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INDEX

1. BIENNIAL REPORTS

1.1 Cultivar adaptation

1.2 Crop modelling

1.4 System analysis

1.5 Weed science

1.6 Entomology

1.7 Pathology

1.8 Nematology

1.9 Technology transfer

BIANNUAL REPORTS

CULTIVAR ADAPTATION (1 April 2012 to 30 September 2012)

DETAILS

PROJECT NUMBER	M101/10
PROJECT TITLE	Evaluation of medium- and long-season maize hybrids for different production systems
PROJECT MANAGER	Vacant (MA Prinsloo)
CO-WORKER(S)	Internal D De V Bruwer, DJ Muller, D du Toit, JL Snijman External Seed industry, cooperatives, GSA, farmers, PDAs, ARC-IIC
PROJECT STATUS	Continue
DURATION	01/04/1999 to 31/03/2015

ACTIONS TAKEN TO DATE

The maize production area is divided into a western and eastern region for more accurate evaluation and recommendation purposes. Private seed companies nominated 50 medium and long-season maize cultivars for evaluation at 79 localities in the eastern and western production regions under dry land conditions and 5 localities for disease study purposes resulting in a total of 84 trials. Evaluation included incidence of diseases, some agronomical traits and grain yield. Sixty nine trials were planted by co-workers and 15 trials by ARC-GCI.

PROGRESS MADE

Eighty out of 84 trials from the western and eastern areas were planted. Four trials could not be planted due to little or late rain at the beginning of the season. Sixty out of the 80 trials from the western and eastern areas were received and statistically analysed. An annual meeting was held with seed companies and other role players, important issues were discussed. Another meeting will be held on the 9th of October to discuss the results before being published. Results for the MIG for 2010/11 season were completed and have been published and distributed to the stakeholders and other organizations. Two popular articles have been published in different local magazines.

RESULTS ACHIEVED TO DATE

Preliminary results for medium and long growing season maize hybrids in the western area resulted in a mean grain yield of 4.54 t ha⁻¹ (minimum 1.07 t ha⁻¹ at Rietgat and maximum 6.91 t ha⁻¹ at Bothaville). PAN 6Q-223, PAN 6Q-445B, PAN 6Q-245, Phb 30Y79B and DKC 77-85BGEN were the top performers with yields of 5.12, 5.06, 5.00, 4.96, and 4.90 t ha⁻¹, respectively. Based on AMMI analysis, the cultivar PAN 5Q-251 was considered the most stable cultivar followed by KKS 4452B and DKC 80-12BGEN over different yield potential conditions. Mean grain yield for the medium and long season maize hybrids in the eastern region was 8.05 t ha⁻¹ (minimum 3.97 t ha⁻¹ at Bethlehem (3) and maximum 12.80 t ha⁻¹ at Delmas (8)). DKC 80-12BGEN, PAN 6P-110, PAN 6Q-308B, LS 8535B and DKC 80-40BRGEN were the best five hybrids yielding 8.77, 8.76, 8.76, 8.75 and 8.74 t ha⁻¹, respectively. Based on AMMI analysis, the hybrid DKC 78-45BRGEN was considered the most stable hybrid followed by DKC 78-15B and IMP53-13. Preliminary results of multi-seasonal analysis for the last three seasons (2009/10 - 2011/12) in the western and eastern areas are in progress. Preparation of trials for the coming season was completed and seed is in the process of being distributed to co-workers.

PROBLEMS ENCOUNTERED

Some seed companies are still not giving the national cultivar trials priority in their assistance resulting in less trials been done than committed. Some of the data received were again not completed according to the required protocol. It is a consistent problem retrieving results in time and in a prescribed format.

DETAILS

PROJECT NUMBER		M101/11
PROJECT TITLE		Evaluation of short- and ultra-short-season maize hybrids under irrigation
PROJECT MANAGER		Vacant (MA Prinsloo)
CO-WORKER(S)	Internal	D De V Bruwer, DJ Muller, D du Toit, JL Snijman
	External	Seed Industry, farmers, cooperatives, GSA, ARC-IIC
PROJECT STATUS		Continue
DURATION		01/04/2007 to 31/03/2015

ACTIONS TAKEN TO DATE

By the end of each season, maize producers need to decide which cultivars they want to plant during the following season. Since the introduction of short- and ultra-short-season maize hybrids it was realised that these cultivars perform quite differently from existing medium- and long-season cultivars. Short- and ultra-short-season cultivars are usually planted at much higher densities compared to the other cultivars and they are mostly cultivated under conditions of sufficient water supply or under irrigation. Twenty three trials were prepared for planting under irrigation in the eastern and western areas and consisted of 26 varieties. An additional nine trials were evaluated for disease incidence.

