Euphytica (2005) 145: 123–132
DOI: 10.1007/s10681-005-0625-4

Environmental classification of maize-testing sites in the SADC region and its implication for collaborative maize breeding strategies in the subcontinent

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Received 7 December 2004; accepted 7 July 2005

Key words: genotype-by-environment, maize, mega-environment, sequential retrospective pattern analysis

Summary

When evaluating genotypes, it is efficient and resourceful to identify similar testing sites and group them according to similarity. Grouping sites ensures that breeders choose as many variable sites as possible to capture the effects of genotype-by-environment (GE) interactions. In order to exploit these interactions and increase testing efficiency and variety selection, it is necessary to group similar environments or mega-environments. The present mega-environments in the Southern African Development Community (SADC) countries are confounded within each country, which limits the exchange of germplasm among them. The objective of this study was to revise and group similar maize-testing sites across the SADC countries that are not confounded within each country. The study was based on 3 years (1999–2001) of regional maize yield trial data and geographical information systems (GIS) parameters from 94 sites. Sequential retrospective (Seqret) pattern analysis methodology was used to stratify testing sites and group them according to their similarity and dissimilarity based on mean grain yield. The methodology used historical data, taking into account imbalances of data caused by changes over locations and years, such as additions and omission of genotypes and locations. Cluster analysis grouped regional trial sites into seven mega-environments, mainly distinguished by GIS parameters related to rainfall, temperature, soil pH, and soil nitrogen with an overall $R^2 = 0.70$. This analysis provides a challenge and an opportunity to develop and deploy maize germplasm in the SADC region faster and more effectively.

Abbreviations: SADC, Southern African Development Community; GIS, geographical information systems

Introduction

Maize (*Zea mays*) is grown in major agroecological zones in southern Africa covering over 12 million hectares and is the staple food for more than 200 million inhabitants in the region (FAOSTAT, 2003). The 12 million hectares of land is highly variable in terms of soil characteristics, rainfall, and maximum temperature. In order to manage this variability, it is necessary to group similar locations or mega-environments where maize germplasm will perform similarly and target adapted genotypes to similar locations. Plant breeders have used mega-environments to identify the number of testing locations and the type of germplasm to use in each mega-environment (Peterson, 1992).

Identifying mega-environments based on genotypes is rendered difficult due to the fact that over the years, plant breeders change genotypes and locations due to factors such as poor performance of some genotypes and lack of resources. Testing sites must be similar to the representative samples of production areas targeted by plant breeders in order to be effective in selection (Cooper et al., 1993). However, testing sites are usually not representative of production areas because the testing locations are chosen based on political boundaries,

resources and convenience (Hamblin et al., 1980). Testing locations are critical when estimating the variance due genotype × location × year interaction. These changes bring imbalances or incomplete designs that are difficult to analyze or interpret. Environmental conditions, such as rainfall are unpredictable and difficult to estimate compared to repeatable conditions such as general climate and soil (Cooper et al., 1993). Plant breeders and agronomists exploit these repeatable changes by characterizing the key environmental changes that can help them view a mixture of target environments (Cooper & Delacy, 1994).

Multivariate techniques have been developed over the years to analyze imbalanced multi-environmental trials (METs) data and to cluster locations using proximity matrices (Delacy et al., 1990). Peterson and Pfeiffer (1989) used the results from METs to stratify wheat-testing locations and group them into mega-environments. DeLacy et al. (1994) using multivariate techniques analyzed data from the International Spring Wheat Yield Nursery (ISWYN) from 184 locations. A dissimilarity matrix of 184 × 184 squared Euclidean distances was used for each pair of locations to develop cluster analysis. The methodology proved to be useful by grouping the 184 sites into six ISWYN mega-environments. On the other hand, these multivariate techniques neglected abiotic factors that were associated with geographical information systems (GIS) variables, such as soils, latitude, and others.

The present maize mega-environments in the Southern African Development Community (SADC) are confounded within each country and does not extend beyond the political boundaries, which limit the exchange of germplasm among the countries. Therefore, the objective of this study was to revise maize mega-environment that are not confounded within each member country and which will extend genotypic comparison across the member countries. The study was based on 3 years (1999–2001) of regional maize yield trials data and GIS parameters. Sequential retrospective pattern analysis provides an opportunity to integrate METs data and GIS parameters to revise testing environments within which germplasm will perform similarly in the SADC region.

