The International *Musa* Testing Programme (IMTP) phase II overview of final report and summary of results

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The establishment of an International *Musa* Testing Programme (IMTP) began in 1989 as a co-operative partnership between National Agricultural Research Systems (NARS), INIBAP, breeding programmes and pathologists from several institutes with the support of UNDP. The aim was to identify in multilocational trials around the world resistant banana and plantain hybrids which would meet local requirements and with which small-scale farmers could replace existing susceptible cultivars. Another objective of IMTP was to stimulate breeding by providing information to breeding programmes on the pathological response of their improved varieties. As a spill-over effect, IMTP also helped to increase the capacity of national organisations to carry out research on bananas and plantains.

The programme began evaluating germplasm from the FHIA breeding programme for resistance to black Sigatoka (*Mycosphaerella fijiensis*). Seven tetraploid hybrids with wide genetic backgrounds were tested along with several reference diploid clones (both wild and edible) that represented the whole range of reaction to black Sigatoka, from highly resistant to highly susceptible. The experiments were established in six countries. The site managers were provided with training, technical guidelines and funding for carrying out the experiments. Four years later, a final document was published that presented the detailed results of IMTP. The recommendation was made to release three clones for distribution: the clones FHIA-01 and FHIA-02, both dessert banana varieties with outstanding performance and high resistance to black Sigatoka, and FHIA-03, a cooking banana also with excellent performance and resistance to black Sigatoka. Over the last ten years these three clones have been distributed to more than 50 countries world-wide.

The success of IMTP phase I encouraged the growth of the programme and INIBAP was requested to develop the initiative further. In 1991, another proposal was submitted to UNDP and approved for a total of three years. The proposal also included support to breeding programmes, virus indexing of the germplasm donated by breeding programmes, support to research on viruses, publication of results, and staff. This time no funds were allocated for the establishment and maintenance of trial sites. However, most NARS decided that given the relevance of IMTP for their programmes they were prepared to finance the trials themselves.

For IMTP phase II, all aspects of the programme were expanded. Instead of evaluating germplasm for resistance to only one pathogen, in this phase germplasm was evaluated for resistance to three diseases, black Sigatoka: *M. fijiensis*, yellow Sigatoka: *M. musicola* and Fusarium wilt: *Fusarium oxysporum* f. sp. *cubense*. Four breeding programmes contributed germplasm, a list of which is provided in Table 1, and the number of testing sites increased from six to 37, despite the fact that the trials were financed at the participating institute's own expense.

The majority of IMTP phase II trials were planted during 1996 and 1997. The complete report includes results from the Fusarium wilt (*Foc*) sites in Australia, Brazil, Honduras, Indonesia, Malaysia, the Philippines, South Africa, Spain, Taiwan, and Uganda, from the black Sigatoka (BS) sites in Cameroon, Costa Rica, Honduras, Nigeria, the Philippines, Tonga and Uganda and from one yellow Sigatoka (YS) site in Colombia.

Although many sites provided data, a complete analysis was not possible due to much missing data following natural catastrophes and incomplete collection of data at some of the sites. These sites included one *Foc* site in Australia, one YS site in Cameroon, three sites in Cuba (one BS, one YS and one *Foc*), five sites in India (two YS and three *Foc*), two *Foc* sites in Indonesia, one *Foc* site in Malaysia, one YS site in St. Lucia and two sites in Thailand (one *Foc* and one YS).

This article is a summary that provides an overview of the IMTP II results. For space reasons we present here only the averages for bunch

Table 1. Improved cultivars included in the Sigatoka and Fusarium resistance trials of IMTP Phase II.

Name of the cultivar	Origin	Genome	Pedigree	Disease	
				Sigatoka	Fusarium
PV-03.44	EMBRAPA[1]	AAAB	Pacovan x Calcutta 4	✓	✓
PA-03.22			Prata Aña x Calcutta 4	✓	
SH-3436-9	INIVIT[1]	AAAA	Somaclonal variant of SH-3436: Highgate x SH-3142	✓	
FHIA-01	FHIA[1]	AAAB	Prata Aña x (Prata Aña x SH-3142)		✓
FHIA-03		AABB	SH-3486 x SH-3320		✓
FHIA-17		AAAA	Gros Michel Highgate x SH-3362		✓
FHIA-23		AAAA	Highgate x SH-3362	✓	✓
GCTCV-119	TBRI[1]	AAA	Giant Cavendish tissue culture variant		✓
GCTCV-215		AAA	Giant Cavendish tissue culture variant		✓

[1] Donor breeding programmes:

EMBRAPA	Empresa Brasileira de Pesquisa Agropecuaria, Brazil
FHIA	Fundación Hondureña de Investigación Agrícola, Honduras
INIVIT	Instituto Nacional de Investigaciones en Viandas Tropicales, Cuba
TBRI	Taiwan Banana Research Institute, Taiwan

weight and disease scores. The full final report includes averages and coefficients of variance of the main agronomic and disease traits, analyses of variance and comparisons of means as well as graphics of all of these plus graphics of the disease evolution across time. To receive copies of the final report please contact the IMTP Coordinator at INIBAP.

Procedure used for the analysis of data

For the Sigatoka sites, the experimental design was a randomised complete block with twelve genotypes, five replicates or blocks and five plants per plot. The experimental unit was the plot of five plants and all the analyses were made with the average of these. For the Fusarium wilt sites the experimental design was a complete randomised design with 22 genotypes and 20 replications, the experimental unit was each replication. In both cases, susceptible and resistant reference clones as well as the local cultivar of the area were included as controls. Site managers were provided with evaluation protocols and they provided the raw data to the IMTP co-ordinator. Raw data from various sites was imported into Minitab v. 12.2 for analyses.

Sigatoka sites

Agronomic traits

For the agronomic traits, a two-way analysis of variance was used with blocks and genotypes as sources of variance. Following the analysis of variance, the means of each genotype were compared with the local cultivar mean using the Dunnett's procedure. A one-side comparison was used. This multiple comparison of means was useful, for example, to determine better yielders or taller clones than the local cultivar.

In this article however, we only present figures with the average of each genotype for bunch weight and number of days to harvest, as well as one graphic illustrating the average bunch weight of the improved cultivars in each site as a general measure of the quality of the site to grow the improved genotypes.