PROGRESS MADE

Fifteen out of the targeted 23 short growing season trials that were planted under irrigation were received and statistically analysed. No data was received for four trials and four trials were written off because of water logging and other factors. An annual meeting was held with seed companies and other role players when important issues were discussed. Another meeting will be held on 9 October to discuss the results before being published. One popular article has been published in a local magazine.

RESULTS ACHIEVED TO DATE

Preliminary results for short growing season trials resulted in a mean grain yield for all localities under irrigation of 13.04 t ha⁻¹ (minimum 10.58 t ha⁻¹ at Potchefstroom and maximum 17.71 ha⁻¹ at Hopetown). PAN 3D-736BR, PAN 3Q-740BR, BG 3492B, P 1615R and Phb 32D96B were the best five hybrids under irrigation and yielded 13.97, 13.39, 13.83, 13.80 and 13.36 t ha⁻¹, respectively. Based on AMMI analysis, the hybrid KKS 8301 is considered the most stable hybrid followed by IMP 50-90BR and DKC 62-84R over different yield potential conditions. The statistical analyses for the last three seasons are in progress. Preparation of the trials for the coming season is in progress.

PROBLEMS ENCOUNTERED

Number of plantings and successful trials decreased since certain seed companies do not commit themselves to planting trials they have promised to conduct at the beginning of the season.

CROP MODELLING

DETAILS

PROJECT NUMBER	M103/16
PROJECT TITLE	Climate and genotype effects for maize grain yield
PROJECT MANAGER	W Durand
CO-WORKER(S)	Internal DL du Toit, T Mathobisa, MA Prinsloo
	External ARC-ISCW
PROJECT STATUS	Continue
DURATION	01/04/2011 to 31/03/2014

ACTIONS TAKEN TO DATE

Climate change is expected to affect agriculture. Stability in yield and quality across environments is a critical breeding goal when dealing with unstable climate. Best variety choice is important to the farmer to maximise yield from a field and before the season starts, using the best variety for planting in the specific area that is best suited to the climate outlook of the season. An informed decision can only be made taking into account historic trends of the different varieties that show the best adaptation for the location, for maturity, vigour, quality and yield. A database which combines all these factors over years, geo-referenced to be linked to specific locations and incorporating climate historic and forecast data can enable better quantification of yields to be expect, even under future climate change scenarios.

PROGRESS MADE

Forty publications containing trial data for commercial maize cultivars from 1989 to the 2009/10 season have been scanned and have been imported into an Excel format and quality checked. All tables have been transposed and normalised to aid the process of linkage to a database. Progress has been made to develop a climate and soils database to be linked to the data. Some of the cultivar trial books from the trials consisting of new cultivars, open pollinated varieties, small scale and short season varieties have also been sourced. However the collection is not yet complete. Some of these books have also been scanned into a raw format.

RESULTS ACHIEVED TO DATE

The required software and hardware has been acquired and installed and has been used to scan pages containing data into raw format. This raw format was imported into Excel spread sheets with all the additional information that will be necessary to transform the data into a database. Investigations have also been made to revive the old original data from the trials that is in a format no longer used in the newer computing systems.

PROBLEMS ENCOUNTERED

Some of the older typesets could not be scanned as the OCR software does not properly recognise its characters and thus had to be captured by hand. Research reports from 2004/05 onward do not allow multiple trials at some sites to be linked to the crop management table. An effort will be made to retrieve this information.

WEED SCIENCE

DETAILS

PROJECT NUMBER		M111/13
PROJECT TITLE		Improved grass control systems in maize
PROJECT MANAGER		E Hugo
CO-WORKER(S)	Internal	MM van der Walt, KE Ramatseng, S Tsamai, RT Nkasha
	External	University of Pretoria
PROJECT STATUS		Continue
DURATION		31/03/2011 to 31/03/2016

ACTIONS TAKEN TO DATE

During the April 2012 to September 2012 time-frame, the following actions were taken:

Coordination and planning

- Glasshouse trails were successfully maintained to determine the competitive effect of *Digitaria sanguinalis* on maize in two soil types.
- Efficacy of herbicides to control *D. nuda* and *D. sanguinalis* was tested in a glasshouse trial in two soil types.
- Data capturing was successfully completed.

