PROTOCOLO INTEGRADO DO ESTADO
Fls. 1
Mov. 1

Folha 1

ESTADO DO PARANÁ

ePROTOCOLO

Órgão Cadastro: UEM
Em: 11/01/2023 10:31

Protocolo:
19.920.144-1

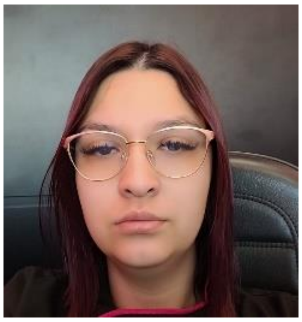
Interessado 1: COORDENAÇÃO DO PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA E MELHORAMENTO / UEM
Interessado 2:
Assunto: ENSINO SUPERIOR
Cidade: MARINGA / PR
Palavras-chave: CURSOS STRICTO SENSU
Nº/Ano -
Detalhamento: INSCRIÇÃO DE MARIA FERNANDA DE SOUZA DIAS MAIOLI NO PROCESSO DE SELEÇÃO AO CURSO DE DOUTORADO DO PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA E MELHORAMENTO (PGM) DA UNIVERSIDADE ESTADUAL DE MARINGÁ (UEM), PARA
Código TTD: -

Para informações acesse: https://www.eprotocolo.pr.gov.br/spiweb/consultarProtocolo

UNIVERSIDADE ESTADUAL DE MARINGÁ

FICHA DE INSCRIÇÃO PARA CURSO DE PÓS-GRADUAÇÃO
Doutorado em Genética e Melhoramento
015/2022-PGM

Dados pessoais



Cód. Inscrição: 6/2022-PGM

Nome: Maria Fernanda de Souza Dias Maioli
CPF: 08356325986 **R.G.:** 110194137 SSP PR
Est. cívil: Casado(a)

Data nasc.: 22/09/1993
Nacionalidade: Brasil
Estado Nasc.: PR
Cidade nasc.: Apucarana

Tít. Eleitor: 101416590680
Zona: 070
Seção: 29
Estado: PR

Endereço: Rua Inhaúma **Nº** 731
Bairro: Zona 3 **Complemento:** apt 901
Cidade: Maringá **Estado:** PR **CEP:** 87050170

País: Brasil **E-mail:** mahfer527@gmail.com
Celular: (43)999204005 **Fone Res.:** (43)999204005 **Fone Com.:**

Declaro conhecer e aceitar as normas estabelecidas em edital para o processo seletivo de candidatos para o programa de DOUTORADO EM GENÉTICA E MELHORAMENTO da Universidade Estadual de Maringá

Maria Fernanda

Maria Fernanda de Souza Dias Maioli

Data de Inscrição: 12/20/22 11:36 AM

Data impressão: 20/12/2022

Universidade Estadual de Maringá
Centro de Ciências Agrárias
Departamento de Agronomia
Programa de Pós-Graduação em Genética e Melhoramento

FICHA DE INSCRIÇÃO COMPLEMENTAR

IDENTIFICAÇÃO DO CANDIDATO

NOME COMPLETO MARIA FERNANDA DE SOUZA DIAS	CÓD. INSCRIÇÃO ___/____-PGM

Indique, em ordem decrescente de interesse, os prováveis orientadores, dentre os professores orientadores do Programa de Pós-Graduação em Genética e Melhoramento.
Não fica assegurado ao candidato o atendimento dos professores orientadores escolhidos.

PROVÁVEL PROFESSOR ORIENTADOR

1ª OPÇÃO	Ronald José Barth Pinto
2ª OPÇÃO	
3ª OPÇÃO	

Você aceitará como orientador, outro professor do Programa de Pós-Graduação em Genética e Melhoramento, que não os listados acima?

☒ Sim. ☐ Não.

FORMAÇÃO ACADÊMICA

GRADUAÇÃO

NOME DO CURSO Agronomia		ANO DE CONCLUSÃO 2010
INSTITUIÇÃO Universidade Estadual de Maringá		
PAÍS Brasil	CIDADE Maringá	UF PR

PÓS-GRADUAÇÃO

NOME DO CURSO Pós- Graduação em Genética e Melhoramento		ANO DE CONCLUSÃO 2018
INSTITUIÇÃO Universidade Estadual de Maringá		
PAÍS Brasil	CIDADE Maringá	UF PR

ATUAÇÃO PROFISSIONAL E LOCAL DE TRABALHO

INSTITUIÇÃO	PERÍODO		Tipo de atividade (docência, pesquisa, extensão, promoção e atividade particular). Indique cronologicamente, começando pela mais recente, suas três últimas atividades profissionais remuneradas.
	DESDE	ATÉ	

FONTE FINANCIADORA DE SEUS ESTUDOS

☐ Possuo bolsa de estudo concedida (ou a ser concedida) pelo (a) ....
☐ Manterei vínculo empregatício durante o curso, percebendo meus vencimentos.
☐ Manterei vínculo empregatício durante o curso, sem perceber meus vencimentos.
☐ Não possuo emprego ou bolsa e desejo candidatar-me a uma bolsa do curso.
☒ Não possuo emprego ou bolsa, mas não desejo candidatar-me a uma bolsa do curso.

Obs.: A seleção não implica compromisso de bolsa por parte do curso.

PLANO DE TRABALHO

No quadro abaixo, indique e justifique os motivos de sua escolha pelo Programa de Pós-Graduação em Genética e Melhoramento da Universidade Estadual de Maringá, destacando suas expectativas quanto ao Programa.
Justifique os temas de pesquisa e os prováveis professores orientadores escolhidos.
Apresente, resumidamente, como os conhecimentos a serem adquiridos em seu treinamento poderão repercutir em sua vida.

Meu nome é Maria Fernanda S. D. Maioli e venho declarar o meu interesse em fazer parte do curso de Pós-Graduação em Genética e Melhoramento da Universidade Estadual de Maringá (UEM).

Possuo graduação em Agronomia e Pós-Graduação em nível de mestrado pelo programa de Pós-Graduação em Genética e Melhoramento ambos pela Universidade Estadual de Maringá (UEM). Durante minha graduação e mestrado sempre tive o interesse de seguir a área de pesquisa no campo de genética e melhoramento vegetal.

Acredito que estudar no programa de pós-graduação em Genético e Melhoramento será um grande diferencial para minha carreira. Não apenas pela oportunidade de aprender com o corpo docente, mas também pela troca de informações com os demais alunos.

Concluindo, espero que com o curso em uma instituição e em um programa com o conceito que o PGM apresenta possa produzir estudos que serão inovadores e que tragam frutos tanto para o programa quanto para meu crescimento pessoal, como o trabalho que pretendo realizar que é um trabalho inovador na área, tendo em vista que a análise de GWAS em proteína em milho foi pouco estudada e apresenta grandes perspectivas.

DECLARAÇÃO

DECLARO que este pedido contém informações completas e exatas, que aceito o sistema e os critérios adotados pela Instituição para avaliá-lo e que, em caso de cursar disciplinas de pós-graduação nesta universidade, me comprometo a cumprir fielmente seus regulamentos e os do Programa de Pós-Graduação em Genética e Melhoramento.

Maringá	20/12/2022	Maria Fernanda
LOCAL	DATA	ASSINATURA DO CANDIDATO

DECLARAÇÃO SOBRE RAÇA/COR E NECESSIDADES ESPECIAIS

Em relação à Raça/Cor, eu me considero:

☒ Branca
☐ Parda
☐ Indígena
☐ Preta
☐ Amarela
☐ Não Declarado

Declaro:

☐ Ser portador (a) de deficiência e/ou de necessidades educativas especiais;

☒ **NÃO** ser portador (a) de deficiência e/ou de necessidades educativas especiais.

DECLARO estar ciente de que as informações que estou prestando são de minha inteira responsabilidade e que, no caso de declaração falsa, estarei sujeito às sanções previstas em lei.

Maringá	20/12/2022	Maria Fernanda
LOCAL	DATA	ASSINATURA DO CANDIDATO

REPÚBLICA FEDERATIVA DO BRASIL
REGISTRO CIVIL DAS PESSOAS NATURAIS

CERTIDÃO DE CASAMENTO

Nomes

LUCAS FARINAZZO MAIOLI, CPF Nº 076.031.339-39

MARIA FERNANDA DE SOUZA DIAS, CPF Nº 083.563.259-86

Matrícula

0816610155 2018 2 00036 047 0004607 14

Nomes completos de solteiro, datas nascimento, naturalidade, nacionalidade e filiações dos cônjuges

LUCAS FARINAZZO MAIOLI, nascido aos 06 de abril de 1991, natural de Apucarana-PR, brasileiro, solteiro, engenheiro sanitarista e ambiental, filho de Primo Donizéte Maioli e de Sandra Tereza Farinazzo Maioli; residente e domiciliado em Jandaia do Sul-PR.

MARIA FERNANDA DE SOUZA DIAS, nascida aos 22 de setembro de 1993, natural de Apucarana-PR, brasileira, solteira, estudante, filha de Jansir Dias Paz e de Gildete Aparecida de Souza Dias; residente e domiciliada em Jandaia do Sul-PR.

Data de registro do casamento (por extenso)	Dia	Mês	Ano
Dez de agosto de dois mil e dezoito	10	08	2018

Regime de bens do casamento
Comunhão Parcial de Bens.

Nome que cada um dos cônjuges passou a utilizar (quando houver alteração)
MARIA FERNANDA DE SOUZA DIAS MAIOLI

Averbações/Anotações à Acrescer
Casamento celebrado em Cartório.

ANOTAÇÕES DE CADASTRO

Tipo de Documento	**Número**	**Data Expedição**	**Órgão Expedidor**	**Data de Validade**
RG	9.255.949-1 11.019.413-7	28/03/2001 10/09/2007	SESP PR SESP PR	....
PIS/NIS	....			
Passaporte	....			
Cartão Nacional Saúde	....	....	....	....
Tipo Documento	**Número**	**Zona/Seção**	**Município**	**UF**
Título de Eleitor	0977 4531 0663 1014 1659 0680	070/0042 070/0029	Jandaia do Sul Jandaia do Sul	PR PR
CEP Residencial	86.900-000		Grupo Sanguíneo	***

*As anotações de cadastro acima não dispensam a parte interessada da apresentação do documento original, quando exigido pelo órgão solicitante ou quando necessário para identificação do seu portador.

Nome do Ofício
Cartório de Registro Civil

Oficiala Designada
Melissa Cassoli Pereira Pires

Município / UF
Município e Comarca de Jandaia do Sul-PR

Endereço
Rua Luiz Vignoli, nº 730 - Loja 01
CEP 86.900-000 – Fone: (43) 3432-7572
crcjandaia@yahoo.com.br

O conteúdo da certidão é verdadeiro. Dou fé.

Jandaia do Sul-PR, 10 de agosto de 2018.

Angela Cristina Campaner
Escrevente Substituta

FUNARPEN
SELO DIGITAL N°
`IccVm.wjQ4j.vW6tn`
Controle:
`8R3Nx.C6p4k`
Consulte esse selo em
http://funarpen.com.br

REGISTRO CIVIL
PESSOAS NATURAIS
Bel. Melissa Cassoli Pereira Pires
OFICIALA DESIGNADA
JANDAIA DO SUL

FUNARPEN AA 003418697 P

MINISTÉRIO DA FAZENDA

Receita Federal
Cadastro de Pessoas Físicas

COMPROVANTE DE INSCRIÇÃO

Número
083.563.259-86

Nome
MARIA FERNANDA DE SOUZA DIAS

Nascimento
22/09/1993

VÁLIDO SOMENTE COM COMPROVANTE DE IDENTIFICAÇÃO

CÓDIGO DE CONTROLE
92E3.0930.BB21.C76A

A autenticidade deste comprovante deverá
ser confirmada na Internet, no endereço

www.receita.fazenda.gov.br

Comprovante emitido pela
Secretaria da Receita Federal do Brasil
às 13:28:07 do dia 17/02/2012 (hora e data de Brasília)
dígito verificador: 00

REPÚBLICA FEDERATIVA DO BRASIL

SECRETARIA DE ESTADO DA SEGURANÇA PÚBLICA
INSTITUTO DE IDENTIFICAÇÃO DO PARANÁ

RG: 11.019.413-7

POLEGAR DIREITO

Maria Fernanda de Souza Dias

ASSINATURA DO TITULAR

CARTEIRA DE IDENTIDADE

Calcografia Banknote

VÁLIDA EM TODO O TERRITÓRIO NACIONAL

REGISTRO GERAL: **11.019.413-7** DATA DE EXPEDIÇÃO: 10/09/2007

NOME: **MARIA FERNANDA DE SOUZA DIAS**

FILIAÇÃO: JANSIR DIAS PAZ
GILDETE APARECIDA DE SOUZA DIAS

NATURALIDADE: ÁPUCARANA/PR DATA DE NASCIMENTO: 22/09/1993

DOC. ORIGEM: COMARCA=JANDAIA DO SUL/PR, DA SEDE
C.NASC=8724, LIVRO=36A, FOLHA=92

CURITIBA/PR

LUIS FERNANDO V. ARTIGAS
DIRETOR - IIPR

ASSINATURA DO DIRETOR

É PROIBIDO PLASTIFICAR

LEI Nº 7.116 DE 29/08/83

Calcografia Banknote

JUSTIÇA ELEITORAL

TRIBUNAL SUPERIOR ELEITORAL

CERTIDÃO

Certifico que, de acordo com os assentamentos do Cadastro Eleitoral e com o que dispõe a Res.-TSE nº 21.823/2004, o(a) eleitor(a) abaixo qualificado(a) está QUITE com a Justiça Eleitoral na presente data .

Eleitor(a): **MARIA FERNANDA DE SOUZA DIAS**

Inscrição: **1014 1659 0680** Zona: 070 Seção: 0029

Município: 76350 - JANDAIA DO SUL UF: PR

Data de nascimento: 22/09/1993 Domicílio desde: 03/02/2011

Filiação: - GILDETE APARECIDA DE SOUZA DIAS
- JANSIR DIAS PAZ

Ocupação declarada pelo(a) eleitor(a): ESTUDANTE, BOLSISTA, ESTAGIÁRIO E ASSEMELHADOS

Certidão emitida às 19:04 em 20/12/2022

Res.-TSE nº 21.823/2004:
O conceito de quitação eleitoral reúne a plenitude do gozo dos direitos políticos, o regular exercício do voto, salvo quando facultativo, o atendimento a convocações da Justiça Eleitoral para auxiliar os trabalhos relativos ao pleito, a inexistência de multas aplicadas, em caráter definitivo, pela Justiça eleitoral e não remitidas, excetuadas as anistias legais, e a regular prestação de contas de campanha eleitoral, quando se tratar de candidatos.
A plenitude do gozo de direitos políticos decorre da inocorrência de perda de nacionalidade; cancelamento de naturalização por sentença transitada em julgado; interdição por incapacidade civil absoluta; condenação criminal transitada em julgado, enquanto durarem seus efeitos; recusa de cumprir obrigação a todos imposta ou prestação alternativa; condenação por improbidade administrativa; conscrição; e opção, em Portugal, pelo estatuto da igualdade.

Esta **certidão de quitação eleitoral** é expedida gratuitamente.
Sua autenticidade poderá ser confirmada na página do Tribunal Superior Eleitoral na Internet, no endereço: http://www.tse.jus.br ou pelo aplicativo e-Título, por meio do código:

ØGH6.WQAN.ELSH.WBXO

* O literal Ø no código de validação representa o número 0 (zero).

REPÚBLICA FEDERATIVA DO BRASIL

TÍTULO ELEITORAL

NOME DO ELEITOR
MARIA FERNANDA DE SOUZA DIAS

DATA DE NASCIMENTO
22/09/1993

Nº INSCRIÇÃO — D.V.
1014 1659 0680

ZONA
070

SEÇÃO
0029

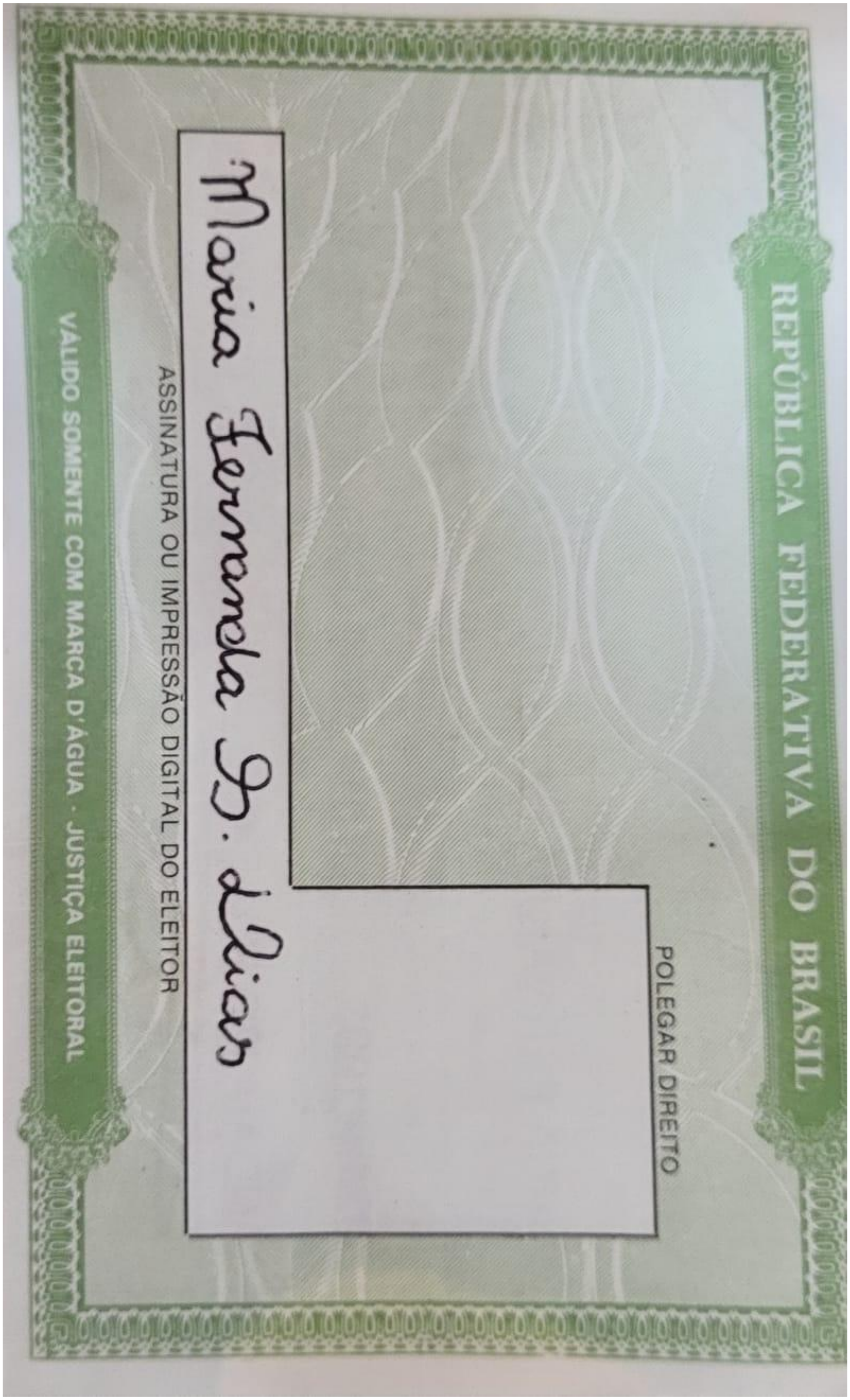
MUNICÍPIO / UF
JANDAIA DO SUL/PR

DATA DE EMISSÃO
03/02/2011

JUIZ ELEITORAL

Des. Irajá Romeo Hilgenberg Prestes Mattar

VÁLIDO SOMENTE COM MARCA D'ÁGUA · JUSTIÇA ELEITORAL



REPÚBLICA FEDERATIVA DO BRASIL

Maria Fernanda G. Dias

ASSINATURA OU IMPRESSÃO DIGITAL DO ELEITOR

POLEGAR DIREITO

VÁLIDO SOMENTE COM MARCA D'ÁGUA · JUSTIÇA ELEITORAL

Universidade Estadual de Maringá

RECONHECIDA PELO DECRETO FEDERAL N.º 77.583, DE 11/05/76, PUBLICADO NO DIÁRIO OFICIAL DA UNIÃO DE 12/05/76
MARINGÁ - PARANÁ

O Reitor da Universidade Estadual de Maringá,
no uso de suas atribuições e tendo em vista a conclusão do Curso de Agronomia
no ano letivo de 2015, confere o título de

Engenheira Agrônoma

a

Maria Fernanda de Souza Dias

brasileira, natural do Estado do Paraná, nascida no dia 22 de setembro de 1993
R.G. n.º 11.019.413-7 - PR

e considerando o termo de Colação de Grau lavrado no dia 18 de fevereiro de 2016, outorga o presente diploma, a fim de que possa gozar de todos os direitos e prerrogativas legais.

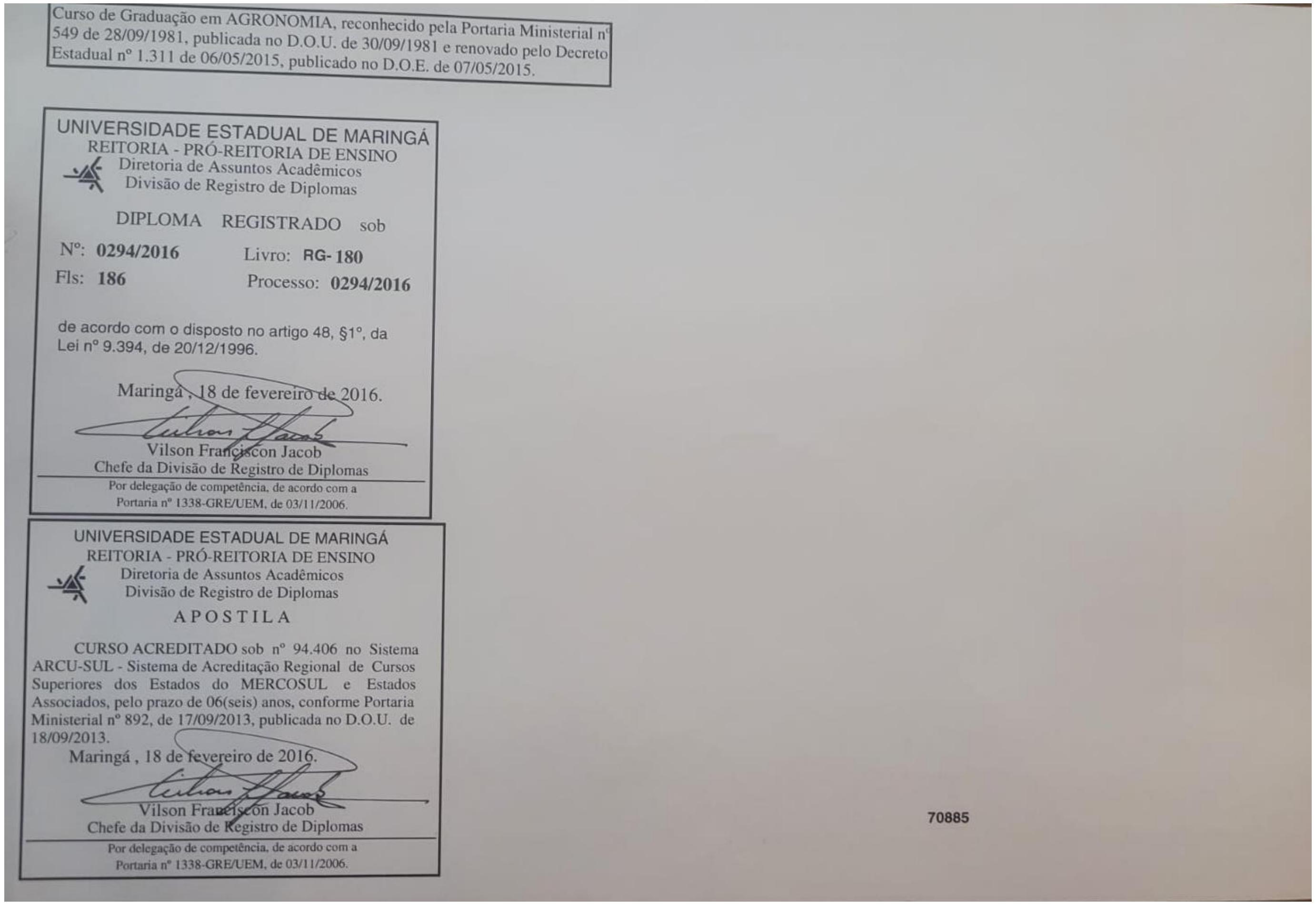
Maringá , 18 de fevereiro de 2016.