Infection index, disease development time (DDT) and youngest leaf spotted (YLS)

The infection index was recorded at three stages during the plant cycle, at six months after planting, at bunch emergence and at harvest. In the complete report, an analysis of variance was carried out for each evaluation time. Then, all treatment means were compared, first to the susceptible reference mean and then to the resistant reference mean. Two consecutive two-sided Dunnett tests were used with the aim of detecting firstly those genotypes that presented a more, an equally or a less susceptible phenotype than the susceptible control and secondly, genotypes that were more, equally or less resistant than the resistant control.

In this summary we present a graphic for the average infection index and YLS per genotype in three representative countries: Cameroon, Costa Rica, and Tonga. In the complete report a graphic illustrating the progression of the infection index during the plant cycle is presented to compare all genotypes at each location. The complete report also includes tables with averages and coefficients of variation of DDT and YLS.

Reference clones used for the analyses

Calcutta IR 124 was planted in all trials as the highly resistant clone. However it was not used for the comparisons of means as it is a clone with a hypersensitive response and its infection index is always zero. Evidently everything will be less resistant than Calcutta.

Pisang Lilin, another resistant landrace, was also planted in all trials as the highly resistant reference clone. Unfortunately due to problems with tissue culture, very weak dwarf somaclonal variant plants of this accession were used at all locations. These plants could not, therefore, be used as a reference clone as intended.

Pisang Ceylan, a landrace that has been selected to be the partially resistant reference for the next round of IMTP, was also planted in all trials of IMTP phase II. This clone was, in the absence of other suitable resistant clones, used as a resistant control for the Dunnett multiple comparisons of means.

Pisang Berlin was used as the susceptible reference clone. In one or two trials where this clone was not planted, the analysis was carried out using Niyarma Yik as the highly susceptible reference clone.

Fusarium wilt sites

Agronomic traits

For the agronomic traits, a one-way analysis of variance was used with genotypes as the source of variance. Following the analyses of variance, the means of each genotype were compared with that of the local cultivar. A one-side Dunnett comparison of means with a control was used in the same way as in the Sigatoka analyses (see above for explanation). As was also the case with the Sigatoka sites, a dual graphic is presented summarising the average bunch weight per site and per improved genotype across sites. The complete analysis is presented in the report.

Internal symptoms

The internal symptoms score was also analysed using a one-way ANOVA. The one-side Dunnett test was performed using the Fusarium susceptible reference clone specified by the protocol. A different reference clone was used depending on the Fusarium race present at the site. In this article however, we only present a table summarising the averages of the internal symptoms (rhizome) on sites infested with race 1 of *Foc* (Table 2). We also present in this summary two dual graphics (one per *Foc* race) showing the averages of the internal symptom scores averaged per site and per genotype across site.

External symptoms

The Fusarium evaluation protocol also specified scoring seven external symptoms once a month, beginning three months after planting, with the aim of visualising whether there was a clear evolution of the symptoms. The final results therefore present a graphic of the evolution of each external symptom per genotype along the experiment.

Diversity of Foc across IMTP trial sites

Samples of dried discoloured vascular tissue from the pseudostems of infected plants were prepared by staff at each site and sent to the Plant Pathology Unit, DPI, Indooroopilly, Qld, Aus-

Table 2. Averages of rhizome discoloration score of improved cultivars, reference clones and local cultivars. IMTP II trial sites infested with *Foc* race 1.

Genotype	Rhizome discoloration score		
	Brazil	Honduras	Philippines
FHIA-01 (AAAB)	1.47	1.00	4.14
FHIA-03 (AABB)	2.65	1.00	5.60
FHIA-17 (AAAA)	1.00	1.00	5.78
FHIA-23 (AAAA)	1.18	1.00	4.13
GCTCV 119	1.00	1.00	2.00
GCTCV 215	1.00	1.00	5.63
PA 03.22	1.15	1.07	5.00
PV 03.44	1.00	1.00	4.86
Gros Michel	2.40	1.20	6.00
Bluggoe	3.29	1.39	6.00
P. Ceylan	2.05	1.06	3.88
Williams	1.00	1.00	
Local cultivars			
FHIA-18		1.00	
Latundan			5.70
Prata Anã	2.78		

Complete data is provided in the IMTP II final report.

tralia for analysis. *Foc* was isolated from affected tissue and monoconidial cultures prepared for each isolate. To characterise isolates of *Foc*, vegetative compatibility groups (VCG) analysis and volatile production were carried out at the DPI laboratories and DNA fingerprinting using the DNA amplification fingerprint (DAF) analysis was conducted by Dr. Suzy Bentley at the CRC for Tropical plant pathology laboratories. The results of the analyses are presented in Table 3. These techniques are described in the complete report:

Results

Black Sigatoka

Improved cultivars

Tolerance to black Sigatoka
(M. fijiensis)

The response of the clones being tested against black Sigatoka varied according to the different biotic and abiotic factors present in each country. An analysis of the results obtained indicated that Disease Development Time (DDT) did not provide a reliable parameter for evaluating resistance levels. This may be due to difficulties in interpreting the leaf symptoms in certain situations. For example, when disease pressure is high, the numerous lesions of stage 1 which may occur can coalesce on the leaf closely resembling a necrotic lesion of stage 6. In contrast, the infection index appears to provide a more reliable parameter, allowing a better consistency between countries and a more appropriate basis for the classification of the new hybrids (Figure 1).

In this summary, the results obtained in Costa Rica, Cameroon and Tonga are presented as representative countries for Latin America, Africa and Asia/Pacific. Hybrids from Honduras (FHIA-23 and SH-3436-9) showed an average infection index close to that obtained for Pisang Ceylan (resistant reference), allowing us to conclude that FHIA-23 and SH-3436-9 are tolerant to black Sigatoka disease (Figures 2, 3, 4). This conclusion is consistent with the Youngest Leaf Spotted (YLS) score obtained in most countries. Hybrids from EMBRAPA, Brazil (PV 03.44 and PA 03.22) had average infection indices that were between those of Pisang Berlin and the local cultivars. Moreover, the YLS average means were, in most countries, lower than that of the susceptible local cultivars, allowing us to consider these as susceptible as the susceptible reference clones.

