2	2	2+	2+	2++	2++	2++	2++	3,4	2+	2+	2+	2+	3	3	2+,3	2	3,4	3,4	
México 309	Ur-5	4	1	2	1	1	1	1	1	1	2+	1	1	1	2+	2	3	4	5	5	5	
México 235	Ur-3+	8	2	2	1	1	1	1	1	1	1	2	2++	1	2	2++	1	1	3	3	3	
CNC	...	16	1	2	3	1	1	1	1	1	2	2+	2+	2+	2	2+	3	2,3	4	4	4	
PI 181996	Ur-11	32	1	1	1	1	1	1	1	1	1	1	1	2+	2	1	1	3	1	1	1	
Testigo (RSG)	...		6	5,6	6	6	6	6	6	6	6	6	6	6	6	6	6	4	6	6	6	
Race identification			4:1	8:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1	13:1

^a Bean rust differential cultivar or lines adopted in third International Bean Rust Workshop in South Africa in 2002 (Steadman, et al. 2002). GGW: Golden Gate Wax, CNC: Comuesto Negro Chimaltenango.

^bOrigin: 1. Morales Chupa, 2. Chilcapamba, 3. Morochos 1, 4. Morochos 2, 5. Cumbas 2, 6. San Antonio de Punga, 7. San Antonio de Punge, 8. Quilotoa 1, 9. Quilotoa 2, 10. Santa Bárbara, 11. Guitarra Huco Palacios, 12. San Miguel, 13. Domingo Sabio, 14. Cumbas 3, 15. Moraspungo, 16. Tumbaco.

Table 3. Rust reaction types of *allpa* genotypes from Cotacachi to two common bean isolates from Cotacachi, Quito-Ecuador, 2011.

Genotype ^a	Isolate ^b		Genotype ^a	Isolate ^b		Genotype ^a	isolate ^b
	9	1		9	1		1
4,1	2	6	69	4	4	2,1	5,6
3	3	4	2,2	4,5	4	8	4
4	3	5	20	4,5	6	10,1	3
7	4	3	11	5	4	12	5
3,1	3,4	5	1	5	6	14	4
13	3,4	5	6	5	5	15	5
5	4	6	9	5	6		
10	4	4	17	5	5		
16	4	5	18	5	5,6		
19	4	5	2	5,6	5		

^a Genotypes derive from mixed populations from the 2009 season and the seeds come from a single plant

^b Isolate 7: race 63:23, isolate 1: race 45:1

Table 4. Rust reaction types of *chakra* genotypes from Cotacachi to two common bean isolates from Cotacachi, Quito-Ecuador , 2011.

Genotype	Isolate		Genotype	isolate		Genotype	isolate		Genotype	isolate
	9	1		9	1		9	1		1
29,2	1	3	28	4	6	46,1	5	6	34	5,6
35	1	5	30	4	5,6	48	5	6	51	5
38,1	1	5,6	36	4	6	50	5	5	59	6
65,1	1	5	43	4	5	57	5	5	60	4
40	2	4	44	4	5	58	5	5	65	6
62	2	4	45	4	5	63	5	5,6	66	4
23	3	5	47	4	5	68	5	5	71	5
26	3	4	53	4	5	24	5,6	5	72	6
32	3	3	64	4	4	25	5,6	6		
48,1	3	3	67	4	5	29	5,6	6		
33	3	5	22,1	4,5	5	31	5,6	6		
39	3	4	30,1	4,5	5	41	5,6	6		
42	3	4	50,1	4,5	5	54	5,6	6		
62,1	3,4	3	52	4,5	5,6	73	5,6	6		
55	3,4	5	58,1	4,5	4	22	6	6		
56	3,4	5	28,1	5	5	37	6	5		
49	4	3	29,1	5	5	38	6	5		
21	4	6	38,2	5	5	67,1	6	5		
27	4	4	46	5	6	70	6	6		
27,1	4	6								

^a Genotypes derive from mixed populations from the 2009 season and the seeds come from a single plant

^b Isolate 7: race 63:23, isolate 1: race 45:1

Table 5. Rust reaction types of *mixturiado* genotypes from Saraguro to two common bean isolates from Cotacachi, Quito-Ecuador , 2011.

Genotype	isolate		Genotype	Isolate		Genotype	isolate		Genotype	Isolate
	9	1		9	1		7	1		1
87	1	2	91,1	4	6	84,1	5	6	83	6
89	1	3	92	4	4	86	5	4	119	3
99	1	4	93	4	6	98	5	5	124	3
105	1	2+	94	4	5,6	98,1	5	4	125	3
111	1	6	101	4	6	104	5	5	133	5
138	1	4	102	4	5	108	5	5	95	5
105,2	2	1	102,1	4	5	118	5	6	100	3
107	2	6	103,1	4	5	128	5	5	103	4
123	2	3	106	4	4,5	130	5	5	132	4
131	2	2	109	4	5	136	5	6		
75	3	5	110	4	4	80	5,6	5		
88	3	4	115	4	5,6	112	5,6	5		
96	3	3	120	4	5	134	5,6	1		
116	3	3	121	4	5	135	5,6	5		
137	3	5	129	4	3	91	6	5		
78	3,4	3	74,1	4,5	6	113	6	6		
78,1	3,4	5	74	5	2++	117	2+	3,2		
97	3,4	3	76	5	5	122	2+	2+,3		
127	3,4	3	79	5	5	126	2+	4		
75,1	4	4	81	5	4	105,1	2++	2++,3		
85	4	3	82	5	5	112,1	2++	3		
90	4	6	84	5	6	114	2++	3		

^a Genotypes derive from mixed populations from the 2009 season and the seeds come from a single plant

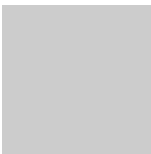
^b Isolate 7: race 63:23, isolate 1: race 45:1



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
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- (B-1) Variation in pest and pathogens
 - (B-2) Assessing genetic vulnerability
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 - (B-4) Economic Value of crop genetic diversity
to manage pest and diseases

Morphopathogenic characterization of *Micosphaerella fijiensis* isolates from *Musa* in Ecuador

Castro, B.

One hundred and twenty isolates of *M. fijiensis* were collected, sixty from each Ecuadorian site: El Carmen, Manabí -- lowland area with a crop pattern characterized by large areas covered with plantain, mainly Barraganete cultivar (AAB) -- and La Maná, located on the Andean slopes -- a very mountainous area where *Musa* spp are cultivated in small plots, the largest being those with Orito (golden finger AA cultivar). Pieces of infected leaves were taken to the Plant Pathology lab of the Pichilingue Research Station from the National Institute of Agricultural Research. Spore discharge on water agar led to single spore isolation on V8Agar and from here to PDA where the observations were made. Morphological criteria used to characterize the cultures were: colony diameter, color and aspect of the cultures, type, size and amount of spores produced. Results to date show certain differences between and within sites: Isolates from La Maná grow slowly and in three weeks average 17 to 21.7mm while those from El Carmen average 20 to 24.7mm. The other conspicuous characteristic was colony coloration, those from La Mana presenting a range of colors from light gray that later turns to pink (light purple) to a mixture of gray with pinkish zones to pure gray or pink. Those from El Carmen there were more variable, with isolates showing a single color, either gray or pink, maintained throughout, while some others were initially gray and then changed to show some pinkish zones like those from La Maná. In order to make a pathogenic evaluation of the isolates, a method to keep the leaf pieces functional was developed by submerging the leaf fragments into two solutions of citric acid (1g/l) and gibberelic acid (1 ml/l) in water for five minutes each and then placing them in a layer of PDA. Bioassays with leaf fragments of 2cm² taken from cultivars William (AAA) and Barraganete (AAB) and inoculated with an ascospore suspension of *M. fijiensis* allowed a complete development of the disease in 50 days. This method will be used to test the pathogenicity of the 120 isolates.

Study of genetic diversity of *Setosphaeria turcica* blight by ISSR

Chen Hong; Ma Jun Hong,; Wang Yun Yue.

The genetic diversity of the 101 strains of *Setosphaeria turcica* from Sichuan, Yunnan were appraised and evaluated by polymerase chain reaction (PCR) – ISSR. Clustering diagram analysis can compare the figure of 101 *S. turcica*'s genetic relationship. The strains of the same geographical origin showed a relatively close genetic relationship, based on ISSR polymorphism by *S. turcica* strains of genetic group closely related with the geographical origin of strains. Traditional varieties and modern varieties separated into different genetic groups, indicating that genetic changes in pathogen and host species have some relevance.

MATERIALS AND METHODS

The source of strain

This experiment has involved a total of 101 single spore *S. turcica* stains, of which nine were from Yunnan, 92 from Sichuan.

Experimental Methods

The 101 strains were examined with the liquid oscillation culture method to reproduction. DNA was extracted by CTAB. DNA was amplified by PCR-ISSR. The PCR amplification was detected by 1.5% agarose gel electrophoresis. Then the IQant capture gel imaging analysis system was used. The adjusted photographs and recorded test results were compared. The bands were recorded which in the image showed as fingerprint in "primer number - Fragment Length". The NTSYSpc 2.10 e analysis software was used and a dendrogram constructed.

CONCLUSIONS

The results showed that PCR was amplified in 93 clear and reproducible bands, of which 73 were polymorphic, equal to 83.9%. Clustering diagram analysis was used to compare the genetic relationships of the 101 *S. turcica*. From the DNA level proof, *S. turcica* from Sichuan and Yunnan was rich in inner genetic polymorphisms. The dendrogram showed that the tested stains' genetic similarity coefficient is 0.61-0.97. Under the 0.718 similarity level in the dendrogram, the strains of different geographical origin belonged to 15 different genetic groups, while the strains of the same geographical origin had relatively close genetic relationships. Based on ISSR polymorphisms, *S. turcica* strains of the same genetic group were closely related with the geographical origin of strains. Under the 0.65 similarity level in the dendrogram, different strains according to host can be divided into five genetic groups. Traditional varieties and modern varieties separated into different genetic groups, indicating that genetic changes in pathogen and host species have some relevance.

DISCUSSION

Composition and distribution characteristics of the S. turcica genetic groups from different areas of Sichuan, and Yunnan

The result indicated that the strains of the same geographical origin had a certain genetic relationship. Whatever the level of genetic similarity, the *S. turcica* groups in Sichuan have shown a very prominent structure. There is more genetic diversity with small genetic groups and specific genetic groups. The strains in Yunnan showed no particular advantage of the genetic groups.

Composition and distribution characteristics of the S. turcica genetic groups from different host species turcicum from Sichuan and Yunnan

Traditional varieties are subject to geographic barriers and have a more complex genetic background and horizontal resistance. The flow is relatively small. However modern varieties' geographical barriers are few, they have a relatively simple genetic background and vertical resistance. The replacement of speed liquidity is large.

Genetic Population Structure of *Exserohilum turcicum* in Yunnan and Sichuan Provinces revealed by ISSR markers

Hong Chen; Jun-Hong Ma; Hua-Xian Peng; Yun-Yue Wang.

In order to characterize the genetic population structure of Northern corn leaf blight fungus in Sichuan and Yunnan provincial project sites, a total of 101 isolates of *Exserohilum turcicum* collected from these two sites were used as an experimental population. The genetic population structures of *Exserohilum turcicum* were characterized by ISSR (inter-simple sequence repeat) marker-based DNA fingerprinting. The results showed that 83.9% of 93 clear and reproducible bands were polymorphic. The isolates were divided into 15 genetic lineages of *Exserohilum turcicum* at the similarity coefficient of 0.718. Fifteen genetic lineages of *E. turcica* were closely related with the geographical origin of strains. Under the 0.65 similarity level, these isolates can be divided into five genetic lineages. They were closely related to corn varieties. The isolates from traditional varieties and modern varieties belong to different genetic lineages. This indicated that genetic variation between pathogen and host varieties had a close relationship.

Contribution to the development of the scientific basis for the use of local *Vicia faba* genetic diversity in the control of pests: Application to *Bruchus rufimanus*

Chlyeh, G.; Sadiki, M.; Atfaoui, S.; Benboujema, F.

Biotic stresses induce important losses in the faba bean crop. The present research aims to contribute to the management of biotic stresses; particularly the faba bean beetle, through the use of local genetic diversity in farms.

This study has a double aim. The first one is to evaluate local knowledge and systems, in addition to analyzing farmers' perceptions concerning faba bean pests. The study was carried out at three sites Ourtzagh, Galaz and Tissa in the Taounate area, Morocco. A survey of 170 farmers was completed to evaluate the contribution of the local genetic richness to the process of integrated defense against damage caused by biotic stresses and related to the varietal profile of each site, including varietal resistance to *Bruchus rufimanus*.

Secondly, a laboratory experiment was carried out to evaluate the importance of the damage caused by the beetle on eight local varieties. The damage caused by the beetle was evaluated on seed germination capacity and seed weight loss, which were used as indicators of varietal level of resistance to *Bruchus rufimanus*.

The results obtained showed that varieties of small size and black color, such as variety 7 (Fouilla Beldia Lbida), variety 8 (Fouillette) and variety 1 (Sbahi khel) are most resistant to attacks of *Bruchus rufimanus* beetle.

Key words: *Vicia faba* L., *Bruchus rufimanus*, varietal resistance, genetic diversity, biotic stress, perception of the farmers, local variety.

Analysis of faba bean (*Vicia faba* L.) seed flow and diversity management practices on-farm

El Badraoui, M.; Belqadi, L.; Ezzahiri, B.; Chentoufi, L.; Sadiki, M.

INTRODUCTION

Faba bean seed is the first and major segment of the crop production chain. It represents the most important factor of production and the least expensive input for traditional production systems. Seed security and food safety are inseparable, particularly for smallholder farmers. Indeed, it carries benefits, since it contains the genetic material that determines the characteristics of the plant: taste, appearance, resistance to pests and diseases, tolerance for various weather conditions and even the capacity retention during storage. Smallholder farmers share a local knowledge that has always been very developed. This knowledge on the management of diversity and diseases is an integral part of cultural heritage, including the local seed system and the system of plant protection that requires preservation. This study aims to analyze the movement of seed in three rural communities of Taounate and practices and strategies adopted by farmers to manage the seed in a traditional system.

MATERIAL AND METHODS

To realize this objective, individual surveys were conducted by a multi-disciplinary team on 179 farms randomly chosen to valorize their local knowledge and intra-specific diversity among traditional varieties maintained by farmers with the aim of reducing the attacks of pests and diseases and therefore reducing pesticide use. These surveys were conducted in three rural communities (Ourtzagh, Galaz and Tissa) located in the region of Taounate. This area is part of the largest and oldest region of faba bean production in Morocco. Statistical analysis consisted of univariate and multivariate analysis. These tests provide a general description of populations and varieties. Hierarchical classification was performed on the data to highlight the linear combinations of characters and classification of varieties by homogeneous grouping of genotypes in the same class. SPSS (Statistical Package for the Social Sciences) was used for carrying out the various statistical analyzes.

RESULTS AND DISCUSSION

Data analyses shown in Tables 1 to 4 indicate that all the components of seed systems in the informal sector are mainly in the hands of farmers and consist of activities based on traditional practices; they share and exchange to satisfy their own seed needs. Selection practices, treatment, packaging and storage affect seed quality and thus the quality of the crop production. Farmers of the three communities depend on diverse sources of seed supply to meet their needs. The most

frequent sources of seeds are: parents, neighbors, friends outside the village, local market, and non-local markets. More than 50% of the farmers believe that seed from the local market is a vector of disease transmission.

Table 1: Percentage of farmers adopting different selection criteria for quality seed in the three communities Ourtzagh, Galaz and Tissa

Criteria	Ourtzagh	Galaz	Tissa
Seed selection on general aspect	34	19	34
Selection of large seeds	57	44	38
Planting of healthy seeds only	9	23	8
Selection of seeds with normal color		9	5
Choice of uniform seeds		6	14

Table 2: Percentage of farmers' post-harvest method for storing the bean seed in the three communities Ourtzagh, Galaz and Tissa

Method	Frequency		
	Ourtzagh	Galaz	Tissa
Seed treatment against pests			
No treatment	77	76	60
Pesticide application	13	8	10
Seed treatment with other products	22	16	30
Storage			
No preparation of seeds for storage	33	29	18
Specific preparation (place & material)	67	71	82

Table 3: Seed traffic analysis in the three towns: Ourtzagh, Galaz and Tissa

Sources of faba bean seed	Ourtzagh	Galaz	Tissa
Autoproduction	53	55	60
Neighbours	18	9	15
Villages		1	
Seed companies	18	3	1
Parents	1		
Neighbours outside village	1		
Local market (souk)	25	24	23
Non-local market	2	8	1

Table 4: Beliefs of farmers regarding disease transmission by seed

Level of Agreement	Ourtzagh	Galaz	Tissa
1 : Strongly agree	20	25	20
2 : Moderate agreement	31	25	25
3 : Undecided	15	13	32
4 : Slightly cons	8	4	3
5 : Quite cons	26	33	20
Total	100	100	100

Seed systems – rice in China

Xu Furong ; Yang Yayun ; Ai Xinxiang ; Dai Luyuan.

INTRODUCTION

The industrial rice system of China is currently composed of a chief scientist, 29 post-doc scientists, six function laboratories and 25 rice experimental stations. The hybrid rice bred by the Chinese "father of hybrid rice," Mr. Yuan Longping, is another major breakthrough in the Chinese history of rice breeding. Yuan Longping proposed the technical route of super rice research in China, combining plant varietal improvement and utilization of heterosis between subspecies. He also designed model features of a super hybrid rice. As more and more of the target genes were cloned, genes for herbicide, disease and insect resistance, as well as anti-virus and salt tolerance were used for improving the quality of rice. Other rice genes not present in the Chinese rice gene pool have been introduced into rice cells using genetic engineering technology. This has made them genetically stable allowed expression in the host cell to become possible and practical. The China National Seed Group Corporation and other large seed enterprises and seed companies above the county level across the country, were engaged in different levels of rice breeding and seed production, management and other activities. The present research examined the role played the farmer in rice seed systems,

RESULTS

The rice seed system of China has passed through ten stages: System selection (1920-1937), Tall varieties selection (the early 1950s), Use of local varieties (the 1950s), dwarf variety breeding (from the 1950s to the 1970s), hybrid rice breeding (in the 1970s), new plant type breeding and super rice breeding (1981-2006), transgenic breeding (the 1990 to present), molecular marker-assisted breeding and green super rice breeding (2005 to present).

China's rice breeding institutions have included the National Rice Breeding Improvement Center (nine branches), the industrial system of rice-breeding institutions and seed companies. These institutes formed the chain of the rice breeding system.

Farmers play an important role in the rice seed system. Farmers choose which seeds to keep, plant and manage, etc. Their experience in managing local varieties played an important role. Farmers, because their livelihoods depend on agriculture, had the best understanding of local agricultural conditions and the most realistic promotion of varieties, which must be accepted and approved by the majority of farmers. Dwarf, high-yielding varieties and hybrid rice, with its combination of high and stable yield, had better adaptability and were widely accepted by farmers. These varieties endured and were promoted over a very large area. Farmers saved their own seeds for planting the next season.

DISCUSSION

To speed up discovery and innovation of new breeding materials of rice germplasm, it was necessary to explore and apply new breeding theories, methods and means, to breed more variety in yield, quality, resistance and other aspects of significantly superior new rice varieties to satisfy the needs of rice production. Zhang Qifa and LI Zhi-Kang both said some of the current green super rice traits, such as insect resistance and disease resistance have been basically achieved, but the three objectives (no pesticide, less fertilizer, and resistance to drought) can be achieved after about 10 to 15 years. Full use of molecular biology research and actively carrying out the basic theory and technology studies of rice molecular design and breeding in the future would substantially increase China's rice breeding to the next level, allowing China to continue to maintain its leading role in the area of super rice breeding.

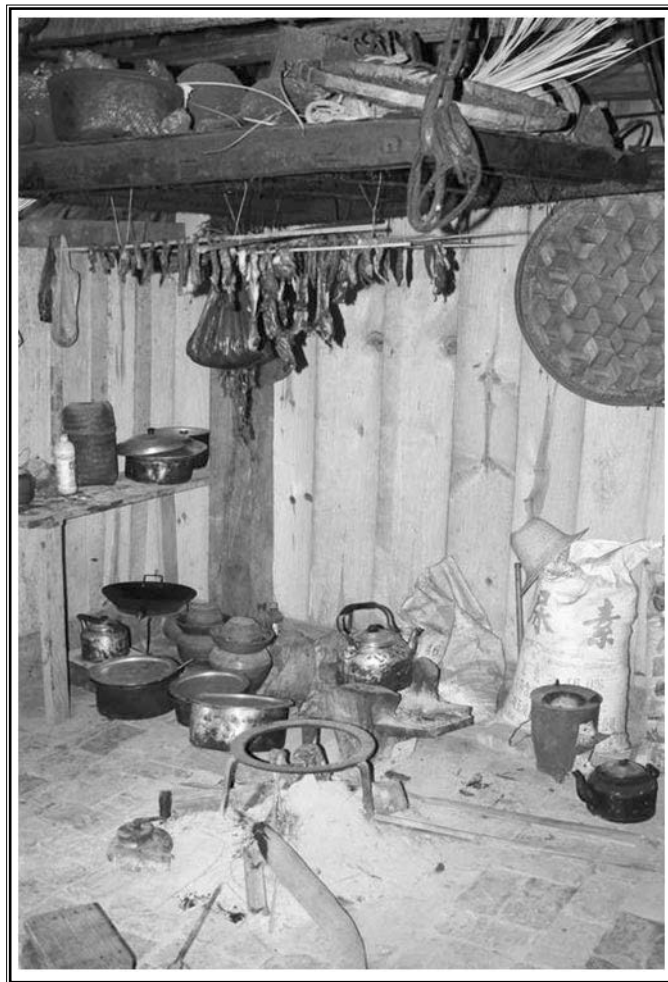


Figure 1: Farmer practice of fumigating seeds to prevent pests



Figure 2: Amoqie (genetic resources)



Figure 3: Mongdelong (genetic resources)

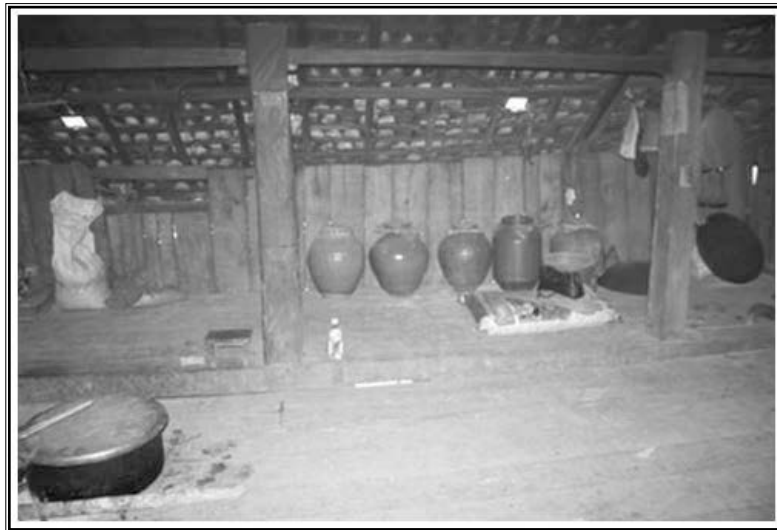


Figure 4: Storage area in Yunnan China

Measuring the economic value of traditional banana varieties for pest and disease management in Uganda

Kwikiriza N.; Katungi, E.; Homa, D.; Mulumba, J.W.; Fadda, C.; Jarvis, D.I.

INTRODUCTION

Uganda is one of the leading producers and consumers of bananas in the world. Bananas are cultivated on about 38% of the total arable land in the country. Production is, however, mainly on small subsistence farms. Uganda enjoys great banana variety diversity at country, community and plot levels. Banana production, however, faces many production constraints and its production has been in decline, the major constraint being pests and diseases. The National Banana Research Program is aware that the effects of some production constraints in some crops can be substantially reduced by using the existing diversity within the crop varieties. This has attracted attention of researchers to using this approach in the management of pests and diseases in bananas. The current study was carried out in Nakaseke and Bushenyi districts. One sub-county was selected from each district: Nakaseke subcounty from Nakaseke District and Kabwohe from Bushenyi District. In each sub-county, two parishes that were previously used as study sites for the main project were purposely selected, and in each parish, two villages were randomly selected.

METHODS

Data for the study was collected from individual household surveys, using a pretested questionnaire. A systematic random sampling with a random start was employed to select the sample from the compiled lists of households provided by the village leaders from the parishes purposely selected for the study. Sixty respondents were obtained from each sub-county. The sample size was predefined by the project.

Data obtained from two regions were entered in the Excel spread sheet and using the STATA analysis tool, t-tests and chi square values were generated to compare the means. The description included household characteristics, institutional characteristics, banana production constraints, aspects which describe banana diversity, banana management technologies, and market and labor information. Multi-collinearity tests and normality tests were carried out during the selection of the variables that were included in the model. Non-linear models were employed to obtain the effect of the explanatory variables on the yield of bananas and, in particular, the logistic model was employed. Before including banana diversity index as an exogenous variable, it was necessary to carry out an endogeneity test. This is because the decision to include various banana varieties in the plot might well be the conscious decision of farmers to increase yield (endogeneity of diversity). A Durbin-Wu-Hausman endogeneity test was performed before including the banana diversity index as an exogenous variable in the abatement model.

RESULTS

The average educational level of farmers was generally low, 6.6 and 6.5 for Nakaseke and Kabwohe respectively (Table 1). There was a significantly larger total land holding in Nakaseke than in Kabwohe, although a bigger proportion of land (90%) was under crop in Kabwohe compared to 80% in Nakaseke. Banana acreage in Kabwohe was also bigger than that in Nakaseke. The occurrence of *fusarium* wilt and Black sigatoka was significantly higher in Nakaseke than Kabwohe, with over 80% of the farmers having faced these problems in Nakaseke and less than 40% in Kabwohe. Both regions have faced a problem of nematodes but Kabwohe has been more hit by the pest compared to Nakaseke. In both Nakaseke and Kabwohe, family labor was the major input in banana production. The average number of banana varieties in the banana plots was eight in Nakaseke farms and six in Kabwohe, with some farmers having as many as 23 varieties in Nakaseke and 13 varieties in Kabwohe farms. This shows that there is more banana variety richness in Nakaseke banana plots than in banana plots in Kabwohe. Results indicate that there was no significant difference in banana evenness on Nakaseke farms (0.46) and Kabwohe (0.48). The value of the measure of diversity (Herfindahl index), which combines both evenness and richness, was higher in Nakaseke and Kabwohe. Banana yield in terms of bunch size and in kgs/ha was significantly higher in Kabwohe (approximately twice as high) than in Nakaseke. The yields obtained on the major banana plots were 5,066kg/ha for a period of six months or 10.14 ton/ha/year for Nakaseke and 9,081kg/ha for six months or 18.16ton/ha/year for Kabwohe.

Results of model 1, show that the variety diversity (presented as the Herfindahl index) has a negative direct effect on yield but a significant and positive damage abatement effect (Table 2). In other words, although banana variety diversity does not contribute directly to increasing banana yield, it reduces the yield losses caused by biophysical pressures. When a major variety has a bigger share in the plot, overall banana yields are significantly higher but the effect of abating damage caused by biophysical pressures is significantly reduced. On the other hand, the number of banana varieties, a measure of diversity richness, has no significant effect either in increasing yields or reducing the yield losses caused by biophysical pressures. It thus appears that what is important in abating damage in bananas is diversity evenness in the plot—not how many varieties are in the plot. This is an important result since it tells which aspect of diversity is important in reducing yield loss. Older household heads obtain higher banana yields than younger household heads. Education was also found to be significant in influencing yield.