Prof. Dr. Mauro Luciano Baesso
Reitor

Prof. Dr. Ronaldo Augusto de Lara Gonçalves
Diretor de Assuntos Acadêmicos

Paulo
Prof. Dr. Paulo Sérgio Lourenço de Freitas
Coordenador do Curso

Maria Fernanda
Maria Fernanda de Souza Dias
Diplomada



Curso de Graduação em AGRONOMIA, reconhecido pela Portaria Ministerial nº 549 de 28/09/1981, publicada no D.O.U. de 30/09/1981 e renovado pelo Decreto Estadual nº 1.311 de 06/05/2015, publicado no D.O.E. de 07/05/2015.

UNIVERSIDADE ESTADUAL DE MARINGÁ
REITORIA - PRÓ-REITORIA DE ENSINO
Diretoria de Assuntos Acadêmicos
Divisão de Registro de Diplomas

DIPLOMA REGISTRADO sob

Nº: **0294/2016** Livro: **RG- 180**
Fls: **186** Processo: **0294/2016**

de acordo com o disposto no artigo 48, §1°, da Lei nº 9.394, de 20/12/1996.

Maringá , 18 de fevereiro de 2016.

Vilson Franciscon Jacob
Chefe da Divisão de Registro de Diplomas
Por delegação de competência, de acordo com a Portaria nº 1338-GRE/UEM, de 03/11/2006.

UNIVERSIDADE ESTADUAL DE MARINGÁ
REITORIA - PRÓ-REITORIA DE ENSINO
Diretoria de Assuntos Acadêmicos
Divisão de Registro de Diplomas

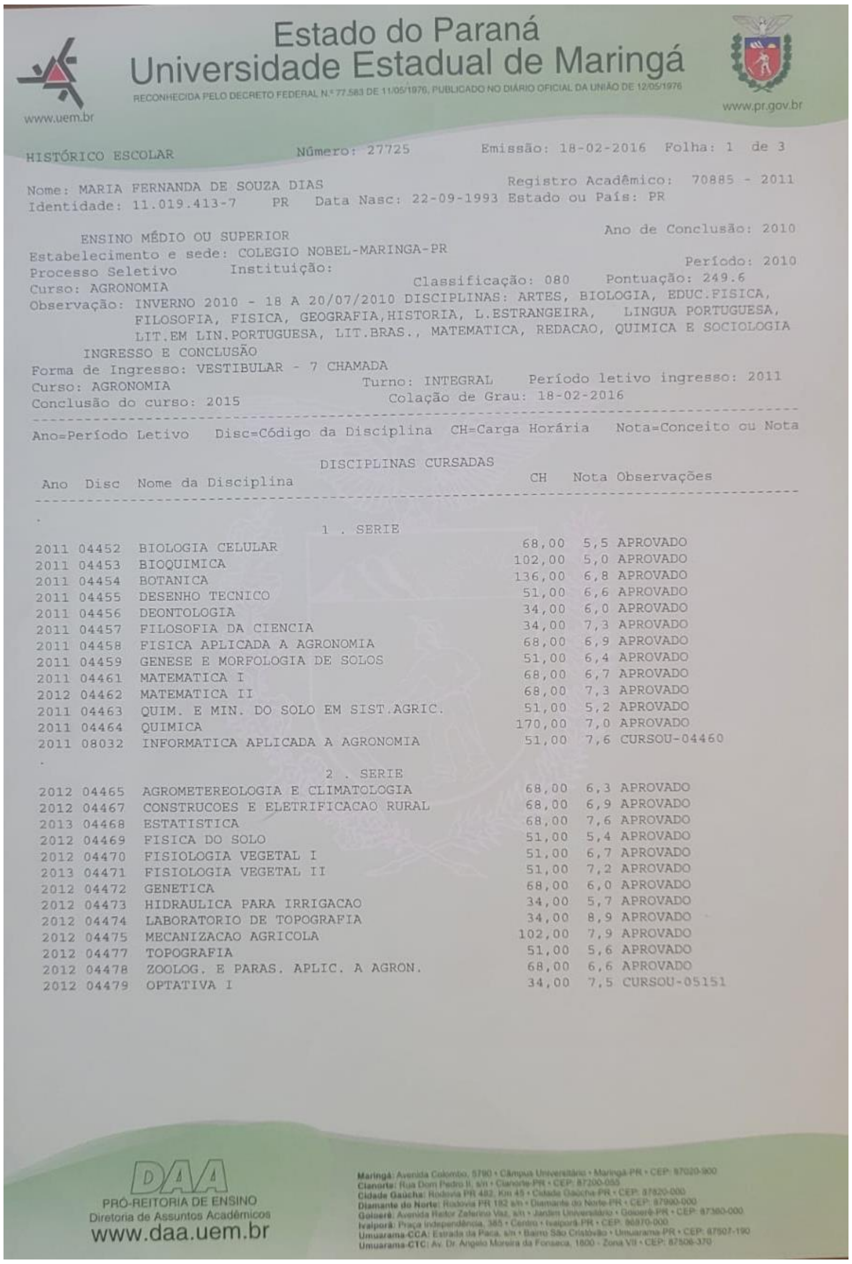
APOSTILA

CURSO ACREDITADO sob nº 94.406 no Sistema ARCU-SUL - Sistema de Acreditação Regional de Cursos Superiores dos Estados do MERCOSUL e Estados Associados, pelo prazo de 06(seis) anos, conforme Portaria Ministerial nº 892, de 17/09/2013, publicada no D.O.U. de 18/09/2013.

Maringá , 18 de fevereiro de 2016.

Vilson Franciscon Jacob
Chefe da Divisão de Registro de Diplomas
Por delegação de competência, de acordo com a Portaria nº 1338-GRE/UEM, de 03/11/2006.

70885



Estado do Paraná
Universidade Estadual de Maringá
RECONHECIDA PELO DECRETO FEDERAL N.º 77.583 DE 11/05/1976, PUBLICADO NO DIÁRIO OFICIAL DA UNIÃO DE 12/05/1976

www.uem.br
www.pr.gov.br

HISTÓRICO ESCOLAR Número: 27725 Emissão: 18-02-2016 Folha: 1 de 3

Nome: MARIA FERNANDA DE SOUZA DIAS Registro Acadêmico: 70885 - 2011
Identidade: 11.019.413-7 PR Data Nasc: 22-09-1993 Estado ou País: PR

ENSINO MÉDIO OU SUPERIOR Ano de Conclusão: 2010
Estabelecimento e sede: COLEGIO NOBEL-MARINGA-PR
Processo Seletivo Instituição: Período: 2010
Curso: AGRONOMIA Classificação: 080 Pontuação: 249.6
Observação: INVERNO 2010 - 18 A 20/07/2010 DISCIPLINAS: ARTES, BIOLOGIA, EDUC.FISICA, FILOSOFIA, FISICA, GEOGRAFIA,HISTORIA, L.ESTRANGEIRA, LINGUA PORTUGUESA, LIT.EM LIN.PORTUGUESA, LIT.BRAS., MATEMATICA, REDACAO, QUIMICA E SOCIOLOGIA

INGRESSO E CONCLUSÃO
Forma de Ingresso: VESTIBULAR - 7 CHAMADA
Curso: AGRONOMIA Turno: INTEGRAL Período letivo ingresso: 2011
Conclusão do curso: 2015 Colação de Grau: 18-02-2016

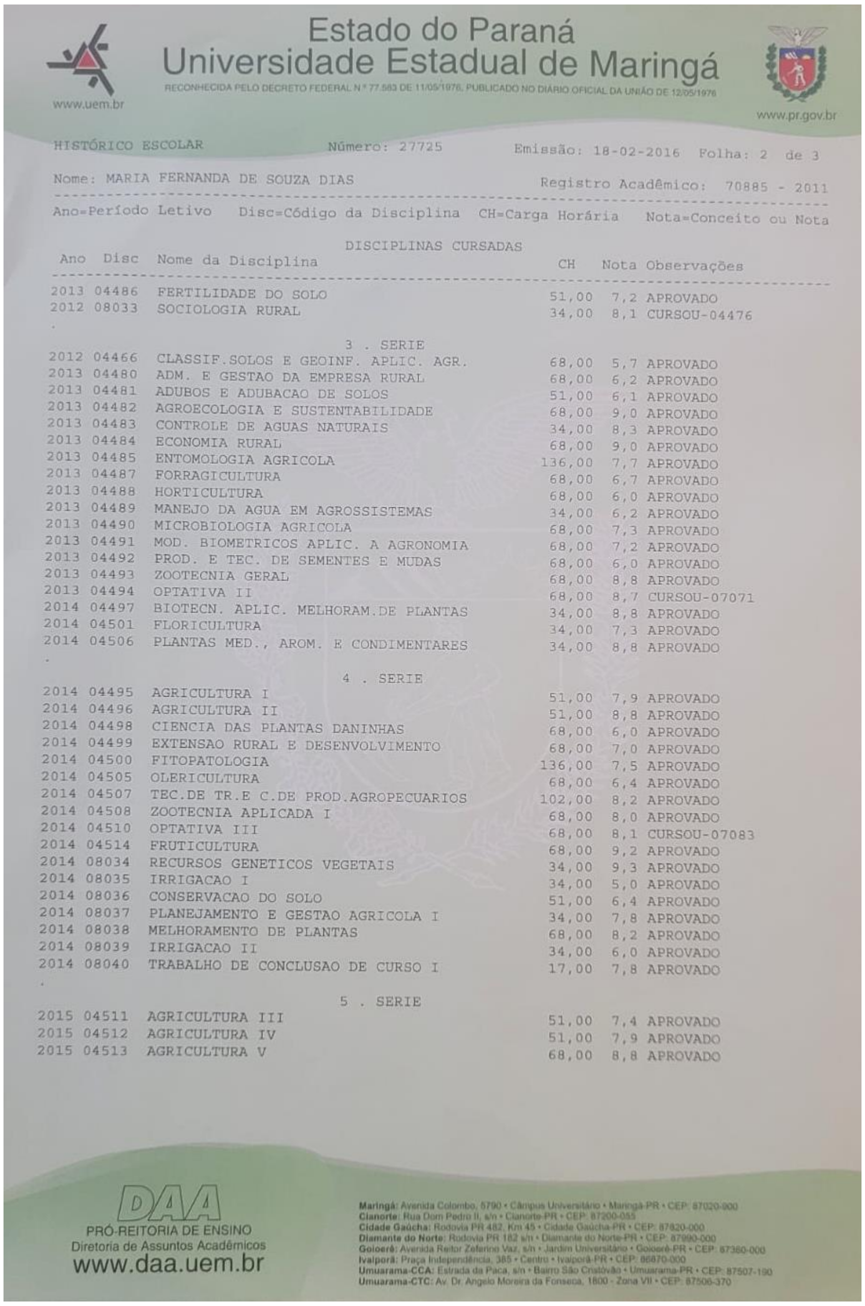
Ano=Período Letivo Disc=Código da Disciplina CH=Carga Horária Nota=Conceito ou Nota

DISCIPLINAS CURSADAS

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
.					
		1 . SERIE			
2011	04452	BIOLOGIA CELULAR	68,00	5,5	APROVADO
2011	04453	BIOQUIMICA	102,00	5,0	APROVADO
2011	04454	BOTANICA	136,00	6,8	APROVADO
2011	04455	DESENHO TECNICO	51,00	6,6	APROVADO
2011	04456	DEONTOLOGIA	34,00	6,0	APROVADO
2011	04457	FILOSOFIA DA CIENCIA	34,00	7,3	APROVADO
2011	04458	FISICA APLICADA A AGRONOMIA	68,00	6,9	APROVADO
2011	04459	GENESE E MORFOLOGIA DE SOLOS	51,00	6,4	APROVADO
2011	04461	MATEMATICA I	68,00	6,7	APROVADO
2012	04462	MATEMATICA II	68,00	7,3	APROVADO
2011	04463	QUIM. E MIN. DO SOLO EM SIST.AGRIC.	51,00	5,2	APROVADO
2011	04464	QUIMICA	170,00	7,0	APROVADO
2011	08032	INFORMATICA APLICADA A AGRONOMIA	51,00	7,6	CURSOU-04460
.					
		2 . SERIE			
2012	04465	AGROMETEREOLOGIA E CLIMATOLOGIA	68,00	6,3	APROVADO
2012	04467	CONSTRUCOES E ELETRIFICACAO RURAL	68,00	6,9	APROVADO
2013	04468	ESTATISTICA	68,00	7,6	APROVADO
2012	04469	FISICA DO SOLO	51,00	5,4	APROVADO
2012	04470	FISIOLOGIA VEGETAL I	51,00	6,7	APROVADO
2013	04471	FISIOLOGIA VEGETAL II	51,00	7,2	APROVADO
2012	04472	GENETICA	68,00	6,0	APROVADO
2012	04473	HIDRAULICA PARA IRRIGACAO	34,00	5,7	APROVADO
2012	04474	LABORATORIO DE TOPOGRAFIA	34,00	8,9	APROVADO
2012	04475	MECANIZACAO AGRICOLA	102,00	7,9	APROVADO
2012	04477	TOPOGRAFIA	51,00	5,6	APROVADO
2012	04478	ZOOLOG. E PARAS. APLIC. A AGRON.	68,00	6,6	APROVADO
2012	04479	OPTATIVA I	34,00	7,5	CURSOU-05151

DAA
PRÓ-REITORIA DE ENSINO
Diretoria de Assuntos Acadêmicos
www.daa.uem.br

Maringá: Avenida Colombo, 5790 • Câmpus Universitário • Maringá-PR • CEP: 87020-900
Cianorte: Rua Dom Pedro II, s/n • Cianorte-PR • CEP: 87200-055
Cidade Gaúcha: Rodovia PR 482, Km 45 • Cidade Gaúcha-PR • CEP: 87820-000
Diamante do Norte: Rodovia PR 182 s/n • Diamante do Norte-PR • CEP: 87990-000
Goioerê: Avenida Reitor Zeferino Vaz, s/n • Jardim Universitário • Goioerê-PR • CEP: 87360-000
Ivaiporã: Praça Independência, 385 • Centro • Ivaiporã-PR • CEP: 86870-000
Umuarama-CCA: Estrada da Paca, s/n • Bairro São Cristóvão • Umuarama-PR • CEP: 87507-190
Umuarama-CTC: Av. Dr. Angelo Moreira da Fonseca, 1800 - Zona VII • CEP: 87506-370



Estado do Paraná
Universidade Estadual de Maringá
RECONHECIDA PELO DECRETO FEDERAL N.º 77.583 DE 11/05/1976, PUBLICADO NO DIÁRIO OFICIAL DA UNIÃO DE 12/05/1976
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HISTÓRICO ESCOLAR Número: 27725 Emissão: 18-02-2016 Folha: 2 de 3

Nome: MARIA FERNANDA DE SOUZA DIAS Registro Acadêmico: 70885 - 2011

Ano=Período Letivo Disc=Código da Disciplina CH=Carga Horária Nota=Conceito ou Nota

DISCIPLINAS CURSADAS

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2013	04486	FERTILIDADE DO SOLO	51,00	7,2	APROVADO
2012	08033	SOCIOLOGIA RURAL	34,00	8,1	CURSOU-04476

.

3 . SERIE

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2012	04466	CLASSIF.SOLOS E GEOINF. APLIC. AGR.	68,00	5,7	APROVADO
2013	04480	ADM. E GESTAO DA EMPRESA RURAL	68,00	6,2	APROVADO
2013	04481	ADUBOS E ADUBACAO DE SOLOS	51,00	6,1	APROVADO
2013	04482	AGROECOLOGIA E SUSTENTABILIDADE	68,00	9,0	APROVADO
2013	04483	CONTROLE DE AGUAS NATURAIS	34,00	8,3	APROVADO
2013	04484	ECONOMIA RURAL	68,00	9,0	APROVADO
2013	04485	ENTOMOLOGIA AGRICOLA	136,00	7,7	APROVADO
2013	04487	FORRAGICULTURA	68,00	6,7	APROVADO
2013	04488	HORTICULTURA	68,00	6,0	APROVADO
2013	04489	MANEJO DA AGUA EM AGROSSISTEMAS	34,00	6,2	APROVADO
2013	04490	MICROBIOLOGIA AGRICOLA	68,00	7,3	APROVADO
2013	04491	MOD. BIOMETRICOS APLIC. A AGRONOMIA	68,00	7,2	APROVADO
2013	04492	PROD. E TEC. DE SEMENTES E MUDAS	68,00	6,0	APROVADO
2013	04493	ZOOTECNIA GERAL	68,00	8,8	APROVADO
2013	04494	OPTATIVA II	68,00	8,7	CURSOU-07071
2014	04497	BIOTECN. APLIC. MELHORAM.DE PLANTAS	34,00	8,8	APROVADO
2014	04501	FLORICULTURA	34,00	7,3	APROVADO
2014	04506	PLANTAS MED., AROM. E CONDIMENTARES	34,00	8,8	APROVADO

.

4 . SERIE

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2014	04495	AGRICULTURA I	51,00	7,9	APROVADO
2014	04496	AGRICULTURA II	51,00	8,8	APROVADO
2014	04498	CIENCIA DAS PLANTAS DANINHAS	68,00	6,0	APROVADO
2014	04499	EXTENSAO RURAL E DESENVOLVIMENTO	68,00	7,0	APROVADO
2014	04500	FITOPATOLOGIA	136,00	7,5	APROVADO
2014	04505	OLERICULTURA	68,00	6,4	APROVADO
2014	04507	TEC.DE TR.E C.DE PROD.AGROPECUARIOS	102,00	8,2	APROVADO
2014	04508	ZOOTECNIA APLICADA I	68,00	8,0	APROVADO
2014	04510	OPTATIVA III	68,00	8,1	CURSOU-07083
2014	04514	FRUTICULTURA	68,00	9,2	APROVADO
2014	08034	RECURSOS GENETICOS VEGETAIS	34,00	9,3	APROVADO
2014	08035	IRRIGACAO I	34,00	5,0	APROVADO
2014	08036	CONSERVACAO DO SOLO	51,00	6,4	APROVADO
2014	08037	PLANEJAMENTO E GESTAO AGRICOLA I	34,00	7,8	APROVADO
2014	08038	MELHORAMENTO DE PLANTAS	68,00	8,2	APROVADO
2014	08039	IRRIGACAO II	34,00	6,0	APROVADO
2014	08040	TRABALHO DE CONCLUSAO DE CURSO I	17,00	7,8	APROVADO

.

5 . SERIE

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2015	04511	AGRICULTURA III	51,00	7,4	APROVADO
2015	04512	AGRICULTURA IV	51,00	7,9	APROVADO
2015	04513	AGRICULTURA V	68,00	8,8	APROVADO

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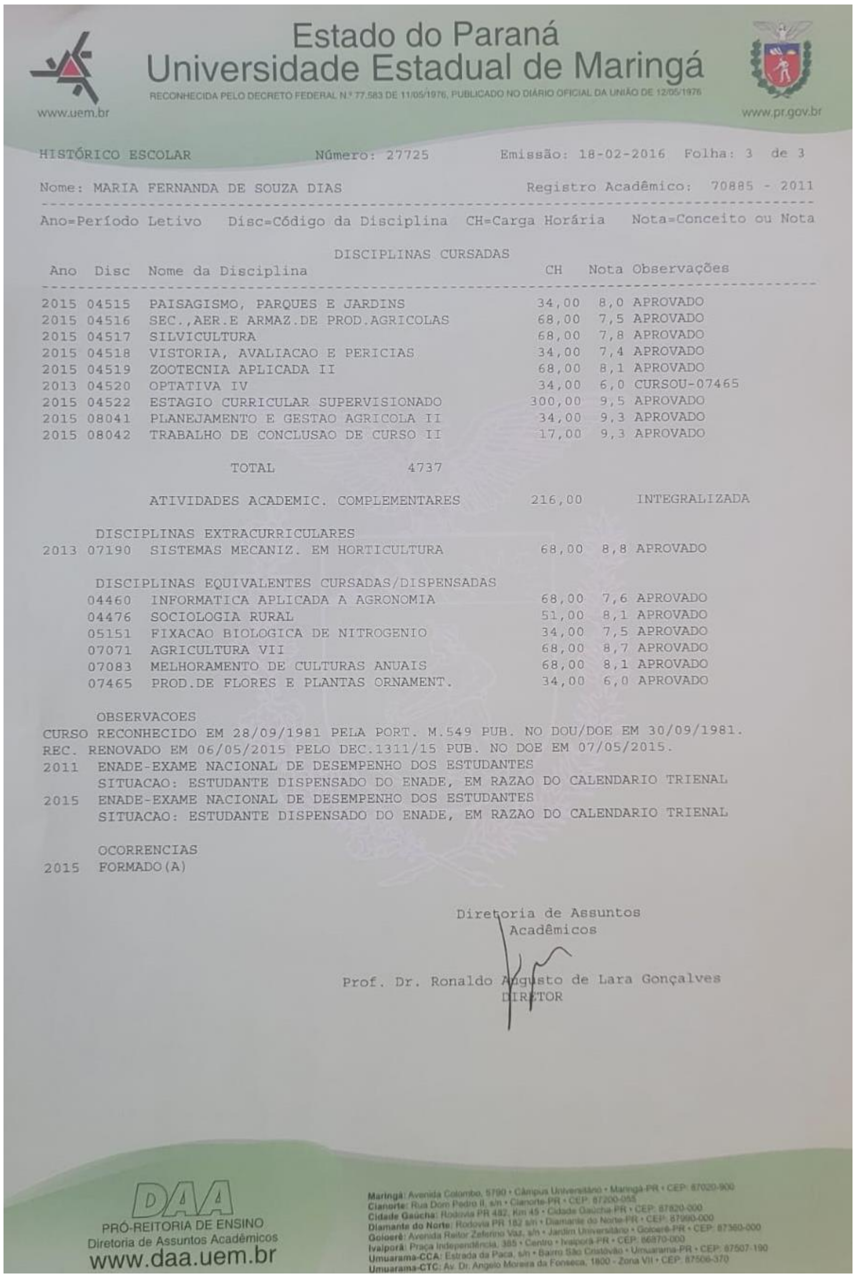
Diamante do Norte: Rodovia PR 182 s/n • Diamante do Norte-PR • CEP: 87990-000
Goioerê: Avenida Reitor Zeferino Vaz, s/n • Jardim Universitário • Goioerê-PR • CEP: 87360-000
Ivaiporã: Praça Independência, 385 • Centro • Ivaiporã-PR • CEP: 86870-000
Umuarama-CCA: Estrada da Paca, s/n • Bairro São Cristóvão • Umuarama-PR • CEP: 87507-190
Umuarama-CTC: Av. Dr. Angelo Moreira da Fonseca, 1800 - Zona VII • CEP: 87506-370



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HISTÓRICO ESCOLAR Número: 27725 Emissão: 18-02-2016 Folha: 3 de 3

Nome: MARIA FERNANDA DE SOUZA DIAS Registro Acadêmico: 70885 - 2011

Ano=Período Letivo Disc=Código da Disciplina CH=Carga Horária Nota=Conceito ou Nota

DISCIPLINAS CURSADAS

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2015	04515	PAISAGISMO, PARQUES E JARDINS	34,00	8,0	APROVADO
2015	04516	SEC.,AER.E ARMAZ.DE PROD.AGRICOLAS	68,00	7,5	APROVADO
2015	04517	SILVICULTURA	68,00	7,8	APROVADO
2015	04518	VISTORIA, AVALIACAO E PERICIAS	34,00	7,4	APROVADO
2015	04519	ZOOTECNIA APLICADA II	68,00	8,1	APROVADO
2013	04520	OPTATIVA IV	34,00	6,0	CURSOU-07465
2015	04522	ESTAGIO CURRICULAR SUPERVISIONADO	300,00	9,5	APROVADO
2015	08041	PLANEJAMENTO E GESTAO AGRICOLA II	34,00	9,3	APROVADO
2015	08042	TRABALHO DE CONCLUSAO DE CURSO II	17,00	9,3	APROVADO
		TOTAL 4737			
		ATIVIDADES ACADEMIC. COMPLEMENTARES	216,00		INTEGRALIZADA

DISCIPLINAS EXTRACURRICULARES

Ano	Disc	Nome da Disciplina	CH	Nota	Observações
2013	07190	SISTEMAS MECANIZ. EM HORTICULTURA	68,00	8,8	APROVADO

DISCIPLINAS EQUIVALENTES CURSADAS/DISPENSADAS

Disc	Nome da Disciplina	CH	Nota	Observações
04460	INFORMATICA APLICADA A AGRONOMIA	68,00	7,6	APROVADO
04476	SOCIOLOGIA RURAL	51,00	8,1	APROVADO
05151	FIXACAO BIOLOGICA DE NITROGENIO	34,00	7,5	APROVADO
07071	AGRICULTURA VII	68,00	8,7	APROVADO
07083	MELHORAMENTO DE CULTURAS ANUAIS	68,00	8,1	APROVADO
07465	PROD.DE FLORES E PLANTAS ORNAMENT.	34,00	6,0	APROVADO

OBSERVACOES

CURSO RECONHECIDO EM 28/09/1981 PELA PORT. M.549 PUB. NO DOU/DOE EM 30/09/1981.
REC. RENOVADO EM 06/05/2015 PELO DEC.1311/15 PUB. NO DOE EM 07/05/2015.
2011 ENADE-EXAME NACIONAL DE DESEMPENHO DOS ESTUDANTES
SITUACAO: ESTUDANTE DISPENSADO DO ENADE, EM RAZAO DO CALENDARIO TRIENAL
2015 ENADE-EXAME NACIONAL DE DESEMPENHO DOS ESTUDANTES
SITUACAO: ESTUDANTE DISPENSADO DO ENADE, EM RAZAO DO CALENDARIO TRIENAL

OCORRENCIAS

2015 FORMADO(A)

Diretoria de Assuntos
Acadêmicos

Prof. Dr. Ronaldo Augusto de Lara Gonçalves
DIRETOR

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Ivaiporã: Praça Independência, 385 • Centro • Ivaiporã-PR • CEP: 86870-000
Umuarama-CCA: Estrada da Paca, s/n • Bairro São Cristóvão • Umuarama-PR • CEP: 87507-190
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ATESTADO N.º 200/2021-DAA/PG

Atestamos que **Maria Fernanda de Souza Dias,** registro acadêmico nº 49113, concluiu os 24 (vinte e quatro) créditos em disciplinas exigidos para conclusão do Curso de Pós-Graduação em **Genética e Melhoramento,** área de concentração: ***Genética e Melhoramento***, em nível de Mestrado, tendo defendido sua Dissertação em 26 de fevereiro de 2018, intitulada: "**Análise da divergência genética de linhagens de milho forrageiro utilizando marcadores microssatélites.",** e sido aprovado (a) pela Banca Examinadora.