Trial activities

Competition trial:

- Soil water content was determined at weekly intervals
- Plant height was determined weekly for maize plants.
- Maize leaf and soil samples were collected for analyses.
- Trial is still being maintained; maize is in the flowering stage.

Herbicide trial:

- Both *Digitaria* spp were sown successfully.
- Herbicide treatments (4) were applied in two soil types (sandy and clay).

Data collection and analyses

- Emergence and total count of both *Digitaria* spp. were done in each of the four herbicide treatments for both soil types.
- Percentage control of each herbicide was determined for both *Digitaria* spp in two soil types.
- Data are being processed and analysed.

PROGRESS MADE

- Competition trial of *D. sanguinalis* is still being maintained in glasshouse.
- Effective control and period of regrowth for both *Digitaria* spp. were recorded.

RESULTS ACHIEVED TO DATE

- Herbicides tested in glasshouse trial gave better control when compared to field trial results. *D. sanguinalis* was fully controlled by acetochlor, s-metolachlor and s-dimethenamid. *D. nuda* control was > 80 % and acetochlor 840 gave the best control. *D. nuda* re-growth was first observed in s-metolachlor treatments at 30 days after spraying (DAS) in clay soil, and 17 DAS in sandy soil.

PROBLEMS ENCOUNTERED

No problems were encountered.

ENTOMOLOGY

DETAILS

PROJECT NUMBER	M131/14
PROJECT TITLE	Deployment of Bt technology for control of the African stem borer, <i>Busseola fusca</i>
PROJECT MANAGER	A Erasmus
CO-WORKER(S)	Internal JBJ van Rensburg, J Truter , SF Grobler , UM du Plessis, LL Ramonyane, MM du Toit
	External Seed industry, North-West University
PROJECT STATUS	Continue
DURATION	01/04/2008 to 31/03/2012

ACTIONS TAKEN TO DATE

The Maize Information Guide (MIG) was released during May 2012 at the NAMPO exhibition and new updates were made under the crop protection section with information and pictures about the most important insect pests of maize and beneficial insects. Two presentations were made during the WEMA DEPT team meeting, Nairobi, Kenya, 3 - 8 June which addressed Insect Resistant Management (IRM) with South Africa as a case study for the rest of Africa. Resistant diapause stem borers were field collected for two weeks in the Vaalharts area during which three students were trained how to collect stem borers. A farmer's day talk was also presented at the National Science week, Rustenburg, 2 August, explaining and highlighting the importance of planting the refuge area to prevent resistance development. The report for Pioneer field and laboratory trails with 12 different entries which were evaluated when inoculated with *Busseola fusca* susceptible larvae, *B. fusca* resistant larvae and *Chilo partellus* was finalised. The field evaluation report for Pannar was compiled in which experimental Bt-hybrids - both alone and stacked with the Roundup Ready gene were evaluated. The "refuge in the bag" (RIB) field trail was finalized and data evaluated by Biometry Department. Susceptible diapause stem borers (98 000) were field collected, 6 August - 7 September in the Ventersdorp area to be used in trails of the forthcoming season. The information captured during the "RIB" trail was compiled in poster format for presentation at the 12th International Symposium on Biosafety of Genetically Modified Organisms (ISBGMO12), St Louis, Missouri, USA, 16 - 20 September 2012. This was the first season in which the RIB strategy was tested, therefore future research will continue. Data captured for the new Bt event (MON89034) field trail were analysed and reported on in a popular publication and radio talk.

PROGRESS MADE

All actions proceeded as planned.

RESULTS ACHIEVED TO DATE

The field trial in which 12 entries with experimental Bt-genotypes presented in four genetic groupings (Pioneer) was evaluated. Ten genotypes that controlled *Chilo partellus* effectively were identified, six genotypes controlled Bt-susceptible *B. fusca* and six genotypes were effective for control of Bt-resistant *B. fusca*. These data relate to stem and whorl feeding. The challenge however is still to control resistant *B. fusca* on the silks. The Pannar trial had no significant differences between hybrids, however this can be due to a lack of sufficient inoculation early season. During the "RIB" field trail large scale larval migration was observed in all treatments. The high rate of migration was particularly evident in MON810 and the control plots. In the MON810 plots the incidence of damaged plants exceeded the percentage refuge planted for 5, 10 and 15 % refuge, but not the 20 % mixture. No significant differences were observed between damage levels in any of the treatments in the MON810 plots. In the MON89034 plots the incidence of damaged plants was lower than the ratio of non-Bt plants present in the particular seed mixture. The 5% seed mixture in the MON89034 plots resulted in significantly reduced incidence of damaged plants compared to other treatments. The level of migration and survival of larvae in field planted seed mixtures will depend on whether the initial infestation takes place on a Bt or non-Bt plant. The likelihood of a non-Bt plant being the point source of migrating larvae is comparatively small due to the low number of such plants in the field. The large scale larval migration observed in this study indicates that the RIB strategy may contribute to exposure of larvae to sub-lethal doses over time. Since the high-dose strategy is employed to kill RS individuals in the population, the tendencies observed in this study may indicate that seed mixtures with non-Bt seed at levels higher than 5% may aid in survival of larvae, confirming previous work that seed mixtures may not be appropriate as IRM strategy for pests that migrate between plants. Research in the RIB strategy is still ongoing. Publication: (Erasmus, A. 2012. Nuwe Bt-geen beheer meliëstamboorder en die chilo-boorder. SA Graan Sept. p 87 - 88) and Radio talk: 8 August 2012, 04:30. Title: New Bt gene controlling resistant