Materials and methods

This study was based on regional maize trials conducted over 3 years (1999–2001) and covering 94 maize-testing locations in the SADC region. Out of the 94 locations, only 52 locations were used in the final analysis. Some locations were dropped if trials were conducted only once in the locations over the 3 years. Geographic information system data were based on long-time average of rainfall, temperature, maximum temperature, and soil characteristics from the FAO soils map (Hodson et al., 2002). The trials included 290 different genotypes of maize open-pollinated varieties (OPVs) and hybrids developed by the International Maize and Wheat Improvement Center (CIMMYT), National Agricultural Research Systems (NARS) and private seed companies. The 290 genotypes were grouped according to vigor and maturity. There were four maturity groups: early to intermediate maturing OPVs (EPOP), intermediate to late maturing OPVs (ILPOP), early to intermediate maturing hybrids (EIHYB), and intermediate to late maturing hybrids (ILHYB). Those genotypes that were tested only once were dropped in the final analysis, which resulted in 163 genotypes. Trials in each country were conducted using an alpha (0, 1) lattice design with three replicates and the number of entries ranging from 25 to 30. Four management schemes were used to implement the trials: well fertilized/rain fed conditions, managed nitrogen stress, managed drought

Table 1. Analysis of variance for maize yield trials across locations and 3 years grouped according to vigour and maturity, forming four replicated trials and grown the Southern African Development Community

	EPOP		ILPOP		EIHYB		ILHYB	
Sources of variation	d.f.	Mean squares	d.f.	Mean squares	d.f.	Mean squares	d.f.	Mean squares
Environments	10	148.03***	22	322.72***	16	814.76***	11	8.26***
Rep (environments)	22	9.45***	46	3.56***	34	8.17***	24	21.69***
Genotypes	23	2.77***	23	7.42***	49	8.46***	65	19.67***
Environment × genotypes	230	1.06***	506	1.36***	784	2.17***	715	4.47***

***Indicates significant differences at 0.001 level of probability.

Table 2. Least square means of maize early to intermediate (EPOP) and intermediate to late maturing open pollinated (ILPOP) varieties grown in 52 locations across the SADC countries for 3 years

Maize open-pollinated varieties	Grain yield (t/ha)
Early to intermediate maturing open pollinated (EPOP)	
ZM301	3.25
GRACE (EWF-2)-#	3.15
Z97EWA-F2-#	3.00
Z97EWB-F2-#	2.86
Z97EWA-F2/Z97EWB-F2	3.27
[EARLY-MID-2/PL16-SR]-#	3.19
[DMRESR-W]#b(EARLY SEL)-#	2.79
[TEWD-SRDRTOLSYN/[NAW5867/P30-SR(S2#)]]##	3.34
[EV7992/POOL16-SR]#bS1SEL-F3	3.28
[EARLY-MID-1/KATUMANI-SR]-#	2.88
[VAR/TEMP.HILANDPOP]-##	2.77
SADVE F1	3.56
SADVI1 F1	3.79
SADVI2 F1	3.78
DTP1-W C6 SEL. PRECOZ F3	3.12
POOL 16 BNSEQ C1 F2	2.99
MATINDIRI-# (Malawi)	3.00
KATUMANI-ST-# (Tanzania)	2.89
KITO-ST-# (Tanzania)	3.13
SYNTHETIC DR-SR-# (CIMMYT-Kenya)	3.10
SYNTHETIC-NUE-SR-# (CIMMYT-Kenya)	3.30
LOCAL CHECK 1 CCD	2.80
LOCAL CHECK 2: CHITIBU	3.15
LOCAL CHECK 3: SUNDWE	2.73
Intermediate to late maturing open pollinated (ILPOP)	
Z97SYNGLS(A)-F2-#	3.68
Z97SYNGLS(B)-F2-#	3.79
AC969A-SR(Best FS)]F2	3.54
[MID.ALT.QPM]C2F2-#	3.29
[WHITE QPM]C2F2-#	3.17
[TUXP.SEQC6]C1	3.89
[TSEQZIM]C2F2	3.69
[ZM601DEN]C3F2	3.32
[SUWAN1-SR/COMPE1]C1-#	3.86
INTAC1F1/INTBC1F1	3.46
LATAC1F1/LATBC1F1	3.90
DRAC0SYNF1/DRBC0SYNF1	3.74
SADVL F1	4.25
MASIKA-# (Malawi)	3.75
MCHOSANJALA-# (Malawi)	2.83
KAKHOMERA-# (Malawi)	3.17
KAFUMBA-# (Malawi)	3.23
SUNDWE-# (Malawi)	3.59
CHITIBU (Malawi)-#	3.55
STAHA-# (Tanzania)	3.26
TMV-1-# (Tanzania)	3.21
TASEQ-# (CIMMYT-Kenya)	3.62
LOCAL CHECK 1: KEP	3.20
LOCAL CHECK 2: KEP	3.24