DISCUSSION

From this study, important results emerge. Overall, results show that an increase in banana diversity has a significant abatement effect, with a potential of reducing banana yield loss. This is in agreement with the findings from most previous studies carried out on annual crops (Burdon 1987; Burdon and Jarosz 1989). It can be concluded that even with perennial crops where pests and diseases accumulate, diversity can still contribute significantly to abating yield loss. The study findings also indicate that the most important aspect of diversity for abating yield losses in bananas is evenness. This means that farmers ought to mix varieties in relatively equal proportions to attain the maximum benefit of abating yield losses caused by biophysical pressures.

However, results also show that maintaining high banana diversity is associated with yield trade-offs. Controlling for its abatement effect, high banana diversity seems to directly reduce banana yield. This means that without biophysical pressures, specializing in a few varieties with a high-yielding genetic potential may increase returns to management and enhance efficiency

in resource utilization. This is likely to be optimal for well-to-do farmers who have the ability to bear risks. This category of farmers constitutes less than 10 percent of the total banana farmers in Uganda, and the social benefits of yield loss abatement on the remaining farmers resulting from adoption of spatial diversity are likely to be great. Therefore, within the current banana production environment of limited abatement agents and high biotic stress, enhancing diversity appears to be an important option despite trade-offs.

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Table 1 Summary statistics


Characteristic	Nakaseke	Kabwohe	Overall
Years of formal education attained by the household head	6.63	6.37	6.50
Total land (acres) owned by the household	6.14**	3.11**	4.64
Total land (acres) allocated to banana production	0.94***	1.67***	1.30
Average number of banana mats in banana plots	168.38***	489.46***	327.57
Average number of banana varieties in banana plots	7.90***	5.68***	6.80
Yield of bananas in kg/acre	2,026.39***	3,632.34***	2,815.75
Proportion of bananas sold(%)	14.25***	35.33***	24.71
Number of crops intercropped with bananas	1.88**	1.46**	1.67
Farmers who have experienced banana sigatoka (%)	88.33***	38.98***	63.87
Farmers who have experienced nematodes (%)	52.54*	69.49*	61.02
Farmers who have experienced fusarium wilt (%)	86.67***	27.12***	57.14
Years of fusarium wilt	3.26	4.65	3.6
Years of sigatoka	5.47	6.38	5.74
Years of nematodes	7.30	7.61	7.47
Loss in yield in bananas caused by black sigatoka (%)	27.35***	14.76***	21.11
Loss in yield in bananas caused by nematodes (%)	18.49	18.74	18.62

Table 2 Estimates of the effect of banana variety diversity and other factors on banana yields

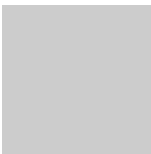
Explanatory variable	Model 1		Model 2	
	Logistic (Herfindahl index)		Logistic (evenness and richness separate)	
	Coefficient	t- value	Coefficient	t-value
Number of varieties			.07	0.86
Share of major variety			5.14	6.8***
Herfindahl index	4.89	4.12***		
District (dummy)	0.82	3.08***	.834	3.1***
Age of household head	0.023	2.89**	0.21	2.71***
Education of household head	.05	1.9*	0.05	1.82*
Total livestock	8.29x10 ⁻⁹	.56	8.12x10 ⁻⁹	.56
Total number of mats	.0006	1.56	.0005	1.4
Number of banana intercrop	.81	3.38***	.47	1.72*
Slope dummy (flat),	.84	2.67***	.82	2.69**
Family labor used as a direct input	.65	4.87***	.52	4.1***
(Costant)	-4.45	-1.89**	-8.1	-1.72*
(Herfindahl index)	-7.12	-1.92*		
(Intercropping)	-0.765	-1.34	-0.22	-0.39
(labor to control pests and diseases)	-0.0005	-0.88	-0.0001	-0.21
Δ (number of different varieties)			-0.22	-0.98
Ø(share of the major banana variety)			-12.1	-2.07**
	Observations =119		Observations =119	
	Adj. R ² = 0.976		Adj. R ² = 0.98	



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:



THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 4



Measuring genetic vulnerability
(Option 5: Glasshouse experiments – Linked to FGD, HH,
Options 1-4)

Introduction: Measuring genetic vulnerability

Brown, T.

From the outset of the project, genetic vulnerability is a key variable and indicator. Reduction in the genetic vulnerability of crops to pests and pathogens is one of its crucial objectives. While this is easily stated in words, our challenge is to develop ways to measure any improvement in vulnerability in farmers' fields.

To some people, increased use of any genetic diversity by farmers equates to a lowering vulnerability. However, we have argued that this is not necessarily so. Unwise use of diversity could select pest populations for higher diversity and lead to the evolution of more virulent pathogens and hence more vulnerable crops. Furthermore, breeders have considered that much of the resistance diversity that is now common in traditional or local varieties is "old" diversity, on which current races of pathogen have had a long time to become virulent. Hence most traditional diversity gives no protection, and it is only very rare resistance genes in remote sources or wild relatives that might be useful against modern races. Thus the use of varietal diversity alone as a measure of vulnerability is open to question. In seeking broadly-based answers to this open question and devising measures of vulnerability, our project enters new ground.

In principle, we recognised three indicators of vulnerability, namely:

- a deficiency of genetic diversity, for genes involved in host-pathogen systems (Variety resistance diversity)
- lack of resistance to invading exotic strains or migrants of pests (Migrational vulnerability)
- lack of resistance to newly arising mutations (Mutational vulnerability)

These measures were conceived in terms of ideal host-pathogen gene-for-gene systems, but we clearly needed procedures that could be extended to quantitative field resistance and to systems that are not well characterized genetically. In this session we pool the wisdom of experience of trying to apply these notions to farms in our project sites.

Resistance of local common bean cultivars from Saraguro to multiple diseases in Saraguro and Gualaceo, Ecuador

Aguilar, M.; Simbaña, L.; Ochoa, J.B.

INTRODUCTION

Rust (*Uromyces appendiculatus* (Pers.) is an important disease of common bean in Ecuador. Farmers spray fungicides to control the disease in susceptible commercial varieties, while resistance to the disease is a breeding objective. Powdery mildew and Common Bean Mosaic Virus (CBMV) are, on the other hand, diseases restricted to areas of lower altitudes, where common bean is not an important crop. However, climate change is expected to create conducive conditions to these diseases and they are potential threats for common bean cultivation in traditional areas.

In Ecuador, most of the common bean is grown in a low-input traditional agricultural system where no modern measures of control are applied, and therefore the resistance operating in the farmer-managed diversity is the basis of the strategy farmers follow to keep disease levels low to avoid serious yield losses. Additionally, the potential threat of new diseases can be also coped with by means of the resistance available in the local crop diversity.

To assess the availability of resistance to multiple pathogens, a study was carried out with the common bean variability from Saraguro in Bulcay-Gualaceo and Cañicapa-Saraguro.

METHODS

A collection of phenotypically similar populations of common bean from Saraguro obtained from farmer mixtures in participatory processes was evaluated with regard to rust, powdery mildew and CBMV in Bulcay-Gualaceo and Cañicapa-Loja. One hundred thirty common bean populations were evaluated in Bulcay and 119 populations in Cañicapa. In both sites the populations were planted in one-row plots 4 m long with 0.80 m. spacing. Two common bean seeds, together with two seeds of maize variety Zhima were planted on the row every 0.6 m (site). After seedling development, a single common bean plant per planting site was allowed to develop for evaluation.

Rust, powdery mildew and CBMV evaluations were done every 14 days since the epidemic initiated. Disease severity (DS) and powdery mildew was evaluated using the Cobb modified scale, that consisted in assessing the foliar area covered by the disease (James, W.C. 1971). Using DS data, the Area Under Disease Progress Curve (AUDPC) was calculated (Shaner, G. and Finney R.E. 1977). Powdery mildew was also evaluated using the Cobb modified scale, while CBMV severity was assessed using a 0-6 scale proposed by Schoonhoven and Pastor-Corrales 1987.

Data of rust, powdery mildew and CBMV severity, as well as AUDPC rust, were submitted to ANOVA analysis and then to a mean analysis using Tukey and Duncan analysis.

RESULTS AND DISCUSSION

In Table 1, results of the common populations evaluated in Bulcay and Cañicapa are shown. Rust was more virulent but less aggressive in Cañicapa than in Bulcay, which suggests that the pathogen populations from these places are different from each other. The high virulence of the Cañicapa rust population appears to be associated with pathogen adaptation to resistance genes present in Saraguro common bean populations, while these genes have not been exposed to Bulcay rust populations. Similar results were observed with Cotacachi isolates and Saraguro common bean populations (Vega and Ochoa 2011). The difference in pathogen populations is confirmed from the plant/pathogen interactions observed between populations 108.2 and 74.1 with Bulcay and Cañicapa pathogen populations. The high aggressivity of rust in Bulcay is most likely associated with the conditions in Bulcay that are highly conducive to rust.

High levels of resistance to rust of most likely major gene nature was observed in some common bean populations. However, the only efficient resistance in both sites is the one in population 74.2. This source of resistance and the ones associated with the plant/pathogen interactions of populations 108.2 and 74.1 are different sources of resistance of major gene nature in Saraguro. Similar plant/pathogen interactions were also observed at seedling stage (Vega and Ochoa 2011), which means that results from the greenhouse and those from the field are associated for common rust.

Partial Resistance (PR) might be present in these populations; however, as in studies from Cotacachi (Espinosa and Ochoa 2011), the levels of PR are difficult to establish as defeated genes express erratically to a highly variable pathogen population. The high variability of rust was already shown in Cotacachi (Vega and Ochoa 2011) and in many parts of the world (Jochua *et al*, 2008).

Resistance to CBMV was also available in the Saraguro common bean populations and varied from low to high levels of resistance (Table 1). CBMV is not an important disease in Saraguro, and the availability of resistance suggests that the disease was probably important in the past, and the resistance has been maintained in the diversity of local cultivars. The source(s) of resistance to CBMV found in this study appears to be different from the one used by breeders and could be important for conventional breeding as well.

Resistant to powdery mildew was of quantitative nature, complete resistance being rare. Populations 112 and 83.1 were completely resistant, but only in Cañicapa. Some levels of resistance, possibly of partial nature, was present in populations 83 and 112 in both sites.

Sources of resistance in the common bean populations from Saraguro are available for the three pathogens. However, the pathogens have already adapted to most of these sources of resistance and they might not be interesting for conventional breeding. However, in the mixture, these sources of resistance appear to interact, with each reducing the negative effect of pathogen populations (Italo, E. and ochoa, J.B. 2011).

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Table 1. Rust, common bean mosaic virus (CBMV) and powdery mildew evaluation of common bean populations from Saraguro evaluated in Bulcay-Azuay and Saraguro-Loja. 2010.

Genotypes	Rust DS ¹		AUDPC ²		CBMV ³	DS of powdery mildew ¹	
	Bulcay	Cañicapa	Bulcay	Cañicapa	Bulcay	Bulcay	Cañicapa
74.3	0a	0	0	0	3.5ab	70.0c-f	50 a-e
102.2	0a	16.7 a-d	0a	551 a-c	1a	70f	60 a-e
76.1	0a	33,3 a-g	0a	1337 a-g	5,7b	80g	60 a-e
75	0a	16.7 a-d	0a	487 a-c	5.0ab	80.0e-f	15 a-d
102.5	3.3ab	16.7 a-d	25a	351 a-c	1.0a	60.0b-f	60 a-e
108.2	5.0a-c	56.7 f-l	38a	2387 l-w	1.6ab	80.0ef	60 a-c
102	13,8b-c	16.7 a-d	234bc	351 a-c	4,3b	70f	60 a-e
91.1	13.0a-d	40 a-l	277ab	1667 c-s	2.4ab	70.0c-f	16.7 a-c
83	16.2a-e	12.5 a-c	309a-c	389 a-c	1.0a	40.0bc	30 a-e
74.2	21.6a-g	1.7 a-b	412a-e	45 a	2.3ab	40.0bc	46.7 a-c
126	23.3a-g	28.3 a-i	475a-f	1003 a-m	2.0ab	60.0b-f	18.3 a-c
94.2	25.0a-h	53.3 e-l	563a-f	2328 k-w	1.0a	60.0b-f	60 a-c
114	30.0a-i	20 a-g	750a-g	723 a-i	2.5ab	30.0ab	46.7 a-c
112	33,3a-i	36.7-a-k	750d	1495 a-r	1,7a	40c	26.6 a-c
84.2	35.0a-j	32.5 a-g	737a-g	1229 a-p	4.0ab	30.0ab	60 a-c
101.1	36.2a-j	40 a-l	834a-h	1683 c-s	4.5ab	90.0f	50 a-c
131	38.7b-k	41.7 b-l	1031a-i	1848 e-t	3.3ab	53.7b-e	60 a-c
74.4	40.0b-k	12.5 a-c	1237a-i	399 a-c	1.0a	40.0bc	60 a-e

Table 1. continues next page

Table 1. continued

Genotypes	Rust DS ¹		AUDPC ²		CBMV ³	DS of powdery mildew ¹	
	Bulcay	Cañicapa	Bulcay	Cañicapa	Bulcay	Bulcay	Cañicapa
90	40.0b-k	50 d-l	1162a-i	2048 f-w	3.5ab	60.0b-f	60 a-c
97	40.9b-k	31.7 a-g	1057a-i	1125 a-o	3.0ab	66.5c-f	60 a-c
112	43.0c-l	40 a-l	1218a-i	1746 d-s	2.3ab	57.7b-e	0
108	43.3c-l	56.7 f-l	950a-i	2387 l-w	5.3ab	90.0f	60 a-c
131.4	43.3c-l	41.7 b-l	1250a-i	1848 e-t	3.3ab	80.0ef	60 a-c
97.4	46.6d-m	31.7 a-g	1375a.i	1125 a-o	1.0a	60.0b-f	60 a-c
112.1	46.6d-m	30 a-g	1150a-i	1064 a-n	4.0ab	50.0b-e	20 a-c
84.1	46.0d-m	26.7 a-f	1105.a-i	846 a-f	3.0ab	80.0ef	60 a-e
80	48.0d-m	10 a-d	1275a-i	251 a-d	4.8ab	90.0f	66.7 a-c
104	50.0d-m	34a-k	1775d-i	1376 a-p	2.6ab	70.0c-f	46.7 a-c
106	50.0d-m	40 a-l	1650b-i	1579 b-s	3.5ab	80.0ef	60 a-c
131.3	50.0d-m	41.7 b-l	1012a-i	1848 e-t	4.0ab	65.0c-f	60 a-c
74	50.0d-m	1.7 ab	1425f	45 a	4,5b	80g	46.7 a-c
84	51.0d-m	21.7 a-g	1381a-i	811 a-j	3.1ab	71.2d-f	60 a-c
74.1	53.0e-n	0a	1402a-i	0a	3.2ab	69.5c-f	50 a-e
101	53.3e-n	35 a-k	1700c-i	1380 a-q	2.3ab	75.5e-f	23.3 a-c
105.1	53.3e-n	13.3 a-c	1600b-i	658 a-d	2.3ab	70.0c-f	60 a-e
118	53.3e-n	11.7 a-d	1050a-i	37 a-d	5.0ab	90.0f	66.7 a-c
94.3	55.0f-o	53.3 e-l	1537b-i	2328 k-w	1.0a	45.0b-d	60 a-c
91	55.0f-o	60 g-l	1218a-i	2477 m-w	4.7ab	90.0f	96.7 a-c
132	56.0f-o	20 a-g	1755d-i	706 a-i	2.2ab	70.0c-f	60 a-c
120	56.6f-o	0a	1450b-i	0a	4.6ab	70.0c-f	55 a-e
75.1	57.1f-o	50 d-l	1569b-i	2103 g-w	2.1ab	61.4c-f	26.7 a-c
103	60.0g-p	36.7 a-k	1825f-i	1437 a-r	2.3ab	50.0b-e	36.7 a-c
113	60.0g-p	3.5 a-c	1687c-i	75 a-b	4.0ab	80.0ef	60 a-c
94	60.0h-p	53.3 ie-l	1800g	2326 k-w	5,3b	90h	60 a-c
78.1	62.0h-p	50 d-l	1830f-i	2163 h-w	3.6ab	80.0ef	53.3 a-c
83.1	62.5h-p	40 a-l	2025	1614 c-s	3.5	60	0a
82	65.0i-r	70 j-l	1987g-i	3285 e-w	4.0ab	70.0c-f	40 a-c
85	70.0j-q	6.7 a	1800e-i	137 a	5.5b	80.0ef	53. a-e

¹Cobb modified scale 0-100

²Calculated using the values of DS

³ 1-6 CBMV scale


Measuring Genetic vulnerability: comparing probabilities of uniformity, mutation and migration across sites in China

Jun-Hong Ma; Xue-Hui Yang; Yun-Yue Wang.

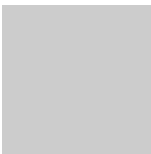
Rice is one of the world's most important food crops. The pursuit of high-yielding rice results in its large-scale monoculture. This also diminishes farmers' capacities to cope with changes in pest and disease infection, and leads to yield instability and loss. In this study, we did resistance spectra analysis and resistance rating for 57 cultivars from Yunnan, Guizhou and Sichuan. Resistance spectra analysis showed in the resistance spectra of cultivars that the frequency of virulence was different in less than 66.67% of the cases. Of these, 62% are traditional cultivars, 38% are modern cultivars. This meant that traditional cultivars might have a broader resistance spectrum. The result of general resistance rating using isolates from Guizhou showed that the resistance ratings of three cultivars was R, of two cultivars was MR, and the remainder was susceptible. These five cultivars are traditional cultivars from Yunnan. This meant we might find new rice germplasm resources with good resistance for breeding. In addition, it indicated that the resistance of cultivars might change because of migration across sites. The twelve cultivars that have the wide resistance spectrum for Yunnan isolates are different from those that had resistance ratings of R and MR. This showed that genetic and pathotypic structure of rice blast fungus population from Yunnan and Guizhou might be different. These glass house experiments will provide further information on the resistance of different varieties and therefore will be the basis for developing recommendations for replacing pesticide use with diversity-rich practices.



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:



THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 5



Quantifying “Genetic diversity management choices” made
by farmers to manage pest and diseases

Quantifying Genetic Diversity Management Choices Made by Farmers to Manage Common Bean (*Phaseolus vulgaris*) Pests and Diseases in Uganda

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INTRODUCTION

In Uganda, the common bean crop is not only used as food, but it is important in cultural functions as well as source of income to farmers. However, over the past twenty years, bean based farming systems have been threatened by natural disasters, including pests and diseases leading to production and diversity decline. Furthermore, the land-races which farmers have maintained for centuries are now thought to be disappearing from farmers' fields. There is now perhaps an increase in the diversity of new genes included in new varieties but the net effect of this is uncertain (Porceddu et al, 1988). The loss of genetic choices, reflected as loss of local crop cultivars, diminishes farmers' capacities to cope with changes in pest and disease infection, and leads to yield instability and loss. The maintenance of a diversity of landraces is the result of a diversity of community based plant genetic resources management practices. Indeed it is this diversity of practices by communities across Africa, often strongly rooted in tradition that drives conservation of crop diversity and which must be maintained to ensure the on-farm conservation of these varieties (UNEP, 2010). In order to understand how farmers are managing pests and diseases, an assessment of the genetic diversity management choices made by farmers in growing common bean was done. The study was carried out in three sites in Uganda namely; Nakaseke, Kabwohe and Rubaya.

METHODS

The data on common bean management practices was collected using participatory diagnosis methods which included FGDs (FGDs) and Household (HH) Surveys. Fifteen FGDs, five per site, were conducted. The FGDs targeted groups of leaders, young men, young women, old men and old women in each site. Each of the groups had a minimum of 10 people. A total of 160 farmers purposively selected to represent the whole target community participated in the FGDs. All the farmers that participated in the FGDs were from the target villages and had to be growing common bean. Farmers of 30 years and below were the young farmers while those above 30 years old were the old farmers. While in these groups, farmers were asked similar questions about practices for managing pests and diseases while growing common bean and some of the underlying perceptions.

In the HH Surveys, 60 households growing common bean per site, were selected randomly. Cluster sampling by village was used to ensure geographic representation across the four target

villages per site representing the whole community. The selected farmers were interviewed using a questionnaire and a deliberate effort was done to ensure that both male and female farmers were involved in equal numbers. In all, 180 bean farmers were interviewed. Individually, farmers were asked about practices for managing pests and diseases in the common bean crop and some of the perceptions underlying these practices. In order to relate the management practices to the diversity and diseases situation on-farm, the name and number of *P. vulgaris* varieties, their area of coverage and disease severity on-farm were recorded from each household. Disease severity was estimated from 30 different points on a farmers' field by assessing three plants front, left and right. The plants were assessed basing on a scale of 1 for low, 2 for moderate and 3 for high severity. The household weighted disease index (WDI) was estimated from the product of the disease index (at the plot level) and the frequency of each variety present in the plot weighed by the percent area covered for each variety at household level Average farm richness was calculated as the average number of varieties per household. Following Magurran (2003), evenness was estimated as a complement of d ($1-D$), where D is the Simpson measure of dominance. The data was encoded in Excel and analyzed using descriptive statistics to produce tables and charts that showed emerging trends and patterns. The relationship between the pest/disease management practices and diversity measures as well as damage indices on-farm were estimated by correlation and regression analysis. The correlation between total area and the number of varieties planted by the respondents was also done to see whether land size is a factor that limits the planting of variety mixtures.

RESULTS

Farmers had several practices to control pests and diseases some of which use intraspecific diversity. These practices are divided into temporal and spatial arrangements of varieties. Spatial arrangements included: Planting variety mixtures in patterns like random, rows, small plots, borders and rows in a plot (Figure 2). Planting mixtures was popular in Kabwohe with sixty eight percent of the respondents and in Rubaya with sixty three percent of the respondents doing it unlike in Nakaseke where it was only thirty percent of the respondents doing it. The correlation between the total land size and the number of varieties planted in Nakaseke was 0.289 at 8.38% level of significance; Kabwohe was 0.375 at 14.05% level of significance and Rubaya was 0.3524 at 12.42% level of significance. Other spartial arrangement practices were; planting each variety in a separate plot carried out in Nakaseke and decreasing the spacing density carried out in Kabwohe and Rubaya. When the different arrangements of varieties on-farm were correlated with the weighted damage indices for Anthracnose and Angular Leaf Spot in Kabwohe and Rubaya, the correlations were very weak and not significant (Table 1).

The temporal arrangements included: planting improved varieties which was most popular in Rubaya (eighty seven percent) followed by Nakaseke (sixty five percent) and least practiced in Kabwohe (50 percent). Crop rotation was the most popular practice in all the sites followed by weeding. Other practices were; scouting(trapping) insects, field sanitation, fertilizing the soil with chemical fertilizers, fertilizing the soil with non-chemical fertilizers, fertilizing the area where seeds are collected and other soil management practices to compensate for loss of nutrients to the plant from pests and diseases. Among practices above, those that use intraspecific diversity to control pests and diseases are planting improved varieties, crop rotation, planting mixtures, decreasing the spacing density and planting one variety per plot (Figure 1 and table 5). Pesticide use was only in Rubaya by 17% of the respondents where they use 2.3kg and 140ml of pesticide per season. The correlations between the number of practices employed by the households to control pests /diseases and the diversity estimates as well as the weighted damage indices were

very weak and not significant (Table 2). The correlation between the amount of pesticides and the weighted damage indices as well as diversity estimates in Rubaya were weak and negative apart from the correlation between amount of pesticides and weighted damage indices for Anthracnose which was moderately strong ($r = -0.414, F = 0.355$) (Table 3).

In order to understand the perceptions of the respondents behind the use of the above practices especially those that use intraspecific diversity, they were asked what they believed about the practices. Forty six percent of the respondents in all sites believed strongly that modern varieties become more susceptible to diseases over time while forty five percent believed that traditional varieties do not become more susceptible to diseases over time. Sixty percent of the respondents in Rubaya and sixty three percent of those in Nakaseke believed strongly that improved varieties become more susceptible to diseases over time yet only 15 percent of the respondents in Kabwohe believed so. Respondents also believed that varieties succumbed to pests and diseases to different levels in the wet and dry years. When the perceived resistance levels of the different varieties during the wet and dry years were correlated with the damage indices for Anthracnose and Angular Leaf Spot in Kabwohe and Rubaya, the correlations for Kabwohe were significant while those of Rubaya were not significant (Table 4) apart from that of damage indices for modern varieties which was moderately significant ($r = 0.429, F = 0.028$). Only respondents in Nakaseke (22%) believed that monoculture is more susceptible to pests and diseases than mixtures; thirty four percent of the respondents in all sites believed that planting more than one variety per plot gives more income yet none of the respondents in all the sites believed that planting more than one variety per plot is more costly than uniform planting. Twenty nine percent of the respondents in all sites believed strongly that if you grow only one variety, you will have more insect attacks than when you grow more than one variety. (Table 6). There were different levels of beliefs in the different statements across the sites as shown in table 7.

DISCUSSION

Genetic diversity management choices used to control pests and diseases vary in the extent to which they are employed in the study sites. Practices using intraspecific diversity were not as many as those not using it possibly because of lack of awareness about the importance of intraspecific diversity amongst the farmers. Planting variety mixtures was more popular in Rubaya and Kabwohe possibly because they want to control pests and diseases but also to maximize and meet their household needs. The market in these two sites also favors mixtures unlike in Nakaseke site. However, it is only Nakaseke respondents (22%) who believed strongly that monocultures are more susceptible to pests and diseases than mixtures. This could mean that most of those planting mixtures in Nakaseke do it to control pests and diseases yet in the other sites, controlling pests and diseases could be secondary. The correlation between land size and number of varieties planted by the respondents was low which meant that land size is not a key determinant of planting variety mixtures. According to Nantale *et al* (2008), beans have been intercropped for quite some time in Uganda and each crop is maintained as a mixture of different genotypes in farmers' fields. Farmers carry out exclusively this practice through selection, production and utilization using different types of knowledge on the crop. Many factors influence the choice of how many and which varieties to grow and in which areas, including the need to minimize risk, maximize yields, ensure nutritional balance, spread workloads and capture market opportunities (FAO, 2010). Planting improved varieties and crop rotation were more common practices in Rubaya compared to the other sites. This could be because crop rotation is one of the good ways of maximizing usage of exhausted soils found in Rubaya as well as trying out new varieties that could carry genes which enable them survive better on poor soils. Rubaya still had the highest

percentage of respondents who believed strongly that improved varieties become more susceptible to diseases over time and this could explain why it is only Rubaya farmers that had taken on pesticide use (17% of the respondents).

The weak correlation between the different arrangements observed on farm and the weighted damage indices (Table 1) could mean that in order to have effective control of diseases and pests on farm through having mixtures of varieties, not any arrangement can be effective. This calls for more rigorous research into which arrangements and which varieties can really work in this regard. The correlations between the number of practices employed by the households to control pests/diseases and the diversity estimates as well as the weighted damage indices were very weak and not significant (Table 2). This could be attributed to the fact that not all practices are effective to the same extent and possibly other factors came into play like the number of people carrying out a particular practice, the area of coverage among others. All these call for more research into which practices are effective, when, where, how and to what extent these should be carried out. The correlation between the amount of pesticides and the weighted damage indices as well as diversity estimates in Rubaya were weak and negative apart from the correlation between amount of pesticides and weighted damage indices for Anthracnose which was moderately strong($r = -0.414, F = 0.355$).(Table 3). The negative nature of the correlation between the amount of pesticides used and the diversity estimates though weak indicates the negative impact that pesticides have on diversity. In the same way, the negative correlation between the amount of pesticide and the weighted damage indices implies that the more pesticides used, the less the severity of diseases but also the less the diversity and that is where the dilemma is. The weakness of the correlation could be attributed to the small percentage of farmers who are using pesticides in Rubaya (17% of the respondents).

Basing on the above, there appears to be quite a good starting point to reducing crop damage on farmers' fields using intraspecific diversity through building on what is already being done but it is also very clear that a number of gaps still exist that require concrete answers as far as the best practices are and how they should be carried out.. We also seem to be on the way to substituting pesticides with diversity because the percentage of people using pesticides is quite small and these can possibly change when they see the benefits of using diversity. Better understanding and support for farmers' management of diversity is still needed; opportunities exist to improve the livelihoods of rural communities through an improved management of diversity (Bajracharya J. *et al*, 2007). Creating an environment that recognizes, respects and learns to build on the positive aspects of these practices is probably the overarching best practice that needs to be recognized and supported through appropriate policies. (UNEP, 2010).