Atestamos ainda, que não acusamos o recebimento do processo do aluno (a) pela secretaria do curso, para providências quanto a emissão do diploma de Mestre.

Diretoria de Assuntos Acadêmicos, aos vinte e três dias do mês de novembro de dois mil e vinte e um.

Sandra Mikuni
Sandra Mayumi Mikuni
Coordenadora Geral
Controle Acadêmico de Pós-Graduação

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HISTÓRICO ESCOLAR DE PÓS-GRADUAÇÃO

NUMERO: 1035
EMISSÃO: 23/11/2021
Folha: 1 de 2

DADOS PESSOAIS

NOME: Maria Fernanda de Souza Dias
REGISTRO ACADÊMICO: 49113
DATA DE NASCIMENTO: 22/09/1993
CIDADE: Apucarana
ESTADO/PAÍS: PR
CARTEIRA DE IDENTIDADE: 11.019.413-7
UF: PR
FILIAÇÃO: Jansir Dias Paz e Gildete Aparecida de Souza Dias

EDUCAÇÃO SUPERIOR

CURSO: Agronomia
INSTITUIÇÃO: Universidade Estadual de Mariangá
ANO DE CONCLUSÃO: 2015
CIDADE: Maringá
ESTADO/PAÍS: PR

PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA E MELHORAMENTO

NÍVEL: Mestrado
ÁREA DE CONCENTRAÇÃO: Genética e Melhoramento
INGRESSO: Março/2016
RECONHECIMENTO: Portaria n.º 609/19-MEC
DATA: 14/03/2019
D.O.U.-DATA: 18/03/2019
SITUAÇÃO DO ALUNO NO CURSO: Em Fase de Conclusão

EXAME DE PROFICIÊNCIA EM LÍNGUA(S)

1-: Inglês	DATA: 17/05/2017	CONCEITO: B	RESULTADO: Aprovada
2-: **********	DATA: **********	CONCEITO: **********	RESULTADO: **********

EXAME GERAL DE QUALIFICAÇÃO DATA: ********** CONCEITO: ********** RESULTADO: **********

DEFESA DE DISSERTAÇÃO/TESE

DATA: 26/02/2018
CONCEITO: **********
RESULTADO: Aprovada
ORIENTADOR(A): Prof. Dr. Ronald Jose Barth Pinto
TÍTULO DA DISSERTAÇÃO/TESE:
Análise da divergência genética de linhagens de milho forrageiro utilizando marcadores microssatélites.
****
****
****
****

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Umuarama-CTC: Av. Dr. Angelo Moreira da Fonseca, 1800 - Zona VII • CEP: 87506-370

NOME: Maria Fernanda de Souza Dias

REGISTRO ACADÊMICO: 49113 Folha: 2 de 2

DISCIPLINAS CURSADAS

PERÍODO	CODIGO	NOME DA DISCIPLINA	CARGA HORÁRIA	CRÉDITOS	% DE FREQUENCIA	CONCEITO	RESULTADO
1º 2016	DAG4094	Métodos de Melhoramento de Plantas	45	003	100	A	Aprovada
1º 2016	DAG4124	Pesquisa	---	--	---	S	Aprovada
1º 2016	DAG4128	Seminário	15	001	100	S	Aprovada
1º 2016	DAG4243	Biometria Aplicada à Genética e Melhoramento	60	004	100	B	Aprovada
1º 2016	DBC4024	Genética	45	003	93	B	Aprovada
2º 2016	DAG4062	Métodos Estatísticos	60	004	100	B	Aprov. c/ Elet.
2º 2016	DAG4089	Genética de Populações	45	003	100	A	Aprovada
2º 2016	DAG4090	Genética Quantitativa Aplicada ao Melhoramento de Plantas	60	003	100	A	Aprovada
2º 2016	DAG4128	Seminário	15	001	100	S	Aprovada
1º 2017	DAG4095	Métodos Não Convencionais Aplicados ao Melhoramento Vegetal	75	004	100	A	Aprovada
1º 2017	DAG4124	Pesquisa	---	--	---	S	Aprovada
1º 2017	DAG4213	Produção de Culturas: Arroz e Feijão	60	004	100	A	Aprovada
2º 2017	DAG4124	Pesquisa	---	--	---	S	Aprovada
2º 2017	DAG4130	Modelos Biométricos	60	004	100	B	Aprovada
2º 2017	DAG4131	Estágio na Docência I	30	002	100	S	Aprovada

Observações

A disciplina cujo resultado indica "Aproveitada como Eletiva" foi cursada no Programa de Pós-Graduação em Agronomia desta Universidade, na condição de aluno não regular, conforme a Resolução nº 84/2017-PGM.

Sandra Mikuni
Sandra Mayumi Mikuni
Coordenadora Geral
Controle Acadêmico de Pós-Graduação

Maria Fernanda de Souza Dias

Endereço para acessar este CV: http://lattes.cnpq.br/7122798798223793
ID Lattes: **7122798798223793**
Última atualização do currículo em 10/02/2022

Engenheira Agrônoma e mestre em Genética e Melhoramento pela Universidade Estadual de Maringá - UEM. Doutoranda em Genética e Melhoramento na área de Melhoramento e Genética Vegetal, pelo Programa de Pós-Graduação em Genética e Melhoramento (PGM) da Universidade Estadual de Maringá - UEM. Tem experiência na área de Agronomia, com ênfase em Melhoramento Vegetal, atuando principalmente nos seguintes temas: Genética quantitativa, melhoramento da cultura do milho, uso de marcadores moleculares. **(Texto informado pelo autor)**

Identificação

Nome	Maria Fernanda de Souza Dias
Nome em citações bibliográficas	Maioli, M.F.S.D.;MAIOLI, MARIA FERNANDA DE SOUZA DIAS
Lattes iD	http://lattes.cnpq.br/7122798798223793
Orcid iD	**?** https://orcid.org/0000-0002-3683-8783

Endereço

Formação acadêmica/titulação

2018	Doutorado em andamento em Genética e Melhoramento (Conceito CAPES 5). Universidade Estadual de Maringá, UEM, Brasil. Título: Análise Genômica Ampla para característica de proteína em milho Orientador: Ronald José Barth Pinto. Coorientador: Carlos Alberto Scapim. Bolsista do(a): Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPq, Brasil.
2016 - 2018	Mestrado em Genética e Melhoramento (Conceito CAPES 5). Universidade Estadual de Maringá, UEM, Brasil. Título: Uso de Marcadores Moleculares SSR para Estimar a Diversidade Genética de Linhagens de Milho Forrageiro, Ano de Obtenção: 2018. Orientador: Ronald José Barth Pinto. Coorientador: Carlos Alberto Scapim. Bolsista do(a): Fundação Araucária de Apoio ao Desenvolvimento Científico e Tecnológico, FAADCT/PR, Brasil.
2011 - 2015	Graduação em Agronomia. Universidade Estadual de Maringá, UEM, Brasil. Título: Levantamento,diagnóstico e planejamento dos Lotes 103-R7 e 42-A - Produtores de Morango orgânico da Fmília Malvezi de Marialva-PR. Orientador: Pr. Dr. Ednaldo Michellon.
2008 - 2010	Ensino Médio (2º grau). Centro de Ensino Nobel, FACULDADE NOBEL, Brasil.

Formação Complementar

Atuação Profissional

Projetos de pesquisa

2015 - 2015
MARCADORES MOLECULARES SSR
Descrição: USO DE MARCADORES MOLECULARES SSR PARA ESTIMAR A DIVERSIDADE GENÉTICA DE LINHAGENS DE MILHO SUBTROPICAIS E TEMPERADAS.
Situação: Concluído; Natureza: Pesquisa.
Alunos envolvidos: Graduação: (1) / Mestrado acadêmico: (1) / Doutorado: (1) .

Integrantes: Maria Fernanda de Souza Dias - Coordenador / Tereza A. Silva - Integrante.

2013 - 2014
Indução de resistência e controle alternativo de doenças
Descrição: Auxilio em pesquisas no campo de Fitopatologia principalmente voltado a indução de resistência e controle alternativo de doenças de plantas com aplicação de extratos e óleo essencial de plantas..
Situação: Concluído; Natureza: Pesquisa.
Alunos envolvidos: Graduação: (1) / Mestrado acadêmico: (1) / Doutorado: (1) .

Integrantes: Maria Fernanda de Souza Dias - Coordenador / Kátia Regina Freitas SchwanEstrada. - Integrante.

2012 - 2013
Resgate e replantio de epífitas e rupícolas da área de supressão da usina hidrelétrica de Mauá.
Situação: Concluído; Natureza: Pesquisa.
Alunos envolvidos: Graduação: (4) / Mestrado acadêmico: (1) .

Integrantes: Maria Fernanda de Souza Dias - Coordenador / Maria Auxiliadora Milaneze Gutierre - Integrante.

Áreas de atuação

1. Grande área: Ciências Agrárias / Área: Agronomia.

Idiomas

Espanhol	Compreende Bem, Fala Razoavelmente, Lê Razoavelmente, Escreve Razoavelmente.
Inglês	Compreende Bem, Fala Bem, Lê Bem, Escreve Razoavelmente.
Português	Compreende Bem, Fala Bem, Lê Bem, Escreve Bem.

Produções

Produção bibliográfica

Artigos completos publicados em periódicos

Ordenar por

Ordem Cronológica

1. EISELE, TAUANA GIBIM ; LAZZARI, DENER ; SILVA, TEREZA APARECIDA DA ; PINTO, RONALD JOSÉ BARTH ; MATSUZAKI, ROBSON AKIRA ; **MAIOLI, MARIA FERNANDA DE SOUZA DIAS** ; ALVES, ALEX VIANA ; AMARAL JUNIOR, ANTÔNIO TEIXEIRA DO . Combining ability and genetic divergence among tropical maize inbred lines using SSR markers. ACTA SCIENTIARUM-AGRONOMY JCR, v. 43, p. e53317, 2021.

Citações: WEB OF SCIENCE 1

2. SAITO, MARCELO AKIRA ; ALVES, ALEX VIANA ; KURITZA, DANILO DE PAULA ; SOUZA, YURE PEQUENO ; **MAIOLI, MARIA FERNANDA DE SOUZA DIAS** ; AMARAL JÚNIOR, ANTÔNIO TEIXEIRA DO ; BENTO, ANTÔNIO CARLOS ; SCAPIM, CARLOS ALBERTO ; PINTO, RONALD JOSÉ BARTH . Influence of agronomic and kernel-related properties on popping expansion in popcorn. Agronomy Journal JCR, v. 113, p. 2260-2272, 2021.

Citações: WEB OF SCIENCE 1

3. **MAIOLI, MARIA FERNANDA DE SOUZA DIAS**; PINTO, RONALD JOSÉ BARTH ; SILVA, TEREZA APARECIDA DA ; RIZZARDI, DIEGO ARY ; MATSUZAKI, ROBSON AKIRA ; SATO, MARCELO AKIRA ; EISELE, TAUANA GIBIM ; GARCIA, GIOVANA DAL LAGO . Partial diallel and genetic divergence analyses in maize inbred lines. ACTA SCIENTIARUM-AGRONOMY JCR, v. 43, p. e53540, 2020.

Citações: WEB OF SCIENCE 1

Trabalhos completos publicados em anais de congressos

1. Santos, H.V. ; KULKA, V. P. ; POSSATTO JUNIOR, O. ; KUKI, M. C. ; ROSSI, E. S. ; **Maioli, M.F.S.D.** . Análise da diversidade genética de linhagens de milho tropicais e temperadas por meio de marcadores microssatélites. In: XXXI Congresso nacional de milho e sorgo:inovações, mercados e segurança alimentar, 2016, Bento Gonçalves. CONGRESSO NACIONAL DE MILHO E SORGO, 2016. v. 31.

Resumos publicados em anais de congressos

1. Silva, H.A. ; BALERONI, A. G. ; SILVA, T. ; Rizzardi, D.A. ; **Maioli, M.F.S.D.** ; UHDRE, R. S. ; DANTE, J. C. . EFEITO DO GENÓTIPO E AMBIENTE NA PRODUÇÃO DE HAPLOIDES PUTATIVOS SELECIONADOS PELA EXPRESSÃO DO MARCADOR FENOTÍPICO R1-NAVAJO. In: 9 Congresso Brasileiro de Melhoramento de Plantas, 2017, Foz do Iguaçu. 9 Congresso Brasileiro, 2017. v. 1. p. 279.

Apresentações de Trabalho

1. Silva, H.A. ; BALERONI, A. G. ; SILVA, T. A. ; Rizzardi, D.A. ; **Maioli, M.F.S.D.** ; UHDRE, R. S. ; DANTE, J. C. . EFEITO DO GENÓTIPO E AMBIENTE NA PRODUÇÃO DE HAPLOIDES PUTATIVOS SELECIONADOS PELA EXPRESSÃO DO MARCADOR FENOTÍPICO R1-NAVAJO. 2017. (Apresentação de Trabalho/Congresso).

Produção técnica

Entrevistas, mesas redondas, programas e comentários na mídia

1. **MAIOLI, MARIA FERNANDA DE SOUZA DIAS**. Popping Effects on Popcorn. 2020. (Programa de rádio ou TV/Entrevista). 🎬

Demais tipos de produção técnica

Eventos

Participação em eventos, congressos, exposições e feiras

1. 9 Congresso Brasileiro de Melhoramento de Plantas.. EFEITO DO GENÓTIPO E AMBIENTE NA PRODUÇÃO DE HAPLOIDES PUTATIVOS SELECIONADOS PELA EXPRESSÃO DO MARCADOR FENOTÍPICO R1-NAVAJO. 2017. (Congresso).
2. Ciência na Praça - Mostra de Atividades da Pós-Graduação da UEM. Cultivares de milhos especiais (tipos e VCU's). 2017. (Exposição).
3. Mini Curso ?New Methodologies for High Resolution Mapping and Development of Molecular Markers. 2017. (Outra).
4. X DIA DE CAMPO DE AGRARIAS. 2015. (Outra).
5. Biotecnologia Aplicada a Produção de Sementes. 2014. (Seminário).
6. Curso de custo de produção. 2014. (Seminário).
7. IX DIA DE CAMPO DE AGRARIAS. 2014. (Outra).
8. VIII CURSO INT. DE COOPERATIVISMO. 2013. (Outra).
9. XXXI CICLO DE DEBATES AGRONOMICOS. 2013. (Simpósio).
10. V SIMPOSIO GRANDES CULTURAS-CAFE. 2012. (Simpósio).

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1. **MAIOLI, MARIA FERNANDA DE SOUZA DIAS**. Popping Effects on Popcorn. 2020. (Programa de rádio ou TV/Entrevista). 🎬

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GENETICS AND PLANT BREEDING

Combining ability and genetic divergence among tropical maize inbred lines using SSR markers

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ABSTRACT. Our objectives were to evaluate general and specific combining ability (SCA) and genetic divergence among tropical maize inbred lines using single sequence repeat (SSR) markers. Thirteen inbred lines were crossed based on a complete diallel scheme. Hybrids and three checks were evaluated in a lattice experimental design. Silk and anthesis flowering, average plant height, average ear height, white spot (*Pantoea ananatis*) and gray leaf spot (*Cercospora zeae-maydis*) severity, and grain yield were evaluated. Significant differences ($p < 0.05$) for general and specific combining abilities were observed for all traits. Based on additive effects, inbred lines 1 (Flash) and 12 (SG 6015) were selected to reduce the flowering period and plant and ear height. Inbred lines 2 (CD 303) and 3 (AG 8080) were selected to reduce disease severity. For the simultaneous increase in grain yield and reduced severity of diseases, line 11 (AG 9090) as a parent or tester in topcross schemes is recommended. According to non-additive effects, crosses 2 (CD 303) × 13 (DKB 747) and 11 (AG 9090) × 12 (SG 6015) were selected for grain yield and future breeding programs. Six groups were identified using SSR markers; a major group contained six inbred lines. Because of the minor relationship between genetic divergence and SCA effects on grain yield limits, the use of the groups for future divergent crosses is recommended.

Keywords: *Zea mays* L.; diallel crosses; heterotic group.

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Introduction

Maize (*Zea mays* L.) is a major food crop and has substantial social and economic importance; it is directly used for human consumption as well as for animal feed and several industrial purposes (Grigulo, Azevedo, Krause, & Azevedo, 2011). Maize breeding programs typically focus on the selection of highly productive and disease resistant genotypes, having greater adaptability and stability (Gralak et al., 2015).

The diallel analysis is one of the most-used tools for obtaining genetic information in maize breeding programs. This controlled mating system enables the estimation of the general combining ability (GCA) and the specific combining ability (SCA), which are associated with additive and non-additive genetic effects, respectively (Griffing, 1956; Cruz, Regazzi, & Carneiro, 2012). According to the parental genetic basis, the diallel analysis results allow the selection of genotypes for the development of new breeding populations (Oliboni et al., 2013; Souza Neto et al., 2015; Bertagna et al., 2018), developing new hybrids for final trials (Aguiar et al., 2004; Silva et al., 2010; Matias Jr., Kuki, Scapim, & Pinto, 2019), or heterotic group descriptions (Silva, Amaral Junior, Gonçalves, Freitas Junior, & Ribeiro, 2011; Gonçalves et al., 2014; Mendes, Miranda Filho, Oliveira, & Reis, 2015).

The development of single-cross hybrids depends on heterosis, which is related to genetic distance and the gene complementation effect (Lippman & Zamir, 2007; Schnable & Springer, 2013), Thus, selection of inbred lines based on genetic effects and heterotic groups is required to obtain superior single-cross hybrids. The identification of divergent parents is one of the first steps to obtain superior hybrids. This procedure has proved to be more reliable when molecular markers are used because they can be very useful in the identification of heterotic groups of genotypes as a consequence of the different allele frequencies of populations (Munhoz, Prioli, Amaral Junior, Scapim, & Simon, 2009; Ndhlela et al., 2015).

Several types of molecular markers are available for breeders and researchers, and new types of polymorphic markers are frequently being developed, enhancing the application of genetic sequencing in breeding programs (Bernardo, 2008; Idrees & Irshad, 2015). Some authors have already shown single sequence repeat (SSR) markers to be more suitable than random-amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), or single nucleotide polymorphisms (SNPs) for genetic divergency and germplasm characterization (Pejic et al., 1998; Vignal, Milan, SanCristobal, & Eggen, 2002; Ravi, Geethanjali, Sameeyafarheen, & Maheswaran, 2003; Varshney, Chabane, Hendre, Aggarwal, & Graner, 2007) primarily because of the reasonable cost-benefit, the high degree of polymorphism provided by a large number of alleles per locus (Vignal et al., 2002; Inghelandt, Melchinger, Lebreton, & Stich, 2010), and highly reproducible results (Jones et al., 1997).

White spot of corn is caused by the microbial complex *Phaeosphaeria maydis* (Rane, Payak, & Renfro, 1966) and *Pantoea ananatis* (Paccola-Meirelles, Ferreira, Meirelles, Marriel, & Casela, 2001; Gonçalves et al., 2013). This disease has occurred in Brazil since the 1990s. However, since 2010, the damage caused by the disease has increased, mainly in second crops and in regions with mild climates. With the increase in the second crop area, the occurrence of white spot has become a limiting factor for sustainable corn production (Cunha, Negreiros, Alves, & Torres, 2019).

The economic damage caused by white spot depends mainly on hybrid susceptibility associated with cultivation in regions with mild temperatures (< 25°C) and high relative air humidity (> 70%) (Fantin & Duarte, 2009). According to Carson (2005), for every 1% increase in the severity of white spot in the R5 maize stage, there was a reduction of 0.23% in grain yield and 0.16% in grain weight.

In São Paulo, Fantin and Duarte (2009) determined the correlation between corn yield and the severity level of this disease in the second crop. In more susceptible cultivars, the authors observed that severity above 25% caused an average decrease of 1,933 kg ha^{-1} in grain yield. The more resistant hybrids exhibited a severity below 1% (Fantin & Duarte, 2009). According to Cota, Costa, Sabato, and Silva (2013), if not controlled, white spot could cause yield reductions of up to 60% in susceptible hybrids.

Maize cercosporiosis, caused by the fungus *Cercospora zeae-maydis* and *C. zeina*, is one of the most important diseases in corn crops worldwide. In Brazil, the disease was first observed in the southwest of the Goiás State in 2000. Currently, it is present in almost all corn plantation areas in southcentral Brazil and occurs at high severity levels in susceptible cultivars, causing losses up to more than 80%.

High relative humidity, the presence of dew, and room temperature between 22 and 30°C are ideal conditions for the pathogen (Ward, Nowell, Stromberg, & Nutter, 1999; Paul & Munkvolk, 2005). Losses ranging from 20 to 60% in grain productivity because of cercosporiosis have been reported in several studies (Donahue, Stromberg, & Myers, 1991; Ward et al., 1999). The use of fungicides to control fungal diseases is especially recommended for special corn, such as sweet corn and popcorn, as well as seed corn production. In other cases, genetic resistance is highlighted as the most efficient alternative (Fantin, Duarte, & Pinto, 2003; Bradley & Ames, 2010).