Agronomic performance

Hybrids from FHIA gave very good yields. Bunches of FHIA-23 and SH-

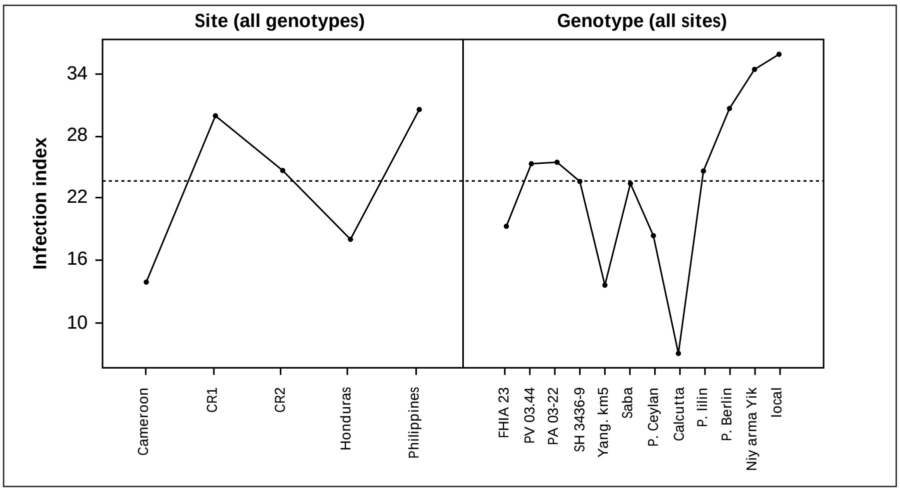

Figure 1. *Means for the infection index at bunch emergence.*

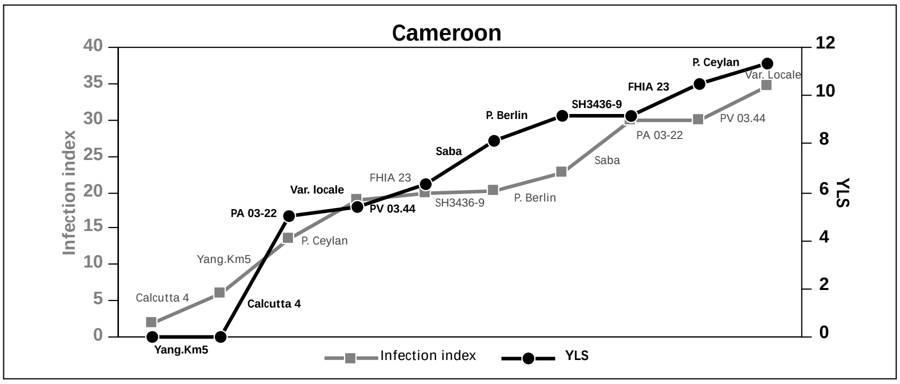

Figure 2. *Black Sigatoka tolerance of different genotypes in Cameroon.*
YLS: Youngest leaf spotted – II: Infection index

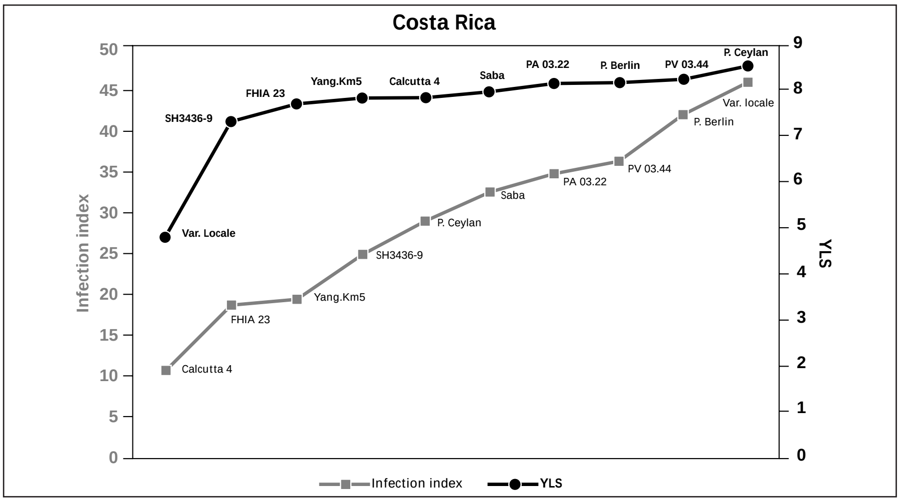

Figure 3. *Black Sigatoka tolerance of different genotypes in Costa Rica.*
YLS: Youngest leaf spotted – II: Infection index

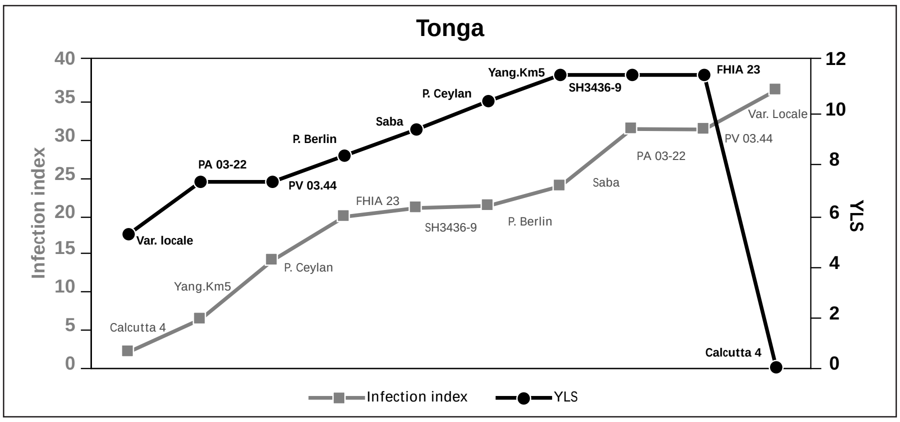

Figure 4. *Black Sigatoka tolerance of different genotypes in Tonga.*
YLS: Youngest leaf spotted—II: Infection index

3436-9 weighed on average 30.6 and 22.3 kg respectively across sites, with a maximum of 39.37 kg in Cameroon and 28.8 kg in Tonga respectively. The yields of the hybrids from EMBRAPA were lower, with average bunch weights of 10.1 and 9.27 kg across sites for PV-03.44 and PA-03.22 respectively. Although the local cultivars differ between countries, it is interesting to note that the average across sites is 16.5 kg, with the maximum 22.78 kg in Tonga. This serves to reinforce the good performance of the FHIA hybrids (Figure 5). However, FHIA hybrids had a longer cycle compared to local references, with an average of 474 and 420.2 days for FHIA-23 and SH-3436-9 respectively (Figure 6).