Table 1 Correlation between the arrangement patterns observed on-farm and the Weighted Damage Index for Anthracnose and Angular Leaf Spot

		WDI ALS	WDI Anthra
Pearson Correlation R	Kabwohe	0.001	0.004
	Rubaya	0.196	0.137
Level of significance F	Kabwohe	0.994	0.973
	Rubaya	0.133	0.295

Table 2 Correlation between the number of practices employed by households to control pests/diseases and the diversity estimates as well as the weighted damage indices

		Richness	Evenness	WDI ALS	WDI Anthra
Pearson Correlation R	Kabwohe	0.142	0.186	0.157	0.067
	Rubaya	0.143	0.183	0.223	0.043
Level of significance F	Kabwohe	0.361	0.231	0.311	0.669
	Rubaya	0.273	0.151	0.086	0.739

Table 3 Correlation between the amounts of pesticides used by some households in Rubaya and the damage indices as well as the diversity estimates

	Richness	Evenness	WDI ALS	WDI Anthra
Pearson Correlation R	0.13	0.257	0.174	0.414
Level of significance F	0.78	0.577	0.708	0.355

Table 4 Correlation between the perceived resistance of varieties during the wet/dry years and the damage indices in Kabwohe and Rubaya

		DI ALS Local Varieties-wet yr	DI ALS Local Varieties-dry yr	DI ALS Modern Varieties dry yr	DI ALS Modern Varieties wet yr	DI Anthra Local Varieties dry yr	DI Anthra Local Varieties wet year	DI Anthra Modern varieties Wet yr	DI Anthra Modern varieties dry yr
Pearson Correlation R	Kabwohe	0.6	0.79	0.86	0.76	0.65	0.77	0.8	0.53
	Rubaya	0.0004	0.014	0.081	0.028	0.081	0.109	0.132	0.429
Level of significance F	Kabwohe	0.00009	0.00003	0.00005	0.00004	0.00002	0.00004	0.00001	0.011
	Rubaya	0.997	0.902	0.691	0.891	0.483	0.341	0.517	0.028

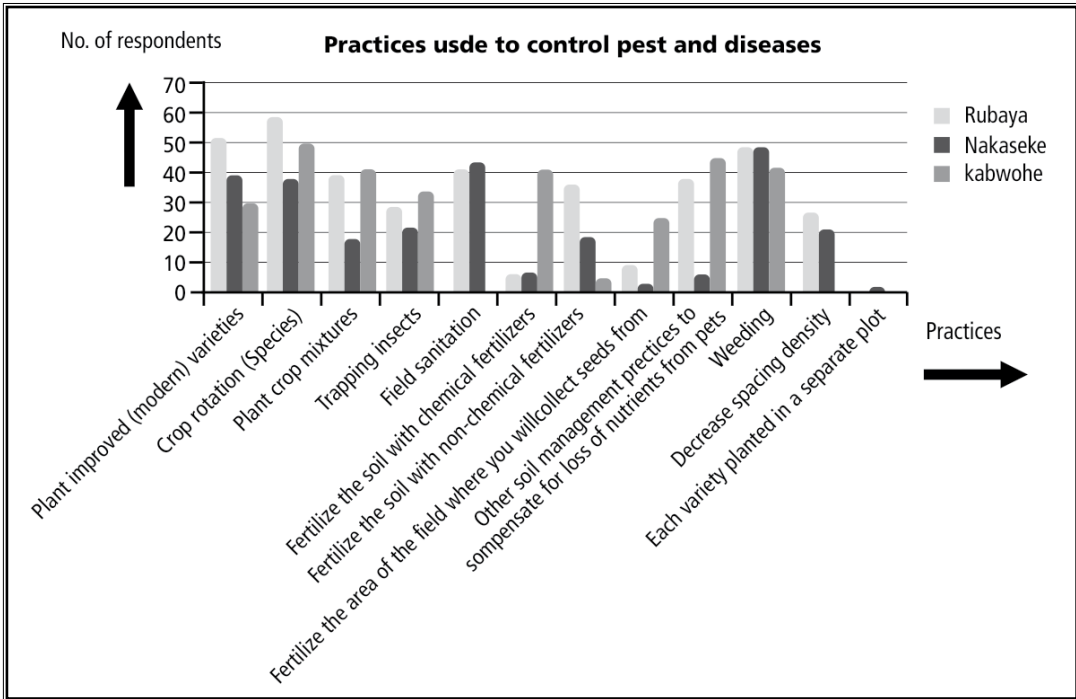


Figure 1 Practices used to control pests and diseases

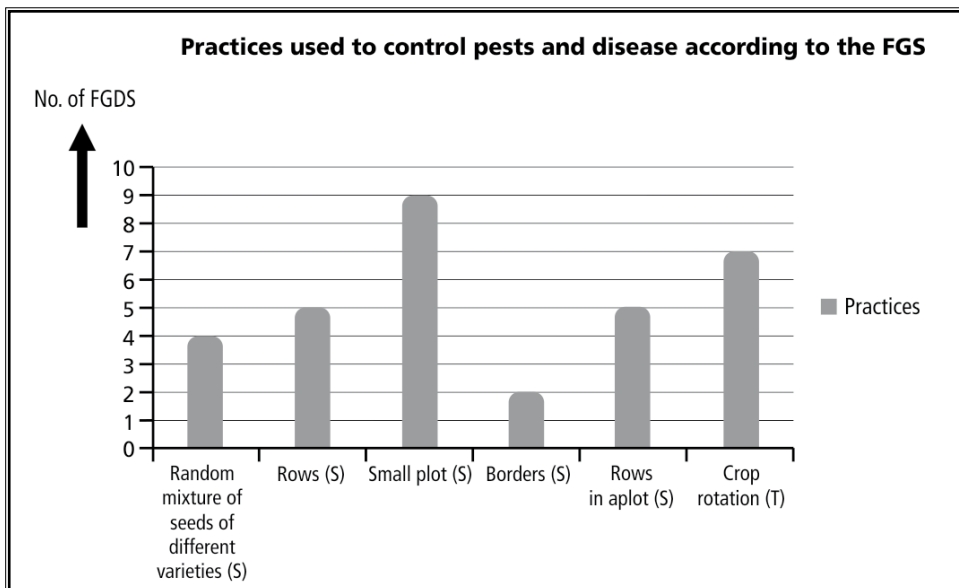


Figure 2 Practices used to control pests and diseases according to the FGS

Table 5 All the practices carried out in the study sites to control pests and diseases

Practice	% of respondents who do it in the site		
	N	R	K
a) Spatial			
Planting crop mixtures (I)	30	63	68
Planting each variety in a separate plot (I)	3	0	0
Decreasing the spacing density (I)	35	45	70
b) Temporal			
Plant improved (modern) varieties (I)	65	87	50
Crop rotation (I)	63	98	83
Scouting (trapping) insects	73	48	50
Field sanitation	73	68	0
Weeding	82	70	70
Fertilizing the soil with chemical fertilizers	68	10	0
Fertilizing the soil with non-chemical fertilizers	32	60	68
Fertilizing the area where seeds are collected	5	15	8
Other soil management practices to compensate for loss of nutrients	10	63	75

Key

N= Nakaseke site

R= Rubaya site

K= Kabwohe site

(I)= Practice uses intraspecific diversity

Table 6 Belief statements about modern and local varieties as well as mixtures

Statements	No. of respondents who agreed to different extents specified		
	N	R	K
a) Modern varieties become susceptible to diseases over time			
Strongly agreed	38	36	9
Slightly agreed	11	8	1
Undecided	4	4	31
Slightly disagreed	1	5	2
Strongly disagreed	3	7	16

Table 6. continued

Statements	No. of respondents who agreed to different extents specified		
b) Traditional varieties do not become more susceptible over time			
Strongly agreed	24	32	25
Slightly agreed	4	8	2
Undecided	3	2	10
Slightly disagreed	10	5	4
Strongly disagreed	11	13	18
c) Varieties become diseased if planted next to diseased plants			
Strongly agreed	38	37	36
Slightly agreed	14	2	3
Undecided	2	2	7
Slightly disagreed	0	4	3
Strongly disagreed	4	15	10
d) Varieties are attacked by insects more often if you grow them year after year			
Strongly agreed	45	40	26
Slightly agreed	1	3	3
Undecided	2	0	9
Slightly disagreed	2	7	4
Strongly disagreed	6	10	18
e) If you grow only one variety, you will have more insect attacks than when you grow more than one variety			
Strongly agreed	7	25	21
Slightly agreed	7	1	1
Undecided	12	2	7
Slightly disagreed	6	5	5
Strongly disagreed	25	25	25
f) Monoculture is more susceptible than mixtures			
Strongly agreed	13	0	0
Slightly agreed	2	0	0
Undecided	1	0	0
Slightly disagreed	2	0	0
Strongly disagreed	6	0	0

Table 6. continues next page

Table 6. continued

Statements	No. of respondents who agreed to different extents specified		
g) Planting more than one variety per plot gives more income			
Strongly agreed	6	15	13
Slightly agreed	3	2	0
Undecided	4	1	0
Slightly disagreed	3	2	1
Strongly disagreed	16	39	11
h) Planting more than one variety per plot is more costly than uniform planting			
Strongly agreed	0	0	0
Slightly agreed	0	0	0
Undecided	0	0	0
Slightly disagreed	0	0	0
Strongly disagreed	0	0	0

Table 7 Perceptions about use of intraspecific diversity

Belief statements	Percentages (%)				
	strongly agree	slightly agree	undecided	slightly disagree	strongly disagree
Modern varieties become susceptible to diseases over time	46.6	11.2	21.9	4.5	14.6
Traditional varieties do not become more susceptible over time	45.5	11.2	8.4	10.7	23.6
Monoculture is more susceptible than mixtures	22 (only in Nakaseke)	3	2	3	10
Planting more than one variety per plot is more costly than uniform planting	0	0	0	0	0
If you grow only one variety you will have more insect attacks than if you grow more than one variety	29.8	5.1	11.8	9	42.1
Planting more than one variety per plot gives more income.	34.3	4.5	4.5	4.5	49.4

Field resistance to rust and yield potential of common bean populations from Cotacachi and Saraguro in Ecuador

Espinoza, Í; Ochoa, J.B.

INTRODUCTION

The climbing common bean types associated with maize are very important crops grown along the highlands of Ecuador. Common bean cultivation is characterized by high intraspecific diversity. Common bean is grown in complex mixtures which appear to be associated with maintaining balance in the agro ecosystem to avoid the negative impact of biotic and abiotic stresses.

Rust caused by *Uromyces appendiculatus* (Pers.) is an important disease in common bean commercial cultivation. However, the disease is less important in the maize-common bean association, probably due to the complex mixtures farmers grow. Genetic resistance operating in these mixtures might explain the stability and the low rust epidemics in traditional agriculture.

Major and minor resistance genes have been described for *U. appendiculatus* (Stavelly, J.R., 1984; Jochua C. et al 2008; Habtu, A and Zadoks, J.C. 1995). These two types of resistance might be interacting with each other in traditional agriculture. A study to evaluate in the field the levels of resistant to *U. appendiculatus* of individual population from Cotacachi and Saraguro were conducted in Cotacachi-Imbabura.

MATERIAL AND METHODS

A representative collection of common bean populations from Cotacachi and Saraguro was studied in Cotacachi-Imbabura. The common bean populations were obtained from participatory diagnostic events and seed fairs by selecting from mixed populations seeds with similar color patterns and shapes. These phenotypic populations were evaluated in Cumbas Conde-Cotacachi in two-row plots of 3 m long with a row spacing of 0.6 m. Two seeds of common bean and two seeds of the local maize variety tzapa were planted together on the row every 0.8 m.

Disease severity (DS) of rust using the Cobb modified scale (James, W.C. 1971) was evaluated every two weeks in the selected plants. The area under disease progress curve (AUDPC) was then calculated using DS data (Shanner, G. and Finney, R.E. 1977). Yield per plant and weight of 100 seeds were evaluated in the selected plants. Yield per hectare was calculated from the yield per plant. ANOVA and mean analysis were performed using the INFOSTAT statistical program.

RESULTS

Disease parameters DS and AUDPC were not in general correlated with yield/plant, yield/ha and weight of 100 seeds. Correlation between DS x yield (+0.41) and DS x weight of 100 seeds (+0.35) for early chakra populations were the only positive correlation. Correlation between DS

and yield/plant (-0.4) for allpas was the only negative correlation observed. In general, positive correlation or the lack of correlation between disease parameters and yield parameters appear more due to differences in productivity and drought tolerance more than to the disease epidemic that long affected the study.

Differences in DS and AUDPC were high in the three types of common bean evaluated. For allpas, the DS varied greatly in terms of the absence of the disease most likely associated with major genes resistance to very susceptible populations. Partial Resistance (PR) might be present in these populations, however the levels of resistance are difficult to establish due to the presence of genes erratically expressed to a highly variable pathogen population, which was already shown in Cotacachi (Vega L and Ochoa J 2011) and in many other parts of the world (Jochua, C. et al 2008). For early chakras, three DS groups were clearly differentiated. Populations within these three groups appear similar. However, for the rest of parameters and for the phenotypic appearance of the seed, they were clearly different. For late chakras, the DS varied greatly from absence of the disease to high susceptibility. PR might be also present but difficult to establish also due to the presence of defeated genes, but also due to the lack of correlation between DS and AUDPC, which was most likely also due to the presence of genes that interfered in the development of the epidemic. Results of mixturiados from Saraguro were very similar to the chakras, showing high levels of resistance associated with major genes, but also different frequencies of intermediate to high levels of DS. The same possible epidemiological effects of defeated genes were also observed with these populations.

The DS average of allpas and early chakras were lower than late chakras and mixturiados, which might be due to the shorter cycle of these populations. The similar DS average of late chakras and mixturiados confirm the similarities of these populations; they have the same growth habit (IV) and phenotypic appearance of the seed.

Variation in disease reaction among populations of the three common bean types was also observed in other studies. High variation was observed in seedling and mixture studies (Vega l and Ochoa; Espinosa and Ochoa). However, in mixtures, the average of DS and AUDPC of the different populations of the mixtures was significantly lower than in plots in all types of common bean evaluated, which shows that the resistance of major and minor genes present in the common bean diversity complement and strengthen each other in the mixture.

Yield per plant and yield per hectare, which represent the yield potential of the common bean populations evaluated varied greatly among populations from very low to high. Yield potential of allpas varied from 102.1 kg/ha to 604 kg/ha, yield potential for early chakras varied from 47,9 kg/ha to 400 kg/ha, yield potential of late chakras varied from 29.2 kg/ha to 891.7 and yield potential of mixturiados varied from 137.5 to 670.8 kg/ha. In general, yield potential of most populations in the four types of common bean is considerably low, which was due to the drought, to which some populations were very susceptible. Some populations, on the other hand, as 1, 62, 40 and 75 of allpa, early chakras, late chakras and mixturiados respectively produced relatively high yield and can be considered resistant. Weight of 100 seeds was not correlated either with disease DS and AUDPC or with potential yield, which means that the populations develop the potential size and weight regardless of the biotic and abiotic stresses.

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Table 1. Severity and AUDPC of rust, yield per plant, yield per hectare and weight of 100 seeds of allpa populations from Cotacachi evaluated under on-farm conditions. Cotacachi, Imbabura-Ecuador.

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant (gr)	Yield/ha (kg)	Weight of 100 seeds
10	0.0a	0a	27.1ab	564.6ab	37.8ab
5	3.3ab	33a	19.6abc	408.3abc	37.3ab
3	4.0ab	80a	16.0abc	333.3abc	33.0ab
9	6.0abc	180abc	8.9bc	185.4bc	36.2ab
7	6.0abc	60a	14.2abc	295.8abc	24.4b
18	6.7abc	200abc	5.5c	114.6c	47.4ab
3.1	6.7abc	133ab	16.4abc	341.7abc	31.2ab
11	10.0abcd	167ab	16.4abc	341.7abc	48.1a
2.1	10.0abcd	200abc	15.2abc	316.7abc	40.1ab
12	10.0abcd	300abc	6.2c	129.2c	30.0ab
4	17.0abcde	510abc	5.2c	108.3c	35.0ab
2.2	18.8abcde	238abc	13.4abc	279.2abc	27.6ab
20	33.3bcde	767abc	4.9c	102.1c	31.3ab
13	36.2bcde	1088bc	6.0c	125.0c	30.6ab
4.1	45.0cde	1425c	5.7c	118.7c	35.0ab
6	56.7de	933abc	13.6abc	283.3abc	24.7ab
1	56.7de	700abc	29.0a	604.2 a	37.9ab
17	62.5e	1350bc	14.5abc	302.1abc	29.5ab
Average	21.6	464.7	13.2	275.2	34.3

¹Cobb modified scale 0-100 (James, W.C. 1971). Evaluated at R7 growth stage.

²Arean Under Disease Progress Curve. Calculated using the values of DS (Shaner, G.. and Finney R.E. 1977)

³ Yield potential: Calculated using plant/yield grown in an area of 0.48 m²

Table 2. Severity and AUDPC of rust, yield per plant, yield per hectare and weight of 100 seeds of early chakra populations from Cotacachi evaluated under on-farm conditions. Cotacachi, Imbabura, Ecuador.

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant	Yield/ha	100 seeds weight
22.1	10	300	2.3b	47.9b	28.4b
44	10	350	5.9b	122.9b	29.6ab
27.1	21.7	642	5.6b	116.7b	36.4ab
36	21.7	575	8.1ab	168.7ab	49.7ab
57	21.7	725	10.5ab	218.7ab	40.8ab
34	21.7	758	6.6b	137.5b	55.7a
62	45.0	1094	19.2a	400.0a	36.0ab
28.1	45.0	1458	5.3b	110.4b	45.2ab
32	45.0	1341	6.9b	143.7b	51.9ab
38.2	45.0	1458	6.4b	133.3b	38.0ab
Average	28.7	870.2	7.7	160.0	41.2

¹Cobb modified scale 0-100 (James, W.C. 1971). Evaluated at R7 growth stage.

²Area Under Disease Progress Curve. Calculated using the values of DS (Shaner, G.. and Finney R.E. 1977)

³ Yield potential: Calculated using plant/yard grown in an area of 0.48 m²

Table 3. Severity and AUDPC of rust, yield per plant, yield per hectare and weight of 100 seeds of late chakras populations from Cotacachi evaluated under on-farm conditions. Cotacachi, Imbabura, Ecuador.

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant	Yield/ha ³	100 seeds weight
40	0.0a	0a	42.8 ^a	891.7 a	52.8abc
26	2.5a	62ab	10.8bcd	225.0bcd	49.7abc
48.1	5.0ab	175a-e	9.8bcd	204.2bcd	43.9abc
62.1	5.0ab	175a-e	7.7bcd	160.4bcd	34.3c
72	5.0ab	125abc	10.1bcd	210.4bcd	54.2abc
29	5.0ab	175a-e	21.2abcd	441.7abcd	47.1abc
43	6.0abc	150abcd	21.4abcd	445.8abcd	51.8abc
55	6.7abcd	200a-f	14.4bcd	300.0bcd	37.9bc
65.1	15.0a-e	525a-g	9.8bcd	204.2bcd	46.8abc
37	10.0a-f	350a-h	19.5abcd	406.2abcd	38.6bc

Table 3. continued

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant	Yield/ha ³	100 seeds weight
49	10.0a-f	325a-g	28.7abc	597.9abc	52.3abc
52	10.0a-f	350a-h	21.7abcd	452.1abcd	54.2abc
29.1	16.2a-g	519a-g	16.4abcd	341.7abcd	50.7abc
58.1	22.5a-h	700a-i	9.1bcd	189.6bcd	46.3abc
71	22.5a-h	612a-h	3.8cd	79.2cd	51.9abc
30.1	18.75a-i	631a-j	16.0bcd	333.3bcd	41.8bc
67.1	21.67a-j	758a-j	8.7bcd	181.2bcd	43.5abc
45	21.67a-j	438a-i	22.0abcd	458.3abcd	62.2ab
35	21.67a-j	758a-j	13.1bcd	272.9bcd	50.8abc
64	27.5a-j	962a-j	9.4bcd	195.8bcd	44.0abc
30	27.5a-j	875a-j	18.0abcd	375.0abcd	52.2abc
25	36.25a-j	1028a-j	22.1abcd	460.4abcd	43.7abc
39	45.0b-j	1488d-j	4.0cd	83.3cd	39.7bc
67	52.0b-j	1558e-j	7.0cd	145.8cd	39.3bc
33	52.0b-j	1364c-j	3.8cd	79.2cd	39.4bc
28	52.0b-j	1750g-j	12.0bcd	250.0bcd	63.3ab
56	53.8c-j	1641f-j	4.0cd	83.3cd	38.6bc
38.1	53.8c-j	1466d-j	10.1bcd	210.4bcd	44.2abc
73	53.8c-j	1706g-j	7.7bcd	160.4bcd	61.8ab
46	56.7d-j	1750g-j	13.2bcd	275.0bcd	50.4abc
46.1	59.0e-j	1680g-j	6.1cd	127.1cd	50.4abc
41	62.5f-j	1838g-j	1.4d	29.2d	38.5bc
70	62.5f-j	1531e-j	6.5cd	135.4cd	50.6abc
50	62.5f-j	1619f-j	8.7bcd	181.2bcd	53.1abc
54	62.5f-j	1706g-j	7.1cd	150.0cd	39.0bc
48	66.0f-j	1715g-j	15.0bcd	312.5bcd	49.4abc
53	66.0f-j	1260b-j	8.1bcd	168.7bcd	31.4c
38	68.3g-j	1429c-j	23.6abcd	491.7abcd	49.2abc
21	68.3g-j	2042hij	14.5bcd	302.1bcd	67.3 a
23	68.3g-j	2275j	2.7cd	56.2cd	63.3ab
65	71.2hij	1838g-j	10.3bcd	214.6bcd	55.0abc
47	71.2hij	2144ij	5.3cd	110.4cd	39.3bc
22	71.2hij	1684g-j	8.9bcd	185.4bcd	34.4c
24	73.0ij	1695f-j	9.9bcd	206.2bcd	38.6bc

Table 3. continues next page

Table 3. continued

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant	Yield/ha ³	100 seeds weight
42	73.0ij	1870g-j	8.1bcd	168.7bcd	46.5abc
31	80.0j	1079a-j	14.9bcd	310.4bcd	50.6abc
50.1	80.0j	1181b-j	10.4bcd	216.7bcd	53.1abc
51	80.0j	2144ij	7.8bcd	162.5bcd	53.3abc
27	80.0j	875a-j	33.7ab	702.1ab	45.8abc
Average	42.1	1106.6	12.7	264.2	47.7

¹Cobb modified scale 0-100 (James, W.C. 1971). Evaluated at R7 growth stage.

²Area Under Disease Progress Curve. Calculated using the values of DS (Shaner, G.. and Finney R.E. 1977)

³Yield potential: Calculated using plant/yield grown in an area of 0.48 m²

Table 4. Severity and AUDPC of rust, yield per plant and weight of 100 seeds of mixturiados from Saraguro evaluated under on-farm conditions. Cotacachi, Imbabura, Ecuador.

Genotypes	Severity rust ¹	AUDPC ²	Yield/plant	Yield/ha ³	weight100 seeds (gr)
88	0.0a	0a	6.6b	137.5b	41.8bc
75	0.0a	0a	43.5a	906.2a	49.4b
79	10.0ab	317ab	10.5ab	218.7ab	45.8bc
75.1	10.0ab	350bc	17.7ab	368.7ab	74.5a
85	10.0ab	350bc	17.0ab	354.2ab	31.6c
74	36.2bc	547bcd	32.2ab	670.8ab	41.9bc
77	38.0bc	1260de	14.1ab	293.7ab	35.0bc
81	45.0bc	1400de	20.7ab	431.2ab	40.2bc
76	52.0bc	665bcd	19.9ab	414.6ab	44.7bc
86	62.5c	1225cde	14.0ab	291.7ab	49.0b
78	66.0c	1208cde	14.5ab	302.1ab	34.4bc
80	68.3c	1750e	20.8ab	433.3ab	42.3bc
84	80.0c	1079cde	24.2ab	504.2ab	41.8bc
82	80.0c	1838e	28.9ab	602.1ab	49.3b
83	80.0c	875b-e	3.6b	75.0b	45.7bc
Average	42.5	857.6	19.2	400.3	44.5

¹Cobb modified scale 0-100 (James, W.C. 1971). Evaluated at R7 growth stage.

²Area Under Disease Progress Curve. Calculated using the values of DS (Shaner, G.. and Finney R.E. 1977)

³Yield potential: Calculated using plant/yield grown in an area of 0.48 m²

Quantifying genetic diversity management choices made by farmers to manage pests and diseases in China

Yang Yayun,; Yu Tengqiong; He Chenxing,; Zhao Zixian; Tang Zhiming; Xu Furong; Dai Luyuan.

INTRODUCTION:

Genetic diversity management choices are defined practices that affect the evolution of crop populations with respect to pest and disease management. They consist of: (i) spatial/temporal arrangements and (ii) selection of and access to planting materials (root material, mother plants, grafted materials). According FGDs and HH surveys, we sought to determine that how farmers in Xiding township use genetic diversity management choices to control pests and diseases of rice and maize.

METHODS:

Seventy households (out of 77 HHs in Xiding Township) that planted maize were investigated in FGDs, while another seven HHs that planted crops other than maize were examined through a HH survey.

Genetic diversity management choices by farmers were determined mainly through quantifying the responses to questions in FGDs and the HH survey.

RESULTS:

The households studied were rich in rice varieties (11 local and 8 modern) and maize varieties (5 local and 3 modern). The five local rice varieties were: Amoque, Paozhugu, Qiebajia, Qiexiu, Qieshu, Qiege, Meleng, Zhangmeleng, Molong, Kaodelong, Duolong, Kejialeng, Abie, Molao, Moduleng And Abai. The modern rice varieties were Gangyou12 and Luyin 46. The varieties of local maize included Selileng, Selebai, Seleleng, Aduxiu and Selile, while three modern maize varieties were Zajiao, Zhengda 615, Zhangda819.

In spatial arrangements of rice, the attitude of farmer to disease was important. In response to questions regarding whether a farmer's field had the same disease damage as a neighbor's field, 90.9% HHs said "yes". With regard to disease damage (or disease/pest attacks) in crops planted in different plots, 77.92% HHs replied that there are no differences. From the first planting of varieties by farmers, intervening years varying by rainfall and temperature made little overall difference in resistance of maize varieties, with farmers noting that resistance remained unchanged in comparison with the first years. No differences were noted between resistance in modern and local rice varieties on a temporal scale. In spatial arrangements of maize, 87.14% of farming HH heads said that disease damage in their fields was similar to that in neighbours' fields and 75.71%

of HH heads found no differences in planted crop damage (or incidence of disease/pest attacks) in different plots. In selection of and access to planting rice materials, 59 (77.62%) of the HH respondents used seed sanitation (cleaning the seeds by taking out unhealthy seeds), 65 (84.41%) of HH respondents put importance on good seed storage conditions (containers, rooms that are resistant to pest and diseases) and 57 (74.03%) HH respondents selected healthy seeds to conserve and plant.

For maize, farmers selected planting material for the following season from the maize population in a fertile field (25.58% of HH respondents), from healthy populations from a field with few pests/diseases (55.74% of HH respondents) (Fig.1), from seeds obtained through plant selection (79.1% of HH respondents), through spike selection (26.68% of HH respondents), through selecting seeds from healthy plants (23.37%), selecting mature seed (63.63%), and selecting seeds during the drying process (44.16%).