The present study is justified because the genetic parameters of the inbred lines to be studied are not known and it is assumed there is genetic divergence between the lines because of their origin. Moreover, our goals were to evaluate the general combining ability (GCA), specific combining ability (SCA), and genetic divergence using SSR markers for the tropical maize available in our maize breeding program.

Material and methods

Field trial and statistical analysis

Thirteen inbred lines selected from different base populations were used as parents in a complete diallel design (Table 1). These genotypes denote the main core of the maize breeding program germplasm for the State University of Maringá and were obtained through several cycles of selfing and selection until a satisfactory level of homozygosis (S_7) was reached. The F_1 hybrids were obtained in the second growing season of 2017, at the Iguatemi Experimental Farm (23° 25′ S, 51° 57′ W, and an altitude of 550 m asl) located at Maringá, Paraná State, Brazil. The 13 inbred lines were grown pairwise using every possible cross in 10 m rows, spaced 0.9 m apart.

The trial area was prepared using a no-tillage system for desiccation of invasive plants using the non-selective contact herbicide Paraquat (4.0 L ha^{-1}). Basic fertilization consisted of 300 kg ha^{-1} of a 08-20-20 formulation. Pest control was performed by the systemic application of an insecticide and contact based on methomyl and chlorantraniliprole, according to needs. Two applications of atrazine and tembotrione were conducted for the control of invasive post-emergence plants. Nitrogen coating was applied 40 days after sowing with 300 kg ha^{-1} of urea.

Table 1. Inbred lines, base population origin, cycle, type of grains, and the company of base population origin for the 13 inbred lines used in the single crosses.

Inbred line	Origin	Cycle	Type of grain	Company
1	FLASH	Very early	Flint	Syngenta
2	CD 303	Early	Semi dent	Coodetec/Corteva
3	AG 8080	Early	Semi flint	Bayer
4	AVANT	Early	Flint	Syngenta
5	AS1560	Early	Semi flint	Bayer
6	FORT	Early	Flint	Syngenta
7	GARRA	Early	Flint	Syngenta
8	A2560	Early	Flint	Bayer
9	DKB 350	Early	Semi flint	Bayer
10	30F33	Early	Flint	Corteva
11	AG 9090	Early	Semi dent	Bayer
12	SG 6015	Early	Semi flint	Limagrain
13	DKB 747	Early	Flint	Bayer

The 78 resulting single-cross hybrids were evaluated against three commercial checks (AS1633, P30F53, and DKB 290), for a total of 81 treatments. The trial was carried out during the 2017/2018 main growing season at the Iguatemi Experimental Farm in Maringá, Paraná State, Brazil, in a 9 × 9 lattice incomplete block design, with three replications. Each plot consisted of two 5 m long rows spaced 0.90 m apart, resulting in a total area of 9 m^2. Each plot was thinned at 30 days to a density of 5 plants m^{-1}, resulting in a population of approximately 55,500 plants ha^{-1} at harvest time.

The following traits were evaluated: days to anthesis (AT); days to silking (SI); average plant height (PH, m), and average ear height (EH, m) of six competitive plants. Additionally, white spot (WS) and gray leaf spot (GLS) severity were evaluated 25 days after flowering using the diagrammatic scale proposed by Agroceres (1996) under natural disease infestation, as well as grain yield (GY, kg $plant^{-1}$) standardized to 13% moisture content.

A two-step analysis was performed for each evaluated trait. The first step consisted of an intrablock analysis of variance with the recovery of interblock information, which is a usual procedure for a lattice experimental design. The following model was used:

$$Y_{ijk} = \mu + r_j + b(r)_{j/r} + t_i + \varepsilon_{ijk}$$

where: Y_{ijk} is the vector from observed data, μ is the overall mean, r_i is the replication effect, $b(r)_{j/r}$ is the nested effect of blocks within replications, t_i is the treatment effect, and ε_{ijk} is the residual effect. Adjusted treatments were considered as fixed effects.

The second step consisted of a diallel analysis, considering model IV proposed by Griffing (1956), where only the F_1 crosses are used in the analysis. The sums of squares of the F_1 adjusted treatments were partitioned into GCA and SCA, according to the model:

$$Y = \mu + g_i + g_j + s_{ij} + \varepsilon_{ijk}$$

where: Y is the vector with the adjusted means for each F_1 cross, μ is the overall mean, g_i and g_j are the GCA effect for the parents in each cross, s_{ij} is the SCA effect related to each specific diallel cross, and ε_{ijk} is the residual effect. Effects were considered significant when $p < 0.05$. All analyses were performed using the Genes (Cruz, 2013) software.

DNA extraction and genetic divergence

The youngest leaves of five plants were sampled from each inbred line approximately 30 days after germination, immediately frozen in liquid nitrogen, and transferred to -80°C freezers. The DNA was extracted using a protocol described by Hoisington, Khairallah, and González-de-Léon (1994), with slight adaptations.

DNA quality was evaluated on 1% agarose gel and quantified using a Picodrop microliter UV/Vis spectrophotometer, and the DNA concentration was adjusted to 10 ng μL^{-1} for amplification.

DNA amplification was performed in a thermal cycler using the Touchdown PCR methodology (Don, Cox, Wainwright, Baker, & Mattick, 1991) and separated using 4% agarose gel (50% agarose and 50% agarose metaphor) in TBE buffer X 0.5 (44.5 mM Tris, 44.5 mM boric acid, and 1 mM EDTA). The gels were exposed to an electric field of 60 volts for approximately 4 hours, stained with 0.5 μg mL^{-1} ethidium bromide solution, and photographed under a UV light. The alleles that were amplified were differentiated using a 100 pb DNA ladder from Invitrogen.

The SSR marker profile for each inbred line was determined by numerical codes related to each allele, where presence/absence was scored as 1 and 0, respectively, according to the multiallelism of each SSR marker (Cruz et al., 2012). Heterozygosity, number of polymorphic loci, and the total number of alleles were assessed using GenAIEx software version 6.5 (Peakall & Smouse, 2012). The polymorphism of each primer (PIC) was evaluated using Power Maker software (Liu & Muse, 2005). Modified Rodger's distance and cophenetic correlation were performed using Genes software (Cruz, 2013).

Results and discussion

Least-square means of the treatments resulted in significant differences ($p < 0.05$) for all evaluated traits (Table 2), indicating differences among the least-square means of the crosses. The experimental coefficients of variation were considered to be of low to medium magnitude for all traits when compared to other reported studies of diallel crosses using inbred lines (Durães et al., 2002; Silva et al., 2010; Conrado et al., 2014; Werle et al., 2014) and also when compared with the reference values proposed by Fritsche Neto, Vieira, Scapim, Miranda, and Rezende (2012) for maize, indicating excellent experimental precision.

Table 2. Results of the diallel analysis of variance of the seven analyzed traits in the diallel crosses conducted at Maringá, Paraná State, Brazil, during the 2017/2018 main growing season.

S.V.[1]	D.F.[2]	Mean square						
		PH	EH	WS	GLS	AT	SI	GY
Treat.	77	0.072*	0.06*	0.77*	1.32*	9.29	11.36*	1.55*
GCA	12	0.36*	0.31*	2.76*	6.29*	41.68*	56.57*	3.01*
SCA	65	0.019*	0.015*	0.40*	0.41*	3.31*	3.01*	1.28*
Residual	136	0.003	0.003	0.992	0.078	2.05	1.86	0.39
Mean	-	2.086	1.054	1.615	1.903	60.190	60.538	6.722
CV (%)	-	2.961	5.412	19.683	19.683	2.383	2.260	9.172
$\hat{\phi}^3$ GCA	-	0.0104	0.009	0.080	0.188	1.20	1.52	0.079
$\hat{\phi}$ SCA	-	0.0053	0.0038	0.1002	0.11	0.42	0.53	0.30

*significant at 5% probability; ns non-significant at 5% probability; [1]S.V.: Source of variation; [2]D.F.: Degrees of freedom;[3]$\hat{\phi}$: quadratic component. average plant height (PH, m); average ear height (EH, m); white spot (WS) severity; gray leaf spot (GLS) severity, days to anthesis (AT); days to silking (SI); grain yield (GY, kg plant^{-1}).

The data presented in Table 2 illustrated that the severity values for both diseases were relatively low based on the Agroceres scale. Despite differences among susceptibility levels, the significance of the GCA and SCA effects indicated that environmental conditions did not favor the occurrence of the diseases evaluated.

Diallel analysis indicated significant differences in GCA and SCA for all evaluated traits (Table 2). This was an important indication of different genetic contributions among inbred lines for the additive effects, andalso a direct result of the differential performance of the single-cross hybrid combinations compared to that expected from the GCA of their parents. According to quadratic component magnitudes, the contribution of the GCA effect was higher for AN, SI, PH, EH, and GLS severity, which was an indication of additive effects that controlled these traits (Table 3). Similar results were also observed by Freitas Jr., Amaral Jr., Pereira, Cruz, and Scapim (2006) and Kuki et al. (2017), who also observed higher importance for the additive effects for PH and EH, as well as flowering period. The contribution of the non-additive effects was higher only for WS severity and GY. Higher importance of non-additive effects was already expected for GY (Pfann et al., 2009; Oliboni et al., 2013; Senhorinho, Pinto, Scapim, Milani, & Nihei, 2015; Bertagna et al., 2018).

According to Cruz et al. (2012), GCA significance was attributed to additive effects, showing there was variability among the evaluated parents for the occurrence of favorable alleles, which could be selected based on genetic effects for the formation superior hybrids and testers in topcross schemes. SCA significance expressed the presence of non-additive gene effects in the related loci that affected the trait because, in the absence of dominance, SCA does not indicate significance in the diallel analysis (Vencovsky & Barriga, 1992).

Table 3. General combining ability estimations ($\hat{g}_i$) for the evaluated traits at Maringá, Paraná State, Brazil, during the 2017/2018 growing season.

Inbred line	$\hat{g}_i$						
	PH	EH	WS	GLS	AT	SI	GY
1	-0.198	-0.149	0.1031	0.256	-2.298	-2.328	0.193
2	0.129	0.120	-0.047	0.141	-0.147	0.622	0.397
3	-0.021	-0.011	-0.013	0.551	-0.324	-0.227	0.276
4	-0.023	0.025	-0.104	0.307	-0.622	-1.300	-0.017
5	-0.039	-0.058	0.410	-0.185	0.307	-0.170	0.080
6	-0.086	-0.068	0.174	0.297	0.20	0.357	0.063
7	0.123	0.162	-0.475	-0.185	2.190	2.164	0.039
8	0.075	0.030	-0,182	-0.675	0.617	0.568	-0.75
9	-0.037	0.004	-0.139	-0.163	-0.59	-1.122	0.056
10	-0.063	-0.119	0.364	0.515	-0.023	0.589	-0.133
11	0.177	0.124	-0.508	-0.944	1.579	1.905	0.276
12	-0.078	-0.088	0.322	0.088	-1.075	-1.542	-0.346
13	0.041	0.029	0.096	-0.003	0.195	0.484	-0.125
DP ($\hat{g}_i$)	0.010	0.0095	0.052	0.046	0,239	0.228	0.104
DP ($\hat{g}_i$ - $\hat{g}_j$)	0.015	0.014	0.077	0.069	0.353	0.336	0.153

1(FLASH), 2 (CD 303), 3 (AG8080), 4 (AVANT), 5 (AS1560), 6 (FORT), 7 (GARRA), 8 (A2560) 9 (DKB350), 10 (30F33),11 (AG9090), 12 (SG6015), and 13 (DKB747). average plant height (PH, m); average ear height (EH, m); white spot (WS) severity; gray leaf spot (GLS) severity; days to anthesis (AT); days to silking (SI); grain yield (GY, kg plant^{-1}).

Maize breeding programs seek hybrids that combine high grain yield, an early cycle, higher disease resistance, and lower estimates of plant and EH. Therefore, GCA enables the best parents to be selected based on the additive genetic effects to form superior single-cross hybrids with a higher frequency of favorable alleles (Cruz et al., 2012).

Considering $\hat{g}_i$ estimations for PH and EH, inbred lines 1, 6, 10, and 12 could be recommended for future crosses with lower plant and ear height, according to their lower $\hat{g}_i$ values compared with other inbred lines (Table 3). Inbred line 11 exhibited the lowest $\hat{g}_i$ values for WS and GLS severity. Additionally, and inbred line 7 could be selected only for WS and inbred 8 for GLS only.

Negative $\hat{g}_i$ values for AT and SI, expressed in days from sowing until the flowering period, basically express how early a genotype flower, which is desirable for breeding programs and farmers. In this scenario, inbred lines 1, 4, 9, and 12 can be used as genitors or testers for reducing both traits in future crosses. Regarding the GY trait, promising genotypes should be selected based on the highest GCA estimations. Considering this, inbred lines 2, 3, and 11 were superior in terms of frequency of favorable genes with additive effects. Furthermore, inbred line 11 was superior for WS, GLS, and GY, and inbred line 1 and 11 were superior for PH, EH, AT, and SI; however, none of the inbred lines used in the diallel scheme was simultaneously superior for all traits (Table 3).

It is important to select hybrid combinations that exhibit favorable $\hat{s}_{ij}$ estimations involving at least one parent with a favorable $\hat{g}_i$ effect on the trait. Thus, the best hybrids would be those for which at least one of the parents was selected based on its $\hat{g}_i$ estimation, thereby presenting a higher frequency of favorable alleles than the average frequency of the parents involved in the crosses (Vencovsky & Barriga, 1992; Cruz et al., 2012).

Tables 4 and 5 show the SCA estimators ($\hat{s}_{ij}$)for GY and maize genetic resistance against the two diseases analyzed in our study: WS and GLS.

According to Cruz et al. (2012), the effect of SCA is interpreted as the deviation of the hybrid from what would be expected based on the GCA of its genitors. Thus, low values of $\hat{s}_{ij}$ indicate that hybrids perform as expected based on their GCA ($\hat{g}_i$) values, whereas high absolute values of $\hat{s}_{ij}$ indicate better or poorer performance than expected. SCA estimates highlight the importance of genes with non-additive effects.

Considering the best-inbred lines selected based on their additive effects, the crosses 2 × 13 and 11 × 12 were the most promising for higher GY because these crosses presented higher and positive $\hat{s}_{ij}$ values, apart from the superiority of inbred lines 2 and 11, which could be selected for their GCA based on their highest additive effects.

Considering the results for the genetic divergence using SSR markers, 89 out of 221 primers were polymorphic for all 13 inbred lines, representing 40.27% of the total. After primer selection, 38 markers were used for the genetic divergence analysis. The number of alleles per locus for the lines ranged from two to six, totaling 114 alleles (Table 6). These results were higher than those described by Dandolini et al. (2008), who reported 27.4% of polymorphic markers using tropical popcorn inbred lines and the number of alleles ranged from two to five.

Table 4. Estimates of the specific combining ability effects ($\hat{s}_{ij}$) for grain yield (GY) and the maize genetic resistance against two important diseases: white spot (WS) and gray leaf spot (GLS).

Parents	Hybrid	WS	GLS	GY	Parents	Hybrid	WS	GLS	GY
1 x 2	1	-0.32139	0.031723	-0.38346	3 x 5	25	0.468122	-0.68063	-0.05293
1 x 3	2	0.305982	0.795696	-0.03669	3 x 6	26	-0.29045	-0.22714	-0.8573
1 x 4	3	0.063106	0.212853	-0.37354	3 x 7	27	0,277526	-0,31595	0.534317
1 x 5	4	-0.04762	0.278532	0.110866	3 x 8	28	-0.46901	0.094341	0.530041
1 x 6	5	0.270927	-0.09236	0.160329	3 x 9	29	0.018644	-033889	-0.18636
1 x 7	6	-0.10687	0.104848	0.050014	3 x 10	30	-0.33288	-0.12743	0.414741
1 x 8	7	-0.31809	-0.45332	0.881338	3 x 11	31	-0.09434	-0.19245	0.107314
1 x 9	8	-0.0767	0.081906	0.632602	3 x 12	32	-0.15988	-0.24081	-0.01067
1 x 10	9	0.320536	0.324909	0.309205	3 x 13	33	0.131941	0.197274	0.101435
1 x 11	10	-0.30958	-0.46774	-0.39422	4 x 5	34	-0.17376	0.022541	-0.88012
1 x 12	11	-0.16168	-0.32684	-0.68274	4 x 6	35	0.128367	0.142705	1.428311
1 x 13	12	0.381377	-0.49021	-0.2737	4 x 7	36	-0.23301	-0.13537	-0.84617
2 x 3	13	0.374955	0.640349	-0.13686	4 x 8	37	-0.04522	-0.42329	0.310487
2 x 4	14	0.251975	0.298329	0.631487	4 x 9	38	0.092683	-0.111	0.595851
2 x 5	15	0.436779	0.172623	0.354263	4 x 10	39	0.107334	0.195094	-0.42098
2 x 6	16	-0.17403	-0.54737	-0.94287	4 x 11	40	0.198106	-0.39252	0.225026
2 x 7	17	-0.2563	0.395359	-0.06129	4 x 12	41	0.116152	-0.44088	-0.04149
2 x 8	18	-0.28195	-0.09972	0.258102	4 x 13	42	-0.27512	0.235904	-0.22182
2 x 9	19	-0.52663	-0.35734	-0.12303	5 x 6	43	0.04551	0.158947	0.664754
2 x 10	20	0.133297	-0.71791	0.666169	5 x 7	44	-0.20094	-0.11913	0.479472
2 x 11	21	0.306159	-0.17935	-0.90339	5 x 8	45	-0.11166	0.275388	0.521329
2 x 12	22	0.191369	-0.06999	-0.47397	5 x 9	46	0.627238	0.382648	-0.98554
2 x 13	23	-0.13423	0.433301	1.114863	5 x 10	47	0.040895	-0.32703	-0.64237
3 x 4	24	-0.23061	0.395636	-0.40704	5 x 11	48	-0.25092	0.195757	0.083635

Table 5. Estimates of the specific combining ability effects ($\hat{s}_{ij}$) for grain yield (GY) and the maize genetic resistance against two important diseases: white spot (WS) and gray leaf spot (GLS).

Parents	Hybrid	WS	GLS	GY	Parents	Hybrid	WS	GLS	GY
5 x 12	49	-0.49706	0.210481	-0.70368	8 x 9	64	0.635879	0.123957	-0.58507
5 x 13	50	-0.33659	-0.57012	1.050323	8 x 10	65	0.814712	0.382732	-0.4509
6 x 7	51	-0.49484	-0.28498	0.781569	8 x 11	66	0.654241	0.716258	0.131808
6 x 8	52	-0.22496	-0.16071	-0.09944	8 x 12	67	-0.20434	-0.04609	-0.26391
6 x 9	53	-0.16915	0.230445	0.689257	8 x 13	68	-0.36078	-0.31986	-0.81144
6 x 10	54	-0.58634	0.426132	0.370493	9 x 10	69	-0.42003	-0.19245	-0.0039
6 x 11	55	0.46663	0.728114	-0.13573	9 x 11	70	-0.14866	0.046447	-0.03373
6 x 12	56	0.614531	-0.033602	0.404351	9 x 12	71	0.086301	0.155803	0.060423
6 x 13	57	0.413801	-0.03776	-2.46371	9 x 13	72	0.044784	0.357309	0.23026
7 x 8	58	-0.08882	-0.08968	-0.42226	10 x 11	73	-0.40664	-0.4582	-0.26906
7 x 9	59	-0.16435	-0.37884	-0.29076	10 x 12	74	0.440765	0.444	0.13336
7 x 10	60	-0.11687	0.006107	-0.30032	10 x 13	75	0.005211	0.044049	0.193563
7 x 11	61	0.302271	0.100932	-0.51525	11 x 12	76	-0.31573	0.016228	1.186799
7 x 12	62	0.220317	0.543621	0.209435	11 x 13	77	-0.40153	-0.11348	0.516802
7 x 13	63	0.861885	0.173092	0.381338	12 x 13	78	-0.33075	0.090509	0.516802
DP ($\hat{S}_{ij}$)	-	0. 166069	0. 147879	0.329239	DP ($\hat{S}_{ij}$)	-	0. 166069	0. 147879	0.329239
DP ($\hat{S}_{ij} - \hat{S}_{ik}$)	-	0. 24530	0. 218432	0.486318	DP ($\hat{S}_{ij} - \hat{S}_{ik}$)	-	0. 24530	0. 218432	0.486318
DP ($\hat{S}_{ij} - \hat{S}_{kl}$)	-	0. 232712	0. 207223	0.461362	DP ($\hat{S}_{ij} - \hat{S}_{kl}$)	-	0. 232712	0. 207223	0.461362

Polymorphism values (PIC) ranged from 0.23 (UMC1714, with two alleles) to 0.72 (MMC0501, with six alleles), with an average value of 0.46 (Table 6). Similar results were also reported by Lopes, Scapim, Mangolin, and Machado (2014) using 15 sweet corn inbred lines in a divergence genetic study, where the authors found 15 out of 100 polymorphic SSR markers with an average PIC of 0.41. The PIC can be used to differentiate markers based on their polymorphisms because the allele loci number and relative frequency of the alleles are used for estimating PIC. According to Botstein, White, Skolnick, and Davis (1980), values higher than 0.5 are considered highly informative, whereas values lower than 0.25 are considered low informative markers.

Table 6. Number of alleles at each of the 38 loci and their polymorphism values (PIC).

Loci	Total number of alleles	PIC
UMC1029	4	0.6300
UMC2080	2	0.3475
BNLG1367	4	0.4822
UMC1585	2	0.3712
UMC1068	4	0.5681
UMC1318	2	0.3648
BNLG1175	5	0.6630
UMC2198	2	0.3161
UMC2025	2	0.3745
UMC1250	2	0.3573
UMC1230	3	0.5818
UMC2257	3	0.4792
UMC1227	2	0.3203
BNLG1297	3	0.5298
UMC2071	3	0.3901
UMC2115	3	0.4184
UMC2164	2	0.3712
UMC2319	2	0.3281
UMC1069	3	0.4204
UMC1714	2	0.2342
UMC2343	3	0.4090
UMC1506	2	0.3729
MMC0501	6	0.7210
UMC2172	2	0.3447
UMC2214	4	0.6533
BNLG1927	5	0.6639
UMC2165	3	0.4958
UMC1399	2	0.3749
UMC1287	3	0.3188
UMC2357	4	0.5839
UMC2047	2	0.3745
UMC1590	5	0.5963
UMC2350	3	0.5876
UMC1656	3	0.4473
UMC1357	3	0.5583
BNLG1046	4	0.6460
UMC1702	2	0.3749
UMC2281	3	0.5709

Genetic divergence between inbred lines was calculated using Roger's modified distance (Goodman & Stuber, 1983) and the 38 polymorphic SSR markers. The dendrogram was constructed using the Unweighted Pair Group Method with Arithmetic Averages (UPGMA) clustering method. Groups were divided with a cut-off value of 0.6868, as suggested by Mojena (1977), with $k = 1.25$, thereby avoiding a possible cofounding factor for group separation.

The UPGMA dendrogram clustered the 13 inbred lines into six different groups (Figure 1), with a higher distance (0.83) between inbred lines 5 and 13 and the lowest distance (0.55) between inbred lines 5 and 6. Group 1 encompassed inbred lines 5, 6, 3, 4, 8, and 7, and was the largest reported group in this study. Group 3 originated by clustering inbred lines 1 and 9, whereas Group 4 included inbred lines 11 and 13. The other inbred lines were allocated solely in different groups. Concerning the main groups 1, 3, and 4, most of that inbred lines were obtained from base populations that originated from Syngenta and Bayer hybrids (Table 1), which suggests a certain similarity between the germplasm of these companies.

The estimated cophenetic correlation coefficient (r) was 0.58, which was similar to that observed by Guimarães et al. (2007) (r = 0.57) and by Alves, Filho, Burin, Toebe, and Silva (2015) (r = 0.58). Ferreira (2008) suggested a value close to 1 provided a better adjustment among distances, although Patto, Satovic, Pêgo, and Fevereiro (2004) recommended a value higher than 0.56 for a good adjustment considering maize inbred lines.