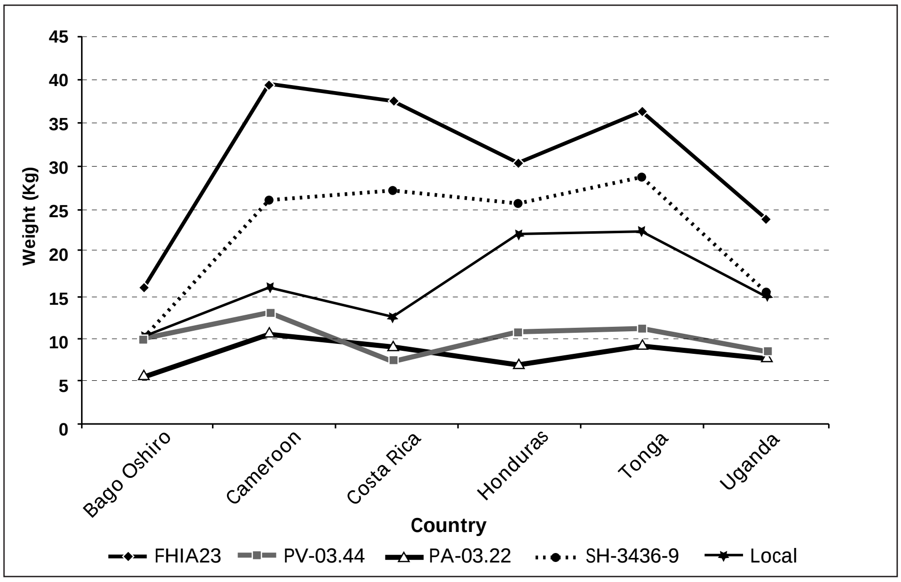

Figure 5. *Bunch weight obtained during IMTP II on different genotypes.*

Discussion

Black Sigatoka tolerance of the same clones showed some significant variations from country to country. Since many factors, including management, soil fertility, pathogen pressure, presence of other pathogens and climatic conditions influence plant tolerance, it is not possible to generalise the results. The effects of these factors, and their role in yield obtained, are not easy to demonstrate or quantify. However, some work has been carried out in this area at CRBP, Cameroon. This work has allowed the influence of black Sigatoka on the bunch weight to be demonstrated. Using the IMTP results for infection index at bunch emergence and the average finger weight across sites and genotype, some good correlations were found, with a coefficient of correlation of – 0.71 (Figure 7). This indicates that the number of parameters for which data is collected could be reduced, thus facilitating data collection and management. It would also reduce the need for visual interpretation of symptoms in the field.

It was also noted that the highly resistant clones Calcutta 4 and Yangambi Km5 presented necrotic lesions of stage 6 in some sites, a result not expected for these clones. This indicates that further studies are required to determine if more aggressive strains of *Mycosphaerella fijiensis* are present, or indeed if a new pathogen species is involved in these cases.

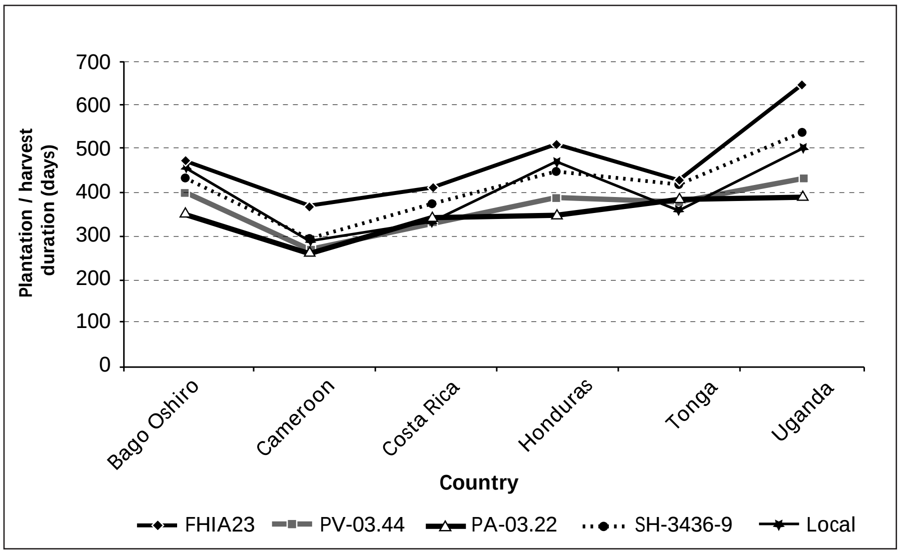

Figure 6. *Days from planting to harvest during IMTP II on different genotypes.*

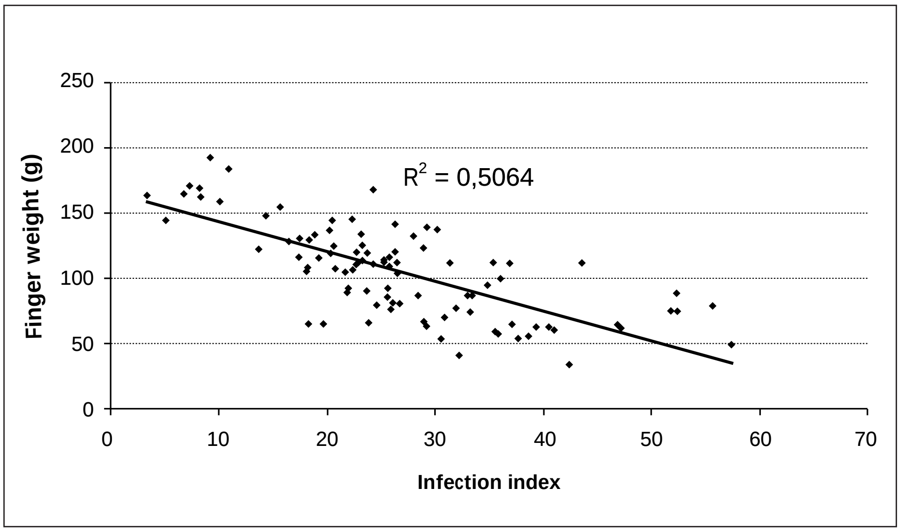

Figure 7. *Correlation between the infection index and finger weight on bananas. Analysis is done using all clones across sites with the IMTP framework.*

Fusarium wilt trials

General considerations

Yields were highly variable and depended on the site as was to be expected. Since many factors, including management, latitude, temperature, pathogen pressure etc. influence the agronomic performance; it is not possible to make many generalisations from the results.

