QTL MAPPING OF RESISTANCE TO SORGHUM DOWNY MILDEW IN MAIZE

A Dissertation

by

AHMED MOHAMED-BASHIR SABRY

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

August 2003

Major Subject: Plant Pathology

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ABSTRACT

QTL Mapping of Resistance to Sorghum Downy
Mildew in Maize. (August 2003)
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Sorghum downy mildew (SDM) of maize is caused by the oomycete *Peronosclerospora sorghi* (Weston and Uppal) C. G. Shaw. The disease can cause devastating yield losses in maize (*Zea mays* L.). Quantitative trait loci (QTLs) mediating resistance to SDM were mapped using both restriction fragment length polymorphisms (RFLPs), and simple sequence repeats (SSRs) in 220 F_2 individual maize progeny derived from a cross between two extremes; highly susceptible inbred parent SC-TEP5-19-1-3-1-4-1-1 (white) and highly resistant inbred P345C4S2B46-2-2-1-2-B-B-B (yellow). The phenotypic expression was assessed on $F_{2:3}$ families in a wide range of environments under natural field infection and in a controlled greenhouse screening method. Heritability estimates of disease reaction ranged from 93.3% in Thailand sit 1 to 48% in Thailand sit 2. One hundred and thirty three polymorphic markers were assigned to the ten chromosomes of maize with LOD scores exceeding 4.9 covering about 1265 cM with an average interval length between markers of 9.5 cM. About 90% of the genome was located within a 10 cM distance to the nearest marker. Three putative QTLs were detected in association with resistance to SDM in different environments using composite interval mapping. Despite environmental and symptom differences, one QTL on chromosome 2 bin 9 had a major effect in all trials and explained up to 70% of the phenotypic variation in Thailand

where the highest disease pressure was experienced. Two other QTLs on chromosome 3 bin 5 and chromosome 9 bin 2 had a minor effect, each explaining no more than 4% of the phenotypic variation. These results revealed one major gene and two minor genes that control sorghum downy mildew resistance. These markers should be very useful in breeding programs in facilitating the introgression of the resistance genes into commercial varieties. Marker-assisted selection for these loci should be useful in incorporating SDM resistance genes in maize across environments, even in the absence of the pathogen.

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TABLE OF CONTENTS

Page

Page

LIST OF FIGURES

FIGURE Page

LIST OF TABLES

TABLE Page

TABLE Page

INTRODUCTION

Sorghum downy mildew (SDM) of maize is caused by the oomycete *Peronosclerospora sorghi* (Weston and Uppal) C. G. Shaw, an obligate pathogen that cannot be cultured in the laboratory. Sorghum downy mildew of maize is a disease of great destructive potential because systemically infected plants seldom produce an ear. Sorghum downy mildew occurs on maize and sorghum in warm, humid areas of the world. The disease has been reported in many African countries, Bangladesh, China, India, Iran, Israel, Philippines, Thailand, Yemen Arab Republic, USA, Mexico, El Salvador, Guatemala, Honduras, Panama, Argentina, Bolivia, Brazil, Uruguay and Venezuela. It may also occur in Italy, Iran, Nepal, Pakistan and Peru. SDM became a global disease of maize during the years of rapid expansion of the use of sorghum for grain and forage. Frederiksen and Renfro (10), Williams (27) and more recently, Craig and Odvody (8) reviewed the work on conventional disease management. Overall, these management practices have been successful in controlling the downy mildews in most of the maize growing regions of the world. There are exceptions, however, including Egypt where SDM of maize remains a serious problem (23).

P. sorghi has both a long-surviving oospore stage and a rapidly repeating asexual reproduction cycle that can create epidemics from limited initial inoculum. The rapid development of an epidemic from a point source represents one of the most challenging aspects of disease management in maize. Therefore, any control strategy to reduce the threat of SDM disease in maize must also consider sorghum management, especially in areas where maize and sorghum production overlaps. This includes the occasional small plot of forage Sorghum frequently found to be extremely susceptible to

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This dissertation follows the style of Phytopathology.

sorghum downy mildew. Sorghum downy mildew can be controlled in sorghum through host resistance, cultural practices, and chemical controls. Approaching disease control in an integrated manner greatly enhances the probability of success. With the integrated approach, the development of genetically resistant maize inbreds to be used for the development of resistant hybrids will provide efficient control of the disease in maize. For practical application, resistance will need to be introduced into materials genetically adapted to the target area.

In Egypt, in so far as it is known, the pathogen responsible for the outbreaks of downy mildew in maize is *P. sorghi*. The only hosts where *P. sorghi* produces large quantities of oospores are various sorghum species, which is the primary host of SDM rather than maize. Close relatives of the pathogen include *P. maydis* and *P. sacchari* for which the primary hosts are maize and sugarcane, respectively. A form found in Thailand seems to have less host specificity. While the Thai form is most often isolated from maize, it is not unusual to isolate it also from sorghum or sugarcane (4).

Although DNA sequences from any of the downy mildew species will hybridize to DNA from each of the others, the restriction digestion patterns have proven to be very uniform within species but to show distinctive patterns between species (29). Based on restriction fragment length polymorphisms (RFLPs), the Thai form is also distinct, so has been referred to as *P. zeae* (28). In addition, polymerase chain reaction (PCR) primers that amplify a mitochondrial DNA sequence found in *P. sorghi*, but not in any of the other *Peronosclerospora* species, have been synthesized (30), making accurate identification of *P. sorghi* a relatively straightforward procedure.

Host plant resistance is the cornerstone for control of downy mildews. It is efficient, economical, and environmentally sound. Prior to the development of the systemic fungicide metalaxyl, genetic resistance was essentially the only reliable control for SDM in maize. Several potential sources of genetic

resistance to sorghum downy mildew have been identified in advanced inbred lines from CIMMYT germplasm. Progeny from segregating crosses of CIMMYT resistant by susceptible lines made in Thailand have been made available from CIMMYT.

There is some possibility that the CIMMYT sources of resistance were also used to develop inbred lines for use in Egypt, some of which show a degree of resistance to sorghum downy mildew. Mapping of resistance genes segregating in selected crosses will help to identify independent sources of resistance. A relatively simple mode of inheritance has been seen for a cross involving two Egyptian inbreds. Three QTLs that contribute resistance to *P. sorghi* were detected in a population of recombinant inbred lines derived from a cross between resistant (G62) and susceptible (G58) inbred lines (1). Two of the loci mapped close together on chromosome 1 while the third one was on chromosome 9.

One of the major difficulties in working with downy mildew resistance in maize has been the difficulty in accurately scoring disease reaction. Plant maturity and amount of inoculum influence the disease. As a consequence, multiple evaluations made in different locations are required for accurate assessment of genetic contributions to resistance. Identification of simply and accurately scored markers for genes that contribute to downy mildew resistance of maize could greatly benefit future efforts to prevent diseases losses.

The research reported in this dissertation arose from a project involving TAMU, CIMMYT and Egyptian collaborators. The specific goals for the dissertation project were:

1) To use the polymerase chain reaction with genus- and species-specific DNA primers to verify that *P. sorghi* is the cause of maize downy mildew in Egypt.

2) To identify crosses between resistant and susceptible parental maize lines with sufficient genetic diversity to permit molecular mapping.
3) To locate alleles that contribute downy mildew resistance based on linkage to segregating DNA markers selected to cover the 10 chromosomes of maize.
4) To compare resistance genes identified when the same cross is evaluated in Texas, Egypt and Thailand.

MATERIALS AND METHODS

Verification of the SDM pathogen and identity of races in Egypt. In order to collect samples of infected maize/sorghum leaves, fields known to be infested with SDM in Egypt were planted with susceptible cultivars. In addition, a set of sorghum differentials QL-3, Tx430, SC170-6, CS3541, Tx7078, Tx2536, and 82BDM499 were planted in the most infested fields of the Agricultural Research Stations at Gemmeiza and Sakha and in some farmer fields at Abtouk. Experiments using the differentials were repeated in 1997, 1998, and 1999 to determine which pathotypes were present and to collect samples where specific pathotypes were identified.

Sixteen samples of diseased plant tissues were collected and DNA was isolated from each sample using the CTAB preparation method (16). *P. sorghi*-specific PCR primers were used to verify the identity of the causal agent of sorghum downy mildew in Egypt (30). All reagents for PCR except primers and deoxynucleotide triphosphates (dNTPs) were purchased from Promega. While dNTPs were purchased from USB, primers were custom made in the Advanced DNA Technology Laboratory in the Biology Department, Texas A&M University. A 20 µl PCR mixture was prepared to give final concentration as follows: 1X reaction buffer, 2.5 mM MgCl, 200 µM each deoxynucleotide triphosphates (dNTPs), and 0.2 µM each primer. Each reaction also contained 10 ng of template DNA, and 0.5 U of Taq DNA polymerase, and was overlaid with 20 µM of mineral oil. The mixtures were subject to PCR amplification in 0.5 mL tubes using a Perkin-Elmer Cetus DNA thermal cycler for 25 cycles. The temperatures and times used for PCR were as follows: in the first cycle, the mixture were denatured at 94 ^{o}C for 4 min, followed by 1 min at 37 ^{o}C for primer annealing, and 1 min at 72 ^{o}C for primer extension. The conditions for the following 24 cycles were the same

as the first, except the time for DNA denaturation was reduced to 1 min. The final extension time for PCR amplification was 7 min at 72 °C.

The sequences of *P. sorghi* species-specific primer sets, in 5`-3` direction, were as follows:

P. sorghi species-specific primers:

primer 1: GAATCATTTTTTATGATAAATTAATAACTA

primer 2: ACATTGTTTATGTAACTTTAATTTATGGTG

PCR products were subjected to electrophoresis in 0.7 "GIBCO-BRL" agarose gel prepared in 1X TAE gel buffer. Gels were stained by adding ethidium bromide to the melted gels to a final concentration of 2μg/ml before pouring gels into gel trays.

Inbred line evaluation. In 1998, 30 inbred lines were evaluated for resistance against *P. sorghi* at UPLB and Cotabato, Philippines (Table 1). The evaluation was conducted in three replications. Plots consisted of single rows, 0.7 m apart and 3m long. The percentage of individual plants with symptoms of sorghum downy mildew was determined 12 and 21 days after planting. The percentage of plants of each inbred infected by *P. sorghi* was the basis for subsequent analysis.

Mapping population. Two inbred maize lines were selected for this initial study; an inbred parent, SC-TEP5-19-1-3-1-4-1-1 (white, P3), which had been identified as being highly susceptible, and an inbred, P345C4S2B46-2-2-1-2-B-B-B (yellow, P2), that was highly resistant to *P. sorghi*. P3 and P2 were crossed to produce the F_1, which was self-pollinated to form a random set of 221 F_2 individuals (Appendix A). Tissue samples were collected from F_2 individual plants before they were self-pollinated to produce $F_{2:3}$ families which were challenged later by sorghum downy mildew to determine the phenotypic character for each family.

TABLE 1. List of inbred lines were evaluated for resistance against *P. sorghi*

No.	Pedigree	Origin
1	Pi21	Philippines
2	Pi31	Philippines
3	Nei9008	Tak Fa, Thailand
4	Nei9203	Tak Fa, Thailand
5	Nei9204	Tak Fa, Thailand
6	Ki3	KU, Thailand
7	Ki14	KU, Thailand
8	AMATLCOHS115-1-2-3-3-1-2-B-B	SW97D309-3
9	AMATLCOHS233-1-1-1-1-2-2-B-B-B	SW97L3004-10
10	P345C3S3B-40-8-1-1-2-2-B	SW97D309-48
11	AMATLCOHS9-1-1-1-1-1-2-B	SW97D308-6
12	AMATLCOHS245-1-1-1-2-2-2-B-B	SW97L3006-9,90
13	P345C4S2B46-2-2-1-2-B-B-B	SW98D1040-37
14	IPB9204-1-3-1-2-4-B	SW97D310-19
15	(24STE-5*24STE-17)-BBBB###-B-1-B-2-B-B-B	TF97R-86
16	(24STE-5*24STE-17)-BBBB###-B-5-B-4-B-B-B	TF97R-106
17	SIN.AM.TSR-76-1-1-B-1-BBBB-5-##-BBBBBBBBB	TF97R-220
18	P24(STE)C2-29-BBBB-#-3-BBBBBBB	TF97R-241
19	G26 C25 HS45-3-4-1-6-BBBB	TF9R-663
20	CML20	SW96L225-20
21	CML270	SW96L225-82
22	CML289	SW96L225-103
23	CML272	SW96L225-84
24	P8	Philippines
25	P12	Philippines
26	Pi23	Philippines
27	Pi27	Philippines
28	Pi35	Philippines

Sample collection and preparation for DNA isolation. Young leaves without necrotic areas or lesions were collected from F_2 individual plants grown in the field in addition to the parents. Tough thick midribs were removed from leaf samples, which were cut into 10 to 15 cm sections and placed in fiberglass screen mesh bags. Sample bags were transferred into ice chest with ice to be freeze dried immediately after being treated with liquid nitrogen. Frozen leaves were lyophilized for 72 hours using $\leq$ 100 microns Hg vacuum with the condenser temperature $\leq$ -60^{o}C. Dried tissue samples

were stored in sealed plastic bags at room temperature for a few days while grinding process took place. A mechanical mill (Tecator Cyclotec Sample Mill, Model 1093) was used for grinding. The fine powder obtained from each sample was stored in individual numbered plastic capped containers. Air tight vials were kept at -20^{o}C until DNA extraction. Sample number "3.106" was lost accidentally which reduced the total number of the population to 220 individuals (Appendix A).

DNA isolation. The CTAB preparation method for isolating genomic DNA described by Hoisington et al. (16) was used with some modifications. Initial sample weight was 375 to 450 mg of ground lyophilized tissue. "Option C" described in the protocol was used for DNA washes. The final volume of TE buffer used for dissolving DNA was 0.3 ml.

UV quantification of DNA. Using a "Beckman DU-65" spectrophotometer, 15 µl of each sample was used in an automated program to measure DNA concentration and calculate the TE volume needed to adjust the concentration of each DNA sample to 0.3 µg/µl as described by Hoisington et al. (16). Also, OD_{260} and OD_{280} readings were used automatically by the program to determine DNA purity.

DNA quality control. DNA quality control was an essential step for checking that the isolated DNA is of high molecular weight. For adequate resolution of RFLPs, native DNA should migrate as a tight band of molecular weight $\geq$ 40 Kb. However, degradation of part of the isolated DNA is inevitable, and the protocol was used is designed to run the DNA under optimal conditions for ascertaining the relative amounts of degraded and high molecular weight DNA.

The isolated DNA was verified to be of high molecular weight and to produce adequate resolution of RFLPs by running 100 ng of each tested DNA sample against Lambda DNA (λ) as a molecular weight marker in a 0.7% agarose gel as mentioned by Hoisington et al. (16). The procedure also allows

for verifying the UV quantification performed above. Because of the large number of samples used in this study, only 20 samples (Table 2) were randomly selected out of the 220 samples to run the DNA quality control test.

TABLE 2. List of the 20 selected samples for digestibility test

No.	Pedigree	No.	Pedigree	No.	Pedigree
1	(DMR P3 x P2)-3.2	77	(DMR P3 x P2)-3.138	159	(DMR P3 x P2)-4.100
29	(DMR P3 x P2)-3.48	89	(DMR P3 x P2)-3.155	166	(DMR P3 x P2)-4.114
39	(DMR P3 x P2)-3.65	100	(DMR P3 x P2)-4.11	178	(DMR P3 x P2)-4.131
47	(DMR P3 x P2)-3.78	114	(DMR P3 x P2)-4.29	187	(DMR P3 x P2)-4.144
55	(DMR P3 x P2)-3.87	122	(DMR P3 x P2)-4.40	197	(DMR P3 x P2)-4.157
62	(DMR P3 x P2)-3.99	135	(DMR P3 x P2)-4.58	214	(DMR P3 x P2)-4.183
74	(DMR P3 x P2)-3.131	148	(DMR P3 x P2)-4.78		

Gel staining. Throughout this study, a solution of 100 µl of 10 mg/ml ethidium bromide in 1000 ml dH_2O was used to stain RFLP gels for 20 minutes with gentle shaking. Gels were destained in dH_2O for 20 minutes before UV was used to view DNA. SSR gels were stained by adding ethidium bromide to the melted gels to a final concentration of 2µg/ml before pouring gels into gel trays.

Testing DNA digestibility. The DNA digestibility tests are essential before setting up large scale digestion experiments. Using the protocol described by Hoisington et al. (16) 2 µg of each of the 20 DNA samples, which were used previously for DNA quality control were tested for DNA digestibility using *Hin*dIII enzyme. A 0.7% agarose gel containing the 20 electrophoresed digested samples in addition to digested λ/*Hin*dIII DNA was visually examined on a UV transilluminator following electrophoresis.

Restriction digests of genomic DNA. 90 µg of DNA from each sample of the 220 samples was aliquoted into two labeled 1.5 ml tubes to be digested separately using two different enzymes, *Eco*RI and *Hin*dIII. The DNA restriction digest protocol used by Hoisington et al. (16) was adopted for this experiment with some modifications. Digested DNA was precipitated using

2.5 volumes of 100% ethanol. After discarding the supernatant, vacuum desiccation was used to evaporate EtOH and dry the samples. 140 µl of TE in addition to 30 µl of sample gel buffer (5X SGB) was used to dissolve samples overnight (16). Fourteen samples, seven for each enzyme, were selected randomly to ensure that digestion was carried out properly (Table 3).

TABLE 3. List of 14 samples, 7 for each enzyme, selected to confirm proper digestion

*Eco*RI		*Hin*dIII	
No.	**Pedigree**	**No.**	**Pedigree**
15	(DMR P3 x P2)-3.23	4	(DMR P3 x P2)-3.5
43	(DMR P3 x P2)-3.71	25	(DMR P3 x P2)-3.39
54	(DMR P3 x P2)-3.85	69	(DMR P3 x P2)-3.117
96	(DMR P3 x P2)-4.7	85	(DMR P3 x P2)-3.151
144	(DMR P3 x P2)-4.74	108	(DMR P3 x P2)-4.20
152	(DMR P3 x P2)-4.87	182	(DMR P3 x P2)-4.137
200	(DMR P3 x P2)-4.164	217	(DMR P3 x P2)-4.189

Preparation of end-labeled Lambda/*Hin*dIII DNA for gel electrophoresis. λ DNA, Gibco BRL λ DNA (Cat. # 25250-010), was digested using *Hin*dIII enzyme and labeled with Digoxigenin-dUTP (Digoxigenin-11dUTP, Boehringer Mannheim, Cat.# 1093088) according to Hoisington et. al. (16).

Digestion of ϕX DNA. ϕX DNA, GibcoBRL ϕX174 FR DNA (Cat. # 25260-027), was digested using *HAE*III enzyme by following the steps mentioned by Hoisington et al. (16).

Restriction digest enzymes. Several restriction endonuclease enzymes were used in this study either to digest DNA from F_2 individuals or to create DNA molecular weight markers. *Eco*RI (Cat. # 1175084), *Hin*dIII (Cat. # 0656321) and *HAE*III (Cat. # 0693944) were supplied by "Boehringer Mannheim GmbH – Germany".

Neutral agarose gel electrophoresis for parental screening. A Large gel, 24 x 20 cm was prepared using the Hoisington et al. protocol (16). It

consists of 0.7% “Seakem LE Agarose” in 1X TAE gel buffer. This agarose gel was used only for parental screening. This gel was formatted in 16 replicates of five lanes: the first two lanes contained DNA from parents digested by *Eco*RI, followed by two lanes containing parental DNA digested by *Hin*dIII, and the fifth lane contained end-labeled λ/*Hin*dIII DNA. After Southern blotting onto non-charged membrane, the membrane was cut into smaller membranes each containing the five lanes mentioned previously (Table 4).

TABLE 4. Gel and membrane format for RFLP parental screening

1	2	3	4	5
end-labeled λ/*Hin*dIII	SC TEP5/ *Eco*RI	P345/ *Eco*RI	SC TEP5/ *Hin*dIII	P345/ *Hin*dIII

Double thick neutral agarose gel electrophoresis. A double thick gel 24 x 20 cm was made of two layers of agarose poured consecutively into the same mold with the four combs in position. For this purpose, “Seakem LE Agarose” was used to prepare 0.7% agarose gels using 1X TAE gel buffer as described by Hoisington et al. (16). The 220 F_2 DNA samples were divided into a set of two membranes formatted as A and B. While format A contained the parents, 116 samples and end-labeled λ/*Hin*dIII DNA in the first and last lanes as a molecular weight marker (Table 5), the rest of the population, which is 104 samples, were contained in format B (Table 6). To produce 6 sets of membranes for each enzyme, 3 double thick gels for each format (A & B) were made per enzyme. After electrophoresis, the two layers were separated and thus yielded two separate, duplicate gels.

TABLE 5. Gel and membrane format A for RFLP

(DMR P3 x P2)-3.155	19	(DMR P3 x P2)-3.92	16	(DMR P3 x P2)-3.47	13	labeled λ/*Hin*dIII	1
(DMR P3 x P2)-3.159	29	(DMR P3 x P2)-3.93	26	(DMR P3 x P2)-3.48	23	SC TEP5	2
(DMR P3 x P2)-4.1	39	(DMR P3 x P2)-3.94	36	(DMR P3 x P2)-3.51	33	P345	3
(DMR P3 x P2)-4.2	49	(DMR P3 x P2)-3.96	46	(DMR P3 x P2)-3.53	43	(DMR P3 x P2)-3.2	4
(DMR P3 x P2)-4.3	59	(DMR P3 x P2)-3.99	56	(DMR P3 x P2)-3.54	53	(DMR P3 x P2)-3.3	5
(DMR P3 x P2)-4.4	69	(DMR P3 x P2)-3.102	66	(DMR P3 x P2)-3.55	63	(DMR P3 x P2)-3.4	6
(DMR P3 x P2)-4.6	79	(DMR P3 x P2)-3.103	76	(DMR P3 x P2)-3.56	73	(DMR P3 x P2)-3.5	7
(DMR P3 x P2)-4.7	89	(DMR P3 x P2)-3.107	86	(DMR P3 x P2)-3.57	83	(DMR P3 x P2)-3.6	8
(DMR P3 x P2)-4.8	99	(DMR P3 x P2)-3.112	96	(DMR P3 x P2)-3.62	93	(DMR P3 x P2)-3.7	9
(DMR P3 x P2)-4.9	001	(DMR P3 x P2)-3.114	07	(DMR P3 x P2)-3.63	04	(DMR P3 x P2)-3.8	01
(DMR P3 x P2)-4.10	101	(DMR P3 x P2)-3.117	17	(DMR P3 x P2)-3.64	14	(DMR P3 x P2)-3.10	11
(DMR P3 x P2)-4.11	201	(DMR P3 x P2)-3.118	27	(DMR P3 x P2)-3.65	24	(DMR P3 x P2)-3.11	21
(DMR P3 x P2)-4.12	301	(DMR P3 x P2)-3.125	37	(DMR P3 x P2)-3.67	34	(DMR P3 x P2)-3.12	31
(DMR P3 x P2)-4.13	401	(DMR P3 x P2)-3.128	47	(DMR P3 x P2)-3.68	44	(DMR P3 x P2)-3.14	41
(DMR P3 x P2)-4.15	501	(DMR P3 x P2)-3.129	57	(DMR P3 x P2)-3.69	54	(DMR P3 x P2)-3.15	51
(DMR P3 x P2)-4.16	601	(DMR P3 x P2)-3.131	67	(DMR P3 x P2)-3.71	64	(DMR P3 x P2)-3.19	61
(DMR P3 x P2)-4.17	701	(DMR P3 x P2)-3.107	77	(DMR P3 x P2)-3.74	74	(DMR P3 x P2)-3.20	71
(DMR P3 x P2)-4.18	801	(DMR P3 x P2)-3.112	87	(DMR P3 x P2)-3.76	84	(DMR P3 x P2)-3.23	81
(DMR P3 x P2)-4.19	901	(DMR P3 x P2)-3.114	97	(DMR P3 x P2)-3.77	94	(DMR P3 x P2)-3.25	91
(DMR P3 x P2)-4.20	011	(DMR P3 x P2)-3.117	08	(DMR P3 x P2)-3.78	05	(DMR P3 x P2)-3.28	02
(DMR P3 x P2)-4.21	111	(DMR P3 x P2)-3.118	18	(DMR P3 x P2)-3.79	15	(DMR P3 x P2)-3.30	12
(DMR P3 x P2)-4.22	211	(DMR P3 x P2)-3.125	28	(DMR P3 x P2)-3.80	25	(DMR P3 x P2)-3.32	22
(DMR P3 x P2)-4.24	311	(DMR P3 x P2)-3.132	38	(DMR P3 x P2)-3.81	35	(DMR P3 x P2)-3.33	32
(DMR P3 x P2)-4.27	411	(DMR P3 x P2)-3.137	48	(DMR P3 x P2)-3.82	45	(DMR P3 x P2)-3.34	42
(DMR P3 x P2)-4.28	511	(DMR P3 x P2)-3.138	58	(DMR P3 x P2)-3.83	55	(DMR P3 x P2)-3.36	52
(DMR P3 x P2)-4.29	611	(DMR P3 x P2)-3.139	68	(DMR P3 x P2)-3.84	65	(DMR P3 x P2)-3.37	62
(DMR P3 x P2)-4.30	711	(DMR P3 x P2)-3.140	78	(DMR P3 x P2)-3.85	75	(DMR P3 x P2)-3.38	72
(DMR P3 x P2)-4.32	811	(DMR P3 x P2)-3.142	88	(DMR P3 x P2)-3.87	85	(DMR P3 x P2)-3.39	82
(DMR P3 x P2)-4.33	911	(DMR P3 x P2)-3.144	98	(DMR P3 x P2)-3.89	95	(DMR P3 x P2)-3.41	92
labeled λ/*Hin*dIII	021	(DMR P3 x P2)-3.145	09	(DMR P3 x P2)-3.91	06	(DMR P3 x P2)-3.42	03

TABLE 6. Gel and membrane format B for RFLP

(DMR P3 x P2)-4.171	19	(DMR P3 x P2)-4.126	16	(DMR P3 x P2)-4.75	13	labeled λ/*Hin*dIII	1
(DMR P3 x P2)-4.172	29	(DMR P3 x P2)-4.127	26	(DMR P3 x P2)-4.76	23	SC TEP5	2
(DMR P3 x P2)-4.173	39	(DMR P3 x P2)-4.129	36	(DMR P3 x P2)-4.77	33	P345	3
(DMR P3 x P2)-4.174	49	(DMR P3 x P2)-4.131	46	(DMR P3 x P2)-4.78	43	(DMR P3 x P2)-4.34	4
(DMR P3 x P2)-4.176	59	(DMR P3 x P2)-4.132	56	(DMR P3 x P2)-4.81	53	(DMR P3 x P2)-4.36	5
(DMR P3 x P2)-4.178	69	(DMR P3 x P2)-4.133	66	(DMR P3 x P2)-4.84	63	(DMR P3 x P2)-4.38	6
(DMR P3 x P2)-4.179	79	(DMR P3 x P2)-4.135	76	(DMR P3 x P2)-4.85	73	(DMR P3 x P2)-4.39	7
(DMR P3 x P2)-4.180	89	(DMR P3 x P2)-4.137	86	(DMR P3 x P2)-4.87	83	(DMR P3 x P2)-4.40	8
(DMR P3 x P2)-4.181	99	(DMR P3 x P2)-4.138	96	(DMR P3 x P2)-4.88	93	(DMR P3 x P2)-4.41	9
(DMR P3 x P2)-4.183	001	(DMR P3 x P2)-4.139	07	(DMR P3 x P2)-4.89	04	(DMR P3 x P2)-4.42	011
(DMR P3 x P2)-4.184	101	(DMR P3 x P2)-4.141	17	(DMR P3 x P2)-4.90	14	(DMR P3 x P2)-4.43	111
(DMR P3 x P2)-4.188	201	(DMR P3 x P2)-4.142	27	(DMR P3 x P2)-4.93	24	(DMR P3 x P2)-4.44	211
(DMR P3 x P2)-4.189	301	(DMR P3 x P2)-4.144	37	(DMR P3 x P2)-4.97	34	(DMR P3 x P2)-4.45	311
(DMR P3 x P2)-4.191	401	(DMR P3 x P2)-4.146	47	(DMR P3 x P2)-4.99	44	(DMR P3 x P2)-4.47	411
(DMR P3 x P2)-4.192	501	(DMR P3 x P2)-4.147	57	(DMR P3 x P2)-4.100	54	(DMR P3 x P2)-4.48	511
(DMR P3 x P2)-4.193	601	(DMR P3 x P2)-4.149	67	(DMR P3 x P2)-4.102	64	(DMR P3 x P2)-4.52	611
(DMR P3 x P2)-4.194	701	(DMR P3 x P2)-4.150	77	(DMR P3 x P2)-4.104	74	(DMR P3 x P2)-4.54	711
labeled λ/*Hin*dIII	801	(DMR P3 x P2)-4.151	87	(DMR P3 x P2)-4.106	84	(DMR P3 x P2)-4.55	811
	901	(DMR P3 x P2)-4.152	97	(DMR P3 x P2)-4.108	94	(DMR P3 x P2)-4.56	911
	011	(DMR P3 x P2)-4.153	08	(DMR P3 x P2)-4.110	05	(DMR P3 x P2)-4.57	022
	111	(DMR P3 x P2)-4.155	18	(DMR P3 x P2)-4.112	15	(DMR P3 x P2)-4.58	122
	211	(DMR P3 x P2)-4.156	28	(DMR P3 x P2)-4.114	25	(DMR P3 x P2)-4.59	222
	311	(DMR P3 x P2)-4.157	38	(DMR P3 x P2)-4.115	35	(DMR P3 x P2)-4.60	322
	411	(DMR P3 x P2)-4.158	48	(DMR P3 x P2)-4.116	45	(DMR P3 x P2)-4.61	422
	511	(DMR P3 x P2)-4.161	58	(DMR P3 x P2)-4.117	55	(DMR P3 x P2)-4.64	522
	611	(DMR P3 x P2)-4.164	68	(DMR P3 x P2)-4.118	65	(DMR P3 x P2)-4.66	622
	711	(DMR P3 x P2)-4.165	78	(DMR P3 x P2)-4.119	75	(DMR P3 x P2)-4.70	722
	811	(DMR P3 x P2)-4.166	88	(DMR P3 x P2)-4.120	85	(DMR P3 x P2)-4.71	822
	911	(DMR P3 x P2)-4.167	98	(DMR P3 x P2)-4.122	95	(DMR P3 x P2)-4.72	922
	021	(DMR P3 x P2)-4.168	09	(DMR P3 x P2)-4.125	06	(DMR P3 x P2)-4.74	033

Southern blotting onto non-charged membranes. The matrixes used were MSI Magnagraph Nylon membranes, non-charged, 0.45 μm pore size, 20 cm x 10 m rolls sold as "Gibco BRL's Biodyne" (Cat. # 10134-013). Construction of a wet blot transfer system and transferring the digested DNA into the membranes were done according to Hoisington et al. protocol (16). Membranes were cross-linked in a "Stratagene UV Crosslinker" using auto setting 120,000 μjoules/cm^2.

RFLP markers. RFLP probes from Brookhaven National Laboratory (bnl) and the University of Missouri at Columbia (umc) were used to detect polymorphism between parental lines and F_2 individuals. The protocol established by Hoisington et al. (16) was adopted for the PCR amplification of inserts from bacterial cultures and labeling the RFLP probes with Digoxigenin-dUTP.

Parental screening using RFLP probes. Parent lines were screened for polymorphism using 160 RFLP markers (Appendix B).

Hybridization and detection of Dig-labeled probes. DNA membranes were hybridized with 60 Dig-labeled RFLP probes using protocols that have been optimized by Hoisington et al. (16) for hybridization in siliconized glass bottles provided by "Robbins Scientific Corp.". Some modifications were applied to these protocols. After hybridizing the membrane with HYB solution that contained the labeled probe, membranes were washed in a solution mix of 0.15X SSC and 0.1% SDS two times each 5 minutes at 54 ^oC. These protocols also were followed for the removal of probe for reuse of membranes. Each one of the 6 sets of membranes for both *Eco*RI and *Hin*dIII were hybridized five times using 5 different RFLP probe (Tables 7 and 8).

TABLE 7. List of RFLP probes used to screen *Eco*RI membranes

No.	Probe ID	No.	Probe ID	No.	Probe ID
1	umc167	11	umc21	21	umc105
2	npi287	12	umc44	22	umc109
3	umc6	13	csu93	23	umc149
4	umc67	14	umc128	24	umc59
5	umc177	15	umc39	25	umc83
6	umc150	16	npi290	26	npi110
7	umc55	17	umc19	27	umc157
8	umc36	18	csu154	28	csu173
9	umc65	19	npi249	29	bnl5.71
10	umc130	20	umc133	30	umc113

TABLE 8. List of RFLP probes used to screen *Hin*dIII membranes

No.	Probe ID	No.	Probe ID	No.	Probe ID
1	csu61	11	csu25	21	umc48
2	csu148	12	umc87	22	umc29
3	umc34	13	umc147	23	bnl6.23
4	umc1860	14	umc104	24	umc156
5	umc68	15	csu155	25	umc10
6	npi277	16	umc81	26	csu54
7	umc107	17	npi232	27	umc154
8	npi238	18	bnl8.17	28	npi285
9	umc32	19	bnl8.23	29	umc132
10	umc17	20	umc168	30	csu86

SSR protocols. A DNA Engine Tetrad thermal Peltier cycler produced by "M J Research, Inc." was used throughout the parental screening, while a 96-Well GeneAmp® PCR System 9700" Silver-plated was used for detecting the polymorphism between the F_2 individuals. All reagents for PCR except primers and deoxynucleotide triphosphates (dNTPs) were purchased from Promega. While dNTPs were purchased from USB, SSR primers were obtained from GenRes except those which were not available were custom made in the Advanced DNA Technology Laboratory in the Biology Department, Texas A&M University. Following the protocol by Hoisington et al. (16) with some modifications, a 15 µl PCR mixture was prepared to give final concentration as follows: 1X reaction buffer, 2.5 mM MgCl, 200 µM

each deoxynucleotide triphosphates (dNTPs), 0.3 µM each primer. Each reaction also contained 40 ng of template DNA, 10% Glycerol, and 1 U of Taq DNA polymerase, and was overlaid with 15 µM of mineral oil. For parental screening Concord™ 96-well Polycarbonate Microplates by "M J Research" were used, while for testing the F_2 population Low-Profile Multiplate Unskirted Microplates were used. Plates loaded with mixtures were subject to PCR amplification for 30 cycles. The temperatures and times used for PCR were as follows: in the first cycle, the mixtures were denatured at 94 ^{o}C for 3 min, followed by 2 min at 56 ^{o}C for primer annealing, and 2 min at 72 ^{o}C for primer extension. The conditions for the following 29 cycles were the same as the first, except the time for DNA denaturation was reduced to 1 min. The final extension time for PCR amplification was 5 min at 72 ^{o}C. Three µl of 5X SGB were added to each amplified sample.

Parental screening for SSRs. Altogether, 496 SSR primer pairs were used to screen the parent lines for polymorphism (Appendix C). Those pairs which identified polymorphisms were confirmed by testing them again with DNA from the parents in addition to the first 22 individuals of the F_2 population (Table 10).

SSR markers. Ninety nine SSR markers were used to detect the polymorphism between the F_2 individuals (Table 9).

Agarose gel preparation for SSR. A 4% large agarose gel, 20 X 28 cm, was prepared by melting 11.2 g SFR agarose (Amresco, Cat # J234) in 280 ml of 1X TAE. Ethidium bromide was added to the melted agarose to a final concentration of 2µg/ml before pouring gels into gel trays. Three gel formats were used to contain the 220 F_2 individuals in addition to the parent lines and the molecular weight marker ϕX174/*HAE*III (Tables 10, 11 and 12).

TABLE 9. List of SSR primers used to screen F_2 individuals for polymorphism

No.	SSR ID	No.	SSR ID	No.	SSR ID	No.	SSR ID
1	bnlg149	26	bnlg1647	51	bnlg1711	76	bnlg1025
2	bnlg1124	27	umc1030	52	bnlg1885	77	bnlg1347
3	umc1071	28	bnlg1035	53	bnlg2305	78	bnlg162
4	bnlg1007	29	bnlg1117	54	bnlg249	79	bnlg1782
5	bnlg1953	30	bnlg1505	55	bnlg1538	80	bnlg1812
6	bnlg1016	31	phi073	56	bnlg1867	81	bnlg1031
7	bnlg1811	32	bnlg1350	57	bnlg2097	82	bnlg1056
8	bnlg1598	33	bnlg1182	58	umc1018	83	phi080
9	dupssr12	34	umc1008	59	nc013	84	bnlg1724
10	mmc0041	35	nc005	60	bnlg345	85	phi068
11	bnlg2123	36	phi026	61	bnlg1521	86	bnlg1401
12	bnlg131	37	umc1031	62	bnlg1740	87	umc1078
13	bnlg1092	38	bnlg1927	63	bnlg1759	88	phi061
14	bnlg1621	39	mmc0321	64	umc1063	89	bnlg1375
15	umc1026	40	umc1051	65	mmc0171	90	bnlg1525
16	bnlg1831	41	bnlg1565	66	umc1066	91	phi118
17	bnlg1893	42	bnlg589	67	bnlg657	92	bnlg1450
18	bnlg2328	43	bnlg1208	68	bnlg1094	93	bnlg2190
19	umc1065	44	bnlg1879	69	umc1001	94	bnlg1720
20	umc1080	45	bnlg2323	70	bnlg155	95	bnlg125
21	bnlg1606	46	bnlg609	71	bnlg1666	96	umc1419
22	bnlg1662	47	umc1019	72	dupssr13	97	umc1265
23	bnlg1721	48	bnlg118	73	phi082	98	umc1407
24	bnlg1144	49	bnlg1306	74	umc1075	99	umc1695
25	bnlg1638	50	bnlg1346	75	bnlg1863		

TABLE 10. Gel format SSR-22 used for confirming the polymorphism between parent using SSR markers in addition to testing the polymorphism pattern in the first 22 individuals of the F_2 population

ϕX174/*HAE*III	97	ϕX174/*HAE*III	35	ϕX174/*HAE*III	72	ϕX174/*HAE*III	1
SC TEP5	08	SC TEP5	45	SC TEP5	82	SC TEP5	2
P345	18	P345	55	P345	92	P345	3
(DMR P3 x P2)-3.2	28	(DMR P3 x P2)-3.2	65	(DMR P3 x P2)-3.2	03	(DMR P3 x P2)-3.2	4
(DMR P3 x P2)-3.3	38	(DMR P3 x P2)-3.3	75	(DMR P3 x P2)-3.3	13	(DMR P3 x P2)-3.3	5
(DMR P3 x P2)-3.4	48	(DMR P3 x P2)-3.4	85	(DMR P3 x P2)-3.4	23	(DMR P3 x P2)-3.4	6
(DMR P3 x P2)-3.5	58	(DMR P3 x P2)-3.5	95	(DMR P3 x P2)-3.5	33	(DMR P3 x P2)-3.5	7
(DMR P3 x P2)-3.6	68	(DMR P3 x P2)-3.6	06	(DMR P3 x P2)-3.6	43	(DMR P3 x P2)-3.6	8
(DMR P3 x P2)-3.7	78	(DMR P3 x P2)-3.7	16	(DMR P3 x P2)-3.7	53	(DMR P3 x P2)-3.7	9
(DMR P3 x P2)-3.8	88	(DMR P3 x P2)-3.8	26	(DMR P3 x P2)-3.8	63	(DMR P3 x P2)-3.8	01
(DMR P3 x P2)-3.10	98	(DMR P3 x P2)-3.10	36	(DMR P3 x P2)-3.10	73	(DMR P3 x P2)-3.10	11
(DMR P3 x P2)-3.11	09	(DMR P3 x P2)-3.11	46	(DMR P3 x P2)-3.11	83	(DMR P3 x P2)-3.11	21
(DMR P3 x P2)-3.12	19	(DMR P3 x P2)-3.12	56	(DMR P3 x P2)-3.12	93	(DMR P3 x P2)-3.12	31
(DMR P3 x P2)-3.14	29	(DMR P3 x P2)-3.14	66	(DMR P3 x P2)-3.14	04	(DMR P3 x P2)-3.14	41
(DMR P3 x P2)-3.15	39	(DMR P3 x P2)-3.15	76	(DMR P3 x P2)-3.15	14	(DMR P3 x P2)-3.15	51
(DMR P3 x P2)-3.19	49	(DMR P3 x P2)-3.19	86	(DMR P3 x P2)-3.19	24	(DMR P3 x P2)-3.19	61
(DMR P3 x P2)-3.20	59	(DMR P3 x P2)-3.20	96	(DMR P3 x P2)-3.20	34	(DMR P3 x P2)-3.20	71
(DMR P3 x P2)-3.23	69	(DMR P3 x P2)-3.23	07	(DMR P3 x P2)-3.23	44	(DMR P3 x P2)-3.23	81
(DMR P3 x P2)-3.25	79	(DMR P3 x P2)-3.25	17	(DMR P3 x P2)-3.25	54	(DMR P3 x P2)-3.25	91
(DMR P3 x P2)-3.28	89	(DMR P3 x P2)-3.28	27	(DMR P3 x P2)-3.28	64	(DMR P3 x P2)-3.28	02
(DMR P3 x P2)-3.30	99	(DMR P3 x P2)-3.30	37	(DMR P3 x P2)-3.30	74	(DMR P3 x P2)-3.30	12
(DMR P3 x P2)-3.32	001	(DMR P3 x P2)-3.32	47	(DMR P3 x P2)-3.32	84	(DMR P3 x P2)-3.32	22
(DMR P3 x P2)-3.33	101	(DMR P3 x P2)-3.33	57	(DMR P3 x P2)-3.33	94	(DMR P3 x P2)-3.33	32
(DMR P3 x P2)-3.36	201	(DMR P3 x P2)-3.36	67	(DMR P3 x P2)-3.36	05	(DMR P3 x P2)-3.36	42
(DMR P3 x P2)-3.38	301	(DMR P3 x P2)-3.38	77	(DMR P3 x P2)-3.38	15	(DMR P3 x P2)-3.38	52
ϕX174/*HAE*III	401	ϕX174/*HAE*III	87	ϕX174/*HAE*III	25	ϕX174/*HAE*III	62

TABLE 11. Gel format SSR-A used for SSR markers

ϕX174/*HAE*III	96	ϕX174/*HAE*III	33	ϕX174/*HAE*III	1
(DMR P3 x P2)-3.159	70	(DMR P3 x P2)-3.87	63	SC TEP5	2
(DMR P3 x P2)-4.1	71	(DMR P3 x P2)-3.89	73	P345	3
(DMR P3 x P2)-4.2	72	(DMR P3 x P2)-3.91	83	(DMR P3 x P2)-3.38	4
(DMR P3 x P2)-4.4	73	(DMR P3 x P2)-3.92	93	(DMR P3 x P2)-3.39	5
(DMR P3 x P2)-4.6	74	(DMR P3 x P2)-3.93	04	(DMR P3 x P2)-3.41	6
(DMR P3 x P2)-4.7	75	(DMR P3 x P2)-3.94	14	(DMR P3 x P2)-3.42	7
(DMR P3 x P2)-4.8	76	(DMR P3 x P2)-3.99	24	(DMR P3 x P2)-3.47	8
(DMR P3 x P2)-4.9	77	(DMR P3 x P2)-3.102	34	(DMR P3 x P2)-3.48	9
(DMR P3 x P2)-4.10	78	(DMR P3 x P2)-3.103	44	(DMR P3 x P2)-3.51	01
(DMR P3 x P2)-4.11	79	(DMR P3 x P2)-3.107	54	(DMR P3 x P2)-3.53	11
(DMR P3 x P2)-4.12	80	(DMR P3 x P2)-3.112	64	(DMR P3 x P2)-3.54	21
(DMR P3 x P2)-4.13	81	(DMR P3 x P2)-3.114	74	(DMR P3 x P2)-3.55	31
(DMR P3 x P2)-4.15	82	(DMR P3 x P2)-3.117	84	(DMR P3 x P2)-3.56	41
(DMR P3 x P2)-4.16	83	(DMR P3 x P2)-3.118	94	(DMR P3 x P2)-3.57	51
(DMR P3 x P2)-4.17	84	(DMR P3 x P2)-3.125	05	(DMR P3 x P2)-3.62	61
(DMR P3 x P2)-4.18	85	(DMR P3 x P2)-3.128	15	(DMR P3 x P2)-3.64	71
(DMR P3 x P2)-4.19	86	(DMR P3 x P2)-3.129	25	(DMR P3 x P2)-3.65	81
(DMR P3 x P2)-4.20	87	(DMR P3 x P2)-3.131	35	(DMR P3 x P2)-3.67	91
(DMR P3 x P2)-4.21	88	(DMR P3 x P2)-3.132	45	(DMR P3 x P2)-3.68	02
(DMR P3 x P2)-4.22	89	(DMR P3 x P2)-3.137	55	(DMR P3 x P2)-3.69	12
(DMR P3 x P2)-4.24	90	(DMR P3 x P2)-3.138	65	(DMR P3 x P2)-3.71	22
(DMR P3 x P2)-4.27	91	(DMR P3 x P2)-3.139	75	(DMR P3 x P2)-3.74	32
(DMR P3 x P2)-4.28	92	(DMR P3 x P2)-3.140	85	(DMR P3 x P2)-3.76	42
(DMR P3 x P2)-4.29	93	(DMR P3 x P2)-3.142	95	(DMR P3 x P2)-3.77	52
(DMR P3 x P2)-4.30	94	(DMR P3 x P2)-3.144	06	(DMR P3 x P2)-3.78	62
(DMR P3 x P2)-4.32	95	(DMR P3 x P2)-3.145	16	(DMR P3 x P2)-3.79	72
(DMR P3 x P2)-4.33	96	(DMR P3 x P2)-3.146	26	(DMR P3 x P2)-3.80	82
(DMR P3 x P2)-4.34	97	(DMR P3 x P2)-3.148	36	(DMR P3 x P2)-3.81	92
(DMR P3 x P2)-4.36	98	(DMR P3 x P2)-3.151	46	(DMR P3 x P2)-3.82	03
(DMR P3 x P2)-4.38	99	(DMR P3 x P2)-3.152	56	(DMR P3 x P2)-3.83	13
(DMR P3 x P2)-4.39	100	(DMR P3 x P2)-3.153	66	(DMR P3 x P2)-3.84	23
(DMR P3 x P2)-4.40	101	(DMR P3 x P2)-3.155	76	(DMR P3 x P2)-3.85	33
ϕX174/*HAE*III	102	ϕX174/*HAE*III	86	ϕX174/*HAE*III	43

TABLE 12. Gel format SSR-B used for SSR markers

ϕX174/*HAE*III	96	ϕX174/*HAE*III	53	ϕX174/*HAE*III	1
(DMR P3 x P2)-4.146	97	(DMR P3 x P2)-4.90	63	SC TEP5	2
(DMR P3 x P2)-4.147	107	(DMR P3 x P2)-4.93	73	P345	3
(DMR P3 x P2)-4.149	127	(DMR P3 x P2)-4.97	83	(DMR P3 x P2)-4.41	4
(DMR P3 x P2)-4.150	137	(DMR P3 x P2)-4.99	93	(DMR P3 x P2)-4.42	5
(DMR P3 x P2)-4.151	147	(DMR P3 x P2)-4.100	104	(DMR P3 x P2)-4.43	6
(DMR P3 x P2)-4.152	157	(DMR P3 x P2)-4.102	114	(DMR P3 x P2)-4.44	7
(DMR P3 x P2)-4.155	167	(DMR P3 x P2)-4.104	124	(DMR P3 x P2)-4.45	8
(DMR P3 x P2)-4.156	177	(DMR P3 x P2)-4.108	134	(DMR P3 x P2)-4.47	9
(DMR P3 x P2)-4.157	187	(DMR P3 x P2)-4.110	144	(DMR P3 x P2)-4.48	101
(DMR P3 x P2)-4.158	197	(DMR P3 x P2)-4.112	154	(DMR P3 x P2)-4.54	111
(DMR P3 x P2)-4.161	208	(DMR P3 x P2)-4.114	164	(DMR P3 x P2)-4.55	121
(DMR P3 x P2)-4.164	218	(DMR P3 x P2)-4.115	174	(DMR P3 x P2)-4.56	131
(DMR P3 x P2)-4.165	228	(DMR P3 x P2)-4.116	184	(DMR P3 x P2)-4.57	141
(DMR P3 x P2)-4.166	238	(DMR P3 x P2)-4.117	194	(DMR P3 x P2)-4.58	151
(DMR P3 x P2)-4.167	248	(DMR P3 x P2)-4.118	205	(DMR P3 x P2)-4.59	161
(DMR P3 x P2)-4.168	258	(DMR P3 x P2)-4.119	215	(DMR P3 x P2)-4.60	171
(DMR P3 x P2)-4.171	268	(DMR P3 x P2)-4.120	225	(DMR P3 x P2)-4.61	181
(DMR P3 x P2)-4.172	278	(DMR P3 x P2)-4.122	235	(DMR P3 x P2)-4.64	191
(DMR P3 x P2)-4.173	288	(DMR P3 x P2)-4.125	245	(DMR P3 x P2)-4.66	202
(DMR P3 x P2)-4.174	298	(DMR P3 x P2)-4.126	255	(DMR P3 x P2)-4.70	212
(DMR P3 x P2)-4.176	309	(DMR P3 x P2)-4.127	265	(DMR P3 x P2)-4.71	222
(DMR P3 x P2)-4.178	319	(DMR P3 x P2)-4.129	275	(DMR P3 x P2)-4.72	232
(DMR P3 x P2)-4.179	329	(DMR P3 x P2)-4.131	285	(DMR P3 x P2)-4.74	242
(DMR P3 x P2)-4.180	339	(DMR P3 x P2)-4.132	295	(DMR P3 x P2)-4.75	252
(DMR P3 x P2)-4.181	349	(DMR P3 x P2)-4.133	306	(DMR P3 x P2)-4.77	262
(DMR P3 x P2)-4.183	359	(DMR P3 x P2)-4.135	316	(DMR P3 x P2)-4.78	272
(DMR P3 x P2)-4.184	369	(DMR P3 x P2)-4.137	326	(DMR P3 x P2)-4.81	282
(DMR P3 x P2)-4.188	379	(DMR P3 x P2)-4.138	336	(DMR P3 x P2)-4.84	292
(DMR P3 x P2)-4.189	389	(DMR P3 x P2)-4.139	346	(DMR P3 x P2)-4.85	303
(DMR P3 x P2)-4.191	399	(DMR P3 x P2)-4.141	356	(DMR P3 x P2)-4.87	313
(DMR P3 x P2)-4.192	4010	(DMR P3 x P2)-4.142	366	(DMR P3 x P2)-4.88	323
(DMR P3 x P2)-4.193	4111	(DMR P3 x P2)-4.144	376	(DMR P3 x P2)-4.89	333
ϕX174/*HAE*III	4212	ϕX174/*HAE*III	386	ϕX174/*HAE*III	343

Marker analysis. The polymorphism detected by either RFLP or SSR marker was scored as follows:

A homozygous maternal genotype

B homozygous paternal genotype

H heterozygote genotype

C paternal genotype when that phenotype is dominant; the F_2 is either heterozygous or homozygous paternal

D maternal genotype when that phenotype is dominant; the F_2 is either heterozygous or homozygous maternal

\- unknown

The program "Map Manager QTX" by Manly et. al. (21) was used to establish linked marker groups and to create a genetic map. Distances between markers are presented in centiMorgans (cM) derived using the Kosambi function (17) with linkage criterion $P<0.00001$.

Field trials. Seed from the self-pollinated 221 F_2 individual plants, together with the two parental lines and two lines related to the two parents, were challenged with *P. sorghi*, the pathogen that causes sorghum downy mildew disease. The evaluation was conducted in four locations including two sites in Thailand, one site at Gemmeiza, Egypt, and one site in Corpus Christi, Texas. The field experimental design in both sits of Thailand and Egypt was randomized block design, of single row plots in three replications. Each row was sown with about 20 seed at a within-row spacing of 0.25 m in 6 m long rows spaced 0.75 m apart. Each replicate was partitioned to 15 blocks and each block contained 15 rows. Because of the limitation of seed quantity the Corpus Christi location was planted in one replication. Disease nurseries were established by planting a highly susceptible sorghum variety as disease spreader in every third row throughout the field at least three weeks prior to the expected date of planting of the tested materials. In Corpus Christi, 20 to 30 seed from each F_2 were planted between rows of infected sorghum. All

materials were subject to natural infection that is dispersed from naturally infected spreaders. Percentage of infected plants was scored three weeks after planting. In Corpus Christi, both local and systemic infection were scored as the percentage of plants showing the respective type of symptoms separately, then the total percentage of infection was scored based on the presence of both of the symptom types. At both Corpus Christi, Texas, and Gemmeiza, Egypt *P. sorghi* Pathotype 1 is predominant, while in Thailand *P. sorghi* Thai strain, which was suggested by Yao (28) to be renamed *P. zeae* is predominant.

Greenhouse trials. In addition to the field evaluation $F_{2:3}$ families were tested for susceptibility in the greenhouse of the Plant Pathology Department, Texas A&M University at College Station. The greenhouse trial was conducted in three replications. Each replication consisted of nine trays. Using 2 1/4" Jiffy Strips, each tray contained twenty five $F_{2:3}$ families in addition to three control pots of sweet corn "Golden Bantam". Each pot was sown with 5 seed on average. Pathotype 3 of *P. sorghi* was used to evaluate $F_{2:3}$ families in the greenhouse. Test trays were inoculated at 6 days after emergence with a conidial suspension adjusted to approximately 1X 10^5/ml H_2O, and applied at a rate equivalent to approximately 1 ml per plant using an atomizer. Conidial suspension was prepared daily as described by Cardwell et. al. (6). Because of the limitation of space in the growth chamber and the inability to prepare 5.4 liter of inoculum to spray all material at once, only two trays were sprayed per day. Percentage of infected plants in each $F_{2:3}$ family was scored 7 and 14 days after inoculation, for local and systemic infections, respectively.

Statistical analysis. The phenotypic data from both field and greenhouse trials were recorded as the percentage of plants showing sorghum downy mildew infection. The percentages covered a wide rang of values between zero and one hundred. Such data generally have what is called a "binomial

distribution" rather than a normal distribution, which causes the variance to be related to the means but in quite a different way. The arcsine transformation is the appropriate transformation recommended by Little and Hills for this type of data (20). This transformation was expected to make the means and variances independent and normally distributed. For field and greenhouse data, analyses of variance were conducted on transformed phenotypic data for individual environments using PROC GLM, SAS Institutes. Analysis of variance was conducted on transformed values of sweet corn controls across all trays used in the greenhouse evaluations to test if there was any significant difference between trays and to detect bias resulting from daily inoculum preparation.

Bartlett's test was used to test for homogeneity between environments before combining data (12). Components of variance for the $F_{2:3}$ families in all locations and across field locations were computed considering all effects (locations, replicates and $F_{2:3}$ families) as random in the statistical model. Transformed entry means were used to compute the combined analyses of variance and covariance across environments as described by Bohn et. al. (3). Estimates of variance components σ^2 (error variance), σ^2_{ge} (genotype-by-environment (G x E) interaction variance), and σ^2_g (genotypic variance) of $F_{2:3}$ families were calculated as described by Searle (24). Heritability (H^2) on a $F_{2:3}$ family transformed mean basis was estimated as described by Hallauer and Miranda (14) where r = number of replications and e = number of environments.

$$H^2 = \frac{\sigma^2 g}{\frac{\sigma^2}{re} + \frac{\sigma^2 ge}{e} + \sigma^2 g}$$

QTL analysis. The analysis of QTLs was performed on the means of $F_{2:3}$ family replicates for the arcsine transformed data within each trial as well as across trials. Means were subtracted from 100 to get means of resistance

percentage for each $F_{2:3}$ family. The program "Map Manager QTXb17" for Windows™ (21) was used to detect significant association between segregating markers and sorghum downy mildew resistance as a quantitative trait using a threshold of $P<0.00001$. Duplicated and very close markers were eliminated before mapping of the QTLs to avoid regression failure.

The "marker regression option" was used to identify all loci associated with sorghum downy mildew as a quantitative trait, which provided also the likelihood ratio statistic (LRS) and P value for the association in addition to confidence intervals and separate regression coefficients for additive and dominance effects. LRS is a measure of the significance of a possible QTL described by Haley and Knott (13). This LRS can be interpreted as a χ^2 statistic or as a LOD score, but the LOD differs from conventional base-10 LOD scores by a factor of 4.6. The likelihood ratio statistic needed for significance is about 20 for an F_2 cross (18).

The interval mapping procedure was used to fit a regression equation for the effect of a hypothetical QTL at the position of each marker locus and at regular intervals between the marker loci. This procedure is based on the work of Haley & Knott (13), Martinez & Curnow (22), and Zeng (32, 33). This procedure also provided the resulting regression coefficient(s) and a likelihood ratio statistic (LRS) that measured the significance of the coefficient(s). Because the population is an intercross population, QTX fitted coefficients for both additive and dominance effects.

The Permutation test described by Churchill and Doerge (7), was used to establish the significance of the LRSs generated by the interval mapping procedures which estimates an empirical genome-wide probability for observing a given LRS score by chance.

Composite interval mapping (CIM) was used for mapping of QTL and estimation of their effects as described by Bohn et. al. (3). Quantitative trait loci other than the one being mapped can be called "background" loci. These

background QTLs have two effects. Those which are not linked to the QTL being mapped behave like additional environmental effects and reduce the significance of any association. Those which are linked to the QTL being mapped bias the estimated location of that QTL. QTX provided the option to include other markers in the regression to reduce the effects of background QTLs.

RESULTS

Verification of the SDM pathogen and identity of races in Egypt. The sixteen samples collected from Gemmeiza, Sakha, and Abtouk Egypt amplified one 1.0 kb fragment that is specific for *P. Sorghi* using the *P. Sorghi* species-specific primers (29).

In Egypt, the 1999 pathotype trials of sorghum downy mildew confirmed the 1997 and 1998 data which identified most samples as pathotype 1 with a trace of pathotype 2 (Table 13). The only difference is that pathotype 2 showed up only at Sakha 1997 then at Gemmeiza in 1998 and at Sakha in 1999.

TABLE 13. The sorghum differentials reaction to sorghum downy mildew as resistant (R), susceptible (S), and trace of infection (S (tr)) in three locations, Gemmeiza, Sakha, and Abtouk in Egypt over three seasons 1997,1998, and 1999.

Cultivar	Gemmeiza			Sakha			Abtouk
	1997	1998	1999	1997	1998	1999	1999
QL-3	R	R	R	R	R	R	R
Tx430	R	R	R	R	R	R	R
SC170-6	R	R	R	S(tr)	R	R	R
CS3541	R	S(tr)	R	S(tr)	R	S(tr)	R
Tx7078	R	R	R	R	R	S	S
Tx2536	S	S	S	S	S	S	S
82BDM499	R	R	S(tr)	R	R	R	R

*This evaluation was conducted for this project in Egypt in 1997, 1998, and 1999 and this data was provided by Elhamy El-Assiuty, Maize and Sorghum Diseases Research Section, Plant Pathology Research Institute, Agricultural Research Center, Egypt.

Inbred line evaluation and development of a mapping population. The choice of parents is crucial in QTL mapping studies because the chances for detection of QTLs increase if the parents are extremes for the traits of interest (19). Hence, since the Philippines is considered to have the most severe incidence of downy mildew; 28 inbred lines were evaluated for

resistance in two sites in the Philippines (Table 14). Data in Table 14 shows that the three inbred lines Nei920, AMATLCOHS223-1-1-1-1-2-2-B-B-B (yellow) and P345C4S2B46-2-2-1-2-B-B-B (yellow), were highly resistant. P345C4S2B46-2-2-1-2-B-B-B was chosen to be crossed with the susceptible female SC-TEP5-19-1-3-1-4-1-1. The self-pollinated F_1 produced 221 seed, which were planted, sampled for DNA and self-pollinated to produce the $F_{2:3}$ families for phenotyping.

DNA preparation. The DNA was extracted from dry sampled tissues from the 221 F_2 individuals, except for one sample ((DMR P3 x P2)-3.106) that was lost through the drying process.

The ratio of OD_{260}/OD_{280} for the 220 DNA samples was between 2.0 and 1.8 except two samples (DMR P3xP2)-4.135 and (DMR P3xP2)-4.149 which were subsequently repurified. DNA quality control was an essential step for checking that the isolated DNA is of high molecular weight, which is required for RFLP analysis. Twenty of the 220 DNA samples were tested on 0.7% agarose gel. Figure 1 shows tight migrating bands of molecular weight $\geq$ 40 Kb as a sign of high quality DNA with almost no degradation.

TABLE 14. Percentage of downy mildew in 28 inbred lines screened in two disease nurseries in UPLB and South Cotabato, Philippines

No.	Pedigree	UPLB		Cotabato	
		12 days	21 days	12 days	21 days
1	Pi21	33	47	55	72
2	Pi31	73	86	75	85
3	Nei9008	3	3	2	2
4	Nei9203	41	44	27	29
5	Nei9204	36	48	51	63
6	Ki3	5	7	11	11
7	Ki14	17	21	52	52
8	AMATLCOHS115-1-2-3-3-1-2-B-B	27	27	21	26
9	AMATLCOHS233-1-1-1-1-2-2-B-B-B	57	65	55	70
10	P345C3S3B-40-8-1-1-2-2-B	31	31	42	50
11	AMATLCOHS9-1-1-1-1-1-2-B	21	21	45	45
12	AMATLCOHS245-1-1-1-2-2-2-B-B	76	88	77	84

No.	Pedigree	UPLB		Cotabato	
		12 days	21 days	12 days	21 days
13	P345C4S2B46-2-2-1-2-B-B-B	3	5	2	2
14	IPB9204-1-3-1-2-4-B	26	26	13	15
15	(24STE-5*24STE-17)-BBBB###-B-1-B-2-B-B-B	.	.	85	85
16	(24STE-5*24STE-17)-BBBB###-B-5-B-4-B-B-B	95	97	100	100
17	SIN.AM.TSR-76-1-1-B-1-BBBB-5-##-BBBBBBBBB	91	94	92	97
18	P24(STE)C2-29-BBBB-#-3-BBBBBBB	86	92	94	94
19	G26 C25 HS45-3-4-1-6-BBBB	81	87	78	82
20	CML20	96	100	77	77
21	CML270	98	100	92	92
22	CML289	93	97	83	83
23	CML272	9	98	71	88
24	P8	47	47	35	36
25	P12	84	84	81	83
26	Pi23	51	61	24	27
27	Pi27	73	71	70	92
28	Pi35	61	61	70	78
29	Check (Sweet Corn)	85	93	89	99

*This evaluation was conducted for this project in Philippine in 1998 and these data were provided by Daniel Jeffers, CIMMYT.

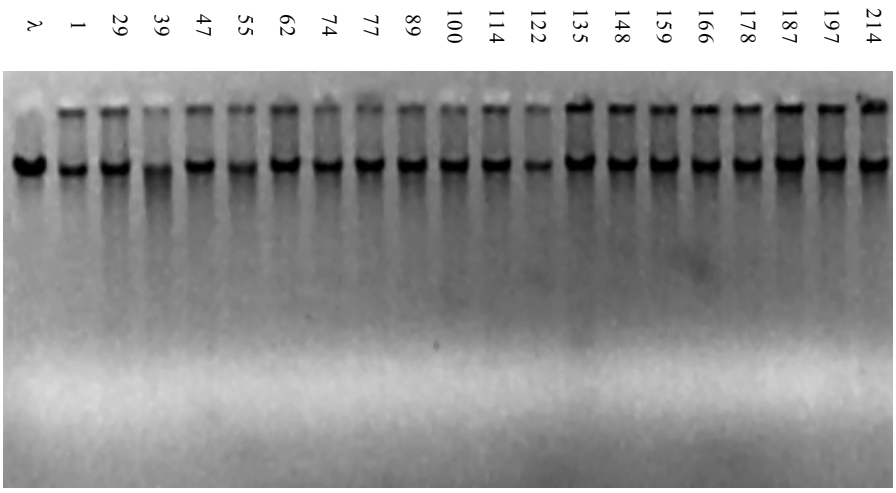


FIGURE 1. A 0.**7% agarose gel for DNA quality test of 20 DNA samples**

A test of DNA digestibility was also conducted before setting up large scale digestion experiments. The 20 DNA samples used for DNA quality test were digested using *Hin*dIII restriction endonuclease to test digestibility. The 20 digested DNA samples were subjected to electrophoresis in 0.7% agarose gel with the results shown in figure 2. This gel shows smears in the lanes of digested DNA migrating down the agarose gel as is expected following digestion.

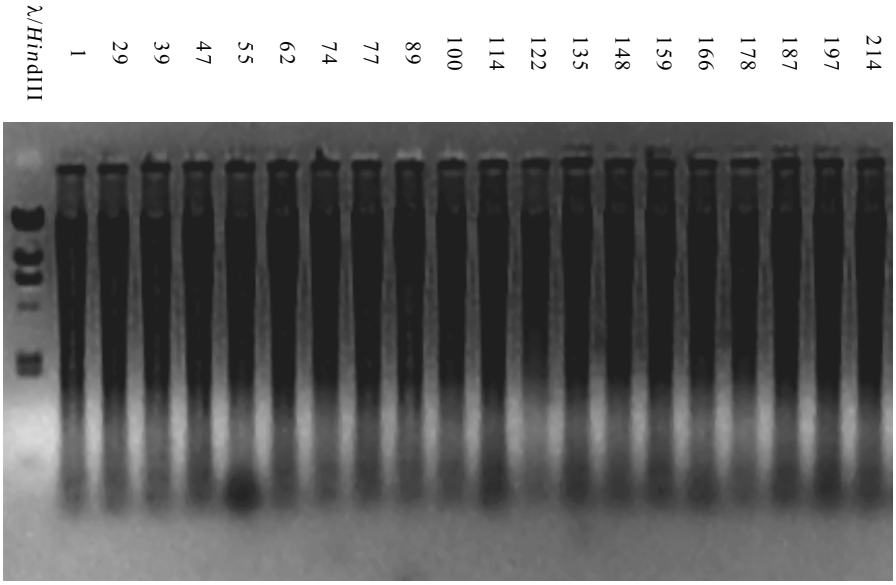


FIGURE 2. A **0.7% agarose gel for testing DNA digestibility of 20 DNA samples**

Based on the results retrieved from DNA digestibility test, DNA digestion was proceeded to include the rest of the 220 DNA samples in addition to P3 and P2 using two separate enzymes *Eco*RI and *Hin*dIII. Fourteen samples, 7 for each enzyme, were selected randomly to confirm that DNA samples were digested properly. All 14 samples showed smears of digested DNA migrating in 0.7% agarose gel (Figure 3). This result was the basis for running digested DNA for all the 220 F_2 individuals in double thick agarose gels and Southern blotting them onto non-charged membranes. Figures 4 and 5 show examples

of pictures for formats A and B for each set of gels. These pictures were taken to confirm the proper separation of digested DNA into gels before Southern blotting them.

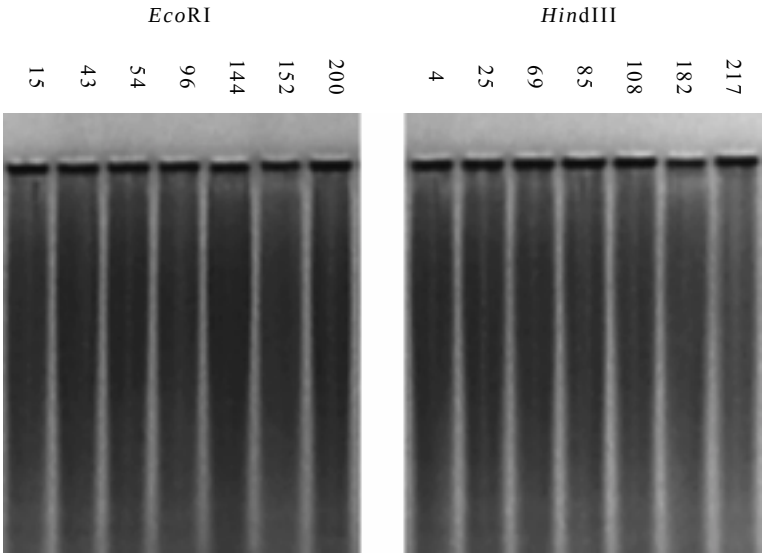


FIGURE 3. A 0.7% agarose gel showing 7 digested DNA samples from each enzyme *Eco*RI and *Hind*III

FIGURE 4. Picture of 0.7% agarose gel containing digested DNA samples from F_2 population following format "A"

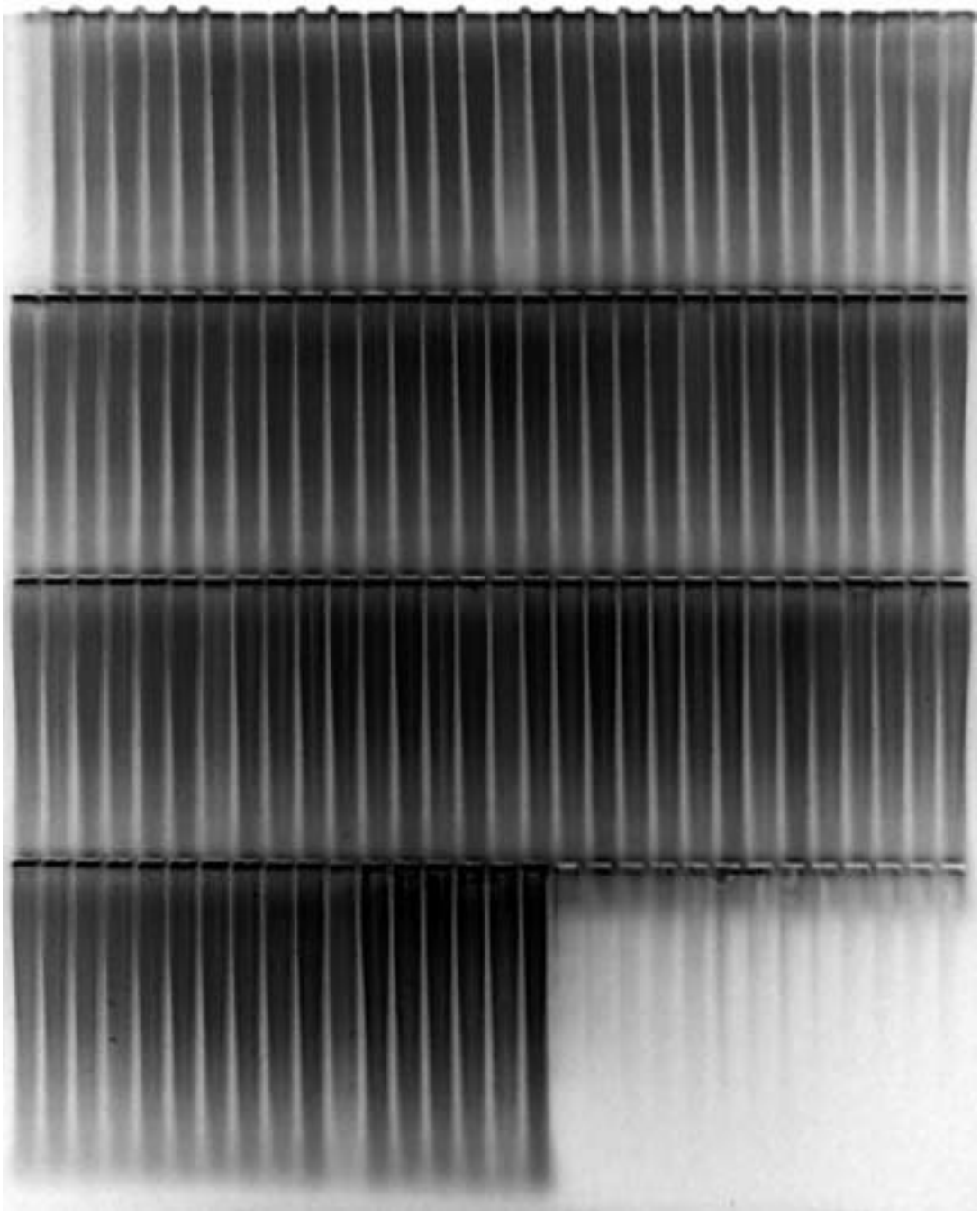


FIGURE 5. Picture of 0.7% agarose gel containing digested DNA samples from F_2 population following format “B”

Parental screening for RFLPs. After digested parental DNA samples were run into 0.7% agarose gels and blotted onto non-charged membranes, it was essential to identify the polymorphic probes before testing the entire population. Out of 160 RFLP probes used to screen parents for polymorphism, only 60 gave adequate polymorphic signals for reliable scoring of segregation. Because of the limitation of presenting 160 pictures in this dissertation, Figure 6 was chosen, as an example, to show a picture of X-Ray film that was exposed to a parental screening membrane hybridized with umc107 RFLP probe.

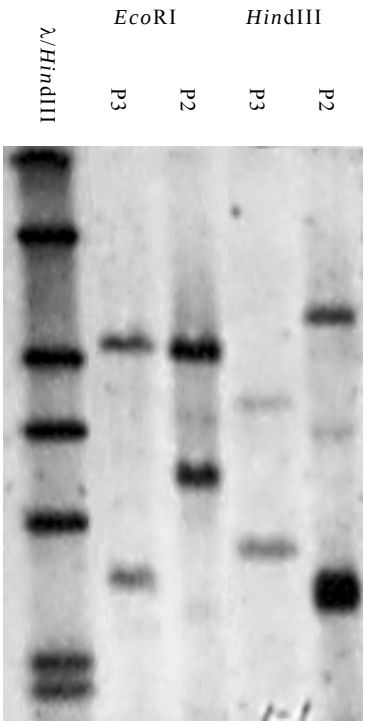


FIGURE 6. Parental screening for polymorphism using umc107 in 0.7% agarose gel. First lane: end-labeled λ/*Hin*dIII; following two lanes: Parents P3 and P2 digested with *Eco*RI; last two lanes: Parents P3 and P2 digested with *Hin*dIII

RFLP markers. The use of double thick agarose gels is a technique designed for large scale RFLP projects. The 60 polymorphic RFLP probes identified from parental screening were hybridized to the 12 sets of membranes. These were probed with 30 polymorphic RFLP probes for each restriction enzyme, *Eco*RI and *Hin*dIII. Because of the difficulty of presenting 120 full page pictures, Figures 7 and 8 were chosen as examples of formats A and B of X-Ray films exposed to the membrane set hybridized with umc107 RFLP probe. Results of the 120 developed X-Ray films were scored as A, B, C, D, H and (-) for missing data and represented in Appendix D.

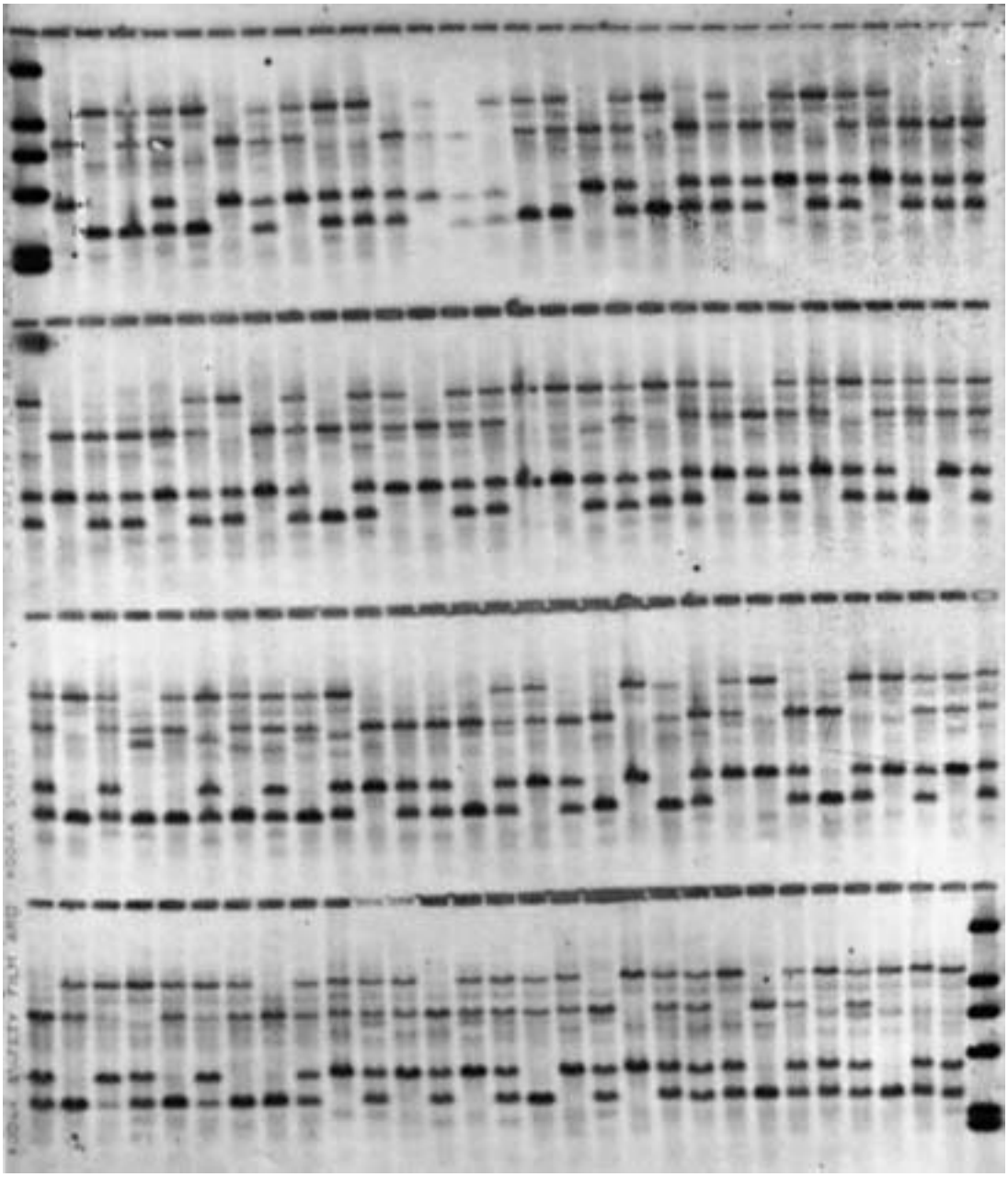
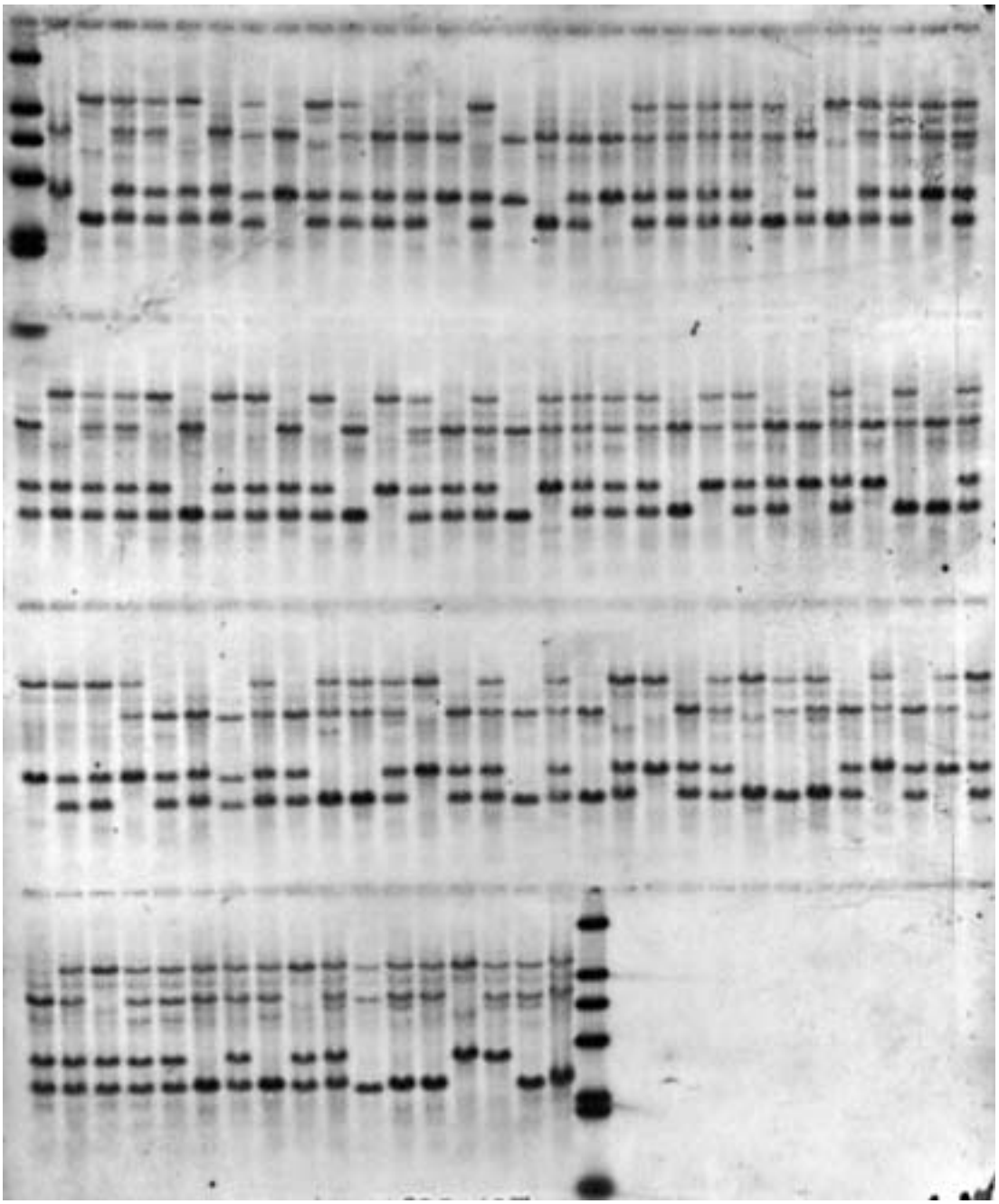


FIGURE 7. X-Ray film exposed to *Hin*dIII membrane format "A" hybridized for the second time using umc107 RFLP probe



FIGUER 8. X-Ray film exposed to *Hin*dIII membrane format “B” hybridized for the second time using umc107 RFLP probe

Parental screening for SSRs. Parental lines were screened for polymorphism using 496 SSR markers. More than 150 of those markers were polymorphic. Only 99 SSR markers were selected to screen the F_2 population based on their mapping location and the confirmation test conducted by testing the first 22 individuals of the segregating population along with the parent lines. Figure 9 provides an example of the 496 gels that showed polymorphic patterns when the parent lines and the first 22 individuals were amplified using bnlg1598 SSR primers.

SSR markers. The total F_2 population was screened for polymorphism using the 99 polymorphic SSR markers. Data were scored as A, B, C, D, H and (-) for missing data and are presented in Appendix D combined with the RFLP genotypic data. Two of the 198 gel pictures are presented in Figures 10 and 11 as examples for the segregating pattern in formats SSR-A and SSR-B using bnlg1598 SSR marker.

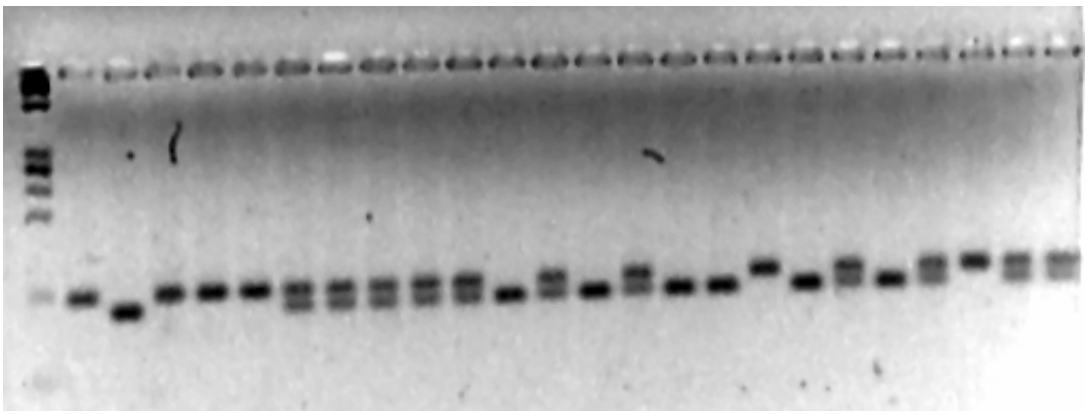


FIGURE 9. Gel format SSR-22 containing from left to right: molecular marker ϕX174/*HAE*III; parent P3; parent P2; the first 22 F_2 individuals

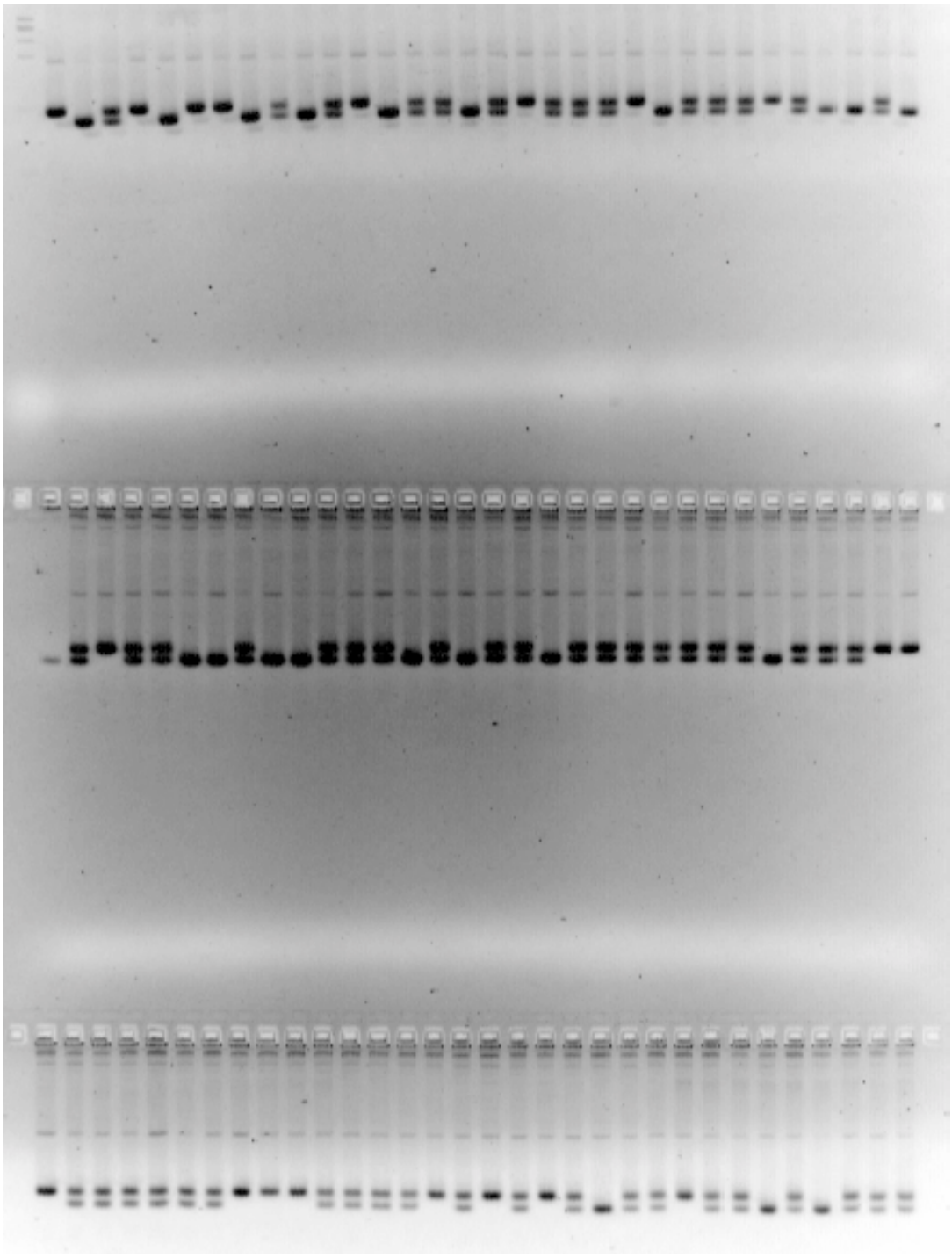


FIGURE 10. Gel format SSR-A containing in the upper row from left to right: molecular marker ϕX174/*HAE*III; parent P3; parent P2; then the rest of the gel contains F_2 individuals

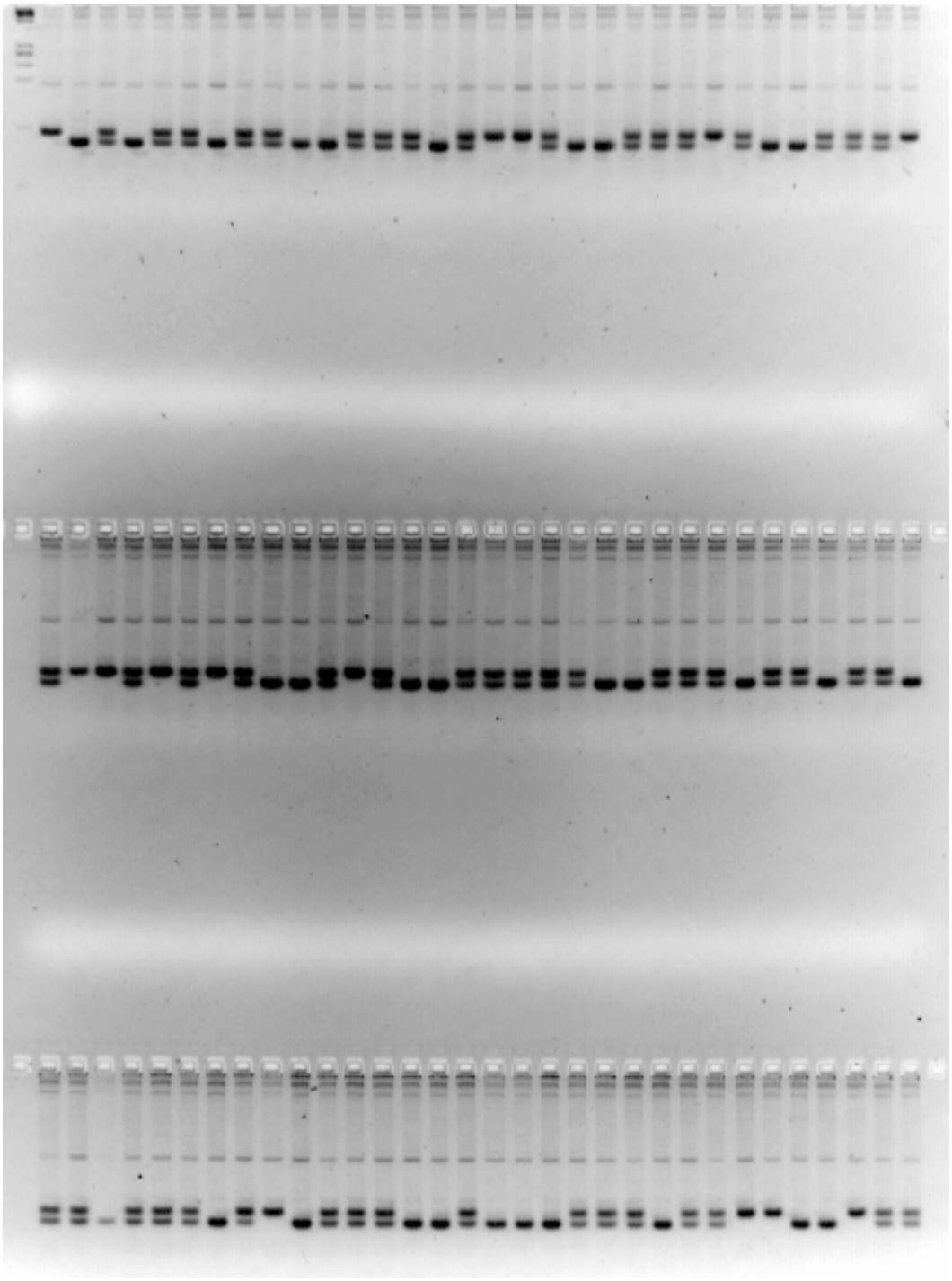


FIGURE 11. Gel format SSR-B containing in the upper row from left to right: molecular marker ϕX174/*HAE*III; parent P3; parent P2; then the rest of the gel contains F_2 individuals

Segregation and linkage of markers. Out of 149 combined RFLP and SSR scored markers, a total of 133 markers were used to construct a genetic map of this population. Three of the 149 markers remained genetically unlinked while 11 dominant markers were not useful. Analyses of the genotype frequencies among the 220 F_2 plants were consistent with the expected Mendelian segregation ratios for all 149 RFLP markers assayed.

All markers were assigned to ten linkage groups using Map Manager QTX" (21). The genetic map shown in Figures 12a-12j with distances indicated in centiMorgans was created using the Kosambi function (17) with linkage criterion $P<0.00001$. All markers were linked to the map with LOD scores exceeding 4.9. The map covered about 1265 cM with 133 markers distributed over all chromosomal regions and classified into ten linkage groups with an average interval length of 9.5 cM. About 90% of the genome was located within a 10 cM distance to the nearest marker. The map is largely in agreement with the most recently published RFLP and SSR maps and data base established for temperate maize by "Maize DB".

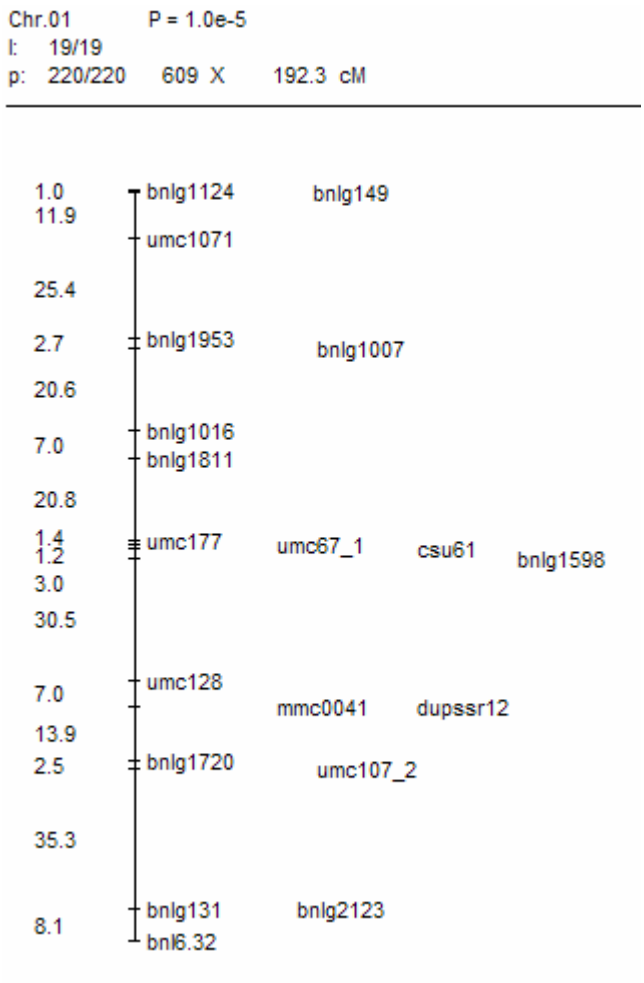


FIGURE 12a. Genetic marker map for chromosome 1

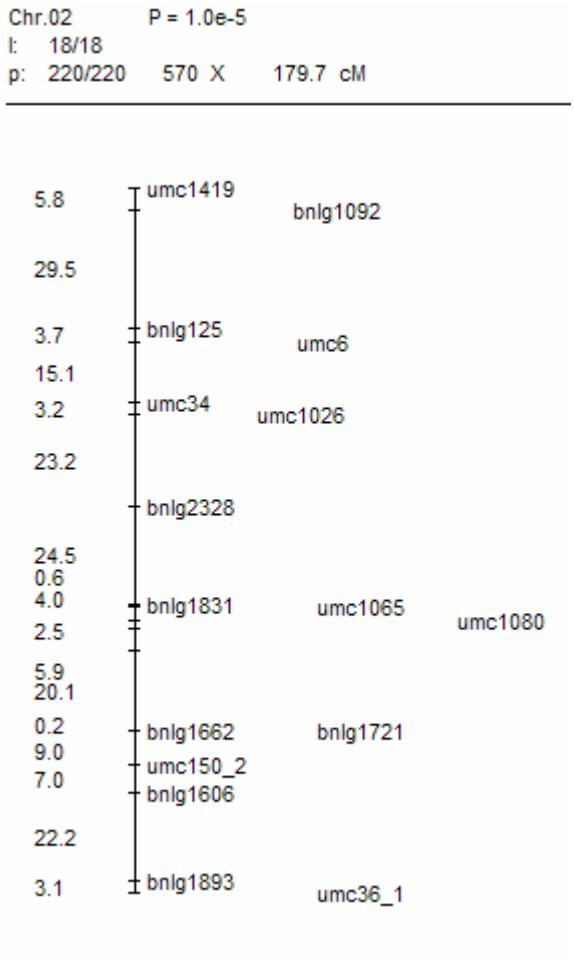


FIGURE 12b. Genetic marker map for chromosome 2

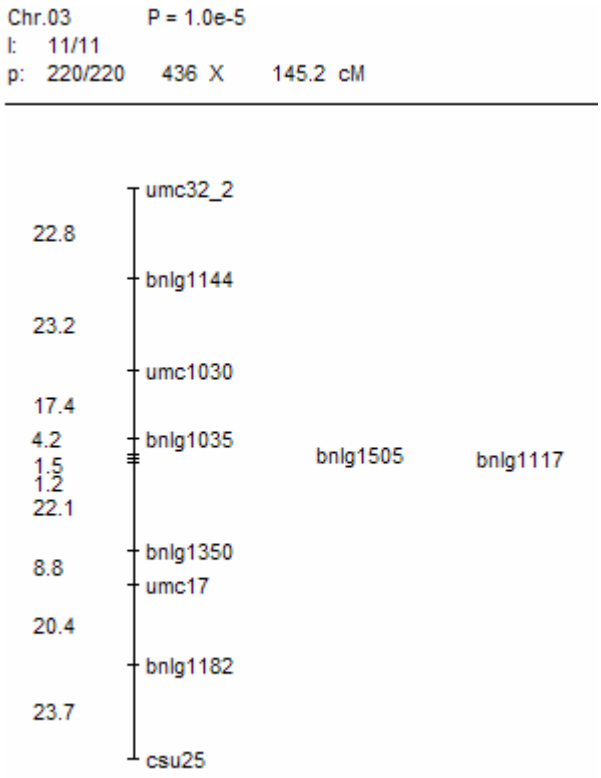


FIGURE 12c. Genetic marker map for chromosome 3

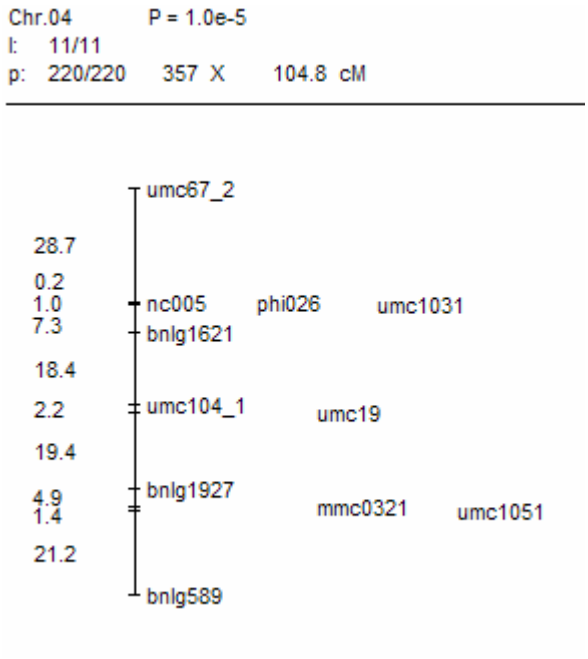


FIGURE 12d. Genetic marker map for chromosome 4

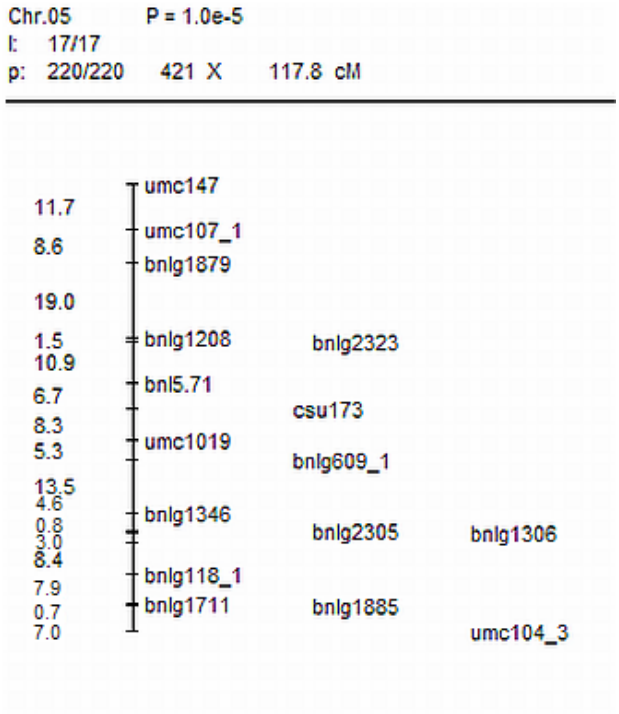


FIGURE 12e. Genetic marker map for chromosome 5

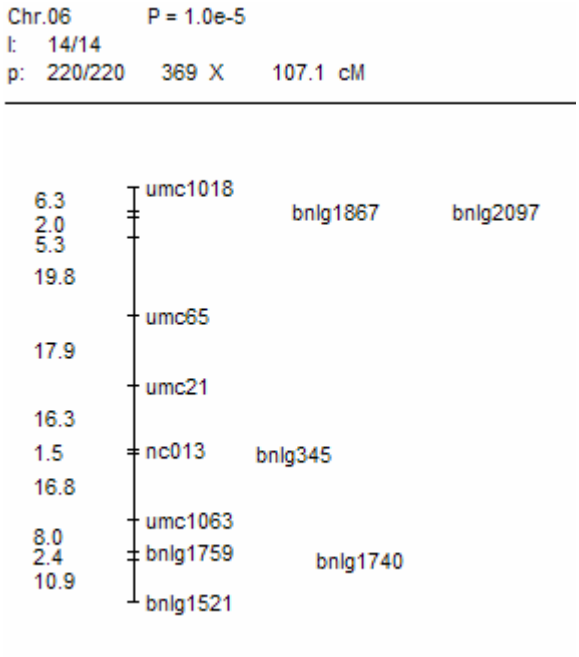


FIGURE 12f. Genetic marker map for chromosome 6

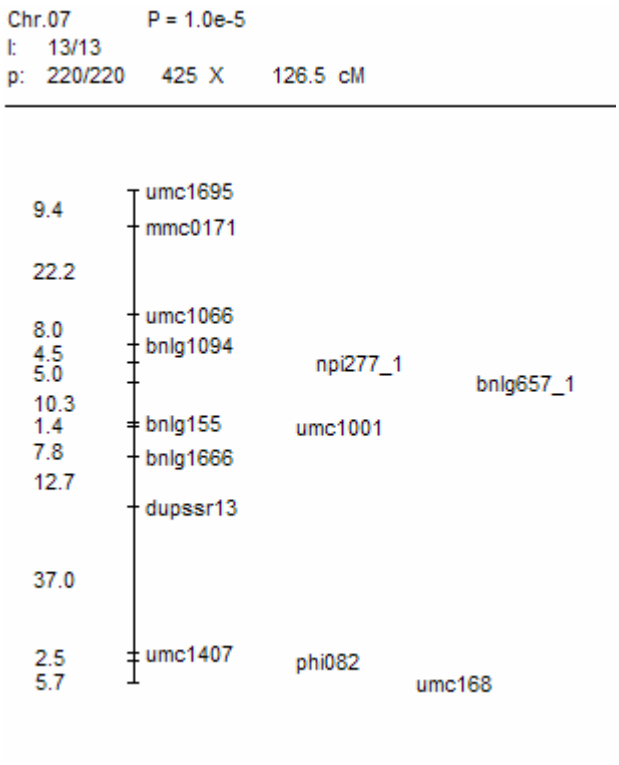


FIGURE 12g. Genetic marker map for chromosome 7

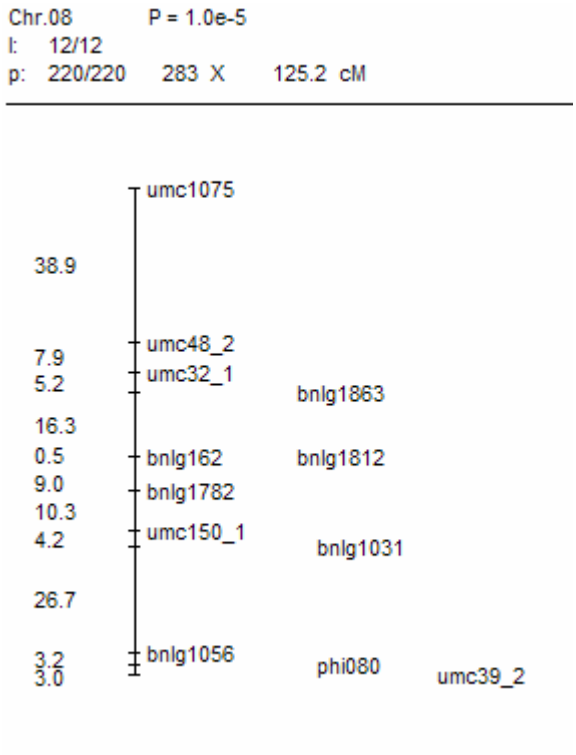


FIGURE 12h. Genetic marker map for chromosome 8