stress, and managed low pH stress. Data were collected on yield performance and other important agronomic traits.

Statistical analysis

Trial data were adjusted for flowering date, using a linear regression analysis, and standardized within each trial before subjecting data to cluster analysis. Sequential retrospective pattern analysis (Seqret) was used for stratification of testing sites according to Mirzawan et al. (1994) and DeLacy et al. (1994). The analysis was implemented using the SEQRET package Version 1.1 (DeLacy et al., 1998). Sequential retrospective pattern analysis requires for its implementation the mean values of genotypes tested in individual site-year environments. The genotypes were considered to be random across the years. Analysis parameters employed in the clustering strategy were incremental sum of squares algorithm, weighted averages, and standard error of the difference (SED) (Ward, 1963). The adequacy of the model was calculated from the R^2 statistic as explained by DeLacy et al. (1996), which is a measure of the effectiveness of the model. Some of the sites were eliminated or allocated to one of the groups based on SED from the nearest centroid.

After identifying the clusters with SEQRET, GIS parameters and trial management information was allocated to different sites in different clusters and a *t*-test revealed which parameters differed significantly among clusters. The entire SADC region was then classified using different combinations of those GIS parameters.

Results and discussion

The analysis of variance for grain yield is shown in Table 1 for the various trials grouped according to maturity and vigor. There were highly significant differences among environments, genotypes and genotype-by-environment interactions across the 52 locations in the SADC region. The means for the genotypes are listed in Tables 2 and 3 according to the maturity and vigor. Generally, the late maturing hybrids yielded higher than the OPVs.

Cluster analysis grouped the 52 maize-testing sites into seven major environments based on yield data (Figure 1). Some of the sites were retained and the rest were eliminated due to lack of comparisons across the 3 years

Table 3. Least square means of maize early to intermediate (EIHYB) and intermediate to late maturing hybrids (ILPOP) varieties grown in 52 locations across the SADC countries for 3 years

Maize hybrids	Grain yield (t/ha)
Early to intermediate maturing hybrids (EIHYB)	
[[NAW 5867/P30-SR]-111-2/[NAW 5867/P30-SR]-25-1]-8-S7/CML205	3.62
[[NAW 5867/P30-SR]-111-2/[NAW 5867/P30-SR]-25-1]-8-S7/CML390	4.15
[[NAW 5867/P30-SR]-111-2/[NAW 5867/P30-SR]-25-1]-8-S7/CML395-B	4.07
[COMPE2/P43-SR//COMPE2] FS#-20-S7/CML390	4.50
[COMPE2/P43-SR//COMPE2] FS#-20-S7/Z97EWB	3.52
[COMPE2/P43-SR//COMPE2] FS#-20-S7/Z97EWA	3.77
[NAW 5867/P49-SR(S2#)//NAW 5867] FS#-48-S7/CML216	4.14
CML205/Z97EWB	3.33
CML205/ZM301	3.32
CML205/Z97EWA	3.45
[[K64R/PL16-SR]-39-1/[K64R/PL16-SR]-20-2]-5-1-2-B-B-B/CML202	3.83
G16BNSEQC0F118-1-1-B-B/CML202	4.20
G16SeqC1F47-2-1-2-1-B-B-B/CML202	3.92
[COMPE2/P43-SR//COMPE2] FS#-20-1-1-B-1-B-B/CML202	4.20
IKENE8149SR-68-2-BBB-6-BB-B-B-B/CML202	4.13
SPLC7F182-1-2-2-B-B-B/CML202	4.23
TS6C1F238-1-3-3-1-2-#-B-B-B/CML202	4.69
[[NAW 5867/P30-SR]-111-2/[NAW 5867/P30-SR]-25-1]-8-1-1-B-1-B/CML202	3.71
[EV7992#/EV8449-SR]C1F2-334-1(OSU8i)-10-7(I)-X-X-X-2-B-B-1-B/CML202	4.11
INTA-191-2-1-2-B-B-B/CML202	4.16
LATA-26-1-1-2-1-B-B/CML202	3.94
G16BNSEQC0F228-2-3-B-B-B/CML202	3.89
G16SeqC1F47-2-1-2-1-B-B-B/CNL206	3.85
DTP1WC6F181-1-#-3-1-1-B-B-B/CNL206	3.88
[[K64R/P30-SR]-82-2/[K64R/P30-SR]-87-4]-7-3-4-B-B-B-B/CNL206	3.13
TS6C1F238-1-3-3-1-2-#-B-B-B/CNL206	4.17
INTB-91-1-2-2-1-B-B/CNL206	3.73
ZM605 C2F1-17-1-B-1-B/CNL206	3.28
[[TUXPSEQ]C1F2/P49-SR]F2-103-2-2-3-B/CNL206	3.07
953WH237	3.55
ZS255	4.13
983WH102	3.52
PAN 473	3.31
PAN 6043	3.15
PAN 6235	3.40
PAN 6321	3.82
PAN 6363	3.47
PAN 6549	2.87
PAN 6561	3.80
CG4141	3.13
CG4585	3.43