Figure 8 provides an overview of the average bunch weight by genotype and by site considering only the improved and local cultivars, Yangambi Km5 and Gros Michel. The most favourable site from the bunch weight point of view was Taiwan where management skills

Table 3. Diversity of *Fusarium oxysporum* f. sp. *cubense* at IMTP phase II trial sites.

Location and VCG	Volatile production	*Musa* genotype
Cudgen, Australia		
VCG 0124	inodoratum	Bluggoe (ABB)
	inodoratum	Calcutta IR 124 (AAw)
	inodoratum	FHIA-02 (AAAB)
	inodoratum	Gros Michel (AAA)
	inodoratum	Ney Poovan (AB)
	inodoratum	Pisang Ceylan (AAB)
Wamuran, Australia		
VCG 0120	odoratum	Bluggoe (ABB)
	odoratum	FHIA-03 (AABB)
	odoratum	FHIA-23 (AAAA)
	odoratum	Gros Michel (AAA)
	odoratum	Igisahira
	odoratum	Pisang Mas (AA)
Cruz das Almas, Brazil		
VCG 0124	inodoratum	Bluggoe (ABB)
VCG 0125	inodoratum	Bluggoe (ABB)
Podavur, Tamil Nadu, India		
VCG 0124/5	inodoratum	Pisang Awak (ABB)
	inodoratum	Silk/Rasthali (AAB)
VCG 01213/16	odoratum	Silk/Rasthali (AAB)
Solok, Indonesia		
VCG 01213/16	odoratum	Bluggoe (ABB)
	odoratum	FHIA-23 (AAAA)
	odoratum	GCTCV 215 (AAA)
	odoratum	Pisang Ceylan (AAB)
	odoratum	Pisang Mas (AA)
	odoratum	Pisang Nangka (AAB)
	odoratum	PV 03-44 (AAAB)
	odoratum	Williams (AAA)
	odoratum	Yangambi Km5 (AA)
VCG 01219	odoratum	Kepok
Selangor, Malaysia		
VCG 01213/16	odoratum	Bluggoe (ABB)
	odoratum	Burro CEMSA (ABB)
	odoratum	FHIA-17 (AAAA)
	odoratum	FHIA-23 (AAAA)
	odoratum	Pisang Berangan (AA)
	odoratum	Pisang Ceylan (AAB)
	odoratum	Pisang Mas (AA)
	odoratum	PV 03-44 (AAAB)
	odoratum	Williams (AAA)
	odoratum	Yangambi Km5 (AAA)
Johor, Malaysia		
VCG 01213/16	odoratum	FHIA-17 (AAAA)
	odoratum	Pisang Mas (AA)
	odoratum	Pisang Awak (ABB)
	odoratum	Burro CEMSA (ABB)
Bago Oshiro, Davao City, Philippines		
VCG 0123	inodoratum	Latundan (AAB)
Sto Tomas, Davao del Norte, Mindanao, Philippines		
VCG 0122	odoratum	Cavendish (AAA)
	odoratum	Pisang Lilin (AA)
Hazyview, Eastern Transvaal, South Africa		
VCG 0120/15	odoratum	Bluggoe (ABB)
	odoratum	Burro CEMSA (ABB)
	odoratum	Chinese Cavendish (AAA)
	odoratum	FHIA-03 (AABB)
	odoratum	GCTCV 215 (AAA)
	odoratum	FHIA-17 (AAAA)
	odoratum	FHIA-23 (AAAA)
	odoratum	Gros Michel (AAA)
	odoratum	Williams (AAA)
	odoratum	Yangambi Km5 (AAA)
Canary Islands, Spain		
VCG 0120/15	odoratum	FHIA-01 (AAAB)
	odoratum	FHIA-03 (AABB)
	odoratum	FHIA-23 (AAAA)
	odoratum	Grande Naine (AAA)
	odoratum	PV 03-44 (AAAB)
	odoratum	Williams (AAA)
	odoratum	Yangambi Km5 (AAA)
Chiuju, Pingtung, Taiwan		
VCG 0121	odoratum	Cavendish (AAA)
	odoratum	Gros Michel (AAA)
	odoratum	PA 03.22 (AAAB)
	odoratum	Pisang Ceylan (AAB)
	odoratum	Pisang Mas (AA)
	odoratum	Yangambi Km5 (AAA)
VCG 01213/16	odoratum	Bluggoe (ABB)
	odoratum	FHIA-23 (AAAA)
	odoratum	Gros Michel (AAA)
	odoratum	PA 03.22 (AAAB)
Kichwamba, Bushenyi District, Uganda		
VCG Unknown - Not Foc	?	Pisang Nangka (AAB)
	?	Williams (AAA)
	?	Yangambi Km5 (AAA)

are highly developed. Second best results were obtained from the Uganda site. It should be noted that this site was in a farmer's field, indicating the high level of management skills of banana farmers in this area.

Internal discoloration of the rhizome was rated from 1 to 6, where 1 - indicated no discoloration; 2 - isolated points of discoloration; 3 - discoloration up to 1/3 of vascular tissue; 4 - discoloration between 1/3 and 2/3 of vascular tissue; 5 - discoloration comprised more than 2/3 of the tissue and 6 - total discoloration.