In post-harvest methods for selecting seeds, most farmers threshed seeds, dried them to discourage pests, and identified specific storage locations such as garages (Fig 2). As for specific seed containers, 17 HHs used bags. Three HHS used bamboo matting for drying the seeds. Seven HHs used dustpan to remove husks, others used fans or windmills to select healthy seeds. The source of seed was 100% from self-saved seeds. Male heads of HHs played important roles in managing rice varieties (Table.1).The farmer used the same methods for managing pests and diseases for both rice and maize. (Fig.3,4, Table2, detail in presentation).

DISCUSSION:

The local rice and maize varieties in Xiding were rich, with many varieties planted for over 70 years, many for hundreds of years, and all these seeds were from the farmers themselves. In managing pest and disease prevention, the farmers practiced IPM strategies even though they did not know the theory behind them. From this article, farmer often choose the health plants and seeds to plant and conserve, and selected seeds during the maturity and drying stages. Male HH heads played important roles in managing varieties. Half of the HHs questioned knew how to

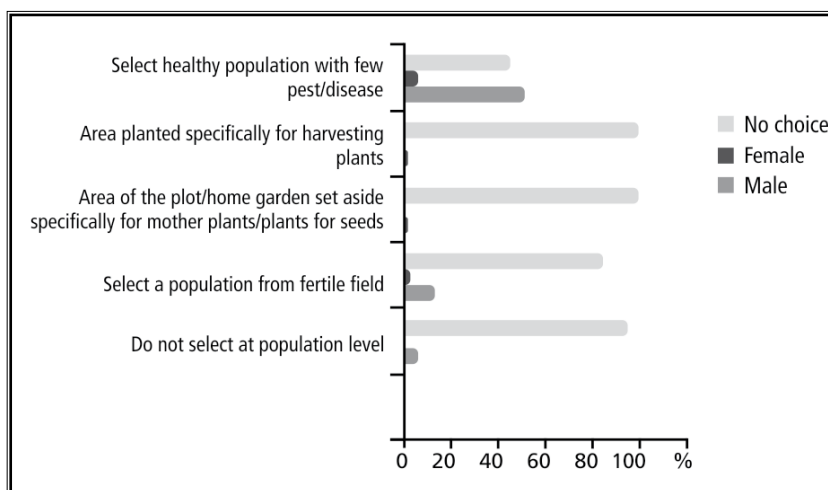


Figure1 Seeds selected from particular plots or areas of the plots (Rice)

practice genetic diversity management to control the diseases and pests in rice and maize, using traditional knowledge from past generations that have planted local varieties for a considerable time. More research is needed on methods used that are consistent with general IPM strategies.

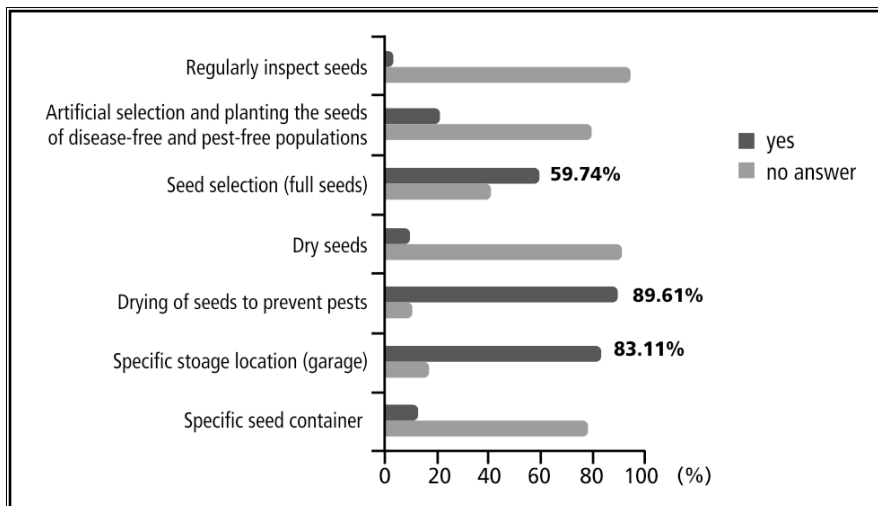


Figure 2 Post harvest methods for selecting seeds (Rice)

Table 1 The role of male heads of HHs in post harvest methods for selecting seeds (Rice)

Respondents	Specific storage location	Drying seeds to prevent pests	Dry seeds	Seed selection (full seeds)	Seed selection and planting disease-free and insect-free seeds
Male head of HH	15.58%	25.97%	1.30%	6.49%	3.90%
Female head of HH	5.19%	11.69%	1.30%	12.99%	2.60%
Self	10.38%	53.25%	6.49%	22.08%	14.29%
No answer	68.85%	9.09%	90.91%	58.44%	79.21%

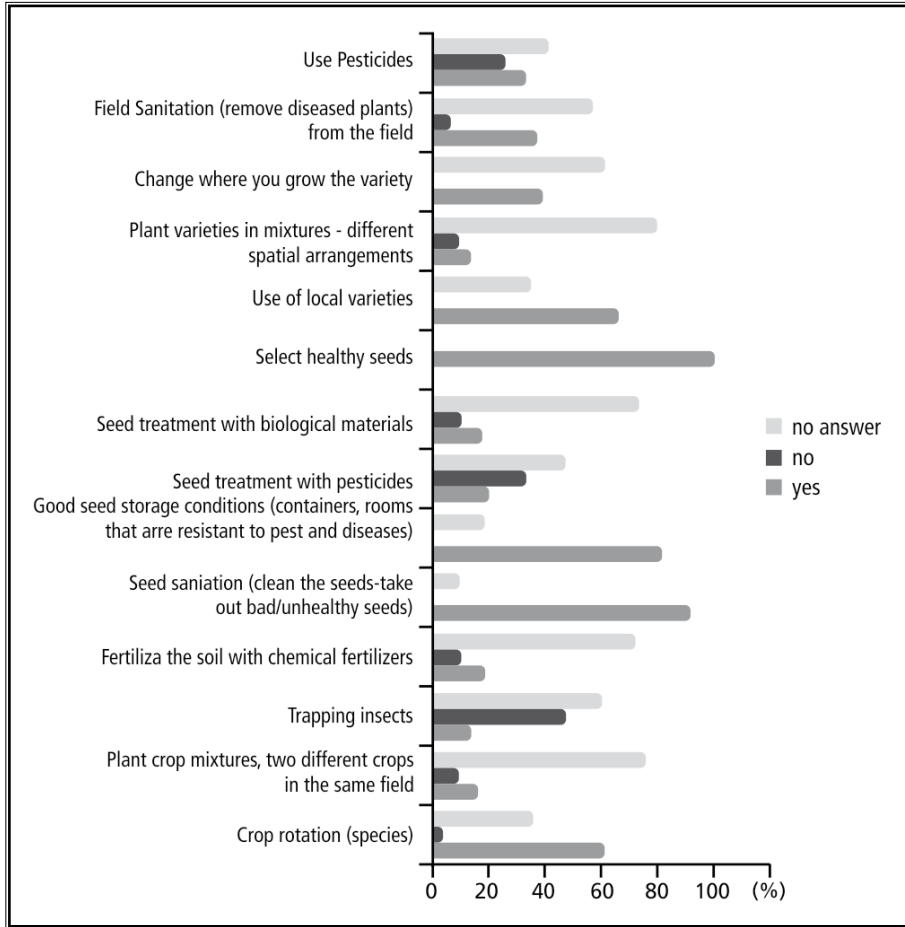


Figure 3 Methods to control pest and disease (Maize)

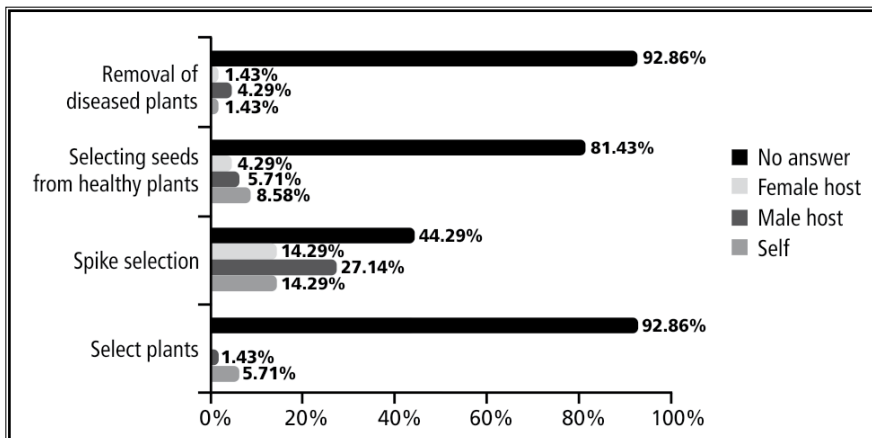


Figure 4 Selection of plants or parts of plants (Maize)

Table 2 The role of Male host of HH in post harvest methods for selecting seeds (Maize)

People	Specific storage location	Dry seed (prevent the pests)	Removal of empty seed	Artificial selection and planting the seeds
Self	45.71%	48.57%	5.71%	11.43%
male host	22.86%	21.43%	8.57%	10.00%
hostess	1.43%	17.14%	17.14%	1.43%
No answer	30%	12.96%	68.68%	77.14%

Management practices of farmers in the project sites using faba bean and barley diversity

Belqadi, L.; Ezzahiri, B.; Taoufiqi, S; Sadiki, M.

INTRODUCTION

Over time, the farmers of the Taounate region developed a body of local knowledge concerning the management of faba bean and barley diversity. A key objective of the work reported here is to understand farmers' practices for using diversity to control pests and diseases.

MATERIAL AND METHODS

In order to analyze these practices for two species, individual surveys were conducted with farmers of three communities: Ourtzagh, Galaz and Tissa.

On hundred seventy three farmers were surveyed on the following aspects:

- Spatial distribution of the varieties in the same plot
- Temporal distribution of the varieties
- Change of seed
- Change of crops in time
- Methods of pest and disease control
- Selection of genetic material for the next season

RESULTS AND DISCUSSION

1) Spatial distribution of the varieties in the same plot: The majority of farmers (more than 90 %) cultivate only one variety of faba bean and barley per plot (Figure 1). The varietal mixture is more frequent for the faba bean crop than for barley in the three sites. Moreover, there is a clear difference in the motives behind the arrangement of several varieties in the same plot by the farmers who practice the varieties mixture for the two crops. This difference is noted both among and within sites. Non-intentional mixtures of the seed, in particular at during harvest and storage operations as well as in the local markets, are frequent.

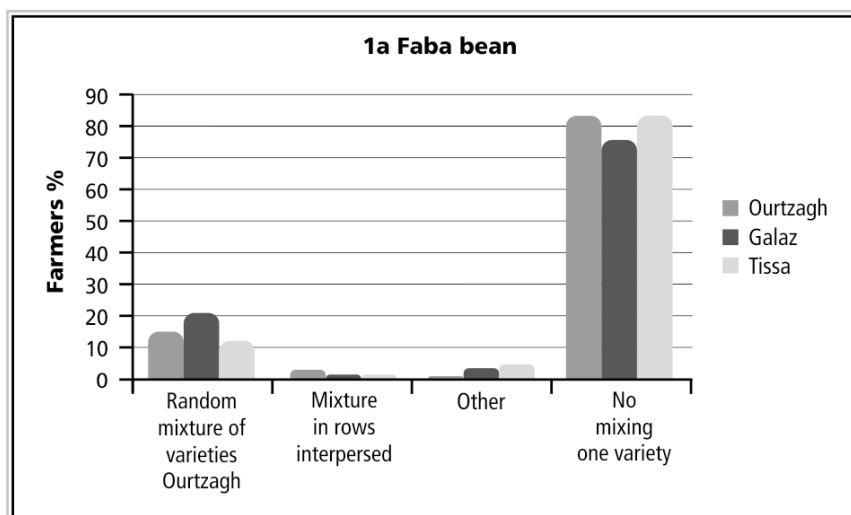
2) Temporal distribution of the varieties: Many reasons were advanced by the farmers to explain the change of the varieties over time (Fig. 2). These reasons reflect unconscious strategies to maintain all the diversity of the genetic material and to introduce new material which can create more genetic diversity for these two species. These reasons are much more important for faba bean than for barley.

3) Change of the seed: More than half of the farmers surveyed do not adopt in their strategies of production the renewal of their seeds, although the majority of these farmers are conscious of the impact of the seed change on the yield, except in the cases of an exhaustion total of seeds. Among farmers who renew their seeds, the most frequent period of renewal ranges between two and four years. The main reasons for change of seeds are: increase in the yield, exhaustion of stock, loss of the germination capacity and the mixture of seeds.

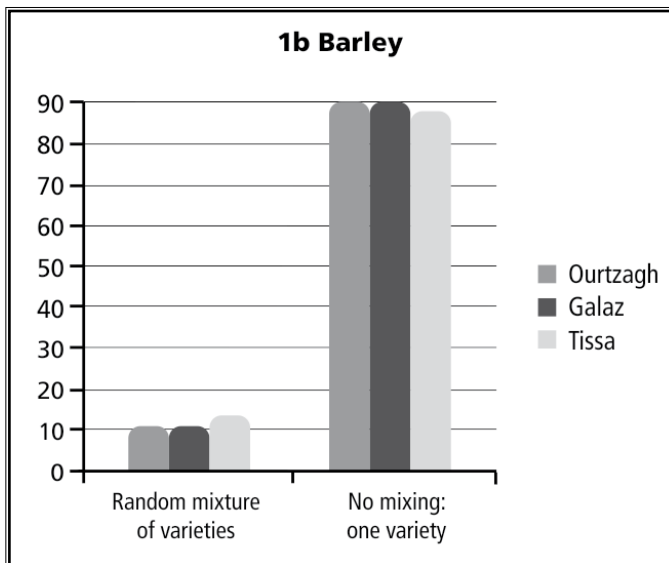
4) Change of the crops in time: All of the farmers surveyed in the three sites change crops in time and advance a number of reasons for doing so which differ between the sites. The farmers are conscious that the change of the crops over time is one of the key factors in obtaining a better yield (Tables 1 & 2).

5) Methods of pest and disease control: The farmers are conscious of control of the pest and diseases not only by application of fertilizers and pesticides but also by using various additional methods, among which crop rotation for faba bean and barley (Figure 3).

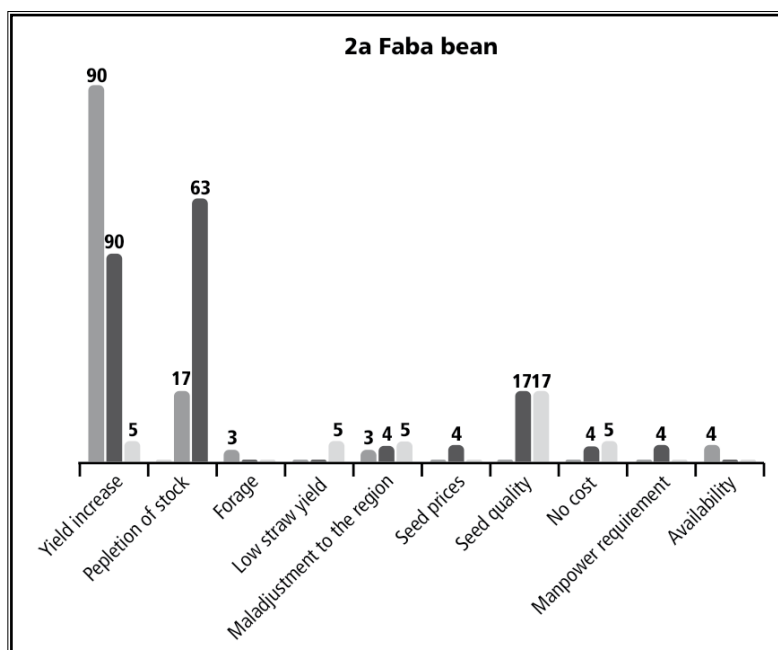
6) Selection of the genetic material for the next season: The various practices of seed selection were analyzed. For faba bean, the selection of seed is practiced and developed compared to barley seed selection. The selection of plots is practiced by a minority of farmers (2 to 4%) among those who practice selection; the overwhelming majority of farmers at Ourtzagh site practice selection by planting faba bean in a specific plot. In Galaz, 11 % of faba bean farmers practice selection on the basis of the best plot on which the seeds will be collected for faba bean as do 12 % of the barley farmers. The results showed that the farmers estimate that when the production of seeds is intended for animal feed, seed selection is an unnecessary step.



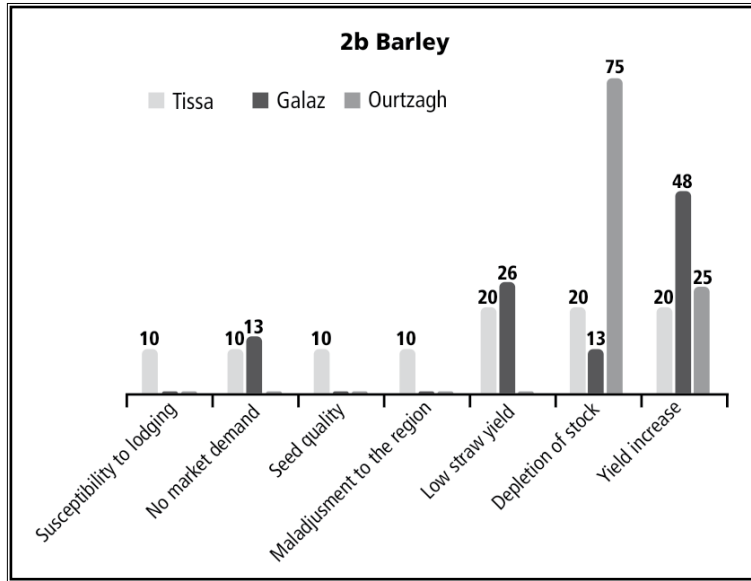
Figures 1a and 1b: Percentage of farmers according to the arrangement of the different methods of mixing varieties in one plot



Figures 1a and 1b: Percentage of farmers according to the arrangement of the different methods of mixing varieties in one plot



Figures 2a and 2b: The reasons adopted by farmers to justify the change of varieties over time



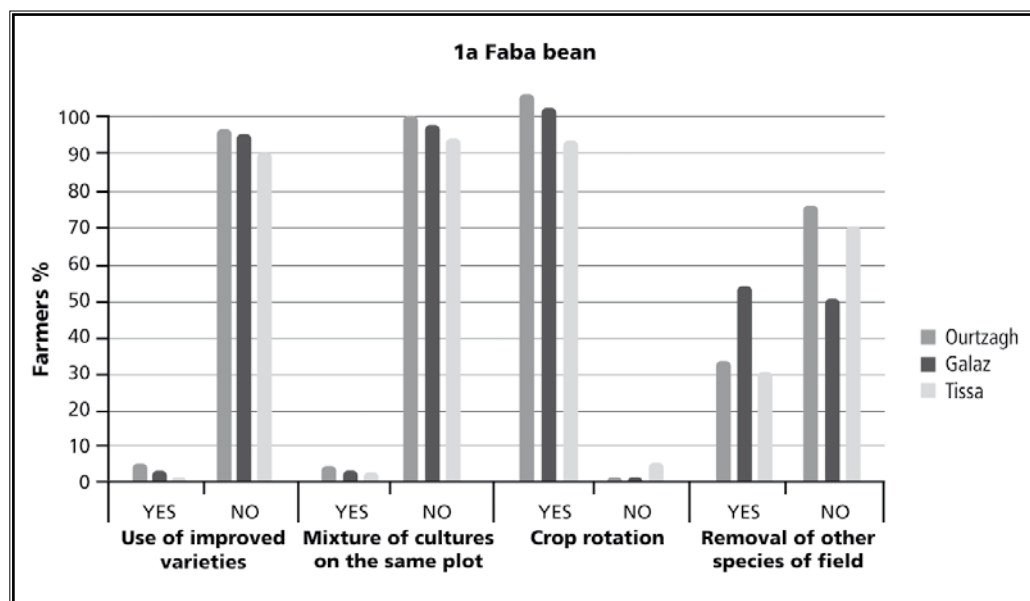
Figures 2a and 2b: The reasons adopted by farmers to justify the change of varieties over time

Table 1: Reasons for changing the allocation of different crop to plots: Faba bean

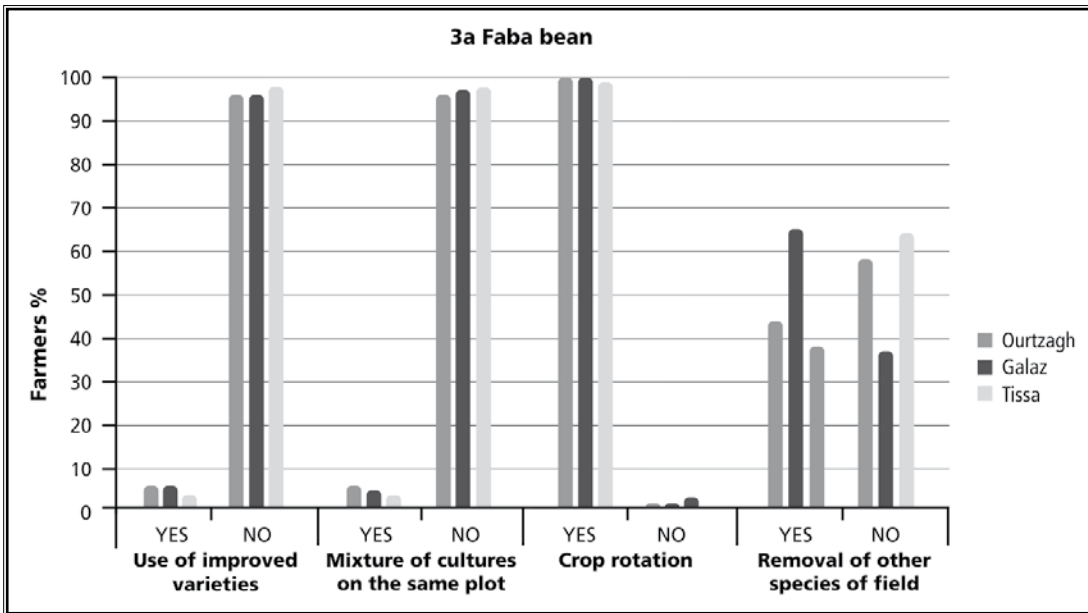
Faba bean	Percentage of farmers (%)		
	Ourtzagh	Galaz	Tissa
Yield increase	23	5	-
Rotation	11	44	56
Animal feed	1	-	-
Disease control	1	-	-
Weed control	64	-	-
Maintaining soil fertility	-	8	10
Tillage, disease control and weed	-	1	-
Yield increase and rotation	-	7	13
Yield increase and maintaining soil fertility	-	-	6
Rotation and disease control	-	-	5
Yield increase, rotation and disease control	-	14	8
Rotation, maintaining soil fertility and disease control	-	21	2
Total	100	100	100

Table 2: Reasons for changing the allocation of different crop to plots: barley

Barley	Percentage of farmers (%)		
	Ourtzagh	Galaz	Tissa
Yield increase	22	5	-
Rotation	10	44	56
Animal feed	1	-	-
Disease control	1	-	-
Weed control	66	-	-
Maintaining soil fertility	-	8	10
Tillage, disease control and weed	-	1	-
Yield increase and rotation	-	7	13
Yield increase and maintaining soil fertility	-	-	6
Rotation and disease control	-	-	5
Yield increase, rotation and disease control	-	14	8
Rotation, maintaining soil fertility and disease control	-	21	2
Total	100	100	100



Figures 3a and 3b: Methods for controlling pests and diseases



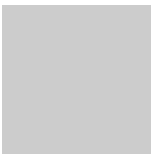
Figures 3a and 3b: Methods for controlling pests and diseases



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION-6



Seed systems - maintaining diversity and
reducing vulnerability

Seed systems, genetic vulnerability and disease movement in Ecuador

Saavedra, E.; Pillaluisa, L.P.; Pazmiño, J.; Ochoa, J.B.

INTRODUCTION

Traditional seed systems have been maintained for generations in Cotacachi. Plants are not selected in the fields, but selection begins at different stages of the crop's growth cycle. To obtain seed for the next season's planting, 65% of farmers select seed during the ripening stage and 35% during harvesting.

MATERIAL AND METHODS

During this investigation of seed systems, information was gathered from five focus group discussions in Cotacachi and Saraguro, as well as from household surveys. In the two sites of Cotacachi and Saraguro, 60 households were selected randomly.

RESULTS

Information gathered in the field from the household surveys and focus group discussions was analyzed. Results showed a variety of criteria were used for seed selection (Table 1); the seed selection procedure is summarized in Table 2. The changes in resistance noted are given in Table 3, while the many sources of seed are listed in Table 4 and in Figures 1 and 2.