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Table 3. (Continued)

Maize hybrids	Grain yield (t/ha)
R201	3.12
SC401	3.03
SC403	3.97
SC405	3.64
SC407	3.86
SC501	3.74
SC513	4.09
SC515	4.00
LOCAL CHECK: KEP	3.50
Intermediate to late maturing hybrids (ILHYB)	
CML202/CML204//CML312/CML206	6.05
CML202/CML395//CML390/CML206	5.97
CML202/CML395//CML312/CML206	6.03
CML202/CML216//CML312/CML206	5.98
CML204/CML216//CML312/CML206	5.98
CML202/CML395//CML390	6.32
CML202/CML395//CML312	6.64
CML312/CML206//CML197	6.51
CML204/CML216//CML312	6.29
CML202/CML216//CML312	6.60
CML202/CML216//CML206	5.66
CML202/CML395//CML197	7.07
CML202/CML204//CML312	6.67
CML390/CML206//CML395	6.07
CML202/CML206	5.75
CML 216/CML197	6.39
CML216/MBR-ET(W)F2-14-S8	6.38
BS19S2no68-1-2-B-B-B/CML202	6.16
M37W/ZM607#bF37sr-2-3sr-6-2-X]-8-2-X-1-B-B-B/CML202	6.11
LATA-F2-138-1-3-1-B-B/CML202	5.56
SNSYNF2[N3/TUX-A-90]-28-1-3-1-BSR-B-B/CML202	6.27
[AC8342/IKENNE{1}8149SR//PL9A]C1F1-500-4-X-1-1-B-B-1-B/CML202	6.03
LPSC4F273-2-2-3-B-B-B/CML202	5.62
[[TUXPSEQ]C1F2/P49-SR]F2-45-5-1-2-B/CML202	6.37
[[TUXPSEQ]C1F2/P49-SR]F2-45-7-5-1-B/CML202	6.82
LPSC4F273-2-2-1-B-B-B/CML206	5.51
LPSC3H144-1-2-2-2-2-#-B-B-B/CML206	5.29
LPSC3H144-1-2-2-2-4-#-B-B-B/CML206	5.10
P43C9-1-1-1-1-1-B-B-B/CML206	6.96
DRB-F2-60-1-1-1-B/CML206	6.33
SC/ZM605#b-19-2-X]-1-2-X-1-1-B-B-B/CML206	6.03
ZSR 923 S4BULK-2-2-X-X-X-X-1-B-B-B/CML206	6.10
[EV7992#/EV8449-SR]C1F2-334-1(OSU9i)-8-2(I)-X-1-2-B-B-1-B/CML206	6.39

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Table 3. (Continued)