Breeding programmes have used the internal discoloration of the rhizome to estimate the resistance of the genotype to *Foc*. Also, this value combined with the agronomic performance is a measure of the tolerance of the accession. However, in the case of IMTP phase II it has been quite difficult to make an overall estimation of the resistance/tolerance of the plant genotype to *Foc* due to large differences on ratings across sites. It is believed that the differences were due not only to the differences in pathogen pressure but to a subjective element of visual interpretation. The internal symptom average for each site can be considered as a general measure of the pathogen pressure confounded with the effect of visual interpretation (Figure 9). This is

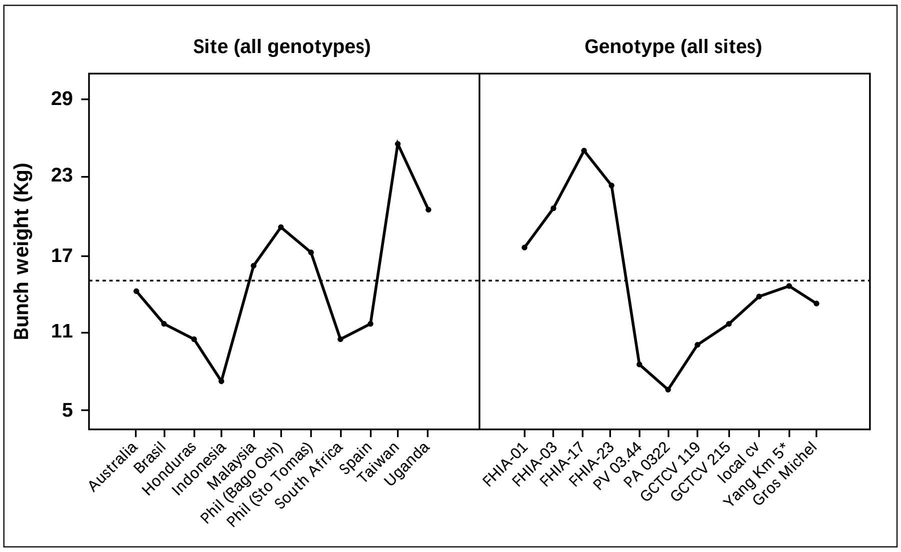

Figure 8. *Means for bunch weight.* Foc *sites.*

particularly true for discoloration averages across sites infested with *Foc* race 1 as there were only three sites infested with this race in the whole IMTP trial and one of them (Bago Oshiro in the Philippines) had exceptionally high averages (Figure 9).

Finally, the results of the VCG analysis are presented in Table 3.

Improved cultivars

Sites infested with Foc *race 1*

There were only three trial sites infested with *Foc* race 1: Brazil, Philippines (Bago Oshiro) and Honduras. As was already mentioned, the site in the Philippines had extremely high averages. However, from the numerous samples that were sent for VCG analysis from this site, only four yielded *Foc*. From these four, three isolates were undetermined VCG and only one belonged to race 1.

The overall averages mentioned below in this summary should therefore be considered with prudence. For comparisons with the reference clone, and resistance/tolerance ratings it is preferable to use the average scores of each genotype within site (Table 2).

The average score considering all genotypes across sites infested with *Foc* race 1 was 2.4. The susceptible reference clone Gros Michel had an average score of 3.2 across sites. The improved genotype with the lowest discoloration score across sites was GCTCV 119. This clone had an overall score of 1.3, which reflects its resistance to *Foc* race 1.

The genotype with the second lowest discoloration score was FHIA-23. This hybrid had an average discoloration score of 2.1 on sites infested with *Foc* race 1. Although this score was below the overall average and it was the lowest for *Foc* race 1 of all FHIA hybrids, it already indicates infection in the corm. Given its excellent bunch weight (Figure 8), this hybrid can be classified as very tolerant. It remains to be tested in the following generations to verify if its tolerance is retained.

FHIA-01 showed an average score of 2.2. Although the scores of FHIA-01 already indicate more than isolated points of discoloration in the vascular tissue, they are still lower than the general average score. Despite its bunch weight being the lowest of the FHIA hybrids, FHIA-01 showed the lowest variance across sites amongst the FHIA hybrids. These results allow us to conclude that FHIA-01 is tolerant to *Foc* race 1, that it performs well under a variety of environments and that it responds positively to good management conditions.

PV 03.44 had an average score of 2.3 on sites infested with race 1, which was just under the general average for these sites. However its bunch weight was usually low with a general average weight of 8.4 kg and a maximum average of 11.3 kg in South Africa.

GCTCV 215 had an average score of 2.5 for race 1 sites, higher than that of GCTCV 119 and slightly higher than the overall average. However it is to be noted that this average is substantially influenced by the exceptional high scores (5.6) recorded in one site in the Philippines (Bago Oshiro). On the other two sites infested with race 1, this genotype had an average score of 1 (no discoloration). Since this genotype was always considered to be resistant to race 1 these contradictory results deserve re-evaluation.

FHIA-17 had discoloration scores which were above average. Its average score was 2.5 across sites. However as in the case of GCTCV 119 it is to be noted that this average is substantially influenced by the exceptional high scores (5.6) recorded in one site in the Philippines (Bago Oshiro). On the other two sites infested with race 1, this genotype had an average score of 1 (no discoloration) which is to be expected for Cavendish clones. FHIA-17 was the best yielding genotype of all across sites. It had an average bunch weight of 25.2 kg. FHIA has reported this genotype to be resistant to *Foc* race 1. These findings indicate contradictory results among sites that merit further investigation.

FHIA-03 had an average vascular discoloration score of 3.08 across sites with *Foc* race 1, the highest score of all the improved genotypes and very similar to that of Gros Michel, the susceptible reference. This score is above the total average score when all the participating genotypes are considered and it certainly indicates susceptibility. Despite its high discoloration score, this hybrid gave some very good bunch weights with an average of 20.4 kg across sites and maximum average of 29.8 kg. It can be said that this genotype shows tolerance in the plant crop cycle. It would be interesting to verify if the tolerance is maintained in further generations.

Sites infested with Foc *race 4*

Unfortunately Williams, the susceptible reference for sites infested with race 4, was a dwarf somaclonal variant that could not be used for comparisons. The average overall discoloration score for the race 4 sites was 2.4 considering all genotypes. GCTCV 119 had an average score of 1.3 across sites infested with race 4. As in sites infested with race 1, it was also the lowest discoloration score of all the improved cultivars across trial sites. Yet indications exist that this genotype can be quite susceptible to *Foc* race 4. Although no infection had been recorded for this genotype in the Indonesian site, samples of this genotype sent previously to QDPI confirmed infection. Its average bunch weight was, on the lower side at 10 kg. This genotype was very variable with good average bunch weights between 15 kg and 22 kg under some conditions and very low (3 kg) in others. It is believed that management practices have a strong influence on the agronomic performance of this genotype.