Table 1 Seed selection criteria

Criteria for choosing high quality seed	Percentage
Select big seeds (includes: large, big ears, large grain, clean corm)	87
Planting only healthy seeds (includes: no pits, no insect larvae, no holes, no spots, healthy appearance)	78
Selection (they did not explain what is selection)	43
Choice uniform seed (including varietal uniformity)	25
Select seed with normal colour (includes: uniform colour for the crop, no discoloration)	18
Planting only seeds with medium size	5

Table 2 Post-harvest seed selection

Post harvest seed selection process	Percentage
Specific storage location	90
No seed treatment at harvesting	75
No seed treatment at storage	45
No specific seed container	32
Seed treatment with ash and herbs	17
Storage in any house place	13
Seed treatment with pesticides	5

Table 3 Changes in resistance

Variety name	Lancha	Patajuro	Kutzo	Pata kuru verde	Redondilla	Pudrición mazorca	Change in resistance	Why
Chaucha	3	2			2		EQUAL	No changes in resistance. All are susceptible
Guandango	2	4	4	3	3	2	EQUAL	
Iruticos	2	4	4	3	3	2	EQUAL	
Killu Sara	2	3	4	3	3	2	EQUAL	
PUKAS	2	3	4	3	3	2	EQUAL	
Morochos	2	5	4	3	4	1	EQUAL	
Tzapas	3	3	4	3	2	3	LESS	Changes in resistance. Less
Yana sara	2	3			3	1	LESS	New damage, probably new diseases
Yura Sara	2	2	4	3	2	3	LESS	White maize is always weak (susceptible to everything)
Chulpi	2	3	4	3	3	4	LESS	Currently susceptible, previously resistant

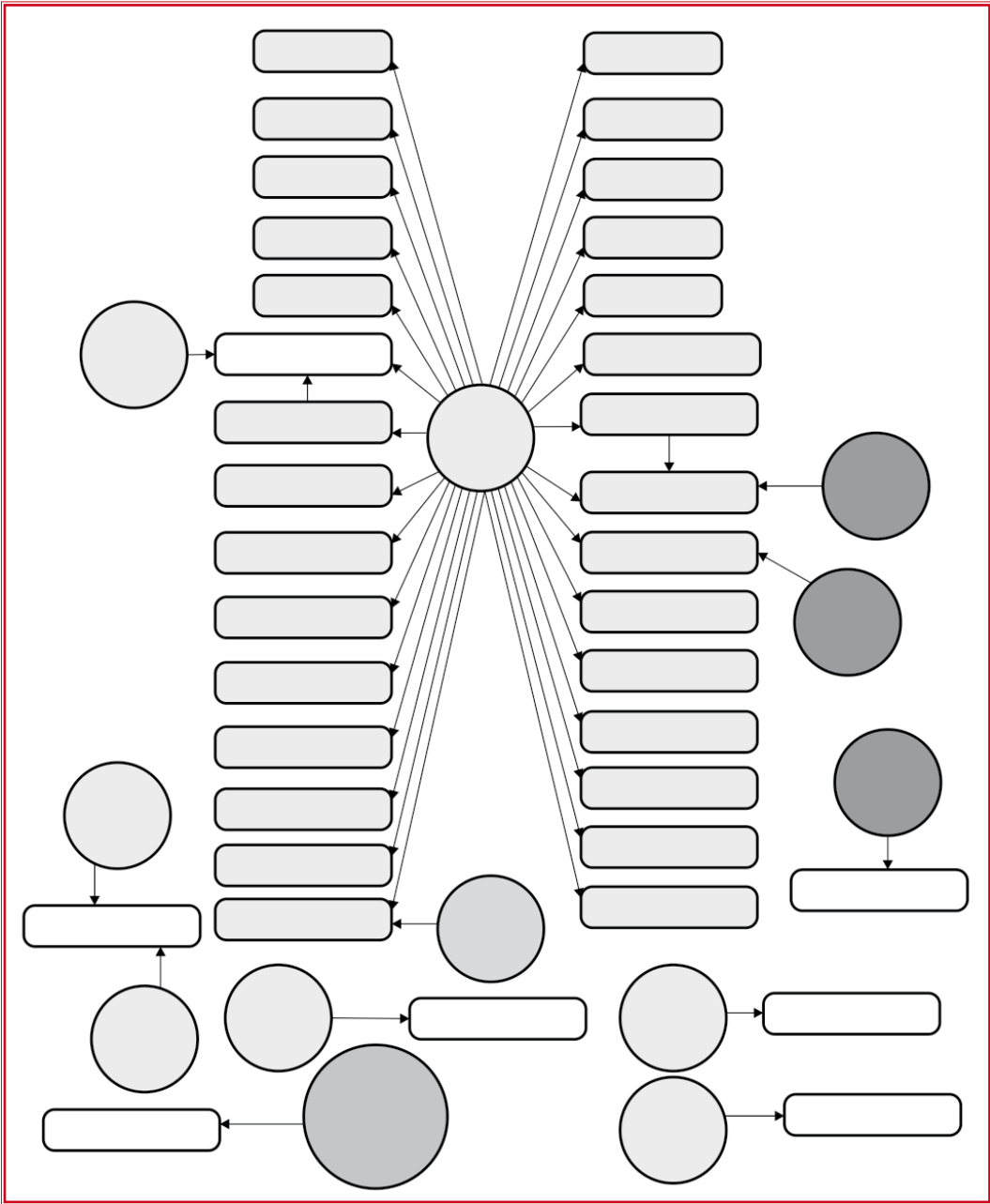


Figure 1 Flow of maize seed in Cotacachi

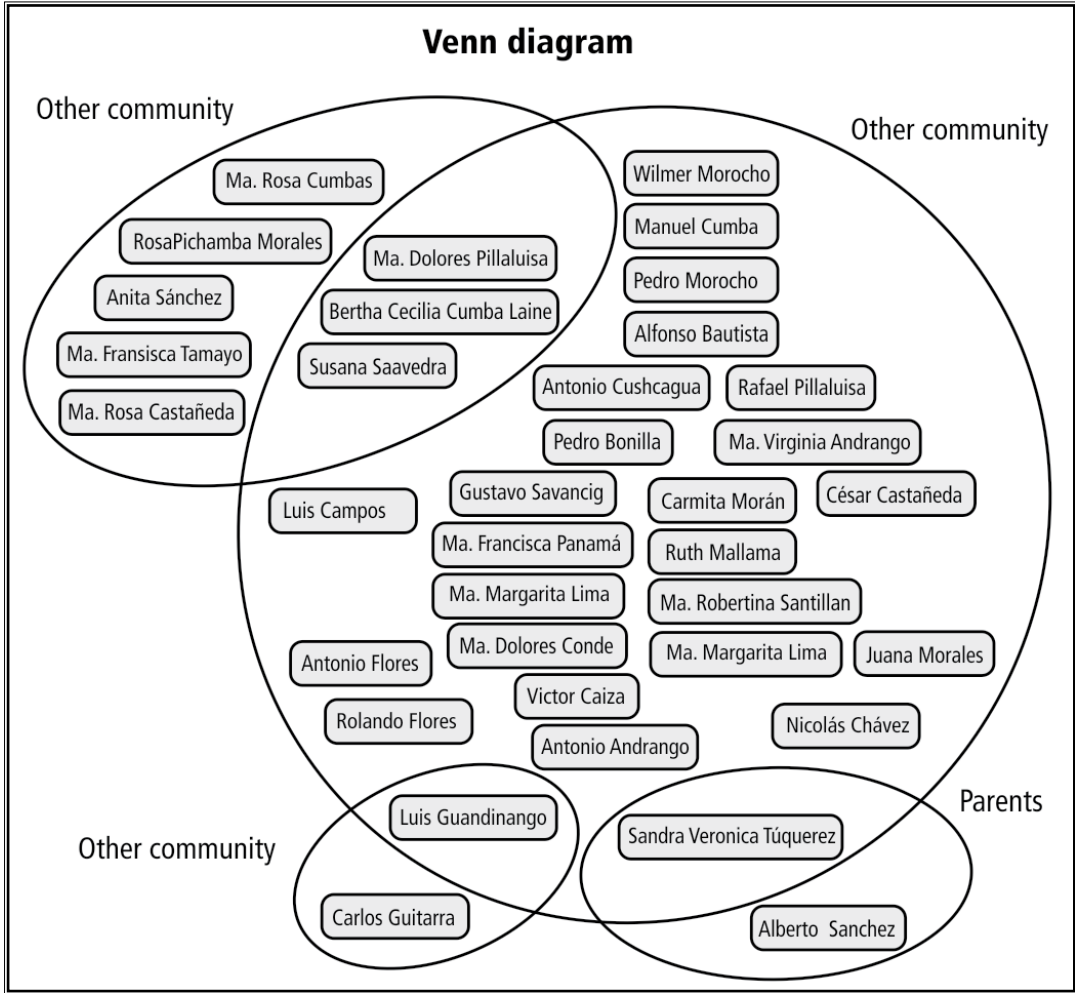


Figure 2 Sources of seeds

Table 4 Results of Seed Source in HH survey

Seed Source	Frequency	Percentage
Self	24	39%
Parents	11	18%
Seed company	5	8%
Neighbour	4	7%
Self and relatives outside the village	2	3%
Self and seed company	2	3%
Local agricultural extension	1	2%
Parents and non-local market	1	2%
Relatives outside the village and seed company-	1	2%
Seed company and parents	1	2%
Self and local agricultural extension	1	2%
Self and neighbor	1	2%
Self and parents	1	2%
Self and parents and local agricultural extension	1	2%
Self and gifts	1	2%
Self and relative in the village	1	2%
Self and seed company & friends outside the village	1	2%
Self and seed company and parents and gifts	1	2%
Very local market	1	2%

Seed systems, genetic vulnerability and disease movement in Uganda

Nankya, R.; Kizwuka, C.; Adokorach, J.; Mulumba, J.W.

INTRODUCTION

In many countries, traditional crop varieties also known as landraces or farmers' varieties contribute significantly to sustainable food production, household nutrition and farmers' incomes. Farmers have traditionally depended upon their own skills and resources to develop the crops that they need. The result has been a complex and continually evolving collection of local crop varieties (landraces) that reflect interactions with wild species, adaptations to changing farming conditions and responses to the economic and cultural factors that shape farmers' priorities. This richness and range of diversity is now under threat because of the changing nature of agricultural production. There are quite a number of factors contributing to this change some of which include the widespread adoption of modern varieties that are products of formal plant breeding, technology change and market-oriented farm production, making farmers less inclined to select for crop characteristics that were once important for local customs and culture (Tripp R. and Wieneke H., 1996).

Plant germplasm is among the most essential of the world's natural resources. Many interventions try to address farmers' seed insecurity although few assess the causes of the genetic vulnerability or understand the farmers' coping strategies. Farmers are the major source of seed in most countries, with the formal seed supply particularly weak in high stress areas. It follows those farmers' seed systems, their saving, selection and exchange practices, associated knowledge and social relationships, are at the heart of strategies for coping with stress. Improved understanding of farmers' vulnerability can assist interventions that support seed systems (McGuire S. J., 2001). In order to understand the common bean seed systems and the associated vulnerability, if any, this study was carried out in three sites in Uganda namely; Nakaseke, Kabwohe and Rubaya.

METHODS

The data on seed systems were collected using participatory diagnostic methods which included focus group discussions and household surveys. Fifteen focus group discussions, five per site, were conducted. The focus group discussions targeted groups of leaders, young men, young women, old men and old women in each site. Each of the groups had a minimum of 10 people. A total of 160 farmers purposely selected to represent the whole target community participated in the focus group discussions. All the farmers who participated in the focus group discussions were from the target villages and had to be growing common bean. Farmers aged 30 and below were the young farmers while those above 30 years old were the old farmers. While in these groups, farmers were asked similar questions common bean seed systems. In the household surveys, 60

households growing common bean per site were selected randomly. Cluster sampling by village was used to ensure geographic representation across the four target villages per site, representing the whole community. The selected farmers were interviewed using a questionnaire and a deliberate effort was made to ensure that both male and female farmers were involved in equal numbers. In all, 180 bean farmers were interviewed. Individually, farmers were asked about the common bean seed systems.

In order to relate the bean seed systems to the diversity and diseases situation on-farm, the name and number of *P.vulgaris* varieties, their area of coverage and disease severity on-farm were recorded from each household. Disease severity was estimated from 30 different points on a farmers' field by assessing three plants front, left and right. The plants were assessed basing on a scale of 1 for low, 2 for moderate and 3 for high severity. The household weighted disease index (WDI) was estimated from the product of the disease index (at the plot level) and the frequency of each variety present in the plot weighed by the percent area covered for each variety at household level. Average farm richness was calculated as the average number of varieties per household. Following Magurran (2003), evenness was estimated as a complement of d ($1-D$), where D is the Simpson measure of dominance. The data was encoded in Excel and analyzed using descriptive statistics to produce tables and charts that showed emerging trends and patterns. The relationship between seed systems and diversity measures as well as damage indices on-farm was estimated by correlation and regression analysis.

RESULTS

Seed selection: Farmers in the study sites considered mainly four factors when selecting seed: area of the plot, plants or parts of plants, post-harvest handling and nature/condition of seed. Selection by area was generally not popular and was practiced most in Nakaseke, followed by Rubaya and not at all in Kabwohe. Selection by plant or part of plant was only practiced in Nakaseke. The most popular post-harvest handling methods included: having specific location for storage, storing in a specific seeds container, treating seeds with local products which are not chemicals, preparing storage facilities, not treating seeds at all and treating seeds with pesticides, although many more practices are carried out (fig 6). Selecting seed according to the nature/condition of seed was what the respondents considered to be the most important criteria. The highly considered criteria under nature of seed was the health of seed (no tunnels/holes, no spots etc), followed by normal colour (uniform colour, standard colour, no discolouration) and big seed (Table 3, Figure 5). The correlation between the number of seed selection criteria used at household level and the diversity estimates (richness and evenness at household level) as well as between the weighted damage indices for Anthracnose and Angular Leaf Spot were all weak and not statistically significant (Table 1).

Seed sources: There were formal and informal seed sources where farmers get most seed from the informal sources. The informal seed sources were self, neighbours and local markets, while the formal seed sources were seed companies, local agriculture extension, NGOs and farmers' associations. Most of the seed was self-provided, followed by that obtained from neighbours, non-local markets and local markets. Other sources are shown in Figure 1. However, respondents got seed from more than one source as indicated in the Venn diagram (Fig. 2) and there was a lot of seed interchange amongst farmers in the villages (figure 3) and in the community in general. The correlation between the quantity of seed from the local market and the weighted damage index for Anthracnose was moderately significant ($r=0.4$, $F=0.08$) in Kabwohe. The other correlations between the number of seed sources per household and the diversity estimates as well as the weighted disease damage indices were weak and not significant (Table 2).

Constraints included varieties not being available when required, seed from neighbors being infested with pests and diseases and poor quality seed from the local agriculture extension. In the seed fairs, farmers did not always want to sell or give away their varieties, the transport cost was high, the variety quality was not always good and the varieties were not available in enough quantities and at the right time. Other limitations were: farmers not always wanting to sell or give away their varieties, seed being very expensive in markets, farmers' preferences not being met because some varieties were no longer available, poor viability of seeds, some varieties losing vigour when grown every season, some sources only sold in big quantities and some farmers not knowing where to buy seed.

Seed change frequency: In Nakaseke, thirty percent of the respondents' seed change frequency ranged from one season to two years, six percent change seed after three to five years and the others changed at no specific time. In Kabwohe, six percent changed seed at no specific time, eight percent changed seed between one season to two years, two percent changed seed between three to five years and the others did not know. In Rubaya, twelve percent of the respondents changed seed between one season and two years yet seventy two percent changed seed between three to five years. The correlations between mean seed turnover and damage indices for local varieties were very significant and negative in Kabwohe and the correlations between the mean seed turn over and the diversity estimates were moderately significant and positive in Kabwohe. In Rubaya, it is only the correlation between the mean seed turnover and the damage indices for Angular Leaf Spot for modern varieties that was significant and negative (Table 3). Reasons for changing seed were: to control pests and diseases, to increase yields, to compare yield of varieties, to maintain soil fertility, to get resistant varieties, land shortage, soil infertility, low yield, market, taste, short maturity period, seed scarcity and to compare permanence of different varieties.

Vulnerability: According to FAO (2010), the extent to which single varieties dominate over large areas could be a useful first indicator for estimating genetic vulnerability, based on the assumption that genetic vulnerability is higher when large areas are cropped with one variety. The household richness in terms of varieties ranged from 1 to 4 in the study sites and the mean household richness for all the sites was 1.9. Ninety five percent of the respondents in Rubaya said they have the same pest and disease damage as their neighbors and five percent said the damage is different due to not planting at the same time and difference in manure application. Ninety two percent of the respondents in Kabwohe had the same damage as the neighbors. The difference in damage here was attributed to the fact that some diseases are soil borne. Eighty two percent of the respondents in Nakaseke had the same damage as the neighbors and ten percent did not know. The difference in damage was attributed to planting good quality seed, planting at different times and difference in the maintenance standards of the gardens.

DISCUSSION

The above results indicate that the respondents have some good level of skill in selecting seed although some of their selection practices could lead to disease movement and increased genetic vulnerability. Farmers select materials for practical reasons that may not always be compatible with the maintenance of genetic diversity (Tripp R. et al 1996). Selection by area was not popular in all the study sites, perhaps because they have relatively small plots (0.5 – 2acres) which they could be taken to have uniform conditions. Selection by plant or part of plant was also not much practiced, perhaps because it is cumbersome. Post-harvest handling practices carried out in all sites are good apart from treating seed with pesticides (environmentally un-friendly) and not treating seeds at all (could lead to disease spreading), but these were the least popular and could be eliminated with awareness about their dangers. Selection of seed according to its condition was

most popular among the respondents where selecting healthy seed was most practiced. The number of seed selection criteria used at household level did not correlate with the richness and evenness of varieties at household level because the selection issues were discussed at a stage when a farmer had already made a decision about the varieties, he had already planted therefore could not affect the richness and evenness of the already planted varieties. There was also no correlation between the number of seed selection criteria and the damage indices for Anthracnose and Angular Leaf Spot possibly because farmers were taking care to plant only healthy seed (basing on appearance) and this could be quite effective in lessening such seed borne diseases as some of their symptoms appear on the seed/pod surface.

In Africa, the majority of farmers mainly get their seeds from informal channels which include farm-saved seeds, seed exchanges among farmers or/and local grain/seed markets where these channels contribute about 90-100% of seed supply depending on the crop (Maredia et al. 1999). This is very true for Uganda, more so for the study sites, and could be attributed to many factors, including the high cost of seed from the formal channels, formal channels not having the varieties wanted by farmers and these channels not being well developed and functional. Commercial (certified) bean seed costs 2 to 4 times what farmers would pay for seed obtained in local markets and yield gains are not commensurate (Rubyogo et al. 2007). There was high exchange of seed within the study sites without much control of the seed quality, which could lead to the spread of seed-borne diseases and pests as well increased genetic vulnerability. While seed exchange can take place over large distances, in many cases it appears to be more important locally, especially within traditional farming systems (FAO, 2010). The frequency of changing seed was very high in Nakaseke and Kabwohe but not as high in Rubaya which could be because in Rubaya, pests and diseases are not so rampant due to the cool climate. Frequent changing of seed would be good for controlling disease movement and genetic vulnerability if only the farmers had control of the quality of seed changing hands. The moderate significance between the quantity of seed from the local market and the weighted damage index for Anthracnose could be a very good indicator that the local market could be the major source of infected seed as it is where seed from any source is sold.

The correlations between mean seed turnover and damage indices for local varieties were very significant and negative in Kabwohe and in Rubaya, it is only the correlation between the mean seed turnover and the damage indices for Angular Leaf Spot for modern varieties that was significant and negative. This could mean that the farmers try to change from diseased to healthy seed thereby lessening the disease incidents and severity. The correlations between the mean seed turnover and evenness/richness were moderately significant and positive in Kabwohe which could imply that seed turnover has a positive effect on increasing diversity. This therefore could imply that changing and exchanging seed can be good with some level of seed quality control. However quality control is still minimal due to ignorance on the part of the farmers, lack of facilities for checking the quality of seed and inadequate/ not enough options from which farmers can choose to get good quality seed. This could one of the reasons why a big percentage of respondents said that they have the same pest and disease damage as their neighbors. Considering the mean number of 1.9 varieties per household as well as the farm sizes and the high rate of exchanging seed without quality control, the level of genetic vulnerability cannot be under estimated.

Table 1 Correlation between the number of seed selection criteria at household level and richness, evenness and Weighted Damage Indices (WDI) for Angular Leaf Spot (ALS) and Anthracnose (Anthra)

		Richness	Evenness	WDI ALS	WDI Anthra
Pearson Correlation R	Kabwohe	0.172	0.043	0.085	0.125
	Rubaya	0.107	0.124	0.134	0.005
Level of significance F	Kabwohe	0.191	0.743	0.518	0.343
	Rubaya	0.413	0.343	0.305	0.968

Table 2 Correlation of the number of seed sources per household, the quantities of seed from major seed sources and WDI ALS, WDI Anthra

		WDI ALS	WDI Anthra
Correlation - Number of seed sources			
Pearson Correlation R	Kabwohe	0.02	0.103
	Rubaya	0.134	0.005
Level of Significance F	Kabwohe	0.877	0.431
	Rubaya	0.305	0.968
Correlation – Quantity of seed from self			
Pearson Correlation R	Kabwohe	0.101	0.231
	Rubaya	0.21	0.051
Level of Significance F	Kabwohe	0.555	0.173
	Rubaya	0.334	0.813
Correlation – Quantity of seed from local market			
Pearson Correlation R	Kabwohe	0.038	0.406
	Rubaya	0.173	0.074
Level of Significance F	Kabwohe	0.875	0.08
	Rubaya	0.451	0.749
Correlation – Quantity of seed from neighbour			
Pearson Correlation R	Kabwohe	0.31	0.297
	Rubaya	0.248	0.174
Level of Significance F	Kabwohe	0.09	0.11
	Rubaya	0.252	0.426

Table 3 Correlations between the mean seed turn over and damage indices/diversity estimates

		Richness	Evenness	DI ALS Local Varieties	DI ALS Modern Varieties	DI Anthra Local Varieties	DI Anthra Modern varieties
Pearson Correlation R	Kabwohe	0.632	0.448	-0.945	-	-0.813	-
	Rubaya	0.0485	0.109	-0.166	0.598	0.098	0.015
Level of significance F	Kabwohe	0.177	0.372	0.004	-	0.049	-
	Rubaya	0.667	0.29	0.136	0.003	0.380	0.945

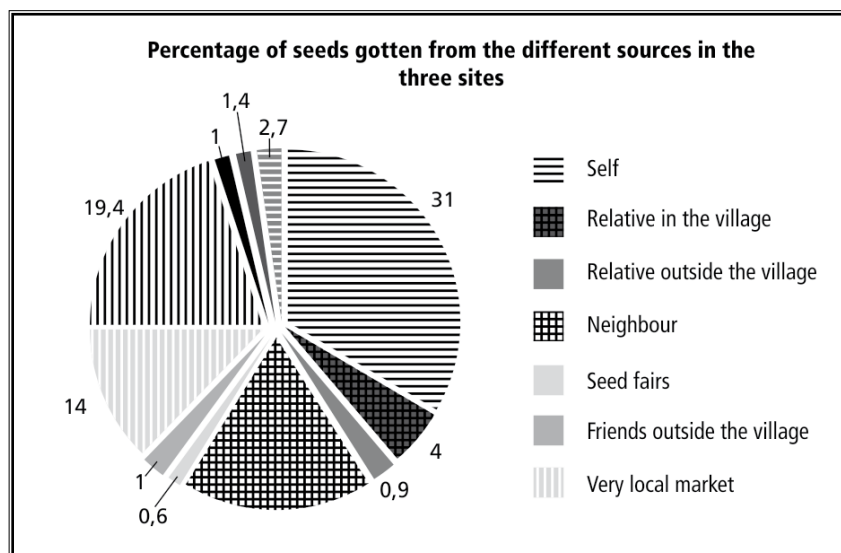


Figure 1 Percentage of seed from different sources in the three sites

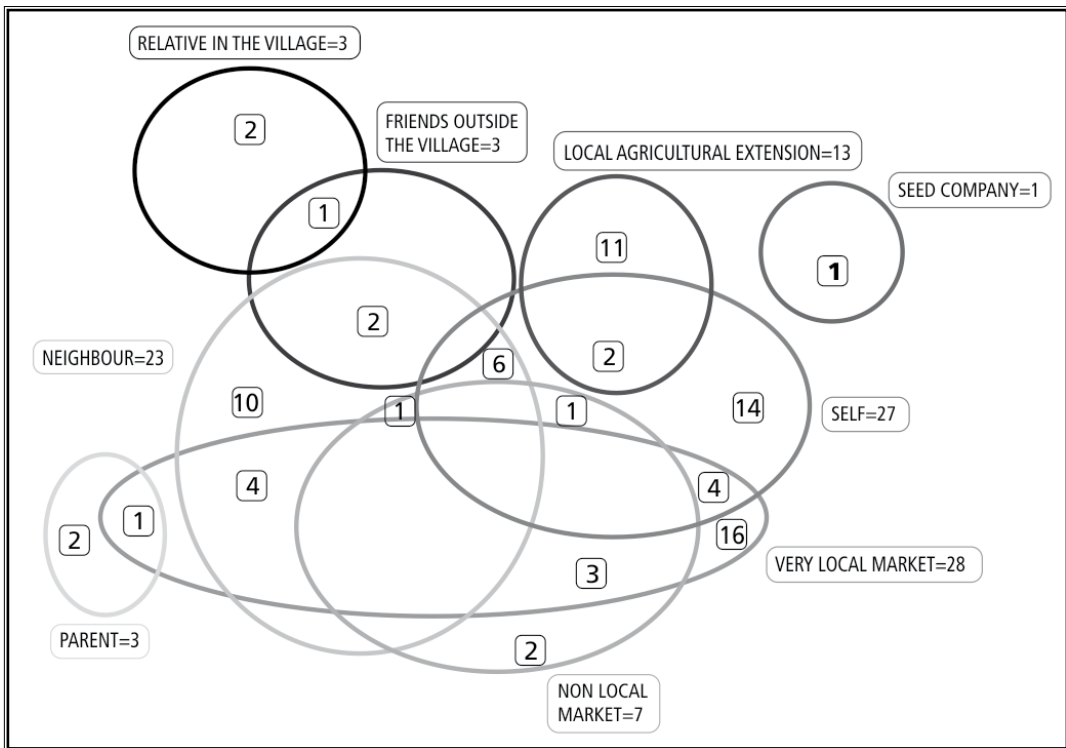


Figure 2 Venn diagram below shows the number of farmers who get seed from the different sources in Rubaya site

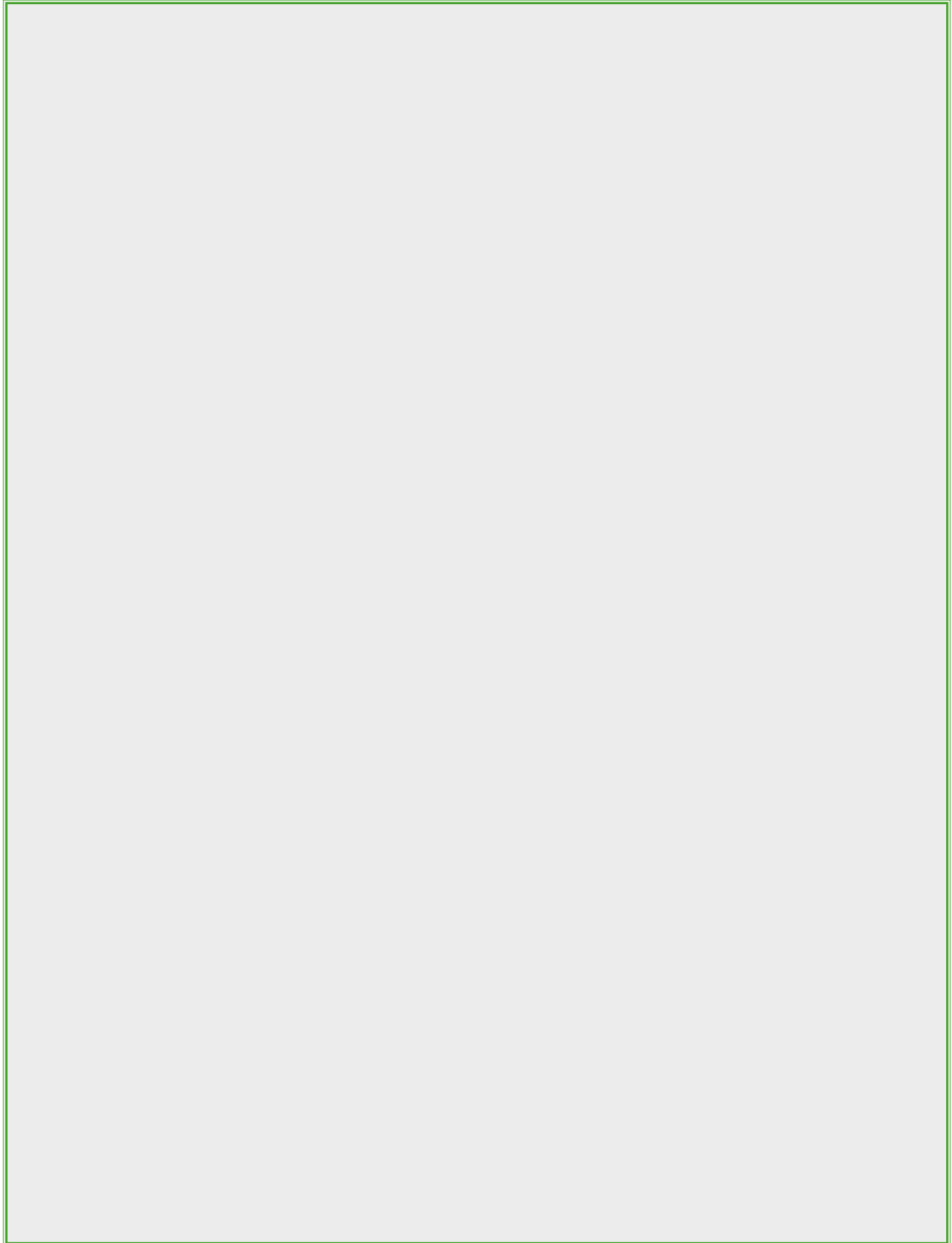


Figure 3 –Seed flow in Nyamirima village, Kabwohe site

Table 4- Prevalent seed selection criteria in the study sites

Criterion	% of respondents who do it in the site		
	N	R	K
a) Area			
Select at population level	28	5	0
Area of plot set aside for mother plants	12	3	0
Select healthy population with few pests and diseases	7	3	0
Area planted specifically for harvesting plants	3	2	0
Select a population from a fertile field	2	2	0
b) Plants or parts of plants			
Removal of diseased plants	67	0	3
Taking out off types	50	0	0
Selecting seeds from healthy plants	27	7	0
Plant selection	7	0	0
c) Nature/ condition of seed			
Normal colour	65	88	87
Big seeds	62	78	60
Uniform seed	47	40	45
Healthy seed	75	97	82
d) Post harvest handling			
Seeds not treated	30	38	7
Treat seeds with pesticides	2	33	7
Treat seeds with other products	55	23	97
Specific seeds container	75	80	38
Prepare storage facilities	15	68	27
Specific location for storage	33	87	98