Maize hybrids	Grain yield (t/ha)
90323(B)-1-X-1-B-B-1-B/CML206	6.75
DRB-F2-180-2-1-B-B/CML206	5.52
INTB-117-1-2-1-1-B-B/CML206	4.89
[[TUXPSEQ]C1F2/P49-SR]F2-45-7-5-1-B/CML206	5.65
INBRED A/CML202	5.25
INBRED A/CML206	5.10
973WH29	5.13
PAN 413	3.85
PAN 6193	4.91
PAN 6195	5.07
PAN 6243	5.77
PAN 6335	5.50
PAN 6479	5.00
PAN 6573	6.03
PAN 6587	5.79
PAN 67	5.55
C8001	5.17
C8016	5.64
C8037	4.55
C8027	6.79
C8040	6.29
SC621	5.90
SC627	6.11
SC709	5.75
ACD12	4.35
ACD21	4.59
ACD31	4.56
ACD42	5.26
ACD51	4.33
ACD62	4.48
DTP2WC4H255-1-2-2-B-B-B/CML197	5.51
M37W/ZM607#bF37sr-2-3sr-6-2-X]-8-2-X-1-B-B-B/P43C9-1-1-1-1-1-B-B-B	7.24
LOCAL CHECK	4.69

(Table 4 and Figure 1). The classification of the sites yielded an $R^2 = 70$. The seven mega-environments differed for GIS parameters as related to rainfall, maximum temperature, soil pH, and soil nitrogen (Tables 5 and 6).

These GIS parameters divided the SADC region into 16 possible combinations (Table 5). The 16 zones were merged and mapped into seven zones equivalent to those identified by cluster analysis (Figures 1 and 2). An eighth zone (Zone H) was added for being the coolest zone ($<24\,^{\circ}$C), which was not represented by maize trial sites (Figure 1). The percentage area of each zone in SADC region is then calculated (Table 6). The largest area was covered by mega-environment E, which is 19.6% of the total area in the SADC region (Table 6) and the smallest was mega-environment H, which accounts for 3.1%, in the region. The largest mega-environment is characterized by low season precipitation and medium to high temperatures, while the smallest mega-environment is characterize by mostly the highlands of Lesotho (Figure 1). Zimbabwe, South Africa, and Swaziland accounts for the second largest

Table 4. The final locations that were retain after using seqret analysis for the characterization and revision of maize mega-environments

Country	Location	Legend	Management type
Angola	Chianga	AngChiLp	Managed low pH stress
Angola	Chianga	AngChiLN	Managed nitrogen stress
Angola	Chianga	AngChi	Well fertilized/rainfed
Angola	Mazozo	AngMaz	Well fertilized/rainfed
Angola	SVicente	AngSVi	Well fertilized/rainfed
Botswana	Goodhope	BotGoo	Well fertilized/rainfed
Lesotho	Mahobong	LesMahLp	Well fertilized/rainfed
Lesotho	Maseru	LesMas	Well fertilized/rainfed
Malawi	Baka	MalBak	Well fertilized/rainfed
Malawi	Chitedze	MalChiDr	Managed drought stress
Malawi	Chitedze	MalChi	Well fertilized/rainfed
Malawi	Lunyangwa	MalLunLp	Managed low pH stress
Malawi	Ngabu	MalNga	Well fertilized/rainfed
Mozambique	Chokwe	MozCho	Well fertilized/rainfed
Mozambique	Sussundenga	MozSusLN	Managed nitrogen stress
RSA	Greytown	RSAGre	Well fertilized/rainfed
RSA	Potchefstroom	RSAPotLp	Managed low pH stress
Tanzania	Arusha	TanAruDr	Managed drought stress
Tanzania	Arusha	TanAruLN	Managed nitrogen stress
Tanzania	WeruWeru	TanWer	Well fertilized/rainfed
Zambia	Kasama	ZamKasLp	Managed low pH stress
Zambia	Magoye	ZamMag	Well fertilized/rainfed
Zambia	Msekera	ZamMse	Well fertilized/rainfed
Zambia	MtMakulu	ZamMtM	Well fertilized/rainfed
Zambia	Nanga	ZamNanDr	Managed drought stress
Zambia	Zamseed	ZamZam	Well fertilized/rainfed
Zimbabwe	Chiredzi	ZimChiDr	Managed drought stress
Zimbabwe	Harare	ZimHarMs	Managed Maize streak virus
Zimbabwe	Harare	ZimHarLN	Managed nitrogen stress
Zimbabwe	Harare	ZimHar	Well fertilized/rainfed
Zimbabwe	Kadoma	ZimKad	Well fertilized/rainfed
Zimbabwe	Makoholi	ZimMakLp	Managed Low pH stress
Zimbabwe	Makoholi	ZimMak	Well fertilized/rainfed
Zimbabwe	RattrayArnold	ZimRat	Well fertilized/rainfed
Zimbabwe	SaveValley	ZimSavDr	Managed drought stress