GCTCV 215 had an average score of 1.7 if data from Indonesia, where only one plant was evaluated, is not considered. This average was the second lowest of all improved genotypes. This so-

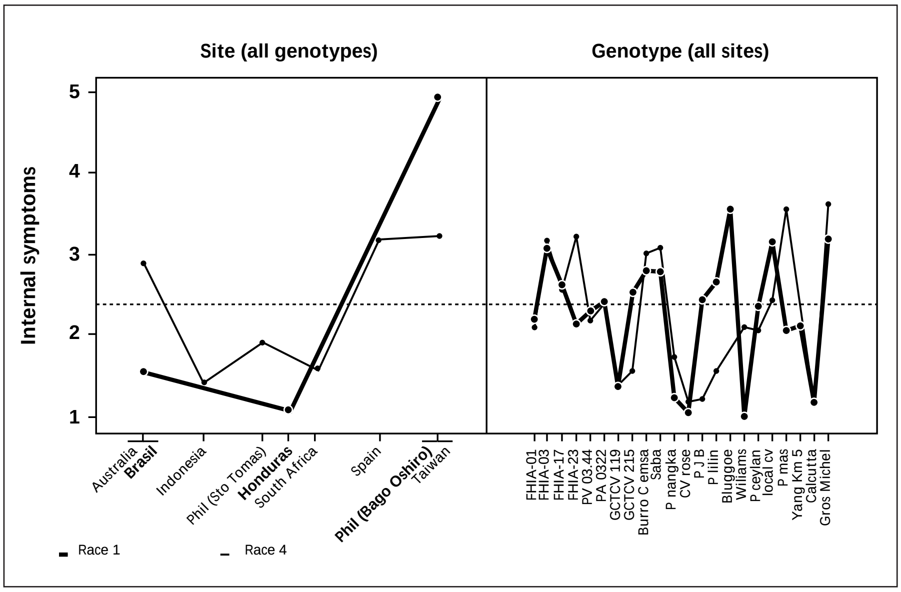

Figure 9. *Means for internal symptoms—*Foc *races 1 and 4.*

race 1 sites and 3.5 for race 4 sites. Two other landraces showed higher than the general average discoloration scores for both types of sites, these were Burro CEMSA and Saba. On sites with *Foc* race 1 Burro CEMSA and Saba had the same general average of 2.8. On sites infested with *Foc* race 4 Burro CEMSA had a score of 2.9 and Saba a score of 3.

Some landraces, e.g. Yangambi Km5 and Pisang Mas had a very specific reaction to the race of *Foc*. Yangambi had a score of 2.1 which was lower than the general average for sites with race 1 but it had a score of 4.1 well above the average for sites with race 4. The difference, although less marked, was also evident for Pisang Mas. On sites with race 1, Pisang Mas had a score of 2.06 while for sites with race 4 it had a score of 3.5. Landraces that consistently had scores lower than the average were Cultivar Rose and Pisang Nangka.

maclonal variant had an average bunch weight of 11.9 kg across sites. However this average increases to 12.7 kg if the data from Indonesia, is not taken into consideration. Since this genotype was always considered to be resistant to race 1 and susceptible to race 4 these contradictory results deserve re-evaluation.

FHIA-01 showed an average discoloration of 2.04 across sites infested with *Foc* race 4. It had an average bunch weight across sites of 17.6 kg and a maximum average of 24 kg with optimum management conditions. Given the good performance of FHIA-01 across sites this genotype can be classified as tolerant to both races 1 and 4 of Fusarium wilt.

PV 03.44 had a score of 2.1. This score was under the overall average. However its bunch weight was usually low with a general average of 8.4 kg and a maximum average of 11.3 kg in South Africa. PA 03.22 also had a low score (2.3) in sites infested with race 4. Similar to PV 03.44, this score was also under the general average across sites and lower than that of the susceptible references. However its bunch weight was also usually very low with an overall average of 6.4 kg and a maximum average of 11.6 kg in South Africa.

FHIA-17 gave an average score was 2.5 across sites, the same for *Foc* race 1 and race 4 sites. This score is above the general average and in Taiwan it had a score of 4.3. Yet FHIA-17 produced the heaviest bunches of all the genotype in these trials. It had an average bunch weight of 25.2 kg across sites and a maximum of 43.8 kg in Taiwan. Our results indicate that it is very tolerant to race 4 during the plant crop. It remains to be tested whether following generations retain this level of tolerance.

FHIA-03 had an average score of 3.09 which means that around one third of the vascular tissue showed discoloration on both types of sites. These scores are above the total average score when all the participating genotypes are considered and they certainly indicate susceptibility. Moreover, in some sites, FHIA-03 had very high discoloration scores (4.3 to 5.7) as in the Canary Islands and Australia. Despite its high discoloration scores, surviving plants of this hybrid gave some very good bunch weights with an average of 20.4 kg across sites and maximum average of 29.8 kg. The only exception to this was in the Canary Islands. In this particular case the data was collected from only 2 plants.

FHIA-23 had an average score of 3.1, well above the general average indicating susceptibility. Moreover in Australia and the Canary Islands it had averages above 4 indicating high susceptibility to sub-tropical race 4. Despite its high discoloration scores, this hybrid was the second best yielding of all FHIA hybrids with an average bunch weight of 22.3 kg and a maximum average of 46.8 kg in Taiwan.

Landraces

Bluggoe was the genotype with the highest discoloration scores on both types of sites. It had a score of 3.5 on race 1 sites and 4.1 on sites with race 4 indicating high susceptibility to both races of *Foc*. The other genotype that showed susceptibility to both races was Gros Michel with a score of 3.2 for

Conclusions

The FHIA hybrids were consistently the best yielding genotypes in these trials. With few exceptions their bunches outweighed bunches produced by all the other improved and local cultivars. The FHIA hybrids also responded well to careful management and to fertiliser application, as in the case of Taiwan. In summary the FHIA hybrids performed well under a range of conditions and responded even better when conditions improved.