stemborers).

PROBLEMS ENCOUNTERED

None.

DETAILS

PROJECT NUMBER		M131/15
PROJECT TITLE		Early-warning system for black maize beetles
PROJECT MANAGER		Vacant (JBJ van Rensburg)
CO-WORKER(S)	Internal	N de Klerk, MM du Toit, LL Ramonyane, LM Moroladi.
	External	Farmers
PROJECT STATUS		Continue
DURATION		01/04/2001 to 31/03/2013

ACTIONS TAKEN TO DATE

Light trap captures were collected and sorted. The data are being used to test the predictive value of the model derived from the previous analyses, based on various seasons' data . Weather data for each site were obtained for long term analysis.

PROGRESS MADE

All captures were collected and counts recorded. Reports of the previous season's captures were sent through to the various farmers. Statistical treatment of long term data is still in progress.

RESULTS ACHIEVED TO DATE

Flight patterns seem to vary with area, the Heidelberg area showing three prominent seasonal peaks compared to one peak in the remaining areas of the monitored area. The long term flight pattern seems to correspond with the expected decline in black maize beetle occurrence. Short term variation in beetle numbers seem to be related to soil moisture levels of the previous season.

PROBLEMS ENCOUNTERED

None.

PATHOLOGY

DETAILS

PROJECT NUMBER	M141/20
PROJECT TITLE	Characterisation of <i>Exserohilum turcicum</i> isolates within South African maize production areas.
PROJECT MANAGER	M Craven
CO-WORKER(S)	Internal JGC Kroukamp, MM Mahlobo, MO Motheketlela, KA Tantasie, TJ Baas, VJ Gobiyeza, RE Terblanche, CFB Weideman, LA Madubanya External B Crampton (UP), I Barnes (UP), M Haasbroek (UP)
PROJECT STATUS	Continue
DURATION	01/04/2011 to 31/03/2016

ACTIONS TAKEN TO DATE

Race identification (Growth chamber studies)

Sixteen isolates have been screened within growth chambers at the Northwest University under optimal conditions (18/22°C, 400 $\mu\text{M m}^{-2} \text{s}^{-1}$, 12 h day/night cycle). Two of these isolates were obtained from sorghum. Seven of the isolates were included to confirm their race allocation based on screening conducted during August- December 2011. The screenings were conducted on the maize differential set obtained from the University of Illinois. The response of the resistance genes was evaluated in two different backgrounds. Near -isogenic lines B68, B68-*HtN*, A632, A632-*HtN*, V26, V26-*Ht1*, V26-*Ht2*, V26-*Ht3*, *Oh43*, *Oh43-Ht1*, *Oh43-Ht2* and *Oh43-Ht3* were selected for the study. Each isolate screening test took 5 weeks to conduct.

Molecular marker screening: (ARC-GCI biotechnology unit)

The aim of the molecular side of the project is to find a fast but repeatable way to distinguish between various races as identified with greenhouse studies using available marker technology. Limited literature is available that mention techniques that have proven to be useful with such studies, but repeatability and reproducibility between laboratories always remain a problem. Two approaches were investigated, all with the aim of finding ways to distinguish between races.