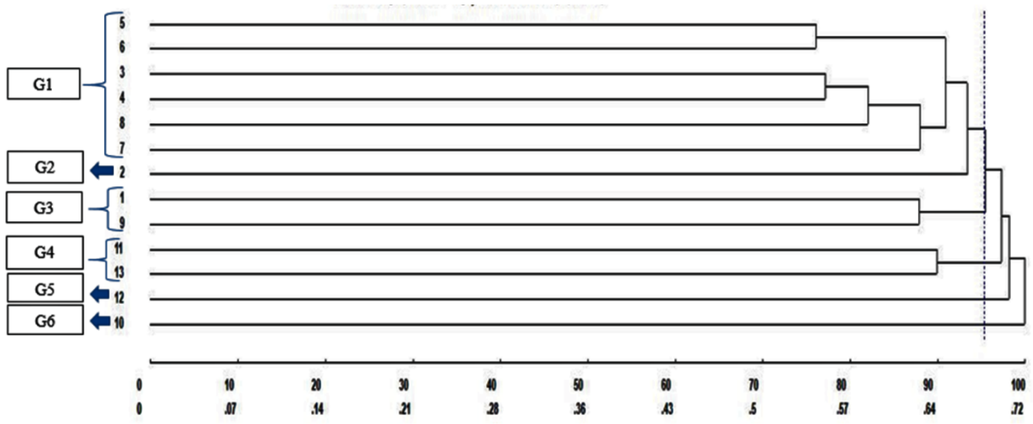

Figure 1. Genetic distance among the 13 tropical maize inbred lines using Rogers's modified distance and clustered using UPGMA. 1 (FLASH), 2 (CD 303), 3 (AG8080), 4 (AVANT), 5 (AS1560), 6 (FORT), 7 (GARRA), 8 (A2560) 9 (DKB350), 10 (30F33), 11 (AG9090), 12 (SG6015), and 13 (DKB747).

Taking into account the 39 hybrids from these companies, for those with positive SCA for GY, 29 had parents from different genetic groups (Figure 1). This indicated that genetic divergence among parents might explain the expression of non-additive effects in hybrids. However, this was not a consistent result because the hybrid with the highest SCA estimation (4 × 6) both had inbred lines clustered in the closest genetic groups. Some authors reported a good concordance among non-additive effects and genetic distances estimated using molecular markers for the flowering period and plant and EH (Lanza, Souza Junior, Ottoboni, Vieira, & Souza, 1997; Sun, William, Liu, Kasha, & Pauls, 2001; Souza et al., 2008), but low or almost no relationship among genetic divergence using SSR markers and phenotypic data for GY, a complex quantitative trait (Guimarães et al., 2007; Paterniani et al., 2008; Munhoz et al., 2009; Fernandes, Schuster, Scapim, Vieira, & Coan, 2015).

The lack of correlation among genetic divergence and SCA for GY observed in this study could be mainly explained by the random choice of SSR markers (Table 7). Thus, the SSR markers used herein were not necessarily associated with QTLs previously identified for any trait. Low genetic map resolution, the complex genetic architecture of traits, and a small number of polymorphic SSR markers available could also have contributed to the low correlation observed. A higher number of polymorphic markers and field trials in different years/seasons should improve these correlations for complex traits (Fernandes et al., 2015), but the costs for a large SSR-mapping panel might limit this analysis.

Table 7. Pearson's correlation estimates of genetic divergence, specific combining ability for grain yield and average grain yield.

Variables	Correlation	Probability (%)
x1 x x2	-0.0969	40.3349
x1 x x3	-0.0735	53.0005
x2 x x3	0.8359	0.0**

** *significant at 1% and 5% probability; ^{ns}non-significant at 5% probability. x1: genetic distance; x2: specific combining ability for grain yield; x3: average grain yield.

Conclusion

Inbred lines 2 (CD 303), 3 (AG 8080), and 11 (AG 9090) were selected based on additive effects and should be used in future hybrid combinations and as topcross testers. Single-cross hybrids 2 (CD 303) × 13 (DKB 747) and 11 (AG 9090) × 12 (SG 6015) were selected based on the non-additive effects and could be used for future breeding programs. Six groups were identified using SSR markers, with the major group containing six inbred lines. The low relationship between genetic divergence and SCA effects for GY limited the use of the groups for future divergent crosses.

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ARTICLE

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Influence of agronomic and kernel-related properties on popping expansion in popcorn

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Abstract

Knowledge about relationships between traits can contribute to raising the efficiency of selection of superior genotypes. The objective of this study was to estimate the correlations, direct and indirect effects of agronomic, chemical and physical traits of kernels on popping expansion (PE) in popcorn (*Zea mays* L.). The trial was carried out in the 2017/2018 growing season, in Maringá - PR, with 49 treatments, which consisted of 43 popcorn, four flint, and two sweet corn. The trial was arranged in a randomized complete block design with three replications. Multiple agronomic, chemical, physical, and popcorn quality traits were evaluated. Analysis of variance was performed to estimate the coefficients of phenotypic and genotypic correlations and the direct and indirect effects of path analysis. The genotypes were partitioned into genotype within each kernel type (popcorn, flint, and sweet corn) and two more contrasts (popcorn vs. [flint + sweet corn]) and flint vs. sweet corn. Positive phenotypic (.76) and genotypic correlations (.81) between popping expansion and pericarp thickness were detected. Kernel length had negative phenotypic (−.75) and genotypic correlations (−.78) with PE. Path analysis indicated that pericarp thickness has a direct and positive effect on PE and that the observed positive correlation with thermal diffusivity of the kernel pericarp and kernel length can be explained by indirect effects of the pericarp thickness. Evaluating kernel length may be most prudent considering economical and practical constraints to popcorn breeding programs.

Abbreviations: CIMMYT, International Maize and Wheat Improvement Center; CV, coefficients of variation; df, degrees of freedom; EH, ear height; Embrapa, Brazilian Agricultural Research Corporation; Fl, flint; G, genotypes; GY, grain yield; IAC, Agronomic Institute of Campinas; IAL, Adolfo Lutz Institute; KL, kernel length; KTh, kernel thickness; KW, kernel width; NE, number of ears; NKR, number of kernel rows per ear; OC, oil content; OPC, open photoacoustic cell technique; OPV, open-pollinated variety; PC, protein content; PE, popping expansion; Pop, popcorn; PTh, pericarp thickness; SC, sweet corn; SH, single-cross hybrid; ThDP, thermal diffusivity of kernel pericarp; TStC, total starch content; UEL, State University of Londrina; UEM, State University of Maringá; W100, 100-kernel weight.

1 | INTRODUCTION

Popcorn (*Zea mays* variety Everta) is a special corn type with the peculiar feature that the kernels expand when heated, resulting in popped flakes. This crop is exploited exclusively for human consumption in a form of a highly popular snack, providing high economic gains, both in the grain production sector and on the popcorn market (Amaral, Jr. et al., 2013; Lyerly, 1942; Senhorinho et al., 2019; Silva et al., 2019).

Similar to other agricultural crops, genotypic variability is the main factor affecting the performance of the target trait of selection, which, in the case of popcorn cultivars, is popping expansion (PE). Owing to efforts in breeding programs, uniform increases in the expansion volume of commercial popcorn hybrids were achieved. For consumers, the number of unpopped kernels is the most important quality criterion of the product, creating a demand for softer and more popped kernels (Tandjung et al., 2005).To this end, some studies were carried out to deepen the understanding of how the kernel physical and chemical traits affect PE and, consequently, popcorn quality, in an attempt to provide information underlying the process of selecting superior genotypes.

Thus, studies focused on physical traits have investigated kernel size and density (Cabral et al., 2016; Carpentieri-Pípolo et al., 2002; Park & Maga, 2002; Rangel et al., 2011; Song et al., 1991), percentage of unpopped kernels (Tian et al., 2001), flake size (Tian et al., 2001), and influence of pericarp thickness (Freire et al., 2020; Mohamed et al., 1993; Silva et al., 1993). In addition, studies related to the kernel chemical composition have determined the protein, starch, and oil contents, as, for example, those of Borras et al. (2006) and Freire et al. (2020). With regard to these aspects, it is worth emphasizing that the physical traits are generally related to the chemical composition (Park et al., 2000). All these research studies were focused on the physical and chemical traits responsible for genotypic variations in the popping and quality of popcorn kernels.

However, little is known about how the thermal diffusivity of the kernel pericarp affects PE. Thermal diffusivity is a specific property of each material, making it possible to characterize it as to the unstable conduction of thermal energy. It can be determined by the ratio between the ability to drive and to store heat from the material (Incropera & Dewitt, 1992). This specific thermophysical property presupposes how fast a body responds to variations in thermal energy to which it is subjected, enabling a better way to represent the conduction of temperature, thermal storage, and the degree of thermal variation of materials. In this respect, it is worth mentioning that the physical trait thermal diffusivity of the kernel pericarp is quite promising to explain PE of popcorn kernels since it elucidates how fast the pericarp will respond to variations in the thermal energy it is subjected to (Incropera & Dewitt, 1992).

Core Ideas

- Pericarp thickness is relevant in the selection of genotypes with greater popping expansion.
- Pericarp thickness has a direct and positive effect on popping expansion.
- Thermal diffusivity of kernel pericarp are indirectly related to popping expansion.
- Kernel length is indirectly related to popping expansion.
- It is more economical and easy to evaluate the kernel length.

In a single study in which the thermal diffusivity of kernel pericarp was included in the group of physical traits in an attempt to understand the relationship with PE in popcorn, Silva et al. (1993) reported a high positive correlation between PE, pericarp thickness and thermal diffusivity of the pericarp. The authors also reported that PE was negatively influenced by kernel weight and starch content. However, it is worth mentioning that these conclusions were based on the evaluation of no more than seven *Zea mays* genotypes in a simple correlation analysis.

Although the magnitude of a correlation is a statistical estimator that is easily computed, care must be taken with its interpretation, since these correlations do not determine the relative importance of the direct and indirect influences of the other traits on the main trait; and therefore, the type of association that controls the trait pair is unknown (Kumar et al., 2015). A viable option to obtain this information is by path analysis, which shows the magnitudes of the direct and indirect effects on the main trait by partitioning the correlation between the traits. It also estimates the residue, which indicates the reliability of the analysis (Cruz et al., 2014).

More specifically, the path analysis proposed by Wrigth (1934) allows a clear interpretation of the direct influence of one trait on another and the interference of other traits with this association. Thus, the influence of each trait involved can be detailed in a previously defined diagram, and the existence of high or low positive or negative correlations among the traits can be explained (Almeida et al., 2018; Vencovsky & Barriga, 1992; Wu et al., 2011).The purpose of this study was to estimate the correlations, as well as the effects of the direct and indirect influence of agronomic, chemical, and physical traits of popcorn kernels on PE, with an aim of elucidating associations of interest for breeding of the crop.

2 | MATERIAL AND METHODS

2.1 | Plant material and experimental conditions

A total of 49 maize genotypes were evaluated, of which 43 were popcorn, four flint, and two sweet corn (Table 1). The trial was carried out in the growing season 2017/2018 on the Experimental Farm of Iguatemi of the State University of Maringá (UEM), in the county of Maringá - PR (23°25′ S, 51°57′ W; at 550 m asl), where the average annual rainfall is 1,500 mm and average temperature 19 °C. The soil of the experimental area was classified as Latossolo Vermelho Distrófico (Brazilian Agricultural Research Corporation (Embrapa), 2018).

The trial was arranged in a randomized complete block design with three replications. Plots consisted of two 5.00-m rows, at a row spacing of 0.90 m and plant spacing of 0.20 m, that is, a total area of 9.00 mš per plot. Two seeds were sown per hole, and thinned to five plants per meter 30 d after emergence, resulting in a plant density of 55,500 plants m^{-1}. The ears of sweet corn were protected with shoot bags to prevent the effect of xenia (effect of pollen on the development and characteristics of the seeds).

The preparation of the experimental area started with the desiccation of the cover crop (bristle oat, *Avena strigosa* Schreb.) and control of the weeds present with the application of paraquat (2.0 L ha^{-1}). In the base fertilization 230 kg ha^{-1} of the formulated N–P–K 08–20–20 were applied. The seeds were treated with insecticide (Cropstar) and sown on 9 Feb. 2017. Two applications of N were also applied, totaling 90 kg ha^{-1} of N in the V4 and V8 stages of corn crop development.

We controlled fall armyworm (*Spodoptera frugiperda*) with two spraying operations with insecticides whose active ingredient was flubendiamide, in the dose of 70 ml ha^{-1} c.p. (commercial product), and beta-cyfluthrin + imidacloprid, in the dose of 500 ml ha^{-1} c.p. The first spraying was done with flubendiamide and the second spraying was done with beta-cyfluthrin + imidacloprid, when the plants were in the V8 stage.

2.2 | Evaluated traits

The following traits were evaluated: ear height (EH, in cm) – mean distance measured with a measuring tape from the soil level to the insertion height of the highest ear, of six healthy plants per plot; number of kernel rows per ear (NKR) – mean number of kernel rows per ear of 10 random ears per plot; number of ears (NE) – sum of all ears per plot, counted after dehusking; 100-kernel weight (W100) – two 100-kernel samples per plot were weighed on a precision scale and averaged; grain yield (GY, in kg.ha^{-1}) – weighing of all threshed kernels per plot, corrected to a standard moisture of 13%; popping expansion (PE, in ml g^{-1}) – relationship between popped popcorn volume and kernel weight (30 g), based on a two-sample mean of each plot. The PE measurements were performed at sample moisture levels between 12.5 and 13.5% (Luz et al., 2005; Maga & Blach, 1992); kernel length (KL, in mm) – mean distance from the tip to the base of 50 kernels; kernel width (KW, in mm) – mean distance measured from one side to the other at the widest point of 50 kernels; and kernel thickness (KTh, in mm) – mean distance, measured between the upper and lower surface of 50 kernels. These traits were measured with a digital caliper on 50 kernels per plot. The mean pericarp thickness (PTh, in mm) was measured with a micrometer. Five (central and peripheral) regions of each pericarp sample of five pericarp samples per plot were measured. The pericarp was removed by hand after soaking the kernels in water for 6 h. Then the pericarps were pressed between two glass slabs for 12 h and stored in a glass desiccator with blue silica gel, ensuring a flat shape and uniform moisture distribution. The thermal diffusivity of kernel pericarp (ThDP, in 10^{-7} m^2 s^{-1}) was determined by the open photoacoustic cell technique (OPC). Basically, this technique consists of recording acoustic waves by means of an electret microphone, which are emitted from the sample when heated by a modulated light source (Rosencwaig & Gersho, 1976) (Figures 1 and 2). Five pericarp samples of each field plot were evaluated. The period of heating cycles and recording of the acoustic waves of the samples lasted approximately 15 min. For the protein content (PC), kernel samples of each plot were ground in a mill and sieved (<0.50 mm). Total N was determined on a dry matter basis by the Kjeldahl method (Association of Official Analytical Chemists, 1995), with a crude protein conversion factor of 6.25 (Villegas et al., 1985); oil content (OC, in %) – determined based on four 2-g subsamples of ground kernels, taken from kernel samples of each plot. For this procedure, a Soxhlet extractor (TE 044) and petroleum ether as solvent were used, as proposed in the analytical standards of the Adolfo

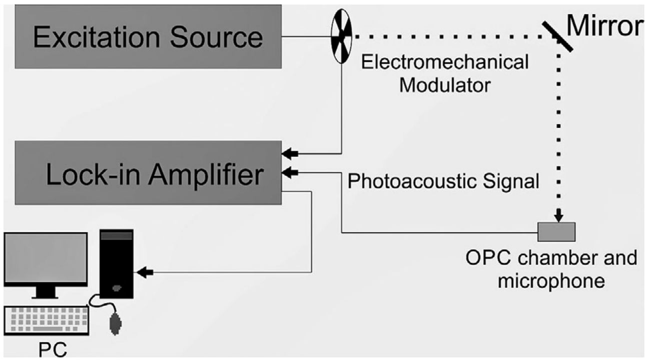

FIGURE 1 Determination of the thermal diffusivity of kernel pericarp by the open photoacoustic cell (OPC) technique

TABLE 1 Description of the genotypes used in the trial

Genotypes[a]	Kernel types	Genetic characterization	Origin
Colombiana	Popcorn	OPV	UEM
Composto Vanin	Popcorn	OPV	UEM
Composto Matheus	Popcorn	OPV	UEM
UNB2UC5	Popcorn	OPV	UENF
Composto Elizete	Popcorn	OPV	UEM
PARA 170 branco	Popcorn	OPV	CIMMYT
CMS 42	Popcorn	OPV	Embrapa
ARZM 07049	Popcorn	OPV	CIMMYT
URUG 298 amarelo	Popcorn	OPV	CIMMYT
SC 016 branco	Popcorn	OPV	UEL
PA 091	Popcorn	OPV	UEM
Viviane	Popcorn	OPV	UEM
RR 046 branca	Popcorn	OPV	UEL
Xuxu Viçosa amarelo	Popcorn	OPV	UEM
Composto Márcia	Popcorn	OPV	UEM
Beija-Flor amarelo	Popcorn	OPV	UFV
Composto Gaúcha	Popcorn	OPV	UEM
Composto Chico	Popcorn	OPV	UEM
Composto misto	Popcorn	OPV	UEM
PR 023	Popcorn	OPV	UEM
PARA172	Popcorn	OPV	CIMMYT
ARZM 13050	Popcorn	OPV	CIMMYT
Viçosa	Popcorn	OPV	UFV
SE 013	Popcorn	OPV	UEM
ARZM 05083	Popcorn	OPV	CIMMYT
SAM	Popcorn	OPV	USA
PA 038 BRANCA	Popcorn	OPV	UEM
Composto Aelton	Popcorn	OPV	UEM
BOZM 260	Popcorn	OPV	CIMMYT
PA 79 branca	Popcorn	OPV	UEM
Boya 462	Popcorn	OPV	CIMMYT
UEM J1	Popcorn	OPV	UEM
Barão Viçosa	Popcorn	OPV	UFV
Composto branco	Popcorn	OPV	UEL
PR 009	Popcorn	OPV	UEL
SC 002	Popcorn	OPV	UEL
Popten	Popcorn	SH	SEEMAX
Poptop II	Popcorn	SH	SEEMAX
IAC 125	Popcorn	TCH	IAC
RS 20	Popcorn	OPV	IPAGRO
PR 017 branca	Popcorn	OPV	UEM
Zélia	Popcorn	OPV	PIONEER
Ângela Branca	Popcorn	OPV	Embrapa
Dow2B433PW	Flint	TH	DOW AgroSciences
DKB 290 PRO3	Flint	TH	DEKALB

(Continues)

TABLE 1 (Continued)

Genotypes[a]	Kernel types	Genetic characterization	Origin
BR 402	Sweet corn	OPV	Embrapa
IAC Doce cubano	Sweet corn	OPV	IAC
IAC Nelore	Flint	IH	IAC
IPR 119	Flint	DH	IAPAR

Note. OPV, open-pollinated variety; UEM, State University of Maringá; UENF, State of North University Fluminence – Darcy Ribeiro; CIMMYT, International Maize and Wheat Improvement Center; Embrapa, Brazilian Agricultural Research Corporation; UEL, State University of Londrina; UFV, Federal University of Viçosa; SAM, South American Mushroom; SH, single-cross hybrid; TCH, topcross hybrid; IAC, Agronomic Institute of Campinas; IPAGRO, Institute of Agronomic Research; TH, triple hybrid; IH, intervarietal hybrid; DH, double-cross hybrid; IAPAR, Agronomic Institute of Paraná.

[a]Maturity: All the genotypes are early.

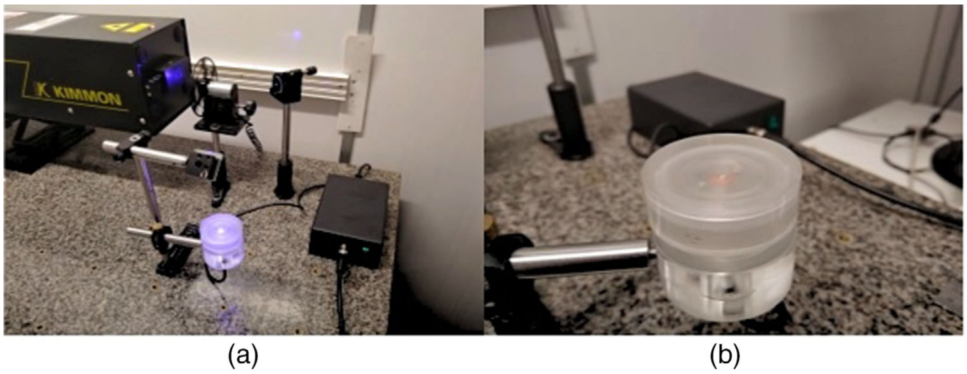
(a) (b)

FIGURE 2 Apparatus used to determine the thermal diffusivity of kernel pericarp via open photoacoustic cell (OPC), (a) operating equipment and (b) photoacoustic chamber with an electret microphone

Lutz Institute (Adolfo Lutz Institute (IAL), 1985). The total starch content (TStC) was determined in dry and ground kernels, by the Lane–Eynon titrimetric method, as described by Adolfo Lutz Institute (Adolfo Lutz Institute (IAL), 1985).

2.3 | Statistical analyses

The analysis of variance followed the model of a randomized complete block design. It was done the partitioning of the genotypes (df and sum of squares [SS]) into genotype within each kernel type (popcorn, flint, and sweet corn) and more two contrasts (popcorn vs. [flint +sweet corn]) and flint vs. sweet corn.

The coefficient of variation (CV) was estimated as follow:

$$CV \quad (\%) = \frac{\sqrt{error\ mean\ square}}{grand\ mean} \times 100$$

The phenotypic (r_f) and genotypic (r_g) correlations between all pairs of traits were estimated by the following expressions:

$$r_f = \frac{Covf\ (x, y)}{\sqrt{\sigma^2_{fx}\ \sigma^2_{fy}}}\ r_g = \frac{Covf\ (x, y)}{\sqrt{\sigma^2_{gx}\ \sigma^2_{gy}}}$$

where $Covf\,(x, y)$ and $Covf\,(x, y)$ correspond, respectively, to the phenotypic and genotypic covariances between traits x and y; σ^2_{fx} and σ^2_{gx} are the phenotypic and genotypic variances of trait x, respectively; and σ^2_{fy} and σ^2_{gy} are the phenotypic and genotypic variances of trait y, respectively.

To avoid the adverse effects of linear relationships between rows or columns of the matrix and of residual correlations in the path analysis, multicollinearity was diagnosed based on an X'X correlation matrix (Montgomery et al., 2001).

Wright's path analysis (1934) was performed based on a single causal model, so that the genotypic correlations (r_g) were partitioned into causal and residual effects, and the causal effects into direct and indirect, by means of the estimates of the equations of standardized partial regression, according to the primary trait model that explains the variation in the basic trait – PE. In this sense, the action of the following traits was considered to be primary: KL, KW, KTh, GY, ThDP, PTh, total starch content (TStC), OC, and PC.

Statistical analyses were performed using the statistical software SAS (2013) (v9.4, SAS, IBM) and Genes (Cruz, 2013), an alpha of 5% probability of error was adopted.

3 | RESULTS AND DISCUSSION

There were significant differences ($p < .05$) between genotypes for all traits (Table 2). The variation coefficients ranged from 3.02% for TStC to 20.51% for PE (Table 2). All estimates were in accordance with those reported elsewhere (Arnhold & Milani, 2011; Fritsche-Neto et al., 2012; Scapim et al., 1995) indicating a high degree of precision with the compared genotypes and a good index of the reliability of the trail. This result was already expected, because, within the popcorn group, there were indigenous open-pollinated varieties without selection, other varieties with few cycles of selection and commercial hybrids of inbred lines. In addition, there were genotypes obtained from several countries in the world, with high genetic variability, resulting in a good starting material for the popcorn improvement (Table 1).