The improved hybrid with the best performance in all the Sigatoka trials taken into account in this evaluation is FHIA-23.

An improved cultivar that deserves special reference is GCTCV 119, which had the lowest discoloration score for both *Foc* races and good yields under good management.

We have tried to combine the bunch weight data with the Fusarium and black Sigatoka reaction data to give an indication of overall and comparative performance of the varieties in different disease situations. It is important to stress that resistance alone is not useful. It needs to be combined with good production, acceptable post-harvest and organoleptic traits. Improved banana varieties contribute not only to reducing disease incidence but also to improving food production.

Full data and analysis of the results will be published shortly. To receive copies of the final report please contact the IMTP co-ordinator at INIBAP.

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Note: Yangambi Km5 is included just as a matter of interest given that it was the accession most requested from the INIBAP Transit Centre. The local cultivar is included as a matter of reference.

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Performance of banana clones under the challenge of Fusarium wilt in Taiwan

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Fusarium wilt caused by *Fusarium oxysporum* f. sp. *cubense* is a serious problem in Taiwan banana production (Su *et al.* 1986). It was estimated that more than 1500 ha., about one-third of the banana growing area in Southern Taiwan, was affected by the disease. Both race 1 (VGC 0123) and 4 (VGC 0121, 01213) of the Fusarium pathogen were reported in Taiwan (Pegg *et al.* 1992). In order to search for different sources of resistance, an IMTP trial for Fusarium wilt organized by INIBAP was conducted in 1996/97 in Pingtung, Taiwan. Twenty-one clones plus a local cultivar were included in the evaluation under the challenge of the disease. This paper is a report of the results of this trial.

Materials and methods

Twenty-one experimental clones (Table 1) were supplied as tissue-cultured plantlets by ITC-INIBAP in 1995. After going through the plant quarantine process, the plantlets were transplanted into pots in the net-house for 5 months. The field trial was established on May 23, 1996 in the diseased nursery with loamy soil at pH 5-5.3 at the Taiwan Banana Research Institute (TBRI), Pingtung, Taiwan (N 22° 42’, E 120° 29’). All clones were well established except for #16 (ITC0001, Pisang Lilin) which died either during the hardening process or at the early stage of growth in the field. A local Cavendish cultivar, Tai-Chiao No. 2 was used as a check reference. Plants were planted on a 2m x 1.5m grid. Fourteen plants of each accession were arranged in a complete randomized design. Each plant was treated as an experimental unit.

Data on disease symptoms and agronomic traits were taken according to the ‘IMTP Phase II Technical Guidelines for Fusarium Sites’ (INIBAP 1994). Disease severity shown by external symptoms included: yellowing of foliage, splitting of pseudostem base, vascular discoloration in leaf base, shortened internodes (rated as 1 to 3) and changes in new leaves (rated as 1 and 2). Data for external symptoms were taken once a month, beginning from the fourth to twelfth month after planting. At harvest or when the plant was completely wilted, internal symptoms were determined by examining the discoloration in the lower portion of the corm (rated as 1 to 6).

For agronomic data, number of days from planting to shooting and to harvest, plant height at harvest (cm), girth of pseudostem at 30 cm from the ground (cm), height of follower sucker at harvest, number of hands and fingers in bunch, average weight of each finger (g) were taken at the time of flowering or at harvest.

Results and discussion

External disease symptoms

Four months after planting, six criteria of external symptoms of Fusarium wilt were recorded in the field. Table 1 is a summary of the data showing the severity and the rate of disease development 12 months after planting. In general, the external symptoms, such as yellowing of foliage, splitting of pseudostem, vascular discoloration and wilting were clear indication of the disease development. Other criteria such as the change of new leaves and shortening of internodes were not distinct. The symptom of petiole buckling was not obvious and therefore not recorded. According to the external symptoms, 21 cultivars can be classified as following:

1. Resistant: SH-3481, SH-3565, SH-3444, GCTCV-119, GCTCV-215, Cultivar Rose, Pisang Jari Buaya, Calcutta IR 124, Williams and Tai-Chiao No. 2 (local cultivar);
2. Intermediate: SH-3649, Pisang Mas, Pisang Nangka, Pisang Ceylan;
3. Susceptible: PV03.44, Burro CEMSA, Saba, Yangambi Km5;
4. Highly susceptible: PA03.22, Gros Michel, Bluggoe.

The highly susceptible clones, PA03.22, Gros Michel and Bluggoe exhibited the most severe symptoms as well as the fastest development of the disease. By the fifth month after planting, about one third of the plants showed yellow foliage and splitting of pseudostem. More than half of plants wilted 8 months after planting. For clones, such as SH-3481, SH-3565, SH 3444, GCTCV-119, GCTCV-215, Cultivar Rose, Pisang Jari Buaya, Calcutta IR 124, Williams and Tai-Chiao No. 2 (local cultivar) showed no or mild external symptoms in all plants investigated.

Internal symptoms

Internal symptom as indicated by the vascular discoloration of the rhizome was examined after the plant has wilted due to the disease or at harvest. The scores of the internal symptom and the frequencies of plants showing different degree of severity are shown in Table 2. According to this observation, the classification of 21 cultivars is as following:

1. Resistant: SH-3481, SH-3565, GCTCV-215, Cultivar Rose, Pisang Jari Buaya, Calcutta IR 124.
2. Intermediate: SH-3444, PV03.44, GCTCV-119, Tai-Chiao No. 2.
3. Susceptible: SH-3649, PA03.22, Burro CEMSA, Saba, Pisang Nangka, Yangambi Km5, Pisang Ceylan, Williams.
4. Highly susceptible: Pisang Mas, Gros Michel, Bluggoe.

Among the resistant cultivars, SH-3481, Calcutta IR 124 and Cultivar Rose did not show any disease symptom in all plants investigated. They can be considered as highly resistant. In GCTCV-215 and Pisang Jari Buaya, about 10% of plants showed internal symptoms and were considered resistant. The diseased plants of susceptible clones, Gros Michel, Bluggoe and Burro CEMSA always showed rotting of the rhizome. Though external symptom was not severe in Pisang Mas in this trial, the occurrence of intensive internal symptom indicated that it is highly susceptible.