Since commencement of the project during April 2011, a total of 85 isolates were provided for this study as single spore cultures. Emphasis was, however, placed on the set of 17 isolates of which 12 were screened in growth cabinets at NWU. DNA was extracted using a Phenol: chloroform isolation method. The quality of the DNA was ascertained on 0.8 % agarose gels preceded by a RNA degradation step. The DNA was quantified using the NanoDrop and standardized to 50 nanograms for PCR analyses. Extracted DNA was placed in storage. Two molecular approaches (or techniques) were investigated:

Sequencing of the intergenic transcribed spacer (ITS) region: Through this technique, ITS regions on the genome of micro-organisms can be used for the characterization of micro-organisms (i.e. to distinguish between isolates or races). The translation elongation factor (EF) as well as the mitochondrial subunit (MS) were the targeted ITS regions. No research has been conducted or reported on in literature with regard to *E. turcicum* and the use of ITS regions to distinguish between isolates. This work is therefore seen as developmental work. Effort to tag the ITS region flanking the fungal ribosomal subunit (5,8 S rDNA) was also carried out whereby we tagged the ITS1-4 region.

Tagging the highly conserved repeat regions: This research is based on documented research used to distinguish between races. It is therefore seen as application research where already reported research is tested within the laboratory for its applicability. Families of short intergenic sequences that contain highly conserved central inverted repeats were accordingly tagged with PCR using reported enterobacterial repetitive intergenic consensus (ERIC) sequence, repetitive extragenic palindromic (REP) elements and the BOX element.

Molecular marker development: (University of Pretoria)

SSR marker technology was implemented for race identification of *Exserohilum turcicum* isolates.

PROGRESS MADE

Race identification (Growth chamber studies)

Fourteen isolates could be race typed. Three of the isolates were not able to cause infection in maize (two of these isolates were from sorghum). Three representative isolates (two from maize and one from sorghum) were identified as *E. turcicum* races by ARC-PPRI mycologists. These three strains will be used as *E. turcicum* reference strains.

Molecular marker screening (ARC-GCI Biotechnology unit)

Optimization of PCR profiles:

MS region: The profile was optimised and it works effectively each time. All the 17 isolates were screened with the MS primer set. To date only 10 of the isolates gave bands on agarose and were sequenced with MS forward and reverse primers. The sequences were blasted first onto the *Setosphaeria turcicum* (anamorph = *E. turcicum*) website and later onto the NCIB website. A phylogenetic tree using the Neighbour joining method was constructed from the sequence data.

EF region: The profile although optimised does not work effectively all the time. All the 17 isolates were screened and the primer set did not yield unique single bands that can be sequenced.

5,8 D rDNA subunit region: Optimization of the PCR for ITS1, 4 and 5 regions was initiated using Qiagen mastermix and Promega Flexi Go Taq. The ITS1-4, 1-5 and 4-5 were tested. No sequencing has yet been done.

ERIC: The profile was optimised and it works effectively each time. All the 17 isolates were screened with the ERIC primer pair. To date all the fingerprints were obtained except for three isolates that consistently did not give amplification results on agarose gels. The fingerprint data were scored with the use of Cross checker software downloaded from the internet as binary (1;0) code. The data were analysed on NTSys to construct a phylogenetic tree based on fingerprint data.

BOX and REP: The profiles are not working despite numerous attempts.

Molecular marker development (UP)

The Internal Transcribed Spacer (ITS) region from DNA extracted from the 26 typed races were amplified, and forward and reverse sequences were obtained for fourteen of the isolates. Preliminary DNA sequence alignments and clustering with known *Exserohilum* sp. ITS regions confirm that all of the isolates are *E. turcicum*. Work is currently underway to conclusively identify the remaining twelve isolates.

A number of diseases may resemble the symptoms characteristic of Northern corn leaf blight to the untrained eye. In order to distinguish *E. turcicum* from other foliar pathogens, we are investigating the potential of developing a molecular tool, such as PCR-RFLP (Polymerase chain reaction – restriction fragment length polymorphism) for pathogen identification. This tool relies on the presence of unique restriction sites within the *E. turcicum* genome (e.g. within the ITS region) which will show a unique banding pattern on an agarose gel after restriction enzyme digestion. Preliminary *in silico* results show that this has the potential to distinguish *E. turcicum* from other foliar pathogens.

Lesions from diseased leaves collected from field trips to Mpumalanga and KZN in February and March 2012 respectively, were surface-sterilized and placed on moist, sterile filter paper to induce conidiation. Single-conidia isolations were conducted and 17 re-isolations have been made from Kwa-Zulu Natal and one from Machadodorp. These isolates will form part of a study on the population structure of *E. turcicum* in South Africa.