According to the contrasts estimates, the group of popcorn was significant, and surpassed, on average, the group (flint + sweet corn) in six traits: EH, 9.08 cm; PE, 18.2 ml g^{-1}; NE, 4.54; ThDP, 0.2 $10^{-7}m^2s^{-1}$; PTh, 16.88 µm; and PC, 1.94% (Table 3). It was also noted that the open-pollinated varieties of popcorn, in the overall majority, were not genetically improved, therefore, it was not expected a high grain yield and lower materials, which are characteristic of commercial hybrids of inbred lines. The highest average number of ears per plant was due to the greater prolificacy of popcorn in relation to the other group (Hallauer et al., 2010). According to Paes (2006), popcorn kernels have thicker pericarps.

The contrast of the group (flint + sweet corn), was significant, and surpassed, on average, the popcorn group in eight traits: KL, 2.60 mm; KTh, 0.29 mm; KW, 1.79 mm; W100, 11.58 g; NKR, 1.0; GY, 2.185 kg ha^{-1}; TStC, 2%; and OC, 1.33% (Table 3). These results were perfectly explainable because they are hybrids of inbred lines and commercial varieties. There was a gradual and continuous breeding process to increase the GY and their components. The OC in corn kernels is relatively low, generally between 3 and 6%, and most studies indicate that the OC depends more on the plant genotype than on the environment (Duarte et al., 2008; Paes, 2008).

Among the 91 pairs of combinations for the 14 traits evaluated, the genotypic correlations ($r_g$of 44 were significant at 1% or 5% probability and higher than the phenotypic correlations (r_f), indicating that the linear association between these pairs of traits was more influenced by genetic than by environmental components (Table 4). Among the significantly correlated genotypic traits, 24 were positive. This shows that these were directly related and allowed conclusions about genetic gains for both traits by practicing selection for only one of them (Table 4). The correlations can have genetic or environmental causes and are fundamental for the distinction and quantification of the degree of genetic and environmental associations among the evaluated traits, once the genetic causes have an inheritable nature and can serve as a guideline in breeding programs (Hallauer et al., 2010). Thus, in this study, only significant correlations higher than .7 or −.7 were analyzed and discussed (Table 4).

Estimates of negative and significant phenotypic and genotypic correlations ($p < .01$) were found between PE and KL ($r_f = -.75$ and $r_g = -.78$) (Table 4). These results indicated that smaller kernels tend to contribute to a greater PE. In an evaluation of 90 popcorn diallel hybrids, Cabral et al. (2016) found similar results to this study for the same traits, but with lower magnitudes ($r_f = -.57$ and $r_g = -.63$). A negative correlation between PE and kernel size was also reported by Lyerly (1942), showing that the expansion volume of medium and small kernels is higher. According to Song et al. (1991), the kernel size has a significant effect on expansion volume and the number of unpopped kernels, and the results of medium-sized kernels (5-mm sieve) are best for both traits. It is therefore worth noting that in popcorn-breeding programs selecting the genotypes with the largest expansion volume, the smallest kernels should be selected.

There was a strong positive genetic correlation between pericarp thickness (PTh) and PE ($r_f = .76$ and $r_g= .81$). The pericarp is the layer of containment and protection of the endosperm. During heating, it has the function of confining the interior pressure of the kernels, and is fundamental in ensuring an adequate popping volume of the popcorn kernels (Sweley et al., 2013). The importance of this layer was pointed out by Silva et al. (1993), who described a 90.4% reduction in PE of popcorn kernels after removal of the pericarp. The strong positive genetic correlation between pericarp thickness (PTh) and PE, suggests that kernels with thicker pericarp contribute to a higher PE (Table 4). Corroborating these results, Mohamed et al. (1993) tested 18 popcorn hybrids and found that the pericarp thickness was directly proportional to PE, obtaining a correlation estimate similar to that of this study ($r = .82$). Similar results were observed by Silva et al. (1993), who reported phenotypic correlation estimates between PE and PTh of $r_f = .81$, although on the basis of only seven *Zea mays* genotypes.

The thermal diffusivity of the pericarp of a genotype is related to the ability to conduct and accumulate thermal energy; thus, genotypes with a high thermal diffusivity coefficient indicate that the pericarp temperature varies more quickly in response to heating or cooling (Incropera & Dewitt, 1992; Mohsenin, 1975). This study showed that the ThDP was positively correlated with PTh ($r_f = .80$ and $r_g = .82$) (Table 4). This result indicated that thermal diffusivity of the pericarp is higher in kernels with thicker pericarps, which in turn favor a greater capacity of PE.

The ThDP was studied by Silva et al. (1993) based on the OPC technique. These authors stated that the kernel pericarp of popcorn has a 2.9-fold diffusivity compared to field corn, suggesting that the matrix of the cell wall of popcorn is structurally better organized. This implies in a greater and

TABLE 2 Summary of the analysis of variance in ear height (EH, cm), popping expansion (PE, ml g^{-1}), kernel length (KL, mm), kernel thickness,(KTh, mm), kernel width(KW, mm), 100-kernel weight(W100, g), number of ears (NE), number of kernel rows per ear (NKR), grain yield (GY, kg ha^{-1}), thermal diffusivity of kernel pericarp (ThDP, 10^{-7}m^2 s^{-1}), pericarp thickness (PTh, µm), total starch content (TStC, %), oil content (OC, %), protein content (PC, %) in the 2017/2018 growing season, in Maringá - PR

***p* values**															
SV	**df**	**EH**	**PE**	**KL**	**KTh**	**KW**	**W100**	**NE**	**NKR**	**GY**	**ThDP**	**PTh**	**TStC**	**OC**	**PC**
G	(48)	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*
G/SC	1	.251	.972	.003*	.659	.92	.269	.213	.438	.791	.662	.202	.009*	.079	.005*
G/Fl	3	.001*	.97	.001*	.678	.003*	.018*	.126	.001*	.001*	.364	.079	.001*	.29	.001*
G/Pop	42	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*	.001*
Pop vs. (SC + Fl)	1	.001*	.001*	.001*	.001*	.001*	.001*	.003*	.001*	.001*	.001*	.001*	.001*	.001*	.001*
SC vs Fl	1	.001*	.988	.003*	.001*	.001*	.001*	.001*	.001*	.001*	.412	.968	.001*	.001*	.001*
Blocks	2	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Error	96	–	–	–	–	–	–	–	–	–	–	–	–	–	–
OA	–	108	18.6	8.9	3.9	6.5	16.9	53	14.5	2,844	0.39	53.9	75	6.2	10.3
SC[a]	–	127.6 ± 6.5	2.6 ± 0.1	10.9 ± 0.6	3.7 ± 0.2	7.7 ± 0.2	19.9 ± 1.4	42.3 ± 5.5	14.5 ± 0.4	2,049.3 ± 335.7	0.2 ± 0.1	38.9 ± 5.4	74.1 ± 3	8.7 ± 0.7	10.6 ± 0.5
Fl[b]	–	86.5 ± 13.3	2.6 ± 0.9	11.4 ± 0.7	4.4 ± 0.1	8.2 ± 0.4	30.6 ± 3	52.1 ± 5.1	15.8 ± 1.7	6,117.6 ±1718.7	0.2 ± 0.1	39.1 ± 8.7	78.1 ± 6.7	6.7 ± 0.9	7.6 ± 0.8
Pop[c]	–	109.3 ± 20.8	20.8 ± 9.9	8.6 ± 0.6	3.9 ± 0.3	6.2 ± 0.5	15.4 ± 2.6	53.4 ± 8.3	14.4 ±1.4	2,575.9 ±757.1	0.4 ± 0.2	55.9 ± 20.2	74.7 ± 3.5	6 ± 1.3	10.5 ± 0.9
CV, %	–	7.4	20.5	4.1	3.9	4	9	11.1	4	17.1	11.9	15.5	3	13.3	3.4

Note. SV, sources of variation; df, degrees of freedom; G, genotypes; SC, sweet corn; Fl, flint; Pop, popcorn; OA, overall average; CV, coefficient of variation.

*Sgnifcant at the .05 probability level.

[a] Averages ± standard deviations per kernel type for sweet corn.

[b] Averages ± standard deviations per kernel type for flint.

[c] Averages ± standard deviations per kernel type for popcorn.

TABLE 3 Contrasts estimates, of 14 traits, evaluated in 49 corn genotypes

Group	Contrasts estimates EH	PE	KL	KTh	KW	W100	NE	NKR	GY	ThDP	PTh	TStC	OC	PC
Pop vs. (SC+Fl)	2,344.9*	4,692.9*	−670.5*	−75.5*	−462.3*	−2,987.5*	1173*	−248.8*	−563,884.5*	50.8*	4,354.3*	−520.4*	−345*	502*
SC vs. Fl	−164.7*	0.11	2.3*	2.7*	1.9*	42.8*	39*	5.1*	16,272.9*	−0.08	0.68	16.2*	−8*	−12.1*

Note. EH, ear height; PE, popping expansion; KL, kernel length; KTh, kernel thickness; KW, kernel width; W100, 100-kernel weight; NE, number of ears; NKR, number of kernel rows per ear; GY, grain yield; ThDP, thermal diffusivity of kernel pericarp; PTh, pericarp thickness; TStC, total starch content; OC, oil content; PC, protein content; Pop, popcorn; SC, sweet corn; Fl, flint.

*Signifcant at the .05 probability level.

TABLE 4 Estimates of the simple genotypic correlation coefficients (r_g) above the diagonal, and estimates of the simple phenotypic correlation coefficients (r_f) below the diagonal, of 14 traits, evaluated in 49 corn genotypes

Traits	EH	PE	KL	KTh	KW	W100	NE	NKR	GY	ThDP	PTh	TStC	OC	PC
EH	–	−.38*	.002	−.54*	−.22	−.29	.07	.01	−.23	−.39*	−.52*	−.22	−.01	.15
PE	−.37*	–	**−.78****[a]	.05	−.62*	−.59*	−.05	−.14	−.54*	.54*	**.81***	−.08	−.30**	.45*
KL	.001	**−.75***	–	.36**	**.81***	**.87***	−.06	.22	**.77***	−.34**	−.47*	.31**	.42*	−.62*
KTh	−.51*	.04	.35**	–	.60*	.68*	−.03	−.26	.46*	.25	.39*	.39*	.01	−.40*
KW	−.22	−.60*	**.79***	.58*	–	**.94***	−.20	−.14	.60*	−.14	−.23	.25	.33**	−.49*
W100	−.28	−.57*	**.86***	.67*	**.92***	–	−.10	.04	**.80***	−.18	−.24	.31**	.25	−.66*
NE	.09	−.04	−.05	−.04	−.17	−.10	–	.03	.26	−.02	−.19	.18	−.13	−.33**
NKR	.02	−.13	.21	−.25	−.14	.03	.06	–	.43*	−.19	−.30**	.17	.01	−.30**
GY	−.21	−.50*	**.75***	.43*	.56*	**.77***	2.9**	.42*	–	−.23	−.34**	.47*	.11	**−.82***
ThDP	−.37*	.53*	−.33**	.23	−.14	−.18	−.02	−.18	−.22	–	**.82***	−.004	−.05	.48*
PTh	−.50*	**.76***	−.44*	.37*	−.21	−.22	−.17	−.28**	−.32**	**.80***	–	.07	−.12	.44*
TStC	−.19	−.06	.26	.35**	.23	.28	.12	.15	.43*	−.007	.06	–	−.01	−.20
OC	−.02	−.27	.38*	.007	.29**	.24	−.11	.01	.11	−.04	−.09	.001	–	−.15
PC	.14	.44*	−.60*	−.37*	−.47*	−.64*	−.28	−.29**	**−.78***	.47*	.43*	−.20	−.14	–

Note. EH, ear height; PE, popping expansion; KL, kernel length; KTh, kernel thickness; KW, kernel width; W100, 100-kernel weight; NE, number of ears; NKR, number of kernels per ear; GY, grain yield; ThDP, thermal diffusivity of kernel pericarp; PTh, pericarp thickness; TStC, total starch content; OC: oil content; PC: protein content.

[a] Bold individual values. Bold averages are discussed in the text.

*Significant by the *t* test at the .05 probability level.

**Significant by the *t* test at the .01 probability level.

faster heat transfer in popcorn kernels, leading to the conclusion that high thermal diffusivity rates associated with thicker pericarps induce a larger volume of popped popcorn (Zerbetto, 1993).

The phenotypic and genotypic correlations were positive between KL and KW ($r_f = .79$ and $r_g = .81$), KW and W100 ($r_f = .92$ and $r_g = .94$), KL and W100 ($r_f = .86$ and $r_g = .87$), KL and GY ($r_f = .75$ and $r_g = .77$), and between W100 and GY ($r_f = .77$ and $r_g = .80$) (Table 4). Similar results were found by Parsons et al. (2020).The higher correlation between KL and W100 indicated that longer kernels were linearly associated with the highest W100 values, evidencing that the selection of genotypes with longer kernels can result in higher W100 and, consequently, a higher GY. Moreover, GY was negatively correlated with protein content (PC) ($r_f = -.78$ and $r_g = -.82$), indicating that high GY values were associated with low protein contents (Table 4).

Although simple correlations are extremely useful in understanding complex traits, it is well known that these associations do not determine the relative importance of direct and indirect influences of other traits on the main trait (Cruz et al., 2014; Kumar et al., 2015; Vencovsky & Barriga, 1992). Therefore, detailed information regarding the cause and effect relationships between the traits under study can be obtained by path analysis, allowing a safer selection of traits that will lead to higher genetic gains in the target trait, in this case, PE.

To improve the reliability of the results of path analysis, the traits were initially subjected to multicollinearity diagnosis (Montgomery et al., 2001). Thus, path analysis was implemented using the explanatory traits KL, KW, KTh, GY, ThDP, PTh, TStC, OC, PC; and PE as dependent trait. The number of conditions for these associations was 99.50, which allowed the classification as weak, that is, multicollinearity is not a problem for the application of the statistical procedure of path analysis (Montgomery et al., 2001). The proposed model fitted satisfactorily, since the determination coefficient was high ($R^2 = .91$). This means that 91% of the dependent trait could be explained by the independent traits (Table 5).

To accelerate genetic gains in breeding programs, it is essential to identify, among the traits strongly correlated with the basic trait, those with the greatest direct effect and in a favorable direction for selection, so that the correlated response to indirect selection is efficient (Coimbra et al., 2005). In this aspect, the trait PTh was the most relevant, since the direct effect (0.84) on the main trait PE was about three times greater than that of the residual effect (unexplained part of the model) (0.30). Also, the magnitude and direction of the genetic correlation estimate, were in line with expectations, indicating that this direct correlation explained the true association between these traits (Table 5). The path analysis confirmed the results obtained by Mohamed et al. (1993) and Silva et al. (1993), who found a high and positive correlation between PTh and PE (0.82 and 0.81, respectively).

The ThDP revealed a direct negative effect of low magnitude on PE (−0.15), not exceeding the magnitude of the residual effect (Table 5 , which showed that this trait may not be the direct cause for variations in PE. According to Vencovsky and Barriga (1992), when the linear correlation coefficient is positive but the direct effect is negative or negligible, the correlation is caused by indirect effects, which are considered in the analysis. In this study it was found that the true causal effect of this correlation was due to an indirect effect (0.69) via PTh (Table 5). Thus, concentrating efforts on direct selection for this trait (ThDP) will not result in satisfactory gains in the main trait (PE).

Similar to ThDP, a strong negative association (−0.78) (Table 4) was observed between PE and KL, although the direct effect was only −0.27. Due to the low magnitude of the direct effect and also because this estimate was not higher than the residual effect, it was not possible to attribute a cause-and-effect relationship (Table 5). However, there is evidence that this correlation, like ThDP, can be explained as a result of the indirect effect via PTh (−0.40). A possible explanation for these results can be the fact that the pericarp of longer kernels tends to be thinner and, consequently, therefore implying a lower capacity to withstand internal pressure, implying in a low popping capacity.

These results corroborate those of Freire et al. (2020), who demonstrated that the progenies with highest PE volume had coarser pericarps. Thus, the importance of kernel pericarp thickness in the complex process of popcorn kernel popping is highlighted, suggesting that this trait can favor gains in PE both in the process of direct and indirect selection. Thus, the breeder could select genotypes with greater pericarp thickness, and would indirectly be selecting those that would favor greater PE.

The traits related to the kernel chemical properties (TStC, OC, and PC), had direct and very low effects on PE (0.03, −0.06, and −0.30, respectively). These values show that these traits were not determinant in explaining PE (Table 5). Similar results were found by Borras et al. (2006), who observed that starch content (divided into amylopectin and amylose) was not significantly correlated with PE in popcorn. On the other hand, Freire et al. (2020) reported that PE is strongly associated ($r = .95$; $p \leq .01$) with a higher starch percentage. It should be noted that the study by Freire et al. (2020) estimated the amylose content, in which popcorn with low expansion capacity (0 and 7 ml g^{-1}) had lower amylose content (21.24 and 20.18%, respectively) and popcorn with high expansion capacity (30 and 35 ml g^{-1}) had a higher amylose content (23.92 and 26.10%, respectively).

Although the results of the correlation analysis indicate the existence of significant and negative genotypic correlation between GY and KW with PE (−0.54 and −0.62, respectively) (Table 4 , the partitioning of path analysis indicated that both traits had lower direct than residual effects on PE

TABLE 5 Partitioning of the effects of the genotypic correlation coefficient in the path analysis of nine explanatory traits of the basic trait popping expansion (PE), evaluated in 49 popcorn genotypes

KL		**KTh**	
Direct effect on PE	**−0.27**[a]	Direct effect on PE	**−0.07**
Indirect effect via KTh	−0.02	Indirect effect via KL	−0.09
Indirect effect via KW	−0.17	Indirect effect via KW	−0.13
Indirect effect via GY	−0.14	Indirect effect via GY	−0.08
Indirect effect via ThDP	0.05	Indirect effect via ThDP	−0.04
Indirect effect via PTh	**−0.40**	Indirect effect via PTh	0.34
Indirect effect via TStC	0.01	Indirect effect via TStC	0.01
Indirect effect via OC	−0.02	Indirect effect via OC	−0.0001
Indirect effect via PC	0.19	Indirect effect via PC	0.10
Total	−0.78	Total	0.04
KW		GY	
Direct effect on PE	**−0.21**	Direct effect on PE	**−0.18**
Indirect effect via KL	−0.22	Indirect effect via KL	−0.21
Indirect effect via KTh	−0.04	Indirect effect via KTh	−0.03
Indirect effect via GY	−0.11	Indirect effect via KW	−0.13
Indirect effect via ThDP	0.02	Indirect effect via ThDP	0.03
Indirect effect via PTh	−0.20	Indirect effect via PTh	−0.29
Indirect effect via TStC	0.01	Indirect effect via TStC	0.01
Indirect effect via OC	−0.02	Indirect effect via OC	−0.01
Indirect effect via PC	0.15	Indirect effect via PC	0.24
Total	−0.62	Total	−0.54
ThDP		PTh	
Direct effect on PE	**−0.15**	Direct effect on PE	**0.84**
Indirect effect via KL	0.09	Indirect effect via KL	0.13
Indirect effect via KTh	−0.02	Indirect effect via KTh	−0.03
Indirect effect via KW	0.03	Indirect effect via KW	0.05
Indirect effect via GY	0.04	Indirect effect via GY	0.06
Indirect effect via PTh	**0.69**	Indirect effect via ThDP	−0.12
Indirect effect via TStC	−0.0001	Indirect effect via TStC	0.002
Indirect effect via OC	0.002	Indirect effect via OC	0.01
Indirect effect via PC	−0.15	Indirect effect via PC	−0.14
Total	0.54	Total	0.80
TStC		OC	
Direct effect on PE	**0.03**	Direct effect on PE	**−0.06**
Indirect effect via KL	−0.08	Indirect effect via KL	−0.11
Indirect effect via KTh	−0.03	Indirect effect via KTh	−0.0001
Indirect effect via KW	−0.05	Indirect effect via KW	−0.07
Indirect effect via GY	−0.09	Indirect effect via GY	−0.02
Indirect effect via ThDP	0.001	Indirect effect via ThDP	0.01
Indirect effect via PTh	0.06	Indirect effect via PTh	−0.09
Indirect effect via OC	−0.0001	Indirect effect via TStC	0.00
Indirect effect via PC	0.07	Indirect effect via PC	0.04
Total	−0.09	Total	−0.30

(Continues)

TABLE 5 (Continued)

KL		KTh	
PC		Determination coefficient (R^2)	.91
Direct effect on PE	**−0.30**		
Indirect effect via KL	0.17		
Indirect effect via KTh	0.02		
Indirect effect via KW	0.11		
Indirect effect via GY	0.15		
Indirect effect via ThDP	−0.07	Residual effect	0.30
Indirect effect via PTh	0.38		
Indirect effect via TStC	−0.01		
Indirect effect via OC	0.01		
Total	0.45		

Note. KL, kernel length; PE, popping expansion; KTh, kernel thickness; KW, kernel width; GY, grain yield; ThDP, thermal diffusivity of kernel pericarp; PTh, pericarp thickness; TStC, total starch content; OC, oil content; PC, protein content.

[a]Bold individual values. Bold averages are discussed in the text.

(−0.18 and −0.21, respectively). Therefore, it can be suggested that these traits have no significant direct or indirect effect on PE (Table 5).

The results, as well as the implications discussed, clearly indicate that adequate determination of simple correlations alone is not informative enough for the study of associations and interrelationships between observed traits and PE.

4 | CONCLUSIONS

Pericarp thickness is a key trait for the selection of popcorn genotypes with greater PE.

The ThDP and KL was indirectly related, via PTh, to PE, and can be an auxiliary strategy in selective processes. Out of these three traits, it is easier and more economical to evaluate KL to achieve greater PE.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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Area

Partial diallel and genetic divergence analyses in maize inbred lines

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ABSTRACT. In this study, we aimed to estimate general and specific combining abilities (GCA and SCA, respectively) and to verify genetic divergence (Rogers distance, Unweighted Pair-Group Method Using Arithmetic Average - UPGMA) using microsatellite markers in maize inbred lines. Using a partial diallel scheme, a total of 19 inbred lines were crossed as (9 x 10), which were derived from the single hybrids SG6015 and P30F53, respectively. The 90 hybrids were evaluated in an incomplete randomized block design with common checks and three replications during the 2017-2018 growing season. Flowering time, average plant height, ear height insertion, average ear diameter, ear length, number of lodged and broken plants, mass of 100 grains and grain yield were measured. According to the analysis of variance, GCA, and SCA were significant ($p < 0.05$) in all the measured traits; inbred line B as well as 1 and 8, derived from the single hybrids SG6015 and P30F53, respectively, were selected due to their higher GCA values in grain yield to be used in crosses as testers, while the single cross hybrid (B x 1) was selected due to their higher SCA value in grain yield to be used in future breeding programs. The molecular marker analysis divided the inbred lines into two groups, where the highest dissimilarity (0.74) was observed between lines A and 9; however, these did not result in a high SCA value, therefore the hybrids obtained by such crossings were not selected for grain yield.

Keywords: *Zea mays* L.; microsatellite markers; genetic distance.

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Introduction

Maize (*Zea mays* L.) is a diploid organism and has 10 pairs of chromosomes. It has great social and economic importance for humans and animals, and in industry (Grigulo, Azevedo, Krause, & Azevedo, 2011). In allogamous plant breeding, generating base populations for inbred lines is essential to obtain superior hybrids (Hallauer, Carena, & Miranda, 2010). In addition, the development of single maize hybrids depends on heterosis, which is related to genetic distance and the gene complementation effect (Lippman & Zamir, 2007; Schnable & Springer, 2013). Thus, selecting inbred lines based on genetic effects and heterotic groups to achieve superior single cross hybrids is necessary. Furthermore, diallel analysis is a widely used tool in breeding programs to obtain genetic information. This controlled mating system enables the estimation of the general and specific combining ability (GCA and SCA, respectively), where GCA reflects the proportion of additive effects related to the parents and SCA reflects the non-additive genetic effects that indicate deviation from a specific cross relative to the expected GCA performance of its parents (Cruz, Regazzi, & Carneiro, 2012). The classic diallel analysis performed in the field is advantageous as several phenotypes, with parental plants and their hybrids can be observed, under field conditions, which would be impractical in a molecular marker analysis. However, field diallel analysis is limited by the number of parents due to the labor-intensive nature of obtaining hybrids via performing multiple manual crossings between parental lines. Moreover, diallels are hindered by the low availability of hybrid seeds, since single hybrid seeds are produced in small ears by plants with inbreeding depression effects. In addition, manual crosses between early and late inbred lines can be difficult to perform with the lack of coinciding flowering times. All these difficulties limit field experiment replications, while increasing the residual mean square in the analysis of variance and lowering the probability of identifying significant differences between treatments. The loss of plant crossings often occurs, which causes data imbalances and complicates the statistical analysis. Finally, the occurrence of genotype x environment interactions is very frequent in the field, as genotypes may have different GCA and SCA values, according to the environmental conditions.