Table 5. Seven clusters delineated by analyzing regional trial data

	High yield, high rainfall environments			Lower yield, low rainfall environments			
	A	B	C	D	E	F	G
Temperature	Low			Medium			High
Rainfall	Wet			Medium		Dry	
Low pH	Acid	Neutral		Acid	Neutral		
Low N/high N				Most low N sites			

Table 6. Characteristics of maize mega-environments in southern Africa as identified through sequential retrospective pattern analysis of multi-environmental trials

Maize mega-environment	Maximum temperature (°C)	Season precipitation (mm)	Sub-soil pH (water)	Area in southern Africa (10^3 ha)
A	24–27	>700	<5.7	46,282
B	24–27	>700	<5.7	28,826
C	24–30	<700		48,291
D	27–30	>700	<5.7	17,166
E	27–30	>700	>5.7	49,589
F	>30	>700		17,146
F	>30	<700		38,403
H	<24			7,897

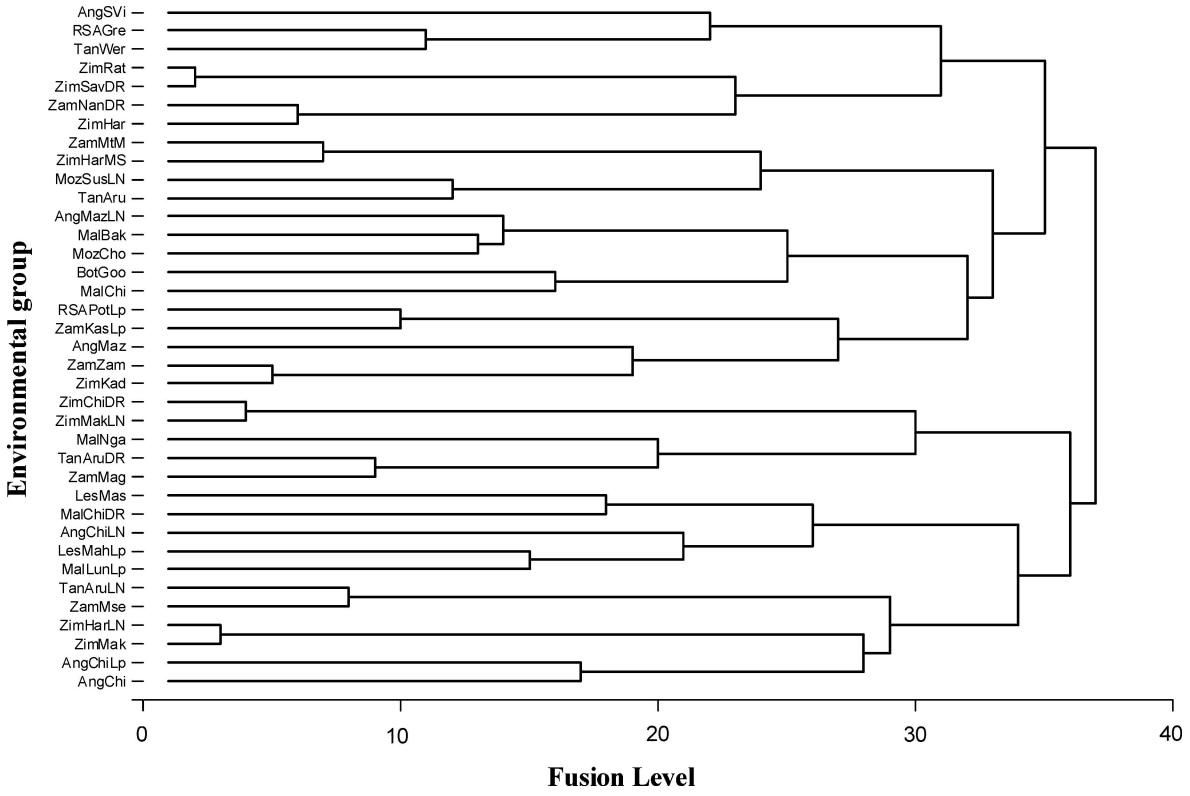

Figure 1. Dendrogram from classification of 38 locations used to develop maize mega-enironments in the Southern African Development Community (SADC) 1999–2001. Based on maize regiona trials. The clustering strategy was based on hierarchical agglomerative classification using squared Euclidean distance as the dissimilarity measure and incremental sum of squares as the clustering strategy.

mega-environment (Figure 1), which has one of the highest rainfall and low temperatures.

Mega-environments A, B, and C are high yielding environments because of high rainfall and medium temperatures compared to mega-environments D, E, and F which are low yielding due to low rainfall and poor soil fertility which contribute to low yields (Table 6).

Implications for maize germplasm development and deployment

This analysis discriminated among maize growing environments in the SADC region that result in different ranking of maize germplasm. The result has different implications:

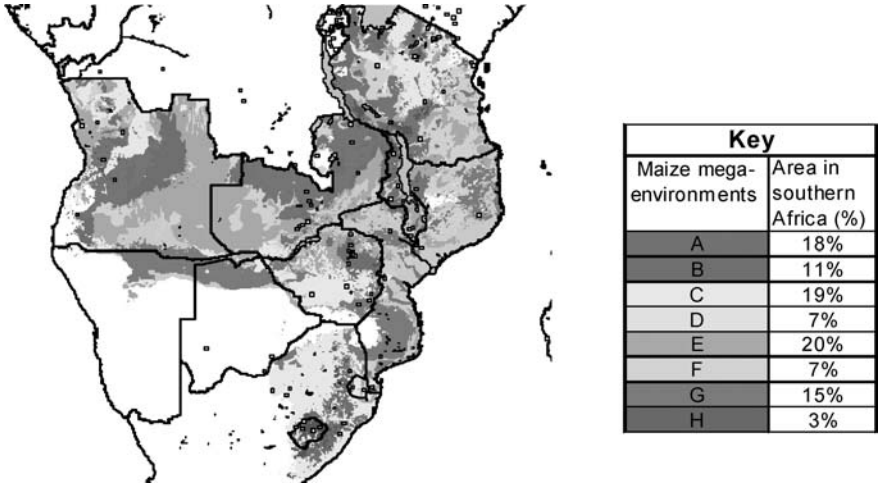

Figure 2. Maize mega-environment in Southern African Development Community delineated by combinations of maximum temperature, season precipitation, and soil pH. The squares indicate trial sites used for defining mega-environments. Climatic and edaphic were from Hodson et al. (2002).