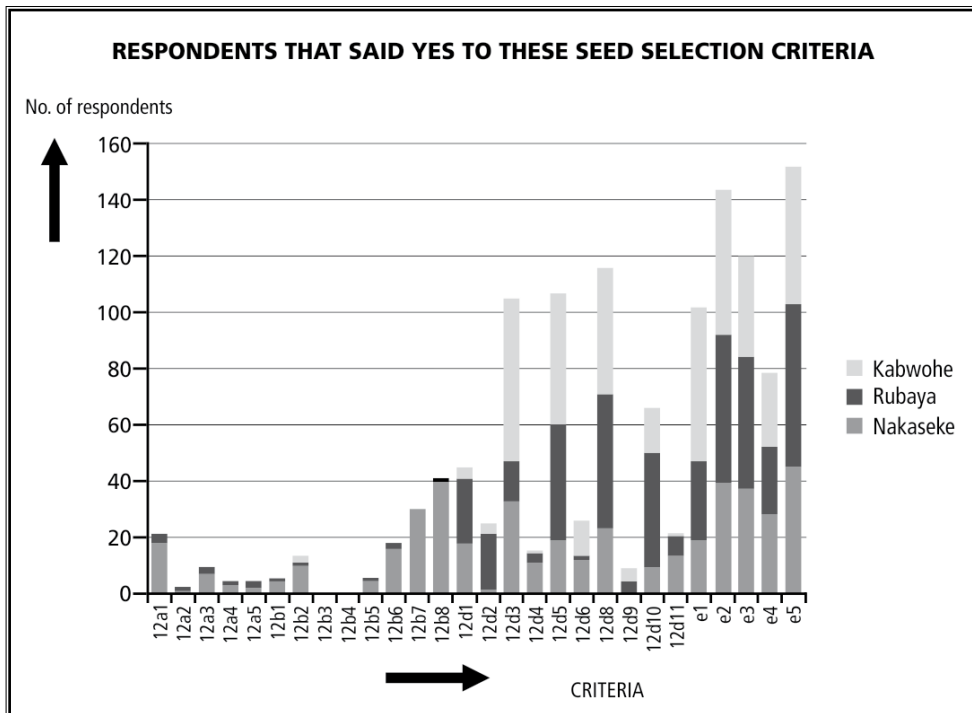


Figure -5: All the seed selection criteria discussed in the survey

12a1 = Do not select at population level
 12a2 = Select a population from a fertile field
 12a3 = Area of plot set aside for mother plants
 12a4 = Area set aside for harvesting plants
 12a5 = Select healthy population with few pests/ diseases by field
 12b1 = Select plants
 12b2 = Select pods
 12b3 = Plant selection
 12b4 = Mark the best plants by putting sticks around
 12b5 = Mark the best plants by putting scare crows close to them
 12b6 = Select seeds from healthy plants only
 12b7 = Taking out off types from the crop
 12b8 = Removal of diseased plants

12d1 = No seed treatment
 12d2 = Treat seeds with pesticides
 12d3 = Treat seeds with other products
 12d4 = No seeds preparation for storage
 12d5 = Specific seeds preparation for storage
 12d6 = No specific seeds container
 12d7 = Specific seeds container
 12d8 = No preparation of storage facilities
 12d9 = Type of preparation of storage facilities
 12d10 = No specific location for storage
 12e1 = Select seeds
 12e2 = Select seeds with normal colour
 12e3 = Select big seeds
 12e4 = Choice of uniform seed
 12e5 = Planting only healthy seed

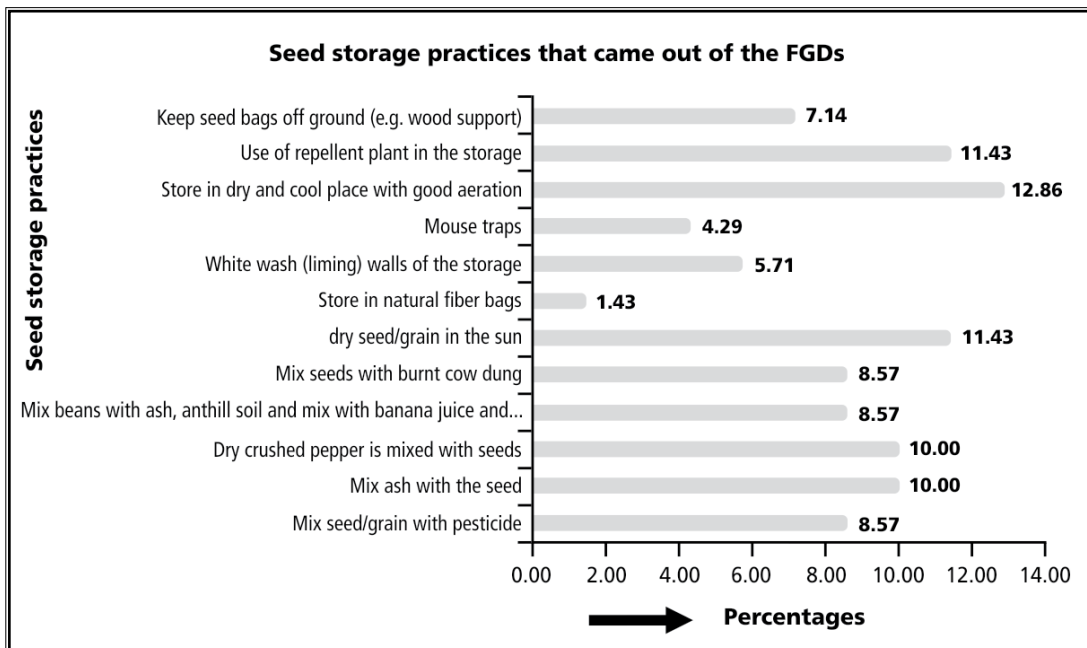


Figure 6: Post-harvest

Analysis of faba bean (*Vicia faba* L.) seed flow and diversity management practices on-farm

Aqtbouz, N.; El Badraoui, M.; Sadiki, M.

INTRODUCTION

In the province of Taounate, agriculture is characterized by a rich traditional production system in terms of local genetic diversity. Indeed, agricultural production is used for both home consumption and for trade between local networks. In this system, the faba bean crop remains a principal component and its cultivation a very strong tradition in this area of Morocco. This system, often closed, opens gradually through the exchange of seeds among neighbors and through marketing regionally and nationally. Moroccan small-holder farmers share a rich and very developed know-how for seed production and management of local varieties as well as their deployment over time and space in various cropping systems. This knowledge, relating to the management of diversity to control diseases, is an integral part of farming and technical inheritance, including local seed systems and systems of plant protection. Combining this local knowledge with scientific progress resulting from research programs is an imperative for providing a basis for sustainable support to on-farm diversity management. Thus the objective of this work is to analyze the seed flow and seed management strategies and practices in a traditional production system of three rural communities of Taounate region.

MATERIAL AND METHODS

To harness this legacy of local knowledge, to understand the perception of farmers in terms of disease, and to analyze the movement of seed within local networks, individual surveys were conducted by a multi-disciplinary team on 179 farms randomly chosen in the three sites of Ourtzagh, Galaz and Tissa in Taounate province. This area is part of the larger and oldest region of faba bean production in Morocco.

RESULTS AND DISCUSSION

Data analyses by univariate and multivariate statistical descriptive methods and ascending hierarchical clustering showed that all the components of seed systems in the informal sector are mainly in the hands of farmers and are based on traditional practices; farmers share and exchange to satisfy their own seed needs (Table 3). These investigations have identified local knowledge in terms of farm management of biotic stresses (such as *Botrytis*). Indeed, farmers are aware of the severity of disease and the importance of resistance in local varietal wealth (Table 1). The analysis of perception shows that they use, directly or indirectly, local genetic diversity for disease management (Table 2). It also follows from these investigations that the practices of diversity manage-

ment in production systems and different decision-making criteria adopted by farmers are the main elements of the evolutionary processes that act on the structural diversity on-farm of local varieties of faba bean. All these practices reflect the needs and preferences of farmers. Selection practices, treatment, packaging and storage are the main components of the local seed system. The origin of the seed is an important factor to take into consideration in predicting conservation of varieties. Farmers of the three communities depend on diverse sources of seed supply to meet their needs. The most frequent are: parents, neighbors, friends outside the village, local markets and non-local markets (Figure 1). Diversification of sources of seed may be dictated by the need to diversify the cultivated material to adapt production to events and uses. It could also indicate that the farmer prospects diversity in search of new germplasm. The investigation of farmers' perception of the origin of faba bean diseases are also focused on disease transmission through seeds bought in the market. More than 50% of the farmers believe that seed of the local market is a vector of disease transmission (Table 4). All levels of the circuit management and seed production is represented by traditional practices adopted and shared by farmers on a closed circuit in most cases, where farmers themselves are the guarantors of maintaining diversity, farm machinery and generators. They condition and act on the genetic structure of varieties used on the one hand and partly on the value of these varieties through seed quality of the other.

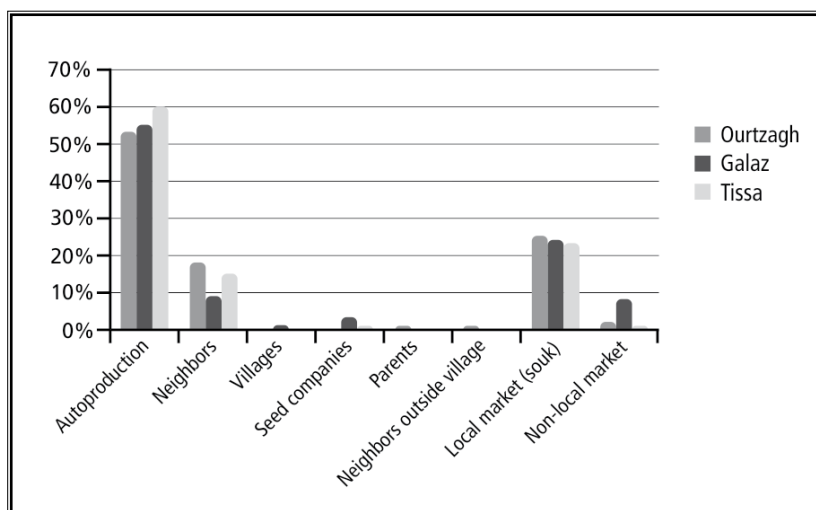


Figure 1: Seed traffic analysis in the three sites of Ourtzagh, Galaz and Tissa

Table 1: Disease scoring by farmers with the range of variation (average, minimum and maximum)

Disease/ Pest	General scoring of diseases/pests according to farmers								
	Average			Minimum			Maximum		
	Ourtzagh	Galaz	Tissa	Ourtzagh	Galaz	Tissa	Ourtzagh	Galaz	Tissa
Anthracnose	2	1	1	1	1	1	2	2	2
Botrytis	2	2	2	0	1	0	3	3	3
Bruchus	1	2	2	1	1	2	1	2	2
Orobanche	3	3	3	0	1	0	3	3	3
Aphids	2	2	2	0	1	0	3	3	3
Rust	1	2	1	0	1	0	3	3	3
White borer	2	2	3	0	1	1	3	3	3
General	2	2	2	0	1	0	3	3	3

Table 2: Percentage of farmers adopting different selection criteria for selecting quality seed in the three communities of Ourtzagh, Galaz and Tissa

Criteria	Ourtzagh	Galaz	Tissa
Seed selection on general aspect	34	19	34
Selection of large seeds	57	44	38
Planting of healthy seeds only	9	23	8
Selection of seeds with normal color		9	5
Choice of uniform seeds		6	14

Table 3: Percentage of farmers' post-harvest methods for storing bean seed in the three communities of Ourtzagh, Galaz and Tissa

Method	Frequency		
	Ourtzagh	Galaz	Tissa
Seed treatment against pests			
No treatment	77	76	60
Pesticide application	13	8	10
Seed treatment with other products	22	16	30
Storage			
No preparation of seeds for storage	33	29	18
Specific preparation (place & material)	67	71	82

Table 4: Beliefs of farmers regarding disease transmission by seed

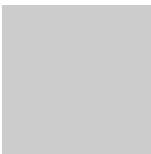
Level of agreement	Ourtzagh	Galaz	Tissa
1 : Strongly agree	20	25	20
2 : Moderate agreement	31	25	25
3 : Undecided	15	13	32
4 : Slightly disagree	8	4	3
5 : Highly disagree	26	33	20
Total	100	100	100



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



POSTER
SESSION-C



Activities to ensure benefit sharing with farmers
(C-1) Policy workshops, recommendations and policy briefs
(C-2) Community genebanks and seed banks

Policy workshops: Protection of the rights of farmers and diversity of local plant genetic resources

Xu Furong; Yang Yayun; Wang Fuyou; Dong Chao; Zhang Enlai; Zhang Feifei; Dai Luyuan.

INTRODUCTION

Xishuangbanna is the southernmost prefecture of Yunnan Province. The prefecture is nicknamed “Aerial Garden” for its luxuriant and multi-layered primitive woods and tropical rain forests, which are teeming with animals and plants. The region has 5,000 kinds of plants or about one-sixth of the total in China. This has earned it renown and the sobriquet “The moonstone on the Crown of the Kingdom of Plants”. In order to better protect biodiversity, we have investigated local policies and regulations related to the research and conservation status. With questionnaires, we want to discover problems and explore solutions to existing problems, eventually rising to the level of laws and regulations, raising government and national awareness, and ensuring sustainable conservation of biological diversity in Xishuangbanna.

METHODS

Using the questionnaire designed for the project, we conducted a survey involving genebank managers, focal points, breeders and local organizations in Yunnan Province.

RESULTS

The results of the survey of eight gene bank managers (such as KIB, XBG and YAAS) by questionnaire (Fig. 1), show that the genebank databases were only partially open to the public. The genetic resources of these crops were mostly of local varieties, accounting for 80% (Fig. 2). The management institutes mainly collected the resources with the aim of selecting for new and specific traits or for research needs, or for rare resources conservation. Policy and mechanisms for accessing the resources included laws and regulations of the state, such as the ‘Seed law of the People’s Republic of China’ and ‘Regulation of crops genetic resources’. Government programmes to promote the access, use, conservation and protection of genetic resources, provide the websites Escience, Agri Data and CGRIS to promote the sharing of crop genetic resources.

In a questionnaire survey of focal points, the competent national authorities included MEP, MoA/SFA and DEP, provincial DoA and FA. Eight international conventions have been ratified by China, including the Convention on Biological Diversity. The Law Committee or the Special Committee under the Standing Committee of the NPC monitors and evaluates the implementation of international treaties in China. Farmers’ rights and participation and their variety have been partially protected by some laws.

In the survey of breeders by questionnaire, eight institutes were investigated. The sources of genetic resources were mainly from local and modern varieties, accounting for 57.10% and 19.10%, respectively. The crop traits of primary concern to breeders were: yield, named by 42.6% of investigated breeders; quality of crop production and resistance. The seeds that breeders obtained mainly through official means accounted for 43.8%, while 26.3% was from unknown local varieties. Seventy-five percent of breeders often cooperated with agricultural research institutes (Fig. 4).

In the survey of local organizations, 12 villages of Xiding County were investigated. In seven communities, farmers who were questioned suggested that farmers' rights were not feasible. Half of the farmers have not had contact with the local government in at least the last six months. There was no policy for sharing the profit from genetic resources with farmers, and no mechanism for avoiding variety stealing by others.

DISCUSSION

According to the results of questionnaires, we need to: make the genetic resources data open to the public; create the policy and executive programmes to obtain and exchange seeds; promote and draw up the laws and regulations to protect farmers' rights and improve farmers' awareness of legal means of protecting their own rights. Breeders, when they make research plans, need to communicate with farmers frequently and sufficiently to share the benefits with the community. With regard to local organizations, the local government should train the farmers and make them participants in policy-making. All the beneficiaries work together to protect agricultural diversity.

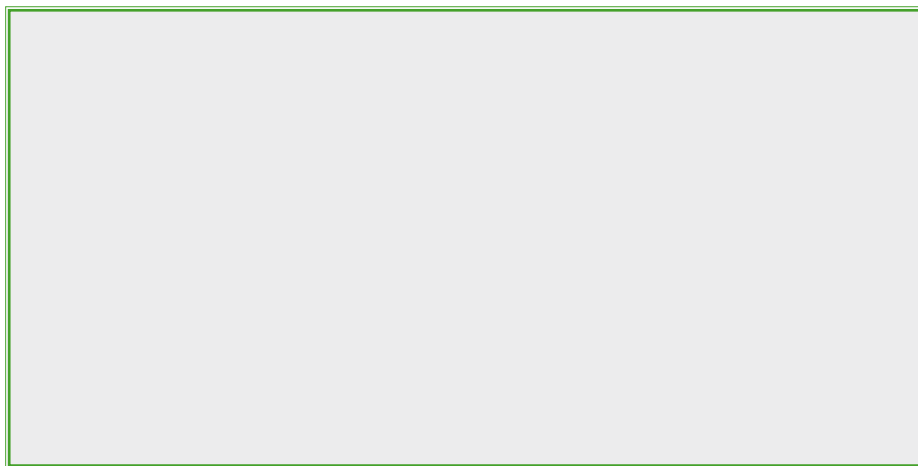


Figure 1 Major collections in Yunnan

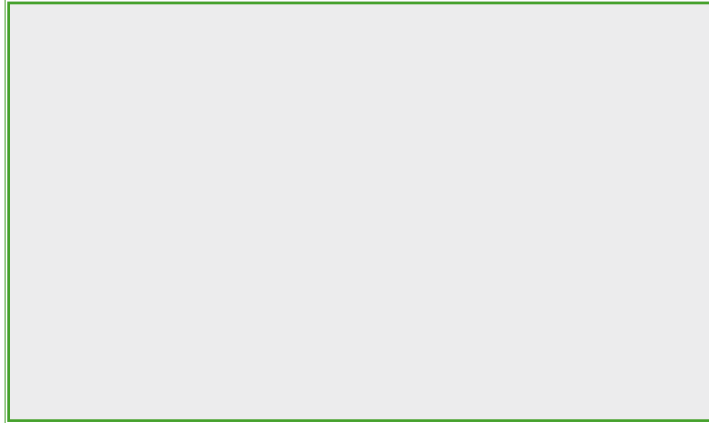


Figure 2 The sources of accessions collected

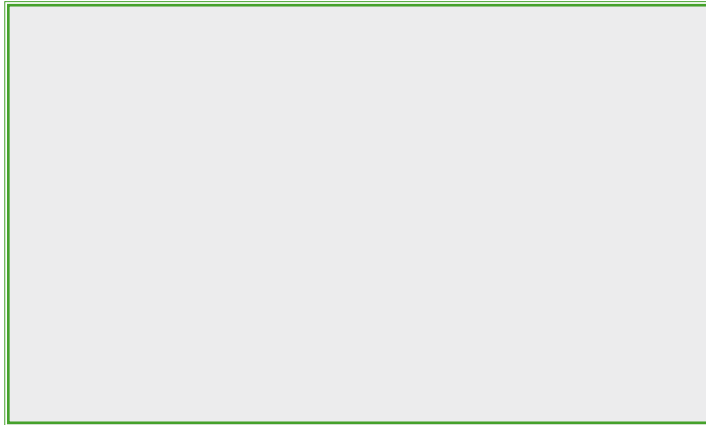


Figure. 3 The sources of breeders' genetic resources

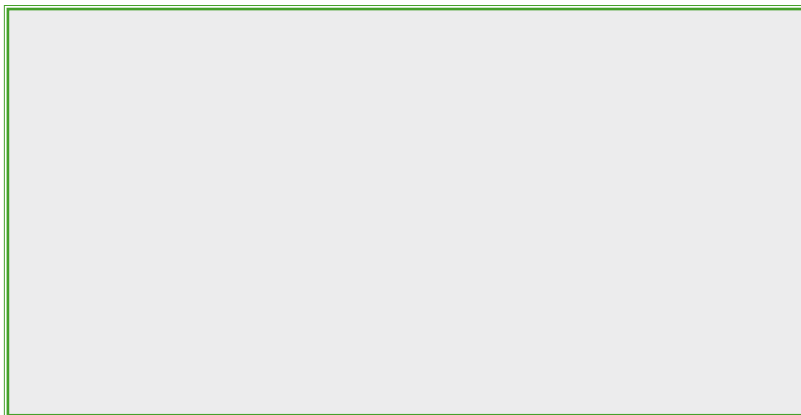


Figure 4 Cooperation of breeders with other institutes

Policy research on farmer's rights and community agrobiodiversity in Yunnan, China

Wang Fuyou

Yunnan, renowned as “the Kingdom of Plants,” has the most plant species of all the provinces of China, with species varying from tropical and subtropical to temperate, and even includes cold zone species. There are about 30,000 advanced plant species in China, among which 17,000 grow in Yunnan, accounting for 56.7% of all plant species in the country. It is thus very important to protect and make the most use of those plant genetic resources, especially communal agrobiodiversity resources, as well as to protect farmers' rights.

Survey on farmers' rights and agrobiodiversity

In June 2010, a survey on farmers' rights and agrobiodiversity was made in Yunnan, China. Eight genebank managers, twelve local organizations and eight breeder institutes were surveyed.

RESULTS

Genebank Managers

Most of the genebanks developed databases of their collections, and began to collect traditional knowledge (TK). However, only parts of the database are shared with the public. Genetic resources are mainly used in academic research, and inadequately in development. There are no specific decision-making mechanisms and performing processes with regard to access to and exchange of genetic resources.

Focal Points

Farmers' rights are recognized partly by China's laws and regulations, i.e. right of exchange and sale of farm-saved seeds of farmers' varieties and breeders' protected varieties. Fewer organizations are lobbying for farmers' rights, and farmers also have little awareness of their rights. Farmers' varieties are recognized by seed policies and their exchange and sale are permitted in rural fairs, but registers of farmers' varieties are not yet developed.

Breeders

Most breeders developed their own databases of genetic resources. However, they only provide data to the focal points on plant genetic resources. Breeders often use local materials and cooperate with farmers on field days and demonstration field stages. Breeders' varieties are protected

by IPRs. In contrast, they only share benefits with farmers through payment during collection. Mechanisms for benefit sharing of genetic resources are not yet developed.

Local Communities

Local communities do not have awareness of their rights, and they do not know how to protect farmers' rights. They do, however, know the importance of genetic resources and traditional knowledge, and would like to protect them. Local organizations' representatives or representatives from other farmers' organizations do not often meet with local government officials.

POLICY WORKSHOP

Biodiversity International held a Policy Workshop on Farmers' Rights and Communal Agrobiodiversity in liaison with Yunnan Academy of Agricultural Sciences, Department of Agriculture of Yunnan, in Xishuangbanna on 20 November 2010. Seventy-three participants attended the workshop:

- Government Officials: Ministry of Agriculture of China, Department of Environmental Protection of Yunnan;
- Farmers of Xiding Town and Tianjian Potato Co-operative of Menhai;
- Genebank managers and breeders: Yunnan Agricultural University, Kunming Institute of Botany;
- Organizations: Beijing Office of UNEP, Chinese Academy of Tropical Agri. Sciences, China Centre for Intellectual Property on Agriculture.

EXAMPLE: Protect local varieties through geographical indications (GIs)

Xiding Little Sticky Potato is one of the local potato varieties, planted for more than one hundred years. The Tianjian Potato Co-operative of Menhai was founded but only "Xiding Local Product, Natural Ecosystem" is written on the cover of the seed package. This label does not belong to the list of products under national IPR protection. The cooperative will apply GIs to the potato.

CONCLUSIONS AND RECOMMENDATIONS

- More subsidies should be given to farmers who conserve and use local varieties.
- More funds should be mobilized and used in the protection of agrobiodiversity.
- A benefit-sharing system must be developed.
- Protection of biodiversity and people's livelihoods should be coordinated.
- All stakeholders should be concerned with the protection of agrobiodiversity.
- Marketing products of the local elite varieties should be through GIs or other IPRs.
- Agrobiodiversity should be publicized and awareness of the public raised.

Community seed bank in China: A first example in Xiding county

Xu Furong; Yang yayun; Dong Chao; Zhang Feifei; Tang Zhimin.

COUNTRY AND SITE(S): *Xiding, China*

INTRODUCTION:

Xiding, one of the selected study sites for the UNEP & GEF sponsored program of “Conservation and Use of Crop Genetic Diversity to Control Pests and Diseases in Support of Sustainable Agriculture”, is in Menghai county (99°56′-100°41′E, 21°28′-22°28′N) of Xishuangbanna Dai Autonomous prefecture, Yunnan Province, China. The Menghai County is located in the southwest of Yunnan Province, with its southwest parts bordering on Myanmar, and the boundary line is of 146.5 km length with the altitude ranging from 535 m to 2429 m. The land area of the county is 5511 km², 93% of which are hilly regions. The plantation area per person is 0.15 ha. According to the census in 2004, the total population was 296,600, of which, 249,800 people lived on agricultural yield. There are many minority nationalities like Dai, Hani, Lahu, Yi, Wa etc in Menghai. The annual average temperature is 18.5 °C, and annual precipitation is 1341.3 mm. The community selected for our ongoing GEF project is Xiding Town, with an altitude of 1310-1740 m. The local crops are mainly paddy, maize, upland rice, tea etc. Due to the specific ecological and geological environment, the plant genetic resources there are of high abundance.

Some traditional varieties are of low temperature-tolerant, disease-resistant, high nutrient characteristic, which are terrific candidates for future research.

RESULTS:

A group led by Mr. Xu Furong from the Institute of Biotechnology and Germplasm Resources, Yunnan Academy of Agricultural Sciences, went to Xiding to survey the understanding of local farmers on the knowledge of the conservation of traditional varieties. After this survey, the suggestion to establish an association to protect the local traditional crop varieties as well as the farmers' rights. With the active support of the Institute of Agricultural Science of Xishuangbanna Dai Autonomous Prefecture, Agricultural Bureau of Menghai County, Xiding Government, Xiding Agriculture Service Center and the local farmers, the “Xiding Crop Germplasm Center” (Fig. 1) was set up at Manwa village committee in Bada, Xiding. Meanwhile, the Xiding Crop Germplasm Management Committee and an Expert Advisory Committee were also established.

A provisional edition of the Xiding crop germplasm center management guideline (Fig. 2) as well as the crop variety registration book (Fig. 3) has been established. With the sponsorship of UNEP & GEF project, we purchased desks, cabinets, containers and other necessary instruments and equipments to store the crop germplasm resources in Xiding. The conservation of the local

rice landrace varieties (Fig. 4) and the maize varieties (Fig. 5) in the 12 villages (Manwa, Manpi, Manpadai, Manpale, Manyankan, Bada, Hesong etc) has completed by now.

During the survey in the 12 villages, we found that some farmers still grow many traditional varieties now. For example, Sha zhe grows 2 upland rice varieties and 1 local maize variety at present; Yan enzhang grows 3 upland rice varieties and 3 local maize varieties right now. To better protect the crop germplasm in Xiding, we suggest giving rewards to the farmers who still grow many traditional varieties for their contribution to the protection of local crop germplasm resources.

DISCUSSION

During the foregoing genetic diversity survey and collection of rice and maize germplasm resources, many cells of the survey form was always left blank, which may due to the following several reasons: (1) they have no idea about the name of the varieties they grew which were descended from their forefathers; (2) they keep grow a variety just because of the good taste of the variety rather than the necessary to protect the diversity of the crop germplasm resources; (3) many of the crop varieties were grown within limited area instead of large-scale field plantation, which made it difficult to estimate the yield of those varieties; Accordingly, we strongly suggest that we should provide some training classes to the farmers there to convince them of the importance to protect crop germplasm resources and help them to understand that they can enjoy their rights as the plant genetic germplasm contributors. Moreover, the local government should come up with some measures or policies to encourage the farmers to protect the varieties on-farm.