Using markers to analyze the genetic divergence can minimize the problems of field diallel analysis, such the genotype x environment interaction. However, its use is indicated only when certain conditions are satisfied, including an adequate laboratory and qualified personnel for handling the markers. When choosing markers, the genome coverage, the capacity to distinguish heterozygous from homozygous genotypes (dominant vs. codominant markers), the need for probe development, the amount of DNA per sample, the genetic information at each locus, and reproducibility need to be considered. These factors can influence the applicability of each type of marker during plant selection. In this study, we examined the results of both the field diallel analysis and the molecular analysis with their potential convergence to verify whether one or both should be taken into consideration. Convergence tends to be greater when marker coverage is broad and inclusive of the maize chromosomes. In the case of microsatellite markers (SSR) markers, results are optimized when the primers are associated with genes encoding traits of agricultural importance. If the used primers are not linked to such genes, the hybrid performance prediction is hindered in the parental molecular analysis. This limitation is even more severe when important agronomic traits are controlled by additive genes.

Recently, different molecular markers have been used to detect heterosis and polymorphisms related to gene similarity in parents (Munhoz Prioli, Amaral Junior, Scapim, & Simon, 2009), which is a main factor that affects heterosis (Hallauer et al., 2010). In this context, SSR are sequences of two to six base pairs that are repeated in tandem and are broadly used for their codominant inheritance and multiallelic nature, which provides valuable information regarding polymorphisms (Souza et al., 2008). Molecular markers have been very useful in breeding programs for genotype clustering in different heterotic groups (Reif et al., 2003). Bertan et al. (2007) reported that the analysis of genetic variability by using genetic and morphological distances is fundamental for efficient breeding programs. In this work, the diallel methodology was employed to quantify the combinatory capacity and facilitate the identification of superior genotypes. We have examined the correspondence between the combinatory capacity estimates obtained from the diallel analysis with the genetic distances of the parents estimated by pedigree information and SSR. We aimed to i) obtain the groups of inbred lines using the unweighted pair-group method using arithmetic average (UPGMA); ii) estimate the dissimilarity matrix using Rogers distance; iii) estimate the GCA and SCA values in the two divergent groups of maize inbred lines to compare with the molecular results; and iv) estimate whether the use of molecular markers can support diallel analyses in the field.

Material and methods

Diallel analysis

A total of nineteen maize inbred lines were selected from the core collection of the State University of Maringá maize breeding program to be used as parents in a partial diallel scheme. Parents were divided according to the population of each inbred line, where nine inbred lines were derived from the commercial single hybrid SG6015 (group I), being coded A to I, whereas the remaining ten inbred lines were derived from the commercial single hybrid P30F53 (group II), being coded as 1 to 10. Pollinations were performed in the growing season of 2016/2017 at Iguatemi Experimental Farm (latitude 23º25' S; longitude 51º57' W, and altitude 550 m asl), located at Maringá, Paraná State, Brazil. The 19 inbred lines were sown as pairs in all possible combinations of a partial diallel in 10 m rows with 0.9 m and 0.20 m spacing between the rows and plants, respectively. During flowering, pollinations were performed manually. The field trial was performed during the 2017/2018 growing season, at Fazenda Experimental de Iguatemi (latitude 23º25' S; longitude 51º57' W and altitude 550 m asl), located at Maringá, Paraná State, Brazil. The region's climate was classified as Cfa, according to the Köppen (1918) classification, with an annual average temperature of 19°C and an annual rainfall of 1,500 mm. The field trial was arranged in an incomplete randomized block design with common treatments, as proposed by Pimentel Gomes and Guimarães (1958). The 90 regular treatments were divided into groups, with three commercial checks used as the common treatment between the groups, and three replications. The hybrids P30F53, DKB 290, and 2B688 were used as commercial checks. Each plot consisted of two 5 m rows spaced 0.90 m apart, resulting in a usable area of 9 m². Each plot was thinned after 30 days to a density of 5 m^{-1}, yielding a population of approximately 55,500 plants ha^{-1} during harvesting. The following traits were evaluated: female (FF, days) and male (MF, days) flowering time; average plant height (PH, m) and ear height insertion (EH, m) from six competitive plants; average ear diameter (ED, m) and ear length (EL, m) from ten ears; number of lodged (NL), and broken (NB) plants per plot; and mass of 100 grains (MG, kg) and grain yield (GY, kg ha^{-1}), which were corrected to 13% moisture. To obtain the analysis of variance and the adjusted means of each evaluated treatment in the field trial, the following statistical model was used:

$$Y_{ijk} = \mu + \tau_i + \beta_j + \theta_k + \delta_{iY_{ijk}} + \varepsilon_{ijk}$$

In the model above, Y_{ijk} is the value for the *i*-th treatment, in the *k*-th replications, and in *j*-th experimental group; μ is the overall mean; τ_i is the fixed effect of treatment i; β_j is the random effect of group j; θ_k is the random effect of replications (k); $\delta_i\gamma_{ij}$ is the random effect of the interaction among groups and treatments, where $\delta_i = 1$ when it is a common treatment (commercial checks), or $\delta_i = 0$ when it is a regular treatment; and ε_{ijk} is the error value. Least square means were estimated through this model and then used as phenotypic inputs for the diallel analysis according to model IV that was proposed by Griffing (1956) and adapted for partial diallel schemes by Geraldi and Miranda Filho (1988):

$$Y_{ij} = \mu + \frac{1}{2}(d_1 + d_2) + g_i + g'_j + s_{ij} + \bar{\varepsilon}_{ij.}$$

In the model above, Y_{ijk} is the average value of the hybrid combination involving the i-th parent of group 1 and the j-th parent of group 2; Y_{i0} is the average of the i-th parent of group 1; Y_{0j} is the average of the j-th parent of group 2; μ is the general average of diallel; d1, d2 are contrasts involving means of groups 1 and 2 and the general average of diallel; $g_i$is the effect of GCA of the i-th parent of group 1; g'_j is the effects of GCA of the j-th parent of group 2; $s_{ij}$is the effect of specific combining ability; and $\bar{\varepsilon}_{ij.}$ is the mean experimental error. All analyses were performed using the statistical software suite SAS (2013) (v9.4, SAS, IBM, USA) and Genes (Cruz, 2013), an alpha of 5% probability of error was adopted.

Genetic divergence using SSR markers

The youngest leaves of five plants were sampled from each inbred line approximately 30 days after germination, immediately frozen in liquid nitrogen, and transferred to -80º C. The DNA was extracted using a protocol described by Hoisington, Khairallah, and Gonzälez (1994) with minor changes. DNA quality was evaluated on a 1% agarose gel and quantified using a Picodrop microliter UV/Vis spectrophotometer, where the DNA concentration was adjusted to 10 ng µL^{-1} for amplification. DNA amplification was performed in a thermal cycler using the Touchdown PCR methodology (Don, Cox, Wainwright, Baker, & Mattick, 1991) and separated using 4% agarose gel (50% agarose and 50% agarose Metaphor CAMBREX) in TBE buffer X 0.5 (44.5 mM Tris, 44.5 mM boric acid, and 1 mM EDTA). The gels were exposed to an electric field of 60 V for about 4 hours, stained with 0.5 µg mL^{-1} ethidium bromide solution and photographed under UV light. The alleles that were amplified were differentiated using 100 pb DNA ladder (Invitrogen, Thermo Fisher Scientific Corporation, USA). Each amplified DNA fragment identified in the gel was considered a distinct polymorphism for each phenotype, where it was considered a single locus with respect to its marker. SSR marker profiles of each inbred line were determined by numerical codes related to each allele, where presence or absence was scored as 1 or 0, respectively, according to the multiallelism of each SSR marker (Cruz et al., 2012). Heterozygosity, number of polymorphic loci in each SSR locus, and the total number of alleles were assessed using GenAIEx software v6.5 (Peakall & Smouse, 2012), while the polymorphism of each primer (PIC) was evaluated using Power Maker software (Liu & Muse, 2005). Genetic distance among the genotypes was estimated using Rogers (1972) distance with the following model:

$$D_R = \frac{1}{m}\sum_l \left[\frac{1}{2}\sum_u (\hat{p}_{1lu} - \hat{p}_{2lu})^2\right]^{1/2}$$

In the model above, *m* is the number of evaluated loci; *p1lu* is the allele frequency *u* in the population *p1*; and *p2lu* is the allele frequency *u* in population *p2*. Dendrogram clustering was performed using UPGMA with Mojena (1977) methodology for defining dendrogram cuts. Cophenetic correlations were also estimated using the Genes software (Cruz, 2013).

Results and discussion

Treatment effects were significant ($p < 0.05$) in almost all evaluated traits (Table 1), with the exception of PH, indicating the average differences among the genotypes. These responses constituted a key element for breeding programs, justifying the partition of variance in the groups of interest in the diallel analysis of variance, which was not performed in PH as its effects were not significant. The coefficients values in the experimental variation ranged from low to moderate in almost all traits, except for the number of lodged and broken plants, when compared to reports of diallel crosses using inbred lines (Durães et al., 2002; Silva et al., 2010; Conrado, Scapim, Bignotto, & Pinheiro, 2014; Werle et al., 2014) and reference values proposed for maize by Fritsche-Neto, Vieira, Scapim, Vieira, and Rezende (2012), indicating acceptable experimental precision. Evidently, the coefficients of experimental variation depend on the evaluated trait, the unit of evaluation, and on the genetic structure of the evaluated populations.

Table 1. Summary of the analysis of variance in female (FF, days) and male (MF, days) flowering, plant height (PH, m), ear height (EH, m), ear length (EL, m) and diameter (ED, m), number of lodged (NL) and broken (NB) plants, mass of 100 grains (MG, kg), as well as grain yield (GY, kg ha^{-1}).

	Residual mean squares										
	DF[7]	FF	MF	PH	EH	EL	ED	NL	NB	MG	GY
Treat.[1]	92	4.07*	4.55*	0.05	0.05*	0.0005*	0.003*	0.96*	66.51*	0.00003*	3671892.1*
Gr.[2]	9	3.27*	6.41*	0.07	0.02	0.0001	0.003*	0.33	11.72	0.00001	4328534.7*
Bl/Gr.[3]	20	5.99*	5.42*	0.16*	0.02*	0.0004	0.002*	0.23	34.49*	0.00002*	3507919.1*
Er.[4]	238	1.59	1.71	0.04	0.01	0.0003	0.001	0.38	14.03	0.00001	1431557.0
Av.[5]	-	59.9	60.18	2.16	1.16	0.162	0.489	0.26	3.37	0.03	7201.109
CV[6]	-	2.11	2.18	9.75	8.78	9.923	6.283	234.4	111.09	9.19	16.6

Grain yield for checks and higher hybrids			
P30F53	6,923.27 kg ha^{-1}	B x 1	10,284.18 kg ha^{-1}
DKB 290	7,557.17 kg ha^{-1}	H x 4	9,799.19 kg ha^{-1}
2B688	5,632.94 kg ha^{-1}	A x 1	9,799.19 kg ha^{-1}

*Significant at 5% of probability; [1]Treatments; [2]Groups; [3]Blocks/Groups;[4]Error; [5]Average among treatments; [6]Coefficient of variation; [7]Degrees of freedom.

The summary results of the diallel analysis of traits FF, MF, EH, EL, ED, NL, NB, MG, and GY are shown in Table 2, which indicated significant differences ($p < 0.05$) in GCA I, GCA II, and SCA effects in all evaluated traits. This indicated the different genetic contribution among the inbred lines in terms of additive effects and the differential performance of the single cross hybrid combinations when compared to what expected from the GCA of their parents. In practical terms, this meant that it was possible to select the best parental inbred lines, followed by the selection of hybrids with high SCA, which were selected from crosses derived from the same common parent that was previously highlighted by its GCA.

Table 2. Summary of the diallel analysis in female (FF, days) and male (MF, days) flowering, ear height (EH, m), ear length (EL,m) and diameter (ED, m), number of lodged (NL) and broken (NB) plants, mass of 100 grains (MG, kg), as well as grain yield (GY, kg ha^{-1}).

	Residual mean square for diallel analysis									
	DF[6]	FF	MF	EH	EL	ED	NL	NB	MG	GY
Treat.[1]	89	4.43*	5.60*	0.04*	0.0005*	0.002*	1.08*	67.01*	0.000029*	3444053.6*
GCA I[2]	8	12.32*	12.65*	0.14*	0.001*	0.007*	1.75*	308.47*	0.00013 *	3178432.4*
GCA II[3]	9	14.67*	21.25*	0.15*	0.001*	0.003*	2.87*	141.70*	0.000081*	10962028.9*
SCA[4]	72	2.27*	2.83*	0.018*	0.0004*	0.0014*	0.78*	30.85*	0.000011*	2533820.17*
DF[5]	238	1.59	1.71	0.01	0.0003	0.001	0.38	14.03	0.00001	1431557.0

*Significant at 5% of probability; [1]Treatments; [2]General combining ability (GCA) for group I; [3]General combining ability (GCA) for group II; [4]Specific combining ability (SCA); [5]Error; [6]Degrees of freedom (DF).

The values of GCA estimates have been summarized in Table 3. Within the first group, the inbred lines 1, 4, 7, 8, 9, and 10 had positive $\hat{g}_i$ values in grain yield, indicating a likely superiority in the quality of their gametes. Within the second group, the inbred lines A, B, F, G, and H had positive values of $\hat{g}_i$ in grain yield, while also exhibiting a certain superiority in their gametes. Maize breeding programs usually seek hybrids that combine high grain yield and earliness (short period of time in days from sowing to silking) with low plant and ear height. Therefore, GCA enabled the best parents to be selected based on the additive genetic effects to form superior single cross hybrids with higher frequencies of favorable alleles (Cruz et al., 2012). In this sense, selecting inbred lines with higher negative values of $\hat{g}_i$ in male flowering, female flowering, plant height and ear height can result in lower seedling-flowering cycles as well as lower to moderate plant and ear height progenies.

Comentado [L1]: Caro conselho editorial, neste parágrafo é possível observar diferença no espaçamento entre linhas, sugiro manter o mesmo espaçamento por todo artigo.
Obrigada

Considering the GCA significance of the EH trait (Table 2), inbred lines D ($\hat{g}_i$ = -0.08), F ($\hat{g}_i$ = -0.06), and H ($\hat{g}_i$ = -0.07) from group I (SG6015 derived) and inbred lines 3 ($\hat{g}_i$ = -0.11) and 5 ($\hat{g}_i$ = -0.08) from group II (P30F53 derived) were selected due to their negative GCA values, since their negative values of EH could result in lower ear height hybrids. In general terms, it also should be desirable to select the most promising genotypes according to their negative estimates of ĝi to reduce the values of traits such as EH, FF, and MF for superior hybrids in future crosses. In FF and MF, inbred lines C (ĝi = -0.7 and $\hat{g}_i$ = -0.57, respectively) and G ($\hat{g}_i$ = -0.46 and $\hat{g}_i$ = -0.18, respectively) from group I and inbred line 2 ($\hat{g}_i$ = -1.54 and $\hat{g}_i$ = -1.75, respectively) from group II had lower values, hence, can be used in future crosses to obtain early progenies. With regards to the number of lodged plants, inbred lines A and D as well as 3, 5, and 6 from groups I and II, respectively, were identified as superior parents given their negative GCA values ($\hat{g}_i$ = -0.30 , $\hat{g}_i$ = -0.30, $\hat{g}_i$ = -0.33, $\hat{g}_i$ = -0.25, and $\hat{g}_i$ = -0.25, respectively), while regarding the number of broken plants, inbred lines B, D, and F as well as 3, 5, and 8 from groups I and II were selected for their negative GCA values ($\hat{g}_i$ = -1.67, $\hat{g}_i$ = -2.28, $\hat{g}_i$ = -1.63, $\hat{g}_i$ = -1.77, $\hat{g}_i$ = -1.43 and $\hat{g}_i$ = -2.09, respectively) to reduce the number of broken plants. In addition, GCA results of groups I and II regarding ear traits revealed that, inbred lines E ($\hat{g}_i$ = 0.007) and F ($\hat{g}_i$ = 0.009) as well as 1 ($\hat{g}_i$ = 0.012) and 8 ($\hat{g}_i$ = 0.010) in groups I and II, respectively, were selected based on higher values of EL, while in terms of ED, inbred lines B ($\hat{g}_I$ = 0.019), C (I_i = 0.022), and I ($\hat{g}_i$ = 0.011) from group I were selected with higher GCA values. Moreover, in terms of MG, inbred lines B ($\hat{g}_i$ = 0.002) and F ($\hat{g}_i$ = 0.003) from group I and 10 ($\hat{g}_i$ = 0.003) from group II could be used in future crosses given their highly positive estimates. Finally, in terms of GY, inbred lines B ($\hat{g}_i$ = 617.5104) as well as 1 ($\hat{g}_i$ = 705.7), and 8 ($\hat{g}_i$ = 864.3) from groups I and II, respectively, had higher GCA values. Since most of the evaluated traits were mainly quantitative, inherited, and influenced by different genes, it was nearly impossible to select a single genotype that performed the best in all traits, highlighting the challenges of plant breeding. Even so, inbred lines B (NB, ED, MG, and GY), C (ED, MF, FF, and MG), 1 (EL, ED, and GY), and 8 (NB, EL, and GY) were consecutively selected for their higher GCA values, representing a direct reflection of a higher frequency of favorable alleles with additive effects. This has great potential for obtaining superior genotypes for maize breeding.

Table 3. GCA[1] estimations ($\hat{g}_i$) for the evaluated traits at Maringá (2017/2018 growing season).

Inbred line	FF[4]	MF[5]	EH[6]	EL[7]	ED[8]	NL[9]	NB[10]	MG[11]	GY[12]
1	1.015	0.559	0.130	0.012	0.012	0.453	3.733	-0.001	705.78
2	-1.541	-1.749	-0.019	-0.001	-0.022	0.009	4.153	-0.004	-1088.33
3	-0.788	-1.194	-0.109	-0.002	0.006	-0.325	-1.773	0.001	-91.81
4	-0.035	-0.120	-0.013	-0.0002	-0.013	0.169	1.338	0.0002	423.07
5	-0.220	-0.453	-0.078	-0.011	0.005	-0.251	-1.427	0.0002	-578.52
6	0.385	0.535	0.022	-0.006	0.009	-0.251	-1.106	-0.001	-761.60
7	0.435	0.584	-0.006	-0.003	0.006	-0.189	-0.304	0.001	118.46
8	0.644	1.115	0.084	0.010	-0.0005	-0.041	-2.094	0.0002	864.31
9	0.225	0.386	-0.070	0.004	-0.010	-0.214	-1.575	0.001	315.49
10	-0.121	0.337	0.060	-0.002	0.006	0.638	-0.946	0.003	93.14
A	0.189	0.185	0.002	0.0004	-0.022	-0.300	0.911	-0.002	88.10
B	0.089	0.474	0.009	-0.010	0.019	0.200	-1.667	0.003	617.51
C	-0.700	-0.570	0.106	-0.004	0.022	0.044	-1.067	0.001	-104.50
D	-0.422	-0.548	-0.079	-0.002	0.003	-0.300	-1.967	0.0003	-288.65
E	1.322	1.363	-0.007	0.007	-0.006	-0.133	7.367	-0.002	-575.75
F	0.633	0.063	-0.063	0.009	0.001	0.333	-2.278	0.003	61.26
G	-0.456	-0.181	0.008	-0.001	-0.008	0.289	-1.633	-0.001	160.45

H	-0.300	-0.770	-0.072	0.0003	-0.021	-0.178	3.222	-0.003	55.51
I	-0.356	-0.015	0.097	0.001	0.011	0.044	-1.067	0.001	-13.92
SD^2($\hat{g}_i$ - $\hat{g}_j$)	0.344	0.356	0.028	0.004	0.008	0.168	1.020	0.001	325.64
SD^3($\hat{g}_i$ - $\hat{g}_j$)	0.326	0.338	0.026	0.004	0.008	0.160	0.967	0.001	308.93

[1]General combining ability (GCA); [2]Standard deviation (SD) for inbred lines 1 to 10; [3]Standard deviation (SD) for inbred lines A to I; [4]female flowering (FF, days); [5]male flowering (MF, days); [6]ear height (EH, m); [7]ear length (EL,m); [8]ear diameter (ED, m); [9]number of lodged plants (NL); [10]number of broken plants (NB); [11]mass of 100 grains (MG, kg); [12]grain yield (GY, kg ha^{-1}).

SCA reflects parent specificity within crosses with regard to the complementation effect between alleles derived from each parent (dominance effect) and the interaction effect between alleles of different loci involved in the trait transmission (epistatic effect). Higher SCA estimates, regardless of the signal, indicate that SCA performance was different from that expected based on the GCA of the parents (Vencovsky & Barriga, 1992). Furthermore, SCA is also related to the genetic distance between parents and reveals the importance of non-additive interactions in hybrid combination (Lippman & Zamir, 2007). According to Cruz et al. (2012), the most promising hybrid combinations must be selected based on estimates of the SCA that most favor the trait in question. In this sense, the best hybrids would be those with at least one selected parent based on its $\hat{g}_i$ estimation, thereby presenting a higher frequency of favorable alleles relative to the average frequency in the parents involved in the crosses (Vencovsky & Barriga, 1992; Cruz et al., 2012). SCA estimations ($\hat{\mathbf{s}}_{\mathbf{ij}}$) for grain yield have been summarized in Table 4. With regard to male and female flowering, one hybrid (E x 2) obtained a greater negative SCA value with one selected parent based on $\hat{g}_i$ estimations, which could be selected for a reduced sowing-flowering cycle. In terms of EL, two crosses (A x 8 and F x 9) were selected with higher SCA values and at least one parent with higher GCA values, while in terms of ED, only one cross (I x 10) had a higher SCA value and one selected parent based on GCA values. However, regardless of the higher correlations that have already been reported in both traits (El-Shouny, Olfat, Ibrahim, & Al-Ahmad, 2005; Suhaisini, Ravikesavan, & Yuvaraja, 2016), no crosses could be simultaneously selected in both traits. Regarding the MG trait, one hybrid was selected with higher SCA values and a parent with higher GCA values (H x 10). Finally, in terms of GY, two crosses (B x 1 and B x 3) showed the highest levels of genetic complementation in enhancing grain yield.

Table 4. SCA[1] estimations ($\hat{s}_{ij}$) in GY[2] at Maringá (2017/2018 growing season).