SSR primers were designed to the sequenced *Setosphaeria turcica* genome. These primers will amplify 10 dinucleotide- and 10 trinucleotide repeats within the fungal genome. Initial experiments indicate that the primers are able to detect polymorphisms between a subset of the 26 *E. turcicum* isolates. Experiments are underway to screen all the SSR primer sets for their ability to detect polymorphisms, and to sequence the amplified SSR fragments. These primers will be used in an attempt to provide a tool for *E. turcicum* race typing, and to investigate the population structure of *E. turcicum* isolates collected from various maize growing regions within South Africa.

RESULTS ACHIEVED TO DATE

Greenhouse/Growth chamber screening of Northern corn leaf blight (NCLB) isolates

The majority of the isolates obtained from maize were capable to overcome resistance provided by the *Ht3* gene. The two isolates obtained from sorghum material did not manage to infect the maize differential set. The effectiveness of the genes was dependent on the genetic background of the differential set. As the B68 and V26 differential sets gave the most consistent reaction to infection, the race identified by these lines will be used to class the races. Six races have accordingly been identified.

Molecular marker screening

MS region: We were able to use the MS1 (forward) and MS2 (reverse) primers to sequence the MS region with the ABI 3130 xl machine. A phylogenetic tree to show the genetic distance of the isolates was drawn with the help of Mega5. The sequences obtained were also blasted onto the *S. turcicum* website. Unfortunately no matches were found which could confirm whether our isolates were *S. turcicum* or not. The sequences were then blasted onto the NCIB website and hits were found. The hits revealed that it was indeed the mitochondrial subunit but could not reveal whether it was *E. turcicum* or not. This is because no sequence data for *E. turcicum* is available yet on the online database. Our unique sequences from this work will be submitted and compared with the on-going *E. turcicum* whole genome sequencing that is currently underway.

EF region: An evolutionary tree was drawn from amplifying the EF region with EF1 (forward) and EF2 (reverse) primer set. Although the PCR profile was optimised it gave challenging results when amplifying the 17 isolate set.

5,8 D rDNA subunit region: No amplification products were obtained for ITS1-5 and ITS4-5. Very faint bands were obtained for ITS1-4 region when using Promega GoTaq flexi enzyme. No other enzymes tested yielded any results. Upon running the results on agarose, 10 of the 17 isolates gave bands. No sequencing was performed as yet.

ERIC: We obtained ERIC fingerprints for all the 17 isolates except for three isolates that do not seem to amplify even after DNA was re-extracted from the petri dishes. After scoring the gel (presence/absence) with the help of Cross checker software, a genetic distance matrix based on Nei (1972) was calculated in NTSys version 2.21. The distance matrix was used to draw up a phylogenetic tree based on UPGMA cluster analysis.

BOX and REP: No amplification products were obtained

Molecular marker development

Conclusive molecular identification has confirmed fourteen isolates obtained from NCLB lesions to be *E. turcicum*.

PROBLEMS ENCOUNTERED

In order to confidently associate SSR markers with a particular race, it will be important to screen the SSRs against at least ten isolates of each race. We currently have available 25 isolates of known race identity, but these belong to different races. We have contacted researchers in the USA and Kenya, and are in the process of trying to obtain more isolates of known races.

DETAILS

PROJECT NUMBER	M141/22
PROJECT TITLE	Survey, screening maize hybrids for resistance to and determination of inoculum source of bacterial leaf streak of maize
PROJECT MANAGER	BC Flett
CO-WORKER (S)	Internal FK Mashinini, JGC Kroukamp
	External Northwest University - Potchefstroom, Pannar Seed Co, Pioneer Hybrid International.
PROJECT STATUS	Continue
DURATION	01/04/2011 to 31/03/2014

ACTIONS TAKEN TO DATE

The occurrence of bacterial leaf streak throughout the South African maize production area was surveyed. Isolates of the bacterium (*Xanthomonas campestris* pv. *zeae*) were collected for characterisation studies and further pathogenicity tests and inoculation studies for genotype screening. 80 isolates were collected from maize leaves showing typical symptoms of bacterial leaf streak disease. Infected plant material was obtained from various localities in South Africa over a period of two months. All isolates were placed on YDA agar and GYCA agar. The plates were incubated at different temperatures ranging from 4 °C to 37°C. Incubation took place over a period of 3 to 6 days. Plates were examined to determine the amount of growth. Standard methods were used for morphological, biochemical and physiological characterisation of all isolates. All tests were repeated at least three times. The ability of the isolates to ferment different carbohydrate sources and their motility was studied. Transmission electron microscopy studies of the 80 isolates were carried out. DNA extractions, 16S rDNA PCR and ITS PCR were conducted. Metabolic fingerprints were created by the use of Biolog GN2 Microplates. The phase II hybrid trial at Hoogekraal planted by Pannar seed was rated.