Figure 1 Xiding Crop Germplasm Center

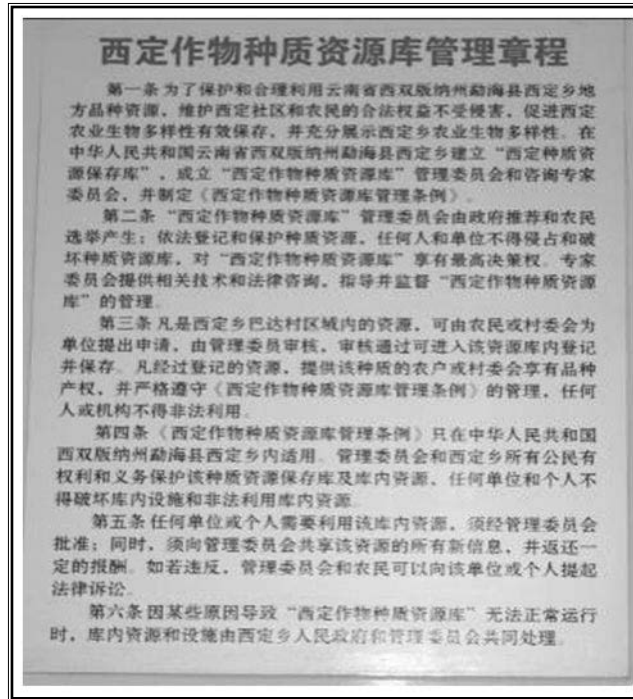


Figure 2 Guidelines of Xiding crop germplasm management (Provisional), the English edition refers to the Appendix

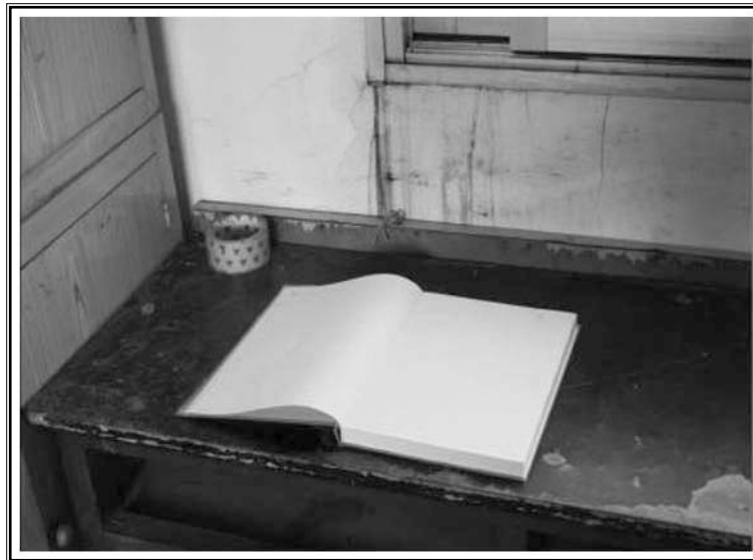


Figure 3 Registration book for crop varieties



Figure 4 Local rice varieties stored in the crop germplasm center
Each container has a tag with the variety name, the name of the provider and the village.



Figure 5 Local maize varieties stored in the crop germplasm center
Each container has a tag with the variety name, the name of the provider and the village.

Appendix:

Management Guidelines of the Xiding Crop Germplasm Centre

1- To better protect and utilize the traditional germplasm resources in Xiding, Menghai County, Xishuangbanla Dai Autonomous Prefecture, Yunnan, China, to protect the legal rights of the farmers and the Xiding Community, to promote the conservation of the crop diversity in Xiding as well as to demonstrate the bioversity in Xiding, the Xiding Crop Germplasm centre, its corresponding management committee and expert advisory committee as well as the management guideline were established.

2- The committee members were recommended by the government or elected by the local farmers. The occupation or damage of the Crop Germplasm Centre by any person or sector was by no means allowed, and the committee has the final decision-making authority. The Expert Advisory Committee is obliged to provide the associated technical and legal consultation, to direct and supervise the operation of the Crop Germplasm Centre.

3- With any crop germplasm that was within the boundary of Bada Village, farmers or village committee could submit their application to the management committee. The germplasm approved by the committee could be registered and conserved in the Crop Germplasm Centre. The provider of the registered germplasm then enjoyed the rights as the contributor of this germplasm which was by no means allowed to be used by any person or institute for illegal purpose.

4- The guideline of the management of the Xiding Crop Germplasm Centre was only applicable to the germplasm within Xiding Town. The committee and all the citizens in Xiding are obliged to protect the germplasm centre and the germplasm in it. Any one or institute who damages the facilities in the germplasm centre or uses the germplasm for illegal purposes will be punished.

5- The use of the germplasm in the Xiding Crop Germplasm Centre by individual or institute should be approved by the committee. Furthermore, the individual or institute who wants to use the germplasm should pay some money for them and share all the new information concerned with the germplasm. The management committee and the farmers there could bring suit against anyone who used the germplasm against the guideline.

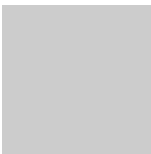
6- The resources and facilities in the crop centre would be conserved by the Management Committee and the Xiding government once the Crop Germplasm Centre failed to run smoothly for some reason.



DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:




THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 7



The damage, diversity, and genetic vulnerability – advantages
of using crop genetic diversity

Damage, diversity and genetic vulnerability - can we say anything yet?

Jarvis, D.I.; Fadda, C.

The project was developed under the hypothesis that by enabling resource-poor farmers to generate and maintain crop populations or sets of crop varieties that are less susceptible to new pathogens or to mutations of existing pathogens, their agricultural production systems would be more resilient to changes in pest and disease infestations, giving poor farmers increased adaptive capacity in their local production systems to buffer against unpredictable environmental change. Thus, crop genetic diversity on-farm would not only reduce current crop loss and maintain yield stability, but also reduce the risk of genetic vulnerability or the potential for crop damage in the future in addition to actual damage now. It was also supposed that by providing rural households and extension services with an alternative to pesticides, many of which pose health hazards, farmers will have reduced need to purchase chemical inputs. Reduced pesticides will also mean that the services of below-ground organisms for improving soil nutrition and soil-forming processes, as well as insect pollinators for improving pollination services, will be enhanced, leading to enhanced ecosystem services that support sustainable agricultural production and improved ecosystem health.

Now after several years of work on the project, it is time to stop and ask ourselves what has been discovered from the work so far to link the planting of a diverse set of crop varieties of a particular crop in the farmer's fields with the damage caused by pests and diseases. Has the project reduced, or is the project on the way to reducing, crop damage in farmers fields? Do we now have evidence that using crop varietal diversity in farmers' fields can be a cost-saving substitute for pesticides?

Integrated Pest Management (IPM) is a widely recognized ecosystem approach to crop production and protection that combines different management strategies and practices to grow healthy crops and minimize the use of pesticides with considerable success. Until recently IPM methods have concentrated on using agronomic techniques to modify the environment around predominantly modern cultures to reduce the need for pesticides, making limited use of the opportunities offered by the effective deployment of the intra-specific diversity of local crop varieties themselves. We now ask the question of whether we been able to enhance the impact of IPM strategies through the use of the intra-specific diversity among cultivars maintained by farmers?

The host/pest or host/pathogen system were selected within this programme to be representative of a much larger set of host/pest or host/pathogen interactions, allowing for scaling up to other similar crops and host/pest systems. Do we still believe this is possible? If so, can we now document the process so that other host/pest systems can benefit?

Do we now have evidence to allow us to direct crop improvement programmes towards moving from extracting genes from local materials to breed exotic varieties towards improving the

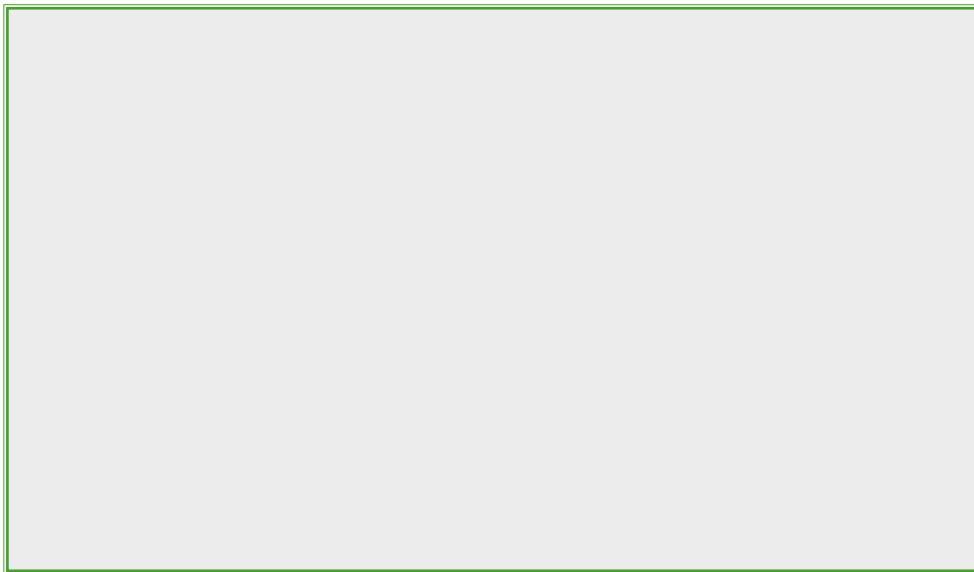
local crop cultivars that are within the farmers' production system (*in situ*), e.g., improving locally resistant landrace materials for other traits, or locally adapted non-resistant landrace materials for resistance? Do we now have enough knowledge to ensure that breeding for mixtures, or breeding for sets of varieties to be grown together, can become part of a national breeding programme? Can we show that this change in breeding protocols is, or has the potential to be, a viable option for breeders (both public and private sectors) in the future?

These are questions that we asked ourselves several years ago when we began this programme. Now is a chance to take stock and see where we are in answering them.

The Disease Damage, Genetic Diversity, Genetic Vulnerability Diagram – Some Reflections

Brown, T.

How are farmers using, and how can they better use, genetic diversity to lessen both the impact and the future threat that pests and pathogens pose to their continued crop productivity? To answer this question, we have amassed a wealth of data from a range of crop systems and biotic pressures. The challenge now is to integrate such information to extract guiding principles. To aid this task, we proposed the following framework sketched as a three-dimensional diagram.



The diagram is a conceptual display of relationships among the key variables that occur in farmers' crops. It has three dimensions. The first is the genetic-diversity axis, which is the independent variable that farmers can manipulate through their choice of seed and variety. The second axis is some measure of damage that arises from biotic pressures in the field. The third axis is the measure of genetic vulnerability or risk of future damage. A point in the 3D space represents the values on each axis measured for an individual farm, field or community and a specific crop host and disease or pest pressure. A mapping of all the study systems would enable the testing

of relationships, and the classification of points into attributes (particular crop breeding system, kinds of pathogen, etc.)

Axes of the DDV diagram

The diversity axis has been extensively considered elsewhere (e.g. Jarvis et al 2008) and diversity can be measured in a number of ways. Variety name richness, evenness and between-farm divergence are our basic measures. In addition, Sherwin *et al* (2009) have argued that the Shannon-Weaver Information is a useful statistic, particularly in hierarchical data with the partition of diversity into components within field, between farms within communities, and between communities.

The damage axis presents challenges in the aggregation of data and their meta-analyses (as discussed elsewhere in these proceedings). Scales are heterogeneous, ranging from specialist disease response types defined for specific systems (e.g. for rust symptom expression) to the measurement of morphological traits. Multidimensional scaling methods such as principal component analysis offer ways to combine many variables into fewer axes. For all measures of damage, the key is that scaling be consistent in direction, that higher scores indicate more disease or damage or higher adversity or outcome of disease. Other variables that belong on this axis include measures of economic impact and pesticide use.

The third axis of genetic vulnerability is the most challenging dimension for measuring (Brown 2008). The table below outlines possible measures and their conceptual bases.

Concept of genetic vulnerability	Measurement
<u>Genetic homogeneity</u> - The area grows one or a few varieties, and they all share a very similar resistance structure	<ul style="list-style-type: none"> • Richness and evenness diversity of varieties • The resistance diversity
<u>Low resilience</u> - The area lacks varieties that respond differently to genetic or environmental variation in biotic pressure in such a way that lessens the average disease burden	<ul style="list-style-type: none"> • Net “beneficial correlation” (defined as negative minus positive correlations) in performance in different disease environments.
<u>Mutational vulnerability</u> – The crop would be susceptible to a new mutant pathotype of the pathogen	<ul style="list-style-type: none"> • Proportion of non-local pathotypes or distinct isolates that can cause disease
<u>Migrational vulnerability</u> - The crop would be susceptible to a new migrant propagule of the pest or disease coming from outside the home area.	<ul style="list-style-type: none"> • Probability that a random migrant pest or disease propagule succeeds • Proportion of plants that become diseased in disease-prone areas other than the home environment

Pair-wise relationships - What insights emerge from the three two-dimensional planes?

1. Diversity – damage

How damage relates to diversity is fundamental for the project, and a large body of information is now assembled. In response to diverse biotic pressures in the HOME environment:

- What is the relative performance of local varieties to modern cultivars?
- What is the overall pattern of relationship between biotic damage suffered and landrace diversity, in individual farmers' fields and in communities?
- With more diversity, is there merely an averaging of damage, or an added benefit about the mean of components?
- Are there differences in relationships for the kinds of crops, or kinds of biotic threats?

2. Diversity – Genetic Vulnerability

- Which kinds of systems display a relationship between diversity and vulnerability?

3. Damage – vulnerability

This relationship could conceivably affect farmers' diversity decision-making. In host populations harbouring large pathogen populations, there is an increased chance of the evolution of new virulence.

- How do farmers respond to crop damage from disease? Will they spray, change varieties, alter cultivation practice, or pray and endure the loss?
- Does damage in the current crop portend worse damage tomorrow?

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Have we taken, or are we about to take, the path to substituting pesticides with diversity?

Wang Yun-Yue

With the advent of modern agriculture, many traditional crop varieties have been replaced worldwide by a few improved, high-yielding varieties, a result of the success of crop breeding and intensive cultivation practices adopted on a massive scale. The cultivation of large areas to single, uniform crop cultivars has contributed tremendously to the world's food production. Yet this practice has also led to serious genetic erosion --, the loss of traditional varieties from agroecosystems, which hinders efforts to improve crop varieties further. Reliance on a narrow spectrum of cultivars grown in monoculture has also been linked to increased pest and disease problems and to vulnerable agroecosystems. Higher yields and greater food security have come at the expense of higher input of pesticides and fertilizers. The potentially damaging consequences of planting large areas to single crop cultivars with uniform resistance to pests and diseases were recognized as early as the 1930s.

Much of the 30% of the world's annual harvest lost to disease and pests occurs in developing countries. Small-scale farmers in developing countries continue to depend on genetic diversity to maintain sustainable production and meet their livelihood needs. Loss of genetic choices, reflected as loss of local crop cultivars, therefore, diminishes farmers' capacities to cope with changes in pest and disease infection, and leads to yield instability and loss.

Pesticide consumption is increasing all over the world, leading to serious harmful impact on human and environmental health, including the associated crop biodiversity. Integrated pest management (IPM) strategies, which have focused on using agronomic management techniques to reduce pesticide use, but concentrate on modifying the environment around predominantly modern cultivars, and have tended to exclude the potential of using within-crop diversity, for example, through genetic mixtures (crop variety mixtures) or the planned deployment of different varieties in the same production environment. A diverse genetic basis of resistance is beneficial for the farmer because it allows a more stable management of pest and disease pressure than a monoculture allows. This is because when resistance in a monoculture breaks down the whole population succumbs, while in a genetically diverse field it is much less likely that different types of resistance will all break down in the same place for comparable pest or disease damage. Here we give an excellent case study that supports the view that intraspecific crop diversification provides an ecological approach to disease control, pesticide reduction and yield increase that contribute to the sustainability of crop production. In Yunnan province in southwest China, a genetically diversified rice crop was planted in large areas. Our system of crop diversity management, using genetic diversity to reduce disease by mixed planting traditional and hybrid rice varieties. Disease-susceptible rice varieties planted in mixture with resistant varieties had 89% greater yield and blast was 94% less severe than when they were grown in monoculture. The practice was so successful that it dramatically reduced the need for fungicides. According to an assessment by

the Yunnan Government and unpublished government economic reports, farmers gain about \$187.5 per hectare from mixed planting. The method has also spread to neighboring region such as Sichuan and Guizhou provinces. Demand for and cultivation of genetically diverse traditional varieties that have been adapted to various agroecosystems and matched with hybrid rice varieties have significantly increased. Our investigation further showed that the cultivated area of traditional rice varieties has also been radically expanded. This method provides a possible solution for effective and sustainable on-farm conservation of traditional rice varieties and brings substantial economic benefits to farmers because it requires low inputs and produces high outputs. We have also conducted experiments with mixed planting of various combinations of crop species, such as wheat and faba bean, potato and maize. These models have shown promise for disease and pest control, pesticide decrease and yield increases, in addition to biodiversity conservation. It is feasible to conserve traditional crop varieties in modern agroecosystems using the crop diversity management model.

The higher levels of biodiversity generated by both intra-specific and inter-specific diversity are already known to be correlated with community and ecosystem stability and resilience. Conservation and use of crop genetic diversity can minimize pest and disease damage, substitute for pesticide use and contribute to sustainable crop production, farmers' livelihoods and environmental sustainability.

Epidemiological Bases of Variety Mixtures for Reduction of Pest and Disease Damage

Murray, T.; Milgroom, M.

The central hypothesis of the current project on the use of variety mixtures to reduce damage from pests and diseases is that genetic uniformity increases vulnerability to pests and diseases, resulting in greater damage. Increasing genetic diversity through directed breeding efforts or mixing of existing varieties should result in less damage because no single component of a mixture will be susceptible to a given pathogen strain or race at the same time, thereby reducing vulnerability. One of the principal assumptions in limiting damage with variety mixtures is that genetic variation exists for resistance to the pest or pathogen of interest within the mixture. There is a significant body of scientific literature on the use of variety mixtures for control of pests and diseases that has identified the epidemiological reasons for their effectiveness.

Three types of mixtures are generally recognized, depending on how they are developed - landraces, variety mixtures, and multiline varieties. Landraces develop in localized areas in response to local selection pressures. The genetic heterogeneity in landraces develops slowly as a result of management by farmers. Variety mixtures result from intentional or unintentional mixing of seed of existing varieties. The individual varieties may be developed by modern breeding programs, locally selected, or a combination of both. The components of intentional mixtures usually have similar agronomic traits but differ in other characteristics such as disease resistance. The amount of genetic heterogeneity in a mixture depends on the components of the mixture. Multiline varieties are mixtures of lines that are developed intentionally by breeders to be grown together. As the name suggests, multiline varieties are composed of multiple lines (2-10 or more), each of which has very similar agronomic characteristics but differs in its disease resistance genes. Multiline varieties are usually developed for diseases in which race-specific resistance exists (see below). As a result, a single multiline variety contains several different resistance genes to a single pathogen, which reduces overall vulnerability of the variety. Multiline varieties are less genetically diverse overall than variety mixtures or landraces, but they may be more diverse for critical disease resistance genes.

In most instances, mixtures reduce disease severity compared to the mean of pure stands of the components in the mixture; this is known as a mixture effect. Mixture effects are the result of three mechanisms. First, the density of any one component is reduced compared to a pure stand. Therefore, inoculum produced on one plant is less likely to be dispersed to another plant of the same genotype on which it will be compatible and cause disease, simply because they are farther apart. Second, the presence of multiple plant genotypes presents a physical barrier to the dispersal of a pathogen between plants of the same genotype. Third, inoculum from one plant genotype that lands on another plant genotype may stimulate induced resistance, even though it does not itself cause disease. Induced resistance purportedly reduces the growth and reproduction of pathogens that do infect and cause disease. This latter mechanism is somewhat controversial, and

its impact as a general mechanism is unclear. Some types of mixtures change the microclimate, making conditions less favorable for pests or diseases in susceptible plants; for example, tall and short varieties in rice mixtures.

The epidemiology of disease in cultivar mixtures is based on the concept of autoinfection. Autoinfection is a term that was initially applied to infection of a plant when inoculum was produced on the same plant. In the context of mixtures, however, autoinfection refers to infection of a plant when inoculum comes from a plant of the same genotype. The critical assumption is that autoinfection will result in disease because the pathogen and host genotypes are compatible, i.e., race-specific resistance will not be effective to inoculum of compatible races already infecting a particular host genotype. The goal in mixtures is to reduce autoinfection, and thereby reduce disease severity (or increase the mixture effect). In mixtures, autoinfection is a function of the plant, the pathogen and how the host genotypes are planted by the farmer. If host genotypes are planted in rows or plots, as opposed to random mixtures of seeds, then the spatial aggregation of plant genotypes results in a larger host genotype unit area (GUA) compared to single plants, with corresponding greater autoinfection and disease. In general for a given crop, smaller GUAs result in less disease because autoinfection is reduced. Similarly, when comparing different crops, those with smaller plants (small GUAs), e.g., rice or barley, will have larger mixture effects than those with larger plants (medium or large GUAs), e.g., beans, maize or bananas. An important characteristic of pathogens for predicting mixture effects is their dispersal gradients. Pathogens that have mostly short distance-dispersal relative to plant size (steep dispersal gradients) will result in a high degree of autoinfection. By contrast, pathogens with longer distance dispersal relative to plant size (shallow dispersal gradients) will minimize autoinfection and have large mixture effects.

There are two types of disease resistance: race-specific and race-nonspecific. Other names for race-specific resistance are vertical, major-gene and qualitative resistance; race-nonspecific resistance is also called horizontal, minor-gene, quantitative and field resistance. Race-specific resistance is often controlled by single, dominant genes and therefore, has been widely used by plant breeders because it is relatively easy to identify and manipulate the trait genetically. In contrast, race-nonspecific resistance often is more difficult to identify and controlled by multiple QTL, making it more difficult to incorporate into new varieties.

Race-specific resistance is very effective in limiting disease development against some but not all races of a pathogen and consequently, host reaction tends to be either resistant or susceptible. Race-specific resistance places heavy selection pressure on races against which it is effective, leading to genetic changes in the pathogen population that result in resistance being "overcome" or "breaking down." In these instances, the resistance gene does not break down, but the pathogen changes genetically so the resistance gene is no longer effective against that pathogen; however, it remains effective against other races of the pathogen. Overall, resistance in varieties with one or a few race-specific resistance genes is not durable and new varieties must be developed continuously to maintain effective resistance.

In contrast, race-nonspecific resistance does not completely prevent disease development, so some disease will be present on resistant plants, though much less severe than on a susceptible plant. As a result, race-nonspecific resistance behaves as a quantitative trait. The great advantages of race-nonspecific resistance are its effectiveness against all races of a pathogen and its durability; once deployed in a variety, it remains effective and does not "break down."

From a variety mixture perspective, it is much more important to have a diversity of race-specific resistance genes in a mixture to reduce its vulnerability to disease than it is to have a diversity of race-nonspecific genes. Because nonspecific resistance is inherently more stable and

less vulnerable to pathogen genetic changes, the mixture effect is less when mixing varieties with nonspecific than specific resistance.

In summary, mixtures can provide effective control of some, but not all, pests and diseases and improve yield stability. Variety mixtures will be most effective when there is pathogen-specific (differential) resistance, when mixtures are grown in larger plots or fields, when the host plant is smaller, when pathogen or pest inoculum originates within the plot or field, and when the inoculum only spreads to other plants in the field (shallow dispersal gradient). Consequently, it's important to understand these attributes of the biology of the pests and diseases of concern when considering the use of variety mixtures to lessen damage.

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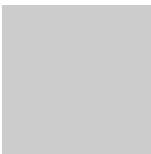
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DAMAGE, DIVERSITY AND GENETIC VULNERABILITY:



THE ROLE OF CROP GENETIC DIVERSITY IN THE
AGRICULTURAL PRODUCTION SYSTEM TO REDUCE
PEST AND DISEASE DAMAGE



Proceedings of an International
Symposium 15-17 February 2011,
Rabat, Morocco



SESSION 8



Policy implications and development actions

Implementation of the Multilateral System of Access and Benefit-Sharing From the International Treaty on Plant Genetic Resources for Food and Agriculture in Ecuador

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ABSTRACT

The publication “El Sistema Multilateral del Tratado Internacional sobre Recursos Fitogenéticos para la Alimentación y la Agricultura: Análisis e implicaciones de su implementación en el Ecuador” aims to provide the reader with a better understanding of the potential consequences of implementing the Multilateral System of Access and Benefit Sharing (MLS) contemplated in the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), especially with regard to possible incentives, disincentives, obstacles and opportunities said implementation might face. The first part develops on the situation of plant genetic resources for food and agriculture (PGRFA) in Ecuador, elaborating primarily on the state of PGRFA use and conservation in the country. However, this portrayal relates mainly to *ex situ* conservation, given that Ecuador does not provide sufficient and appropriate information regarding *in situ* conservation of PGRFA. This part of the document explains how germplasm is introduced and distributed in the country, pointing out that Ecuador has benefitted from the use of germplasm obtained from foreign collections, including in relation to export and mass consumption products. Additionally, it describes the regulatory framework in Ecuador for accessing and using germplasm held in national collections, stressing that the lack of clear applicable norms and procedures has produced a chilling effect on PGRFA conservation and research, mainly due to fear of biopiracy. It also discusses the difficulties that users of PGRFA must face when trying to access germplasm, as well as the existing initiatives and information related to its conservation. Finally, the first part of the document analyzes the current legislation in Ecuador in order to identify both the provisions and arguments that support the implementation of the MLS, as well as those that might pose a legal obstacle to it, concluding that there is a sufficient legislative, regulatory and administrative basis for implementing the MLS in the country.

The second part of the document is rather short and focuses on the incentives for participating in the MLS, the most notable being the free availability of more than 500,000 accessions of crops conserved in international centers and the possibility of participating in the benefit-sharing mechanisms regulated by the Treaty.

Finally, the third part of the document analyzes in depth the possible incentives, disincentives, obstacles and opportunities that are likely to occur when implementing the MLS. As far as the disincentives and obstacles, the most notable consist of intellectual property rights that may limit the free exchange of seeds recognized in the Ecuadorian institution, the lack of information and regulation of access to and conservation of PGRFA, and the administrative structure of the Ecu-

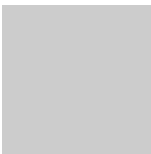
dorian State. In this context, the document includes juridical and administrative measures that may be taken in order to address the difficulties, such as the creation of a *sui generis* regime for plant varieties that excludes Annex 1+ crops from intellectual property protection. With regard to the incentives and opportunities, the possibility of accessing the benefits contemplated under the Treaty is emphasized. Furthermore, it is stressed that the authorities in charge of implementing the MLS must provide the adequate information, support and advice when conceiving, designing and submitting the projects that are considered for funding, especially to small and medium farmers.



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POST PROGRAMME EVENT

Promoting agrobiodiversity with local identities: NUS and typical/local products as a lever for rural development and empowerment of poor farmers and smallscale producers

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Introduction

The mountain zone of Errachidia and Midelt Provinces in the Eastern High Atlas in Morocco is rich in underutilized crops that provide important nutritional and cultural elements. This flora is distinguished by pre-Saharan and Saharan bio climate species. It embodies a natural and cultural inheritance with high added value that could be very important for the development of income-generating activities related to environment and food-diversity protection. NUS (neglected and underutilized species), which are strictly territory-related, hold several advantages for local rural communities: they are highly adapted to a range of agro ecological niches and marginal areas and they are linked to cultural and social values as a part of the cultural identity, which is very strong in this area. Research on the East Atlas regional NUS can show us several uses of these crops applicable to medicine, rural tourism and marketing of origin-linked quality products.