Hybrid		$\hat{s}_{ij}$	Hybrid		$\hat{s}_{ij}$	Hybrid		$\hat{s}_{ij}$
A	1	1048.40	D	1	-904.54	G	1	-576.96
A	2	1145.60	D	2	-275.24	G	2	-143.48
A	3	-478.52	D	3	1937.97	G	3	69.59
A	4	-871.76	D	4	-840.61	G	4	-181.21
A	5	-109.75	D	5	440.26	G	5	692.96
A	6	-880.28	D	6	-899.06	G	6	962.05
A	7	135.16	D	7	131.12	G	7	-1125.55
A	8	31.94	D	8	-134.16	G	8	591.80
A	9	-138.69	D	9	743.09	G	9	-692.12
A	10	117.90	D	10	-198.82	G	10	402.92
B	1	1594.23	E	1	-1889.73	H	1	-596.88
B	2	-295.73	E	2	1085.91	H	2	-1059.13
B	3	1312.07	E	3	-838.18	H	3	-838.01
B	4	-214.07	E	4	803.38	H	4	1953.95
B	5	-1904.64	E	5	-154.46	H	5	-286.87
B	6	-896.88	E	6	149.80	H	6	-499.87
B	7	25.74	E	7	-189.28	H	7	-525.35
B	8	-155.70	E	8	47.95	H	8	557.61
B	9	672.99	E	9	1219.38	H	9	883.98
B	10	-138.01	E	10	-234.77	H	10	410.57
C	1	245.24	F	1	694.03	I	1	386.20
C	2	-688.45	F	2	-102.53	I	2	333.05
C	3	634.87	F	3	-550.68	I	3	-1249.10
C	4	-527.32	F	4	-933.48	I	4	811.11
C	5	935.93	F	5	-342.12	I	5	-0.106
C	6	-399.00	F	6	1389.22	I	6	1.128
C	7	589.34	F	7	508.02	I	7	0.770
C	8	279.79	F	8	530.85	I	8	-0.106
C	9	-1727.08	F	9	91.77	I	9	-1.847
C	10	656.67	F	10	-1285.07	I	10	268.61
SD^3($\hat{s}_{ij}$)								617.86
SD ($\hat{s}_{ij}$ - $\hat{s}_{ik}$)								921.05
SD ($\hat{s}_{ij} - \hat{s}_{kj}$)								926.79
SD ($\hat{s}_{ij} - \hat{s}_{kl}$)								867.69

[1]Specific combining ability (SCA) estimations; [2]Grain yield (GY) (kg ha^{-1}); [3]Standard deviation (SD).

The genetic divergence analysis using SSR markers revealed that 75 out of 195 primers were polymorphic in all 19 inbred lines, representing 34.4% of the total, and 32 primers were selected based on their visual allelic amplification on the agarose gel. In addition, the number of alleles per locus ranged from two to five, totaling 93 different alleles. Primers *Mcm0181* (five alleles) and *Umc 2408* (five alleles) showed the highest number of alleles when compared to other primers.

These results were higher than those described by Dandolini et al. (2008), who reported 27.4% polymorphic markers with a number of alleles that ranged from two to five. Shah et al. (2009) reported an average of only 1.56 alleles per locus when using 10 SSR markers in 17 maize inbred lines. However, when higher numbers of inbred lines and SSR markers are used, it is expected to observe higher numbers of alleles per locus, where Van Inghelandt, Melchinger, Lebreton, and Stich (2010) reported an average of 14.5 alleles per locus when using 359 SSR markers in 1,537 inbred lines. In addition, Yang et al. (2011) found an average of 8.2 alleles per locus in 154 inbred lines and 82 SSR markers, while Malik, Kumar, and Babu (2020) obtained an average of 4.9 alleles per locus when using 46 SSR markers in 47 genotypes.

According to Legesse, Myburg, Pixley, Twumasi-Afriyie, and Botha (2008), lower genetic distances among genotypes could be a limiting factor when identifying polymorphisms by reducing the number of alleles per locus. A possible reason for observing a lower number of alleles per locus in this study could be that group I and group II were consisted of inbred lines selected from single cross hybrids, which were expected to have narrow genetic bases with less alleles per locus. Most of the loci revealed low average values of observed heterozygosity (H_o) relative to the average values of expected heterozygosity (H_e), with 0.284 and 0.216 observed in locus *Mmc 0181* in terms of H_o and H_e, respectively. A total of 13 SSR loci had H_o values of zero, indicating that these loci could be fixed or homozygous in all the estimated inbred lines. In general, the H_e and H_o values ranged between 0 to 0.13 and 0 to 0.19, respectively. Inbred line 2 showed higher values of H_o and H_e (0.131 and 0.199, respectively), whereas inbred line 8 had homozygous loci. According to Nepolean, Sing, Hossain, Pandey, and Gupta (2013), since maize is an allogamous species, residual heterozygosity could be expected at 5 to 10% rates even in advanced selfing generations. Pollen and seed contaminations, microsatellites specific mutations, and the amplification of two similar but distinct SSR regions, could also explain the presence of heterozygotes in advanced selfing generations (Liu et al., 2003; Labora, Oliveira, Garcia, Paterniani, & Souza, 2005; Legesse et al., 2008). Furthermore, inbred line 2 had two specific alleles in loci *Umc 1137* and *Umc 2408*, while inbred line H also had a specific allele for locus *Umc 2410* with 1.0 frequency. Among all the genotyped inbred lines, the average proportion of polymorphic markers was 18.2%, which is a much lower value when compared to the popcorn inbred lines estimated by Liu et al. (2003) and Dandolini et al. (2008). According to Vigourox et al. (2002) and Hamblin, Warburton, and Buckler (2007), it is expected to observe lower allele frequencies in microsatellites, mainly because these genomic regions are highly mutable, where the mutation rate per generation was estimated to range from 7.7^{-4} to 1.1^{-7} (Vigourox et al., 2002).

Furthermore, PIC values can be used to differentiate markers by their polymorphisms, since the allele loci number and relative frequency help estimate PIC (Cruz, Ferreira, & Pessoni, 2011). In this study, PIC values ranged from 0.69 (*Bnlg 1297*, four alleles) to 0.11 (*Umc 1169*, two alleles), with an average value of 0.45. Similar results were also found by Lopes, Scapim, Mangolin, and Machado (2014), using 15 sweet corn inbred lines in a divergence genetic study, where they found 15 out of 100 polymorphic SSR markers had an average PIC of 0.41. Almeida, Amorim, Neto, Filho, and Sereno (2011) obtained PIC values ranging from 0.26 to 0.76 in populations of field corn and teosinte, while Nikolić et al. (2019) found, in their genetic divergence study using 24 maize genotypes, PIC values ranging from 0.57 to 0.89 with an average value of 0.73. In addition, Cruz et al. (2011) highlighted that PIC values reflect whether a marker is informative or not relative to their capacity for genetic divergence analysis. According to Botstein, White, Skolnick, and Davis (1980), values greater than 0.5 or less than 0.25 were regarded as highly or marginally informative markers, respectively. Moreover, the dissimilarity matrix estimated from Rogers distance showed that the highest genetic distance was obtained in inbred lines A x 9 (0.74), whereas the lowest estimation was in inbred lines C x I (0.248). In addition, the UPGMA dendrogram clustered the 19 inbred lines into two different groups (Figure 1), where group 1 encompassed 11 inbred lines (C, I, G, A, D, B, F, H, 4, 8, and 2), while group 2 included eight inbred lines (1, 3, 5, 6, 7, 9, 10, and E). The estimated cophenetic correlation coefficient *(r)* was 0.73, which was higher than what was observed in Guimarães et al. (2007) ($r = 0.57$) and Xia et al. (2004) ($r = 0.63$). Ferreira (2008) suggested a value close to 1 for a better adjustment of distances, whereas Patto, Satovic, Pêgo, and Fevereiro (2004) recommended a value higher than 0.56 for maize inbred lines.

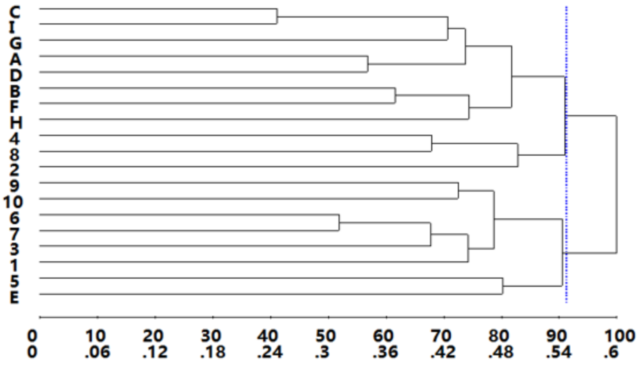

Figure 1. Genetic distance among the 19 maize inbred lines using Rogers distance and unweighted pair-group method using arithmetic average (UPGMA) clustering.

According to the UPGMA clustering and the five highest SCA values in GY, four hybrids (80%) consisting of inbred lines were classified in distinct UPGMA groups, which was not consistent with the hybrid having the highest SCA estimation (H x 4) with both inbred lines clustered in the closest genetic groups. In addition, the largest genetic divergence observed among the inbred lines A x 9 did not necessarily result in a higher SCA valu. In fact, hybrid A x 9 performed poorly in terms of SCA (672.9853) in their grain yield. Sharma and Pankaj (2018) reported a concordance index value of 47% when comparing SSR markers using clustering and heterosis. Despite reports of good concordance in terms of SCA values and genetic distances estimated using SSR markers, Munhoz et al. (2009) and Fernandes, Schuster, Scapim, Vieira, and Coan (2015) found lower concordance or almost no concordance in terms of genetic divergence in grain yield and in other complex quantitative traits. In this work, we found a partial convergence in the molecular genetic distances and the genealogy of diallel parents, in which they both affect the arrangement of parents in the two groups. However, in the grain yield trait, the concordance among the SCA values and the genetic distances estimated by SSR markers was not optimal. For example, the hybrid (A x 9) was generated from parents with greater genetic distances and more heterozygosity, but it was not selected for its total grain yield. This indicated that both analyses were important in phenotyping and genotyping approaches to achieve better selections among hybrids and their parents, so that molecular markers could supplement the diallel analysis made in the field.

Conclusion

i) the molecular marker study divided the inbred lines into two groups; ii) the dissimilarity matrix showed that the largest genetic distance was obtained in inbred lines A and 9; iii) the larger genetic distance trait did not correspond with hybrids that have favorable estimates of SCA and according to the UPGMA clustering, 85% of the five hybrids had parents from different groups, where they all had favorable values of $\hat{s}_{ij}$ in grain yield and iv) this study indicated that both the molecular and diallel analyses were useful, where molecular marker analyses could support diallel crosses in the field.

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Engenheira Agrônoma

ASSOCIAÇÃO GENÔMICA AMPLA (GWAS) PARA CARACTERÍSTICA DE PROTEÍNA EM LINHAGENS DE MILHO TROPICAL

Projeto de pesquisa apresentado como parte das exigências do Programa de Pós-Graduação em Genética e Melhoramento da Universidade Estadual de Maringá, para ingresso no curso de doutorado.

Maringá, dezembro de 2022

INTRODUÇÃO

O milho (*Zea mays* L.) é uma das espécies de maior importância econômica e social, em nível mundial, tanto em área semeada como em volume de produção de grãos. A produtividade mundial para o ano agrícola 2018/2019 estimada foi de 1.147,6 milhões de toneladas, sendo o Brasil o terceiro maior produtor mundial, com 82,3 milhões de toneladas, sendo superado apenas pela China (257,2 milhões de toneladas) e Estados Unidos (392,5 milhões de toneladas) FAO (2019).

Este cereal se caracteriza pelas diversas formas de utilização, que vão desde a alimentação humana e animal, até a indústria de alta tecnologia (Môro e Fristsche-Neto, 2015). O grão apresenta a maior utilização da cultura, sendo este formado por quatro principais estruturas: revestimento de proteção externa (pericarpo), embrião (gèrmen), endosperma e ponta, as quais apresentam composição química distinta na qual a qualidade é dependente do material genético, bem como das condições do ambiente (Pinto et al.,2009).

O grão de milho é composto por amido (60%), além de proteína (cerca de 8%), óleo (cerca de 3,7%), água (15%), açúcares (cerca de 2%), minerais totais (1,5%) e outros constituintes como fibras, minerais e vitaminas (Paes, 2006). Devido ao alto teor de carboidratos é utilizado como fonte energética, possuindo alto conteúdo de amido, disponível de forma facilmente digerível e de baixo custo. Em termos de fonte proteica, seu produto deixa a desejar, por possuir teor médio, apesar disto por ser uma das principais culturas utilizadas e de fácil acesso, programas de melhoramento visando alto teor proteico e melhor qualidade nutricional são interessantes e com aplicações práticas importantes (Paes, 2006; Renk et al. (2021).

A qualidade nutricional é um fator determinante na qualidade geral do grão e consequentemente na produção de alimentos os estudos de melhoramento de milho tem focado em ganho de rendimento, negligenciando valor nutricional do grão (Holmes et al., 2019). Mudar o foco dos programas de melhoramento para características de qualidade requer uma compreensão dos fatores genéticos que contribuem para a variação da característica (Renk et. al., 2021).

O desenvolvimento de marcadores moleculares tem possibilitado o estudo dos genótipo e a obtenção de informações sobre a variabilidade, identificação e localização de genes específicos e sua associação com características fenotípicas. Essas informações permitem a análise do genoma e possui inúmeras aplicações no melhoramento de plantas (Resende, 2008).Estudos sobre características nutricionais, como teor de óleo e proteína, sugerem que o controle genético dessas características é bastante complexo com muitos loci de pequeno efeito contribuindo para a variação fenotípica (Dudley; Lambert, 2004).

Nesse sentido, o uso de marcadores moleculares trouxe a oportunidade o desenvolvimento de técnicas que melhoram a compreensão da base genética de vários traços complexos, como a associação ampla do genoma (GWAS), que identifica variações no genoma que se correlacionam com um fenótipo de interesse. Estudo de GWAS para características de composição de grãos de milho, principalmente relacionado ao teor de proteína, são escassos sendo necessário uma melhor compreensão entre a característica e seu controle genético (Renk et. al., 2021).

OBJETIVO

Identificar regiões do genoma associadas a característica teor de proteína em sementes de milho tropical.

HÍPOTESE DO TRABALHO

O controle genético da característica teor de proteína em grãos de milho complexo com diversos loci contribuindo para a variação fenotípica, o estudo de associação genômica pode permitir um melhor entendimento sobre o valor do teor proteico e seu controle genético, permitindo que programas de melhoramento possam utilizar estas informações em busca de genótipos com melhor qualidade nutricional.

REVISÃO BIBLIOGRÁFICA

A cultura do milho

O milho (*Zea mays* L.)) é uma espécie diploide, alógama, anual e herbácia, pertencente à família Poaceae (Gramineae) e classe das monocotidelôneas. Os genótipos são frequentemente divididos em grupos estabelecidos de acordo com o tipo de grão, sendo mais comuns os milhos dentados, duros, pipoca, doce e ceroso. Os grupos de milho podem ser modificados por meio do melhoramento vegetal (Jugenheimer, 1985).

O grão é a parte da planta mais comercializada, podendo ser colhido na fase leitosa do grão (para silagem) ou após seu amadurecimento fisiológico (para alimentação humana e animal, bem como uso industrial) (Coll et al., 2011). Os grãos de milho podem ser caracterizados quanto à qualidade, quantidade, peso, composição do endosperma, tipo (duro, amassado, doce e pipoca) e textura (semi-dentado e semi-duro) (Brown; Darrah, 2009; Fonseca et al., 2014).

Sua origem tem sido vastamente estudade e existem três principais hipóteses para esclarecer sua origem. A hipótese da "origem comum" sugere que o milho e o teosinto descendem de um ancestral comum. A hipótese da "ancestralidade do teosinto" sugere que o milho descende direta e exclusivamente do teosinto, por meio da seleção praticada pelos humanos A última hipótese sugere exatamente o contrário da anterior, ou seja, postula que o teosinto é originário do milho (Paterniani, 1978).

O milho é considerado um grão essencialmente americano não apresentando evidências fósseis ou históricas de sua existência ou ancestralidade fora das Américas. Alguns estudos sugerem que o centro de origem do milho seria em algum lugar nas montanhas do Peru, Equador e Bolívia. Achados arqueológicos de grãos de pólen e espigas de milho no México tornaram mais provável a hipótese de que o milho se originou no Vale Central do país (Company, 1984).

A evolução no milho é evidenciada pela enorme diversidade genética encontrada, com frequências gênicas mudando entre as gerações (Paterniani; Goodman, 1977). Essas mudanças surgem da seleção, mutação, deriva genética, migração e hibridização. Embora todos os fatores mencionados desempenhem um papel na evolução do milho, os fatores mais importantes foram a hibridização e a seleção (Borém, 2005).

O grão de milho

O milho é um grão encontrado em grandes áreas do globo desde o nível do mar até 3000 metros (Lerayer, 2006). No Brasil, 70-80% do milho é utilizado na alimentação animal devido às suas boas propriedades nutricionais, que contém a maior parte dos aminoácidos, e também por ser um cereal com baixo custo de produção em comparação com outros cereais. Alguns tipos de milho são também empregados na elaboração de silagem, como ingrediente único ou como complemento (Embrapa, 2004).

O grão de milho se divide em endosperma (82,3%), embrião (11,5%), pericarpo (5,3%) e ponta (0,8%). Sendo composto por amido (60%), além de proteína (cerca de 8%), óleo (cerca de 3,7%), água (15%), açúcares (cerca de 2%), minerais totais (1,5%) e outros constituintes como fibras, minerais e vitaminas (Paes, 2006).

As proteínas representam, em média, em 8,5% do endosperma, 18,5% do embrião, 5,0% do pericarpo e 9,1% da ponta (Tosello 1987). As proteínas do milho podem ser divididas em diversas classes, sendo agrupadas de acordo com suas solubilidades, a α-zeína é a de maior concentração em milho normal, representando entre 50% e 60% do total de proteína (Tosello 1987).

As frações proteicas do grão de milho variam de acordo com o tipo de grão, podendo ser alteradas por genes mutantes. São conhecidos vários genes capazes de modificar as frações proteicas do endosperma, o mais difundido é o gene opaco-2 que possui a característica de provocar uma diminuição significativa na síntese de α-zeína, implicando num amento das frações de β-zeína, característica vantajosa do nutricionalmente, devido a α-zeína ser pobre em aminoácidos essenciais como a lisina e o triptofano, enquanto a β-zeína, pussui melhor digestibilidade, disponibilizamdo mais prontamente esses aminoácidos, conferindo ao grão um alto valor biológico (Bjarnasan; Vasal 1992; Moro et al. 1996).

O Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT) com suas pesquisas conseguiram produzir variedades de milho denominadas "Quality Protein Maize" ou simplesmente QPM, que reúnem as boas qualidades do milho normal, e com qualidade proteica similar ao milho opaco-2 (Saldivar; Rooney 1994).

No Brasil, destaque o trabalho desenvolvido pela Embrapa Milho e Sorgo que iniciaram seus estudos em 1984, a partir da introdução de 23 populações QPM oriundas do CIMMYT, lançando a primeira variedade brasileira de milho QPM, a BR 451. Em 1994, esse mesmo programa de melhoramento introduziu no mercado outra variedade QPM, a BR 473, e em 1997, o híbrido duplo QPM BR 2121, ambos de grãos amarelos (Pacheco et al. 1999).

Associação genômica ampla (GWAS)

Estudos de genótipos com a finalidade de se obter informações sobre variabilidade, identificação e localização de genes e suas associações com os fenótipos de interesse foram possibilitados pelo desenvolvimento dos marcadores moleculares, sendo que esses estudos permitiam diversas aplicações no melhoramento (Rezende, 2008).

O uso de marcadores moleculares possibilitou o desenvolvimento de técnicas que visam o entendimento entre características complexas, com muitos loci envolvidos, e características fenotípicas desejáveis. A associação genômica ampla (Genome Wide Association study, GWAS) é uma das ferramentas mais utilizadas nos últimos anos, que visa identificar marcadores polimórficos em desequilíbrio de ligação (LD) com genes que possam influenciar características quantitativas, identificando altos níveis de diversidade em uma população de mapeamento e menores níveis de LD provenientes de eventos históricos de recombinação (Buckler et al., 2009; Yu; Buckler, 2006).

O GWAS é uma abordagem que estuda a relação (associação) entre marcadores genotípicos e QTLs em ligação com a característica de interesse e considera todos os eventos de recombinação que ocorreram ao longo das gerações em um grande número de indivíduos que serão genotipados e fenotipados para estabelecer a associação entre o genótipo e o fenótipo usando análise de regressão simples ou múltipla (Whitt;Buckler, 2003; Gupta et al., 2008; Zhu et al., 2008; Korte;Farlow, 2013). A técnica foi usada pela primeira vez em humanos, atualmente inúmero trabalhos utilizando GWAS foram publicados, em várias espécies, incluindo espécies clássicas como Arabidopsis e rato, além de culturas, vegetais, bovinos, leiteiros e suínos (Hirschhorn; Daly, 2005; Zhu et al., 2008; Hindorff et al., 2009; Korte; Farlow, 2013)

Esse tipo de estudo pode ser um eficiente caminho para dissecar a arquitetura de características complexas e uma ferramenta poderosa para o melhoramento genético de plantas (Rebolledo et al., 2015).

As estratégias GWAS geralmente são compostas por quatro etapas amplas: i) pré-processamento dos dados; ii) geração de novos dados; iii) análise estatística; e iv) pós-analítico. O principal objetivo é identificar e caracterizar a associação entre marcadores (SNPs) (Single Nucleotide Polymorphism), associando o polimorfismo molecular com o fenótipo de interesse. (Reed et al., 2015).

Essa metodologia superou algumas limitações do mapeamento genético tradicional, pois proporciona maior resolução, além de poder utilizar amostras de populações previamente bem estudadas, nas quais as variações genéticas podem ser associadas à variação fenotípica (Brachi et al.,2011).

MATERIAL E MÉTODOS

Material genético

Um total de 285 linhagens de milho tropical serão avaliadas neste estudo; dessas, 162 serão genótipos de milho comum, 110 de milho pipoca e 13 de milho doce. As linhagens a serem utilizadas no trabalho pertencem ao banco de germoplasma da Universidade Estadual de Maringá.

Condições experimentais e característica a ser avaliada

Os experimentos serão conduzidos na Fazenda Experimental de Iguatemi da Universidade Estadual de Maringá (UEM), localizada em Iguatemi – PR distrito do município de Maringá-PR (latitude 23º 25’ S, longitude 51º 57’ O e 550 m de altitude). A região apresenta precipitação média anual de 1.500 mm, com temperatura média de 19 ºC. O solo da área experimental foi classificado como Latossolo Vermelho Distrófico (Brazilian Agricultural Research Corporation (Embrapa), 2018).

As linhagens serão fenotipadas para a característica teor de proteína dos grãos secos e moídos será determinado pelo método de Kjeldahl (Nitrogênio total), conforme recomendação da Association of Official Analytical Chemists (Association of Official Analytical Chemists (A.O.A.C.), 1995). As amostras de grãos provenientes de cada parcela de campo serão moídas durante 60 segundos em um moinho de faca a 15000 r.p.m., sendo utilizada uma peneira de 0,5 mm. Posteriormente, serão analisadas subamostras de 0,2g do grão moído, as quais serão condicionadas em tubos de ensaio, junto com 2g de uma mistura catalítica (sulfato de cobre e selênio em pó) e 5mL de ácido sulfúrico concentrado. Os tubos serão aquecidos em um bloco digestor, para a fase de digestão da matéria orgânica. O aquecimento será gradual até atindir a temperatura de 350ºC, permanecendo nesta temperatura por 2 horas. Após a digestão, será realizada a fase de destilação da amônia liberada, pela reação com hidróxido de sódio (50%), a qual será recolhida em solução de ácido bórico a 4%. A titulação será realizada em solução padrão de ácido clorídrico (1 N), sendo recuperado 99,7% de nitrogênio. Para a determinação de proteínas total, multiplica-se o conteúdo de nitrogênio pelo fator 6,25, com base na matéria seca.

Análise genética

O DNA genômico foi isolado de folhas jovens de cinco plantas de cada linhagem de milho tropical (285 linhagens), aproximadamente 30 dias após a germinação. A extração de DNA foi realizada de acordo com o protocolo estabelecido por Chen e Ronald (1999).

Análise estatística

A estrutura populacional será inferida usando a abordagem de agrupamento Bayesiana baseada em modelo implementado pelo programa InStruct (Gao et al.,2007)

O Desequilíbrio de ligação (LD) será estimado por meio dos coeficientes de correlação das frequências alélicas (r^2) considerando todas as combinações possíveis dos alelos. O valor crítico de r^2 será calculado de acordo com o método utilizado por (Breseghello; Sorrells ,2006).

A análise de associação do genoma será realizada usando um modelo linear misto (MLM) em TASSEL 5.2 (Bradbury et al., 2007).

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