PROGRESS MADE

Xanthomonas campestris pv. *zeae* is the causal agent of bacterial leaf streak of maize which was first reported in South Africa in 1949 and hasn't been reported elsewhere. Very little is known about this specific pathovar and therefore it is necessary to initially compile a characteristics profile of this pathogen. The aim of the study was to make use of molecular, biochemical and physiological methods to determine the specific characteristics of *Xanthomonas campestris* pv. *zeae*. Once we are certain of the organism and its variation we can continue with further studies on development of an inoculation technique for inoculating maize plants with *Xanthomonas campestris* pv. *zeae*. Screening of genotypes for resistance/susceptibility to bacterial leaf streak planted in the 2011/12 season was carried out.

RESULTS ACHIEVED TO DATE

Initial results of two honors students determined the optimum temperature and medium for growth of the bacterium in culture on 9 isolates collected during the 2010/11 season. The 80 different isolates collected in the 2011/12 season were characterised using carbon utilization patterns determined by the Biolog GN2 Microplate system. Bacterial DNA was extracted by means of a DNA kit. DNA was of high quality and concentration as determined by the Nanodrop spectrophotometer. The 16S rDNA, 23S rDNA and ITS sequences were amplified (by PCR) to determine authenticity through sequencing. BOX and ERIC PCR fingerprinting were conducted to highlight differences in the genetic composition of the 80 isolates, as these techniques possess greater differentiation power, to possibly identify the presence of several strains. The BOX and ERIC PCR techniques did illustrate banding pattern differences between isolates (indicating possible different strains or species) and the two compared pathovars of *Xanthomonas campestris*. Results obtained from the biochemical characterisation agreed with the results from the molecular characterization discussed below. To further ensure the identification of the 80 isolates collected these were sequenced at Inqaba Biotech. Only 3 isolates were found to be *Xanthomonas campestris*, 6 were *Pseudomonas* species and the remaining 73 were found to fall into the *Pantoea* spp grouping. There is a possibility that this may be a newly reported disease in South Africa and studies are underway to identify these isolates using PCR techniques using probes. Data from the Hoogekraal phase II cultivar trial has been collected and is being processed to determine resistance in local cultivars. However publication of this data is being held back until clarity on the causal organism has been obtained. Sufficient isolates have been collected to begin work on various other aspects of the project.

PROBLEMS ENCOUNTERED

The primary problem encountered was the assumption that the entire maize industry has made that the symptoms seen were caused by *Xanthomonas campestris* pv. *zeae* and this appears to be an incorrect assumption. Results from the PCR tests to confirm the species of *Pantoea* will determine the future progress of this project.

DETAILS

PROJECT NUMBER		M141/23
PROJECT TITLE		Screening maize hybrids for resistance to cob and tassel smut
PROJECT MANAGER		BC Flett
CO-WORKER (S)	Internal	TM Ramusi, FK Mashinini,
	External	Pannar Seed Co
PROJECT STATUS		Continue
DURATION		01/04/2011 to 31/03/2016

ACTIONS TAKEN TO DATE

Medium- to long-season and short-season hybrids were planted at two localities (Greytown and Standerton) for resistance to cob and tassel smut. Two rows were planted of which one was inoculated and the other was an uninoculated control row. A random block design with three replicates was used for each trial. Trials were inoculated at planting. Ratings were carried out at physiological maturity and data was captured and is ready for analysis.

PROGRESS MADE

Progress this season appears to have been successful as infection levels were adequate. Once data has been analysed it will be published in the popular press and the last 3 seasons data will be analysed to determine G x E interactions. This data will be published in a scientific journal should the data be adequate.

RESULTS ACHIEVED TO DATE

Significant variations in hybrid resistance to cob and tassel smut were observed over the three successful seasons we have screened. This data is published in local popular journals. Unfortunately the publication of such data has not prevented the spread of the disease into new production areas.

PROBLEMS ENCOUNTERED

None.

DETAILS

PROJECT NUMBER		M141/24
PROJECT TITLE		Screening maize hybrids for resistance to Diplodia ear rot
PROJECT MANAGER		BC Flett
CO-WORKER (S)	Internal	MT Ramusi, FK Mashinini,
	External	Pannar Seed Co, Monsanto SA, UFS
PROJECT STATUS		Continue
DURATION		01/04/2011 to 31/03/2016

ACTIONS TAKEN TO DATE

Medium- to long-season and short-season Phase 2 hybrids were planted over four localities for evaluation of resistance to Diplodia ear rot. The aim of this study is to identify maize hybrids resistant and/or susceptible to Diplodia ear rot over four localities (Potchefstroom, Greytown, Petit and Vaalharts) using the technique developed by Flett & McLaren (1994). Trials were inoculated using a technique developed by Flett & McLaren (1994). The trials have been harvested, rated, yields measured and grain moistures are being completed.