METHODS

In order to involve small farmer target groups in agrobiodiversity conservation and local variety protection, our approach follows four steps:

1) Research on local NUS and added value local products. A detailed survey of the aromatic and medicinal plant (MAP) chain has been carried out. The objective was to select a restricted list of potential MAPs to be economically exploited and cultivated. The research-action methodology employed foresaw the direct engagement of people, involved through workshops and the implementation of practical activities during the training, to facilitate the process of learning by doing. The survey was conducted in three Administrative Divisions: Rich, Assoul and Imilchil, whose territories are part of the PNHAO (Parc National du Haut-Atlas Oriental).

2) List of MAP, the knowledge and use of which should be improved for their environmental, cultural and commercial value. As a result of the survey, a list of MAP used in traditional medicine, a list of MAP marketed at local, regional and national level, a list of MAP operators to be trained and a catalogue of MAP to be exploited through different income-generating activities, have been drafted. A list of products and handicrafts to be promoted has been elaborated as well. According to the results of the survey, a restricted list of about fifteen MAP with a potential for regional markets

(rosemary, thyme, wild fennel, caper, pistachio, Artemisia, a species of mugwort, wild mint, sage, juniper tree, almond tree, walnut tree, caper) has been constructed.

3) *Through a participatory approach, identify needs and pilot projects to be carried out.* The survey carried out permitted the researchers to investigate the knowledge and know-how of local communities, in particular for their cultural and identity-bound added value in the field of natural resources and neglected traditions. The added value of MAP is almost neglected among new generations, and consequently their exploitation (commercial or not) is underutilized. This common perception is contrasted by the high number of economic opportunities MAP give to the people engaged in their exploitation. This is the reason why one of the main needs assessed was the promotion of information on the potential of MAP. Data collected during the survey were presented to local farmer cooperatives and associations in the framework of several workshops and meetings, during which target groups expressed needs and proposed some pilot projects that have been evaluated and launched.

4) *Launching of the cultivation of wild fennel (in two sites), technical assistance aiming at the preservation of almond tree, and enhancement of local honey production.* Two pilot sites have been identified to launch, for the first time in this region, the cultivation of wild fennel (which, according to data analysis could potentially improve families' medium revenue by 75%). Furthermore, a survey on almond production and training on almond tree cultivation methods (in order to improve product's quality and quantity) have been carried out.

RESULTS

The analysis of collected data permitted researchers to verify that in the case of *wild fennel* (*Foeniculum vulgare*), for example, a family dedicates 10 full days of work in order to produce a hundred kilos. Each family normally can collect and produce 300 kilos per year. The medium prize of one kilo paid by the intermediary is 50 dirham, which means 15,000 dirham per year (about 1.500 Euro). Considering that the medium income generated by agricultural activities is about 3.100 dirham, it means that this MAP exploitation could potentially improve the medium revenue by 75%. But, at present, no more than 20-30 families per district are doing business with wild fennel exploitation.

Two local associations (a farmers' one in Sidi Boukil and a women's one in Gourrama) have been selected to be directly involved during the construction and management of a greenhouse for the reproduction of plants and the planting of wild fennel seeds. Direct beneficiaries of the action numbered about twenty during the first year and now number about fifty. Local association members have been trained to better manage their natural resources, and they have been made aware of the importance of belonging to an organization such as a cooperative. Most of the Sidi Boukil association members are establishing a cooperative to exploit and enhance natural resources, especially MAP.

Another product with a high potential in the local, but also in the national and international, markets has been identified: the **almond tree** in the area of Amellagou (district of Assoul). Almonds are a typical product of this region (in 13 villages extending over a surface of about 35 km) and they are appreciated all over Morocco. Almost every family is involved in the production of almonds, and the production last year amounted to 300 tons for the area involved. A survey in this target area has been carried out, identifying several weaknesses in almond production in the region. Above all, the lack of farmer coordination and organization, as well as the lack of technical skills (such as pruning and grafting), have been underlined. Training events have been organized

to provide farmers (both men and women) with technical assistance and to raise awareness of the practical utility (for example, improved commercialization) of being organized in a cooperative.

Beekeeping is another sector with high potential for local development. **Honey** produced in this area is renowned all over the country. Climate, local know-how and traditions make this honey different from other similar products. In addition, in this mountainous area we can find the yellow bee, a Saharan variety. Its honey is excellent and very expensive in regional and national markets. Ten organizations of honey producers (both associations and cooperatives) were given the opportunity to exhibit their honey and their production equipment. After this event, three existing cooperatives established a federation in order to combine their strengths.

DISCUSSION

The main objective of this program is to address the marginalization of farmers by enhancing neglected local crops and fostering local agrobiodiversity. The understanding of cultural values related to NUS, together with NUS quality and quantity production improvement and market access promotion (both at local and national level), are specific objectives.

The surveys carried out showed a lack of awareness of local natural resources and farmers' organizational potential. On the basis of the collected data, our work was designed to address the main needs as assessed. Through several workshops, practical training sessions and a participatory approach in identifying pilot projects to be carried out, beneficiaries (about 70 farmers) are now more aware of their biodiversity and local resources. In fact, a locally-based association involved in our activities is now establishing a cooperative to exploit and enhance local aromatic and medicinal plants and other local products. Furthermore, almond producers from Amellagou started pruning and grafting their trees, which they had never done before. The link between products and producers is now stronger in this region.

Mycotoxins in cereals: a food safety concern in traditional varieties

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Mycotoxins are chemical contaminants produced as secondary metabolites of fungal origin in specific biotic-stressed conditions in a wide variety of food and feed commodities. Mycotoxins are produced by fungi of the *Aspergillus*, *Penicillium* and *Fusarium* genera. Due to the wide range of matrices susceptible to mycotoxin, their contamination represents a worldwide problem that is amplified in developing countries of Africa, Asia and South America where the contamination occurs in staple foods such as ground nuts and cereals.

FAO states that approximately 25% of the crops worldwide are contaminated by mycotoxins. Epidemiological correlations between several mycotoxins and diverse health problems have already been established. For example, aflatoxins, one of the the most potent carcinogens, have been shown to be related to acute toxicosis (and also death), liver cancer, morbidity in children suffering from kwarhiorkor and, more recently, stunting. Esophageal cancer and neural tube birth defects have been statistically correlated with exposure to fumonisins. Those two mycotoxins are major contaminants in maize and barley.

For small-scale farmers in developing countries, the mycotoxins pass from field to storage to consumption without any regulatory oversight and without any test of the extent of contamination. Very often the farmer is not aware of or sensitive to the possibility of mycotoxin contamination, in particular in the absence of visible and unacceptable levels of mould, since the farmer concern is more focused on crop yield and nutritional content instead of a food safety concern. Moreover, small farmers are often driven towards adopting new varieties without adequate information on whether the variety has resistance to mycotoxin contamination in their production systems.

For large- or medium-scale farmers, economic and trade problems can originate from the need to export large quantities of food to the EU, where the key hurdle are the stringent EU regulations and standards; this in turn may have consequences on the health of the local population due to the obligation to export the highest-quality goods, leaving the more contaminated for internal consumption, where legislation is lacking or controls are less stringent.

A great potential for managing the mycotoxin problem, either directly or indirectly, lies in genetic resistance. A large amount of research has been devoted to the development of new maize and other crop varieties resistant to aflatoxin and other mycotoxin development. Yet although native resistance for mycotoxigenic fungi has been found to exist at least in maize, little work has been done to examine differences in mycotoxin resistance among local crop varieties.

Assessing the degree of resistance to mycotoxin formation and levels of these local crop varieties, which are already being assessed for their resistance to other pathogens, would contribute to obtaining a more complete scenario of pros and cons of growing a traditional variety in a given

area, providing a more complete scientific tool for assessing the value of using traditional varieties versus other practices in terms of preventing post-harvest losses and health problems.

In this presentation, the objective of assessing the mycotoxin scenario under a traditional agricultural input system is suggested as an idea for potential projects and the subject of grant proposals.

CYCAS-MED Project: Impact of climate change on crop yield in Mediterranean areas

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INTRODUCTION

Future climate scenarios indicate a general increase in temperature and decrease in rainfall for the Mediterranean area, with a significant increase in aridity conditions for Morocco. However, it is well known that climate models give predictions of average climate conditions rather than probabilities of extreme events. Prolonged drought conditions negatively affecting crop yields are predicted to be more likely from 2030. Vulnerability to climate change will depend on crops, with rainfed crops much more vulnerable than irrigated crops.

CYCAS-MED (*Crop Yield and Climate Change Impacts: Adaptation Strategies to Desertification Processes in MEDiterranean Areas*) is an international cooperation project based on the application of a set of integrated methodological strategies aimed at (i) developing tools and methodologies for assessing the impact of climate change on Mediterranean regions and evaluating the specific impact on agricultural areas threatened by desertification, and (ii) identifying the most appropriate socio-economically sustainable adaptation strategies to cope with the negative effects of climatic change.

CYCAS-MED was carried out in cooperation with the Laboratoire d'Agrométéorologie et Systèmes d'Informations Géographiques, Centre Régional de la Recherche Agronomique, Institut National de la Recherche Agronomique, INRA-CRRA, located in Settat, Morocco.

METHODS

CYCAS-MED research activities were devoted to:

- 1) Describing the climatology of the study area and quantifying possible climate trends;
- 2) Developing an agro-climatic classification system at national and local scales for agricultural areas, with particular attention to the Chaouia Ouardigha province (Northwestern Morocco);
- 3) Analyzing relationships between the variability of observed weather and the variability of observed cereal productions with the aim of quantifying the impacts of climate change and desertification on food cereals productions at local scale;
- 4) Providing breeding guidelines for yield potential and adaptation to future drought conditions in cereals, with a specific focus on soft and durum wheat varieties;
- 5) Evaluating the economic impacts of adaptation strategies to climate change at local and farm-level scales using different tools and climate scenarios.

Climate analysis was performed using data from 26 weather stations for the periods 1961-1990 and 1971-2000, and selecting data sets longer than 20 years. From temperature and rainfall data, several meteorological and biometeorological indices at different time scales were calculated (temperature and rainfall statistics, evapotranspiration, maximum number of consecutive dry days, heat wave duration index, growing degree days, length of the growing period, etc. With the purpose of developing an agro-climatic classification system, observed and future climate variability data were combined with geographic and soil information at different spatial scales using land capability and a land suitability for agriculture classification systems, which classifies agricultural land into a range of quality and potential productivity.

The impacts of climate variability and changes on durum wheat and cereal productivity in Morocco were assessed running a crop growth and development simulation model and using a statistical approach.

RESULTS

The climate analysis showed a significantly increasing trend for temperature (minimum, maximum and average daily values) for most sites using the Mann-Kendall test. Rainfall data were much more difficult to analyze due to the large number of missing data.

The agro-climatic classification study produced maps of land capability at national level and land suitability for agriculture at local level for both the actual and the future climate of Morocco.

This project included the following activities related to climate variability and climate risk tasks:

(1) Data on soils and climate of study areas and long agronomic data series for durum wheat data (genotypes, phenology and agronomic management) were used to calibrate and validate the crop simulation models CERES-Wheat, implemented in the software package DSSAT v. 4.0. (2) The model performance was evaluated in terms of productivity (grain yield), development (anthesis date), and quality (unit kernel weight) using several statistics (RMSE; Index of Agreement, Modeling Efficiency, etc.). (3) In addition, the potential effect of future climate scenarios on wheat production and quality using the CERES-wheat model and different climate scenarios was evaluated.

Data on soils and climate, and long agronomic data series for cereals (corn, wheat, barley) were used to analyze the relationship between climate and crop yield variability, using a simple and general FAO model implemented in the AgrometShell tools. Weather observations and observed yields were statistically linked in a so-called Weather Yields Function (WYF) using a statistic threshold stepwise method. In addition, long-time series of synthetic weather data according to current and future climate were produced using a Stochastic Weather Generator (SWG). In conclusion, a comparison of weather and yield characteristics under current and climate change conditions was performed.

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Empowering Sahelian Farmers to leverage their crop diversity assets for enhanced livelihood strategies

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INTRODUCTION

Small-scale farmers in developing countries depend on genetic diversity, in the form of traditional crop varieties, to maintain sustainable production and meet their livelihood needs. Decrease in genetic diversity, reflected as limited access to suitable genetic diversity, therefore, diminishes farmers' capacities to cope with changes in their environment. National and international plant breeding efforts focus on high-yielding varieties and specific agronomic traits. Modern seed systems are established to produce certified seeds for such elite materials. These systems do not take into account traditional cultivars and local genetic diversity. In the high-risk environment of the Sahelian countries of West Africa, local seed systems maintain significant levels of diversity, while allowing further development and adaptation to meet changing conditions. Farmers rely essentially on informal seed systems built around production of their own seed, kept in an evolving diversified gene pool through networks of exchange and selection. Seventy percent of Sahelian farmers depend on traditional seed systems for their food production. Despite its sustainability and its large adoption, traditional seed systems do not receive due attention from national and international research efforts and do not benefit from government support. Therefore strengthening of seed system health and resilience in the Sahelian West Africa region is crucial for reducing the vulnerability of rural and urban populations facing global climate change. A portfolio of seed of desired local crops and varieties with preferred traits and associated knowledge needs to be competitive, reliably available and accessible within reasonable proximity to people, and in time for critical sowing periods.

METHODOLOGY

The project that was implemented in Burkina Faso, Mali and Niger in West Africa aimed at empowering farmers by strengthening their human, social, natural and political capitals. The project activities were organized into two major components, research and capacity building. The activities are coordinated by international and national partners. Bioversity provided overall coordination to the project while coordination at national level was provided by national research institutions (INERA, IER and INRAN). In addition, the inter-university component was coordinated by ICRAF. A Regional Project Steering Committee was set up that met annually to examine progress and to approve planned activities. In addition, the project benefited from strong and diverse support at the national level by national research and development institutions: INERA (Burkina Faso), IER (Mali), INRAN (Niger) and extension services, national universities (Ouaga & Bobodioulasso in Burkina Faso, Katebougou and Bamako in Mali and CRESA, Niamey in Niger),

IFAD loan projects (FODESA, PPILDA, PICOFA, PDRT), national and local NGOs and farmers' groups. The project also benefited from inputs at the international level by ICRISAT, European universities (Italy, Belgium, Switzerland), FAO and the international NGO Enda Intermondes.

Initially the project activities were implemented in three sites per country, but many other sites were added by additional loan projects and farmers' groups. Diversity Field Fora (DFF), composed of male and female farmers, were organized in project teams (25-30 members) to assess crop genetic diversity. The DFF approach, a new innovation platform in high non-heritability environments¹ in West Africa, was used to strengthen the capacity of farmers to analyze and manage their own crop plant genetic resources. In DFF, farmers' groups in low heritability environments test both improved and local cultivars. Seeds of the selected cultivars are multiplied and disseminated within and outside the groups. The informal seed systems supply an evolving diversified gene pool through exchange and selection to allow continued adaptation to changing conditions. The approach takes into account that the preferred selection criteria by women and men farmers differed. This participatory approach generated options that farmers are able to use instead of technology transfer from outside sources. In addition, seed fairs were organized to share information and planting materials among farmers, researchers and extension agents.

RESULTS

Natural Capital

Crop production was improved in the project sites by using cultivars selected by farmers with their selection criteria and through discussions with researchers and extension agents: millet (11), sorghum (12), cowpea (6) and bambara groundnut (2) in Mali. Crop production was also improved by using quality seeds of local cultivars or improved varieties selected in DFF (farmers are trained in seed multiplication), by sharing information and planting materials through seed fairs, and by conserving genetic resources in community genebanks for future use. Newly domesticated crops are tested by women. Women farmers in Niger produced and sold seeds of domesticated *Cassia tora* and *Cerathoteca sp.* The local domestication practices led to more nutrient rich genetic diversity being available for use.

Human Capital

Weekly meetings at DFF helped strengthen farmers' capacities to improve: the deployment of diversity; the adoption of appropriate planting/seeding density (sorghum); pest and disease management (timely uprooting and burning of striga plants. use of local products to control insect pests on plants and in storage etc); quality seed production (millet, sorghum, cowpea); and the initiation of community gene banks and seeds (Petaka, Dan Saga and Thiougou). Training of facilitators and students on crop diversity conservation on-farm using the DFF approach resulted in 28 facilitators being trained in on-farm conservation methodologies, 24 students trained in various aspects of on-farm conservation based on DFF, and numerous researchers, extension agents and lecturers were familiarized with the DFF approach and methodologies. In addition,

¹ Low heritability environments are environment where seedling establishment and breeding adaptive varieties is difficult due crop growing environments being quite heterogeneous, and to environmental conditions, such as unpredictability, or the uncertainty in seasonal distribution of in the Sahel.

the DFF approach was incorporated in training modules at the University of Niamey (CRESA). Furthermore, the University of Pisa in Italy has DFF on its agenda for its new training module development.

Social Capital

The adoption of the DFF approach was an appropriate platform for exchange and consensus building in local development strategies in Mali. Local authorities in Sadien, Sokoro and Bombora in Mali witnessed that DFF, apart from increasing agricultural productivity, also contributed to peace and social cohesion in local communities.

Political capital

The Diversity Seed Fairs (DSF) were used to sensitize local authorities on the role and contributions of crop diversity to increasing agricultural productivity. Through the DSF, decision makers are convinced that the efforts of local communities to conserve and enhance crop genetic diversity are valuable and they are better prepared to provide needed support to farmers. In addition, through weekly meetings at DFF, farmers are informed about international and national conventions and legislation relevant to the exchange of plant genetic resources (CBD, IT) or seed regulation.

DISCUSSION

Farmers and facilitators improved management practices for crop biodiversity and participatory selection methods for crop varieties. A training manual on the conservation of crop biodiversity on farms was produced for facilitators, technicians and university students. A partnership was created among farming communities, universities and research institutions to improve the training of university students in crop biodiversity, conservation and utilization. Farmers' experiences and innovations were recognized and valued through exchange visits and SFs. Some farmers in Mali and Niger developed skills in seed production and formed seed producer associations. Farmers in Niger also learned how to produce hybrid seeds of sorghum. Farmers are now equipped to share their visions and experiences with other partners, and researchers are gradually revising their approach by paying more attention to farmers' views and innovations.

DFFs and SFs strengthened social cohesion in the participating villages. Farmers in some villages in Burkina Faso, Mali and Niger formed associations to design and implement new activities for their benefits. These associations, which were funded by individual contributions and joint production activities, strengthened and improved production capacities and also assisted members in case of urgent need. The training programmes of the DFFs offered opportunities for farmers' associations to discuss technical and other issues. Exchange visits among project sites allowed farmers to discuss local solutions to common and local problems: the visit to Nepal was particularly useful because it allowed Sahelian farmers to see and discuss plant genetic resource management techniques of farmers in different social, political and environmental conditions.

Some landraces were reintroduced and local crop biodiversity increased substantially in the project sites. Farmers improved their skills for testing and selecting crop varieties, reintroduced some cowpea landraces that had disappeared from some villages in Mali, and multiplied popular varieties of millet in Niger.

Traditional rules for managing plant genetic resources were documented. Village chiefs control access to "sacred forests", which are rich in plant genetic resources. Some technicians, researchers

and farmers learned about national and international legal instruments regarding the exchange of genetic resources. The International Treaty on Plant Genetic Resources for Food and Agriculture was translated into Haoussa for farmers in Niger, and some local authorities in Mali decided to include DFF in their development plans.

Table 1: Number of selected varieties in Burkina Faso, Mali and Niger by farmers involved in the Diversity Field Fora approach. Brackets indicate local cultivars. NT indicates that no testing was conducted.

Varieties	Country		
	Burkina Faso	Mali	Niger
Millet	2 (1)*	6 (4)	3 (1)
Sorghum	1 (0)	4 (2)	3 (2)
Cowpea	4 (2)	5 (2)	2 (1)
Bambara groundnut	NT	2 (2)	NT
Peanut	2 (1)	1 (0)	2 (1)
Chinese senna	NT	NT	2 (2)
Okra	2 (1)	NT	NT

Table 2 Some preferred selection criteria according to gender

Preferred selection criteria by gender		
Crop/Trait	Preference	
	Men	Women
Millet		
Height	Tall	Medium
Panicle size	Long	Long
Grain size	Big	Medium
Growth cycle	Medium	Short
Cooking qualities	Market demand	Suitable for local dishes and drinks
Cowpea		
Growth cycle	Short	Short
Grain color	Market demand	White
Insect resistance	Field	Field and in storage
Cooking qualities	Market demand	Short cooking time, good taste

Table 3: Self Sponsored DDF in Mali

Village	01	02	03	04	05	06	07
Bogoro	X	X	X		X	A	A
Sadien	X	X	X		A	A	A
Sokoro	X	X	X		A	A	A
Diagani	X	X	X		X	A	A
Bomboro	X	X	X		X	X	X
Somo	X	X	X			X	X
Nougosso	X		X				

N.B: X means project implementation during the year and A means DFF activities are self-funded by farmers

In situ/On-farm conservation and use of temperate fruit tree genetic diversity in cultivated and wild ecosystems in Central Asia

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INTRODUCTION

Central Asia is a home for many globally important agricultural crops and is considered by N. I. Vavilov as one of the five most important centres of origin of cultivated plants. There is a rich specific diversity of plants, amounting to 8,100 species, of which 890 are endemic. About 400 of these are listed in the IUCN "Red Data Book" as endangered.

Particularly important crops in Central Asia are the temperate fruit species. Apple (*Malus* sp.), apricot (*Armeniaca vulgaris*), peach (*Persica vulgaris*), pear (*Pyrus* sp.), plum (*Prunus domestica*), grape (*Vitis vinifera*), almond (*Amygdalus communis*), pistachio (*Pistacia vera*), pomegranate (*Punica granatum*), and fig (*Ficus carica*) are among the best known crops cultivated in the region where, over the course of several centuries, the diverse natural and climatic conditions have helped farmers produce varieties adaptable to drought and resistant to a number of environmental stress factors. These locally-developed traditional varieties have been shown to be essential components of crop production in difficult environments.

Wild populations of fruit species such as apple (*Malus* spp.), pear (*Pyrus* spp.), plum (*Prunus* spp.), almond (*Amygdalus* spp.), pomegranate (*Punica granatum*), grape (*Vitis* sp.), as well as other wild relatives of fruit crops, still grow and are cultivated in forests throughout the region. Many of them are used as rootstocks. Their resistance to biotic pressures (insects and disease) make them valuable genetic resources for reducing crop vulnerability on-farm and providing genetic material for crop improvement. Many of these species are also important nutritional resources for local people.

Diversity in situ and on farm

Expedition missions, focus group discussions and household surveys conducted in 2006-2010 within the regional project "In situ/On farm Conservation and Use of Agrobiodiversity in Central Asia," coordinated by Bioversity International in Kazakhstan, Kyrgyzstan, Tajikistan, Turkmenistan and Uzbekistan, demonstrated that the process of evolution is still ongoing in the wild populations of fruit species. Focus group discussions organized in forest sites demonstrated that 112 promising forms with economically valuable traits were distinguished by forest dwellers and included 27 forms of *Malus siversii*, 16 of *Prunus armeniaca*, 28 of *Juglans regia*, 19 of *Pistacia vera*, 11 of *Prunus cerasifera*. This local diversity possesses valuable traits such as early maturation, resis-

tance to spring frosts, tolerance to salinity and drought, and fruit-bearing in the off-season, all of which could be valuable traits for breeding improved commercial varieties.

Rich diversity of fruit crops is still maintained in farmers' orchards. 160 local varieties of grapevine, 145 of apple, 103 of apricot, 32 of pear, 26 of pomegranate and 15 of mulberry were morphologically described by national project teams. Along with widely-spread local varieties of grape such as Husayni, Karajanjal, Kishmish, Kattakurgan, and Choros, farmers are also growing such rare and unique varieties as Olomon tuydi, Chumchuk tili, Kara kulcha, Shohona, Hamirak. Local apricot diversity includes varieties such as Kandaki, Bobo rajabi, Arzami, Hurmoi, Soinchalak, Safedak and Akbari. Dried apricots, known as "uruk", "kaysa", "kuraga" and "pashmak," as well as salted apricot seeds, are very popular among local people and are the main source of income for many farmers in Tajikistan and Uzbekistan. Early ripening local varieties of apple such as Rahshoki, Peshpasak, Gulseb, Pahtaseb, Hazaraspskiy and Boysun kysyl olma are in great demand at local markets in late spring and early summer seasons when there is a strong need for nutrients in the diet after cold winter.

Helping the farmers in conservation and use

Unfortunately, the introduction of uniform high-yield varieties, the use of chemical fertilizers and pesticides and increased mechanization have reduced the area of agricultural lands on which many valuable landraces and local cultivars of these species are maintained. In order to mitigate genetic erosion of the local diversity of fruit crops, the national project teams established 54 fruit tree nurseries, including 11 in Kazakhstan, 7 in Kyrgyzstan, 9 in Tajikistan, 10 in Turkmenistan and 16 in Uzbekistan. Eight hundred thousand saplings of local varieties of temperate fruit crops have been produced yearly in these nurseries and distributed among farmers. These nurseries are also used as demonstration sites for training farmers on fruit tree grafting technologies. Sixty-five demonstration plots were established in orchards of farmers/custodians of diversity: 12 in Kazakhstan, 7 in Kyrgyzstan, 14 in Tajikistan, 10 in Turkmenistan and 22 in Uzbekistan. Farmers' field days, training events and workshops were organized in these demonstration plots where farmers could gain knowledge on 430 local varieties and promising fruit crops and their wild relatives. These demonstration plots are also providing mother material for grafting fruit trees.

Empowering community and rural institutions for on-farm/in situ conservation and sustainable use of cultivated and wild tropical fruit diversity in Asia

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SUMMARY

On-farm (*in situ*) conservation of cultivated plants refers to management of landraces/cultivars and occasionally cultivated wild relatives (as in the case of fruit species like mango) in the very place where they developed their present-day characteristics. Tropical and sub-tropical fruits are an important part of culture in Asia because of their nutritional and use values. Over the years, farmers have selected unique varieties and developed a range of production and management practices to conserve and sustainably use tropical fruit species diversity. Fruit tree varieties and related good practices innovated by farmers in their home gardens and semi-commercial orchards are important assets and represent genetic resources that are still under-utilized and neglected considering their potentially lucrative market value. This paper describes a participatory and innovative method for assessing the fruit genetic diversity in farming communities in order to develop both livelihood options and conservation actions based on diversity available to farmers. The amount and distribution of citrus, mango, rambutan and mangosteen species diversity was assessed in 36 communities from India, Indonesia, Malaysia and Thailand. The study used the participatory four cell analysis technique to: measure richness and evenness of fruit tree species diversity; to identify common, endangered, unique or rare fruit species and/or varieties; to identify potential livelihood options; and to develop community-led conservation action plans for threatened and endangered species and varieties. Analysis revealed that traditional fruit diversity is still widely found in most Asian countries but is seriously threatened by a range of socio-economic pressures and government policies. This tool helps to assess the level of threat and develop actions to counter these threats by making communities aware of diversity loss and then facilitating the effective and efficient selection of appropriate on-farm (*in situ*) conservation or livelihood interventions per variety and species as part of a community-based biodiversity management (CBM) approach. CBM emerged as a strategy for realizing on-farm management of genetic diversity that integrates knowledge and practices into local farming and social systems. Researchers have identified 10 clones of *Citrus grandis*, eight clones of *Mangifera indica*, two clones of *Nephelium* spp. (*lappaceum* and *ramboutan-ake*) and two clones of *Garcinia atroviridis* and *G. forbesii* from all four countries that have favorable traits. These selected varieties are propagated by the community and sold/distributed for further promotion and conservation. This paper describes, through examples, a few of good practices of conservation and sustainable

use of cultivated and wild tropical fruit tree species in Asia that at the same time help farmers to benefit directly from growing tropical fruit species.

Keywords: *good practices, in situ/on-farm conservation, tropical fruit species, sustainable livelihoods, agricultural biodiversity, participatory assessment tool, community biodiversity management*