It provides a basis for choosing the location and optimum number of testing sites for future evaluation and release of maize germplasm in the SADC region. Future testing of germplasm could be limited to key benchmark sites in each mega-environment. Evaluation under low and high soil N and under low and high soil pH would have to be included in those mega-environments where these stress factors are relevant in farmers' fields.

This analysis is important for revealing the areas within SADC where a certain variety could be deployed. Mega-environments cut across country limits. A variety performing well in a certain mega-environment in one country would be suitable for growing in the same mega-environment across the entire SADC region. This provides a scientific rationale for regional release of maize varieties and could lead to farmers across the SADC region benefiting much faster from breeding progress. Such an approach would be valid for any maize germplasm with a minimum adaptation to the SADC region (as evaluated in this study). It may not apply for germplasm that strongly differs from the 290 maize genotypes evaluated in this study, such as temperate maize germplasm.

Site similarities will also help breeders to develop germplasm that have wide adaptation, although genetic potential for specific adaptation will become more important as environments become more unique.

In summary, this environmental classification provides a rationale for NARS and regional breeding programs to move towards maize breeding programs that are more resource and time-efficient in developing and delivering improved maize varieties to farmers in the SADC region. More effective and sustainable research is needed to build up on the findings of this research in order to create an effective classification tools for breeders to use in the region. Strong regional collaboration can increase access to valuable germplasm while reducing costs for research and information generation.

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