PROGRESS MADE

Data is presently being captured and will be analysed within the next two months. Greytown had the highest infection levels, followed by Petit, Potchefstroom and Vaalharts.

RESULTS ACHIEVED TO DATE

This is a new project and first data will be published once it has been analysed using the technique developed by Flett & McLaren (1994). This data will be published in a popular article.

PROBLEMS ENCOUNTERED

No problems to date.

NEMATOTOLOGY

DETAILS

PROJECT NUMBER M151/80
PROJECT TITLE Effect of weeds on plant-parasitic nematode population levels in agricultural systems.
PROJECT MANAGER KN Ntidi
CO-WORKER(S) Internal L Bronkhorst, Research Assistant (vacant), SS Kwena, R Jantjies, AEJ du Toit, CMS Mienie, APN du Toit
External ARC-PPRI, Dept. of Agriculture, fish and forestry, farmers
PROJECT STATUS Continue
DURATION 01/04/2010 to 31/03/2013

ACTIONS TAKEN TO DATE

Three field trials were conducted during the 2011/2012 season in which the host suitability of weeds with regard to root-knot nematodes was investigated. Data for nematode soil and root samples have been analysed and identified. High root-knot infestation was recorded on *Hibiscus trionum*, *Cynodon dactylon* and *Solanum retroflex* and lowest numbers were recorded on *Datura ferox*, *D. stramonium* and *Chenopodium murale*. Detailed results of both the glasshouse and field trials (50g roots, 5g roots and soil) will be given in the final report.

PROGRESS MADE

All actions proceeded as planned.

RESULTS ACHIEVED TO DATE

Data derived from this project have been transferred at the following meetings that were attended:
Posters: 2nd Gauteng Department of Agriculture and Rural Development Research Symposium held on the 6 June 2012. Title: Plant-parasitic nematodes a threat to local subsistence producers in the Gauteng Province.

Farmer's days attended and presented at:

- Gaseatlana farmer's day (Maize production) held on the 9th May 2012.
- Barberton (Potato production) farmer's day on the 15 June 2012.
- Morokweng Maize production information day 10 July 2012.
- Mjindi Trust-Barberton (vegetable production) farmer's day 03 August 2012.
- Ikageng Extension 7 (vegetable production) farmer's day 08 August 2012.

PROBLEMS ENCOUNTERED

None.

TECHNOLOGY TRANSFER

DETAILS

PROJECT NUMBER		M181/10
PROJECT TITLE		Maize Information Guide (MIG)
PROJECT MANAGER		SM James
CO-WORKER(S)	Internal	MA Prinsloo, SH Ma'ali, D de V Bruwer, AA Nel, AEJ Saayman-du Toit, MM van der Walt, E Hugo, JBJ van Rensburg, BC Flett, W Deale, UM Du Plessis, A Schoeman, E Ncube, M Craven, A Erasmus
	External	None
PROJECT STATUS		Continue
DURATION		01/04/2001 - 31/03/2015

ACTIONS TAKEN TO DATE

The MIG 2012 was printed in April and launched at the National Maize Producers Organisation (NAMPO) exhibition during May 2012. The release of the booklet was conducted in the presence of media, stakeholders and interested public and received positive reviews in magazines such as Landbouweekblad, SA Grain as well as Farming SA. This year marked the 19th edition of the guideline. This year 4 500 copies of the booklets were printed and nearly 2 300 copies posted to SA Grain members alone. The remaining copies were sent out to various farmers and organisations on the address list. The MIG 2012 was also made available to the public on the ARC website.

PROGRESS MADE

A meeting was held on 27 August to plan for the MIG 2013 as well as to compile an array of new and relevant information for the Maize Industry. It is anticipated that there will be a meeting held in early November to finalize some of the contents to appear in the MIG 2013.

RESULTS ACHIEVED TO DATE

The booklet was successfully completed and distributed to all relevant stakeholders. The advertisers who had advertised in the MIG 2012 were sent reminders to encourage prompt payment.

PROBLEMS ENCOUNTERED

No significant problems were encountered during the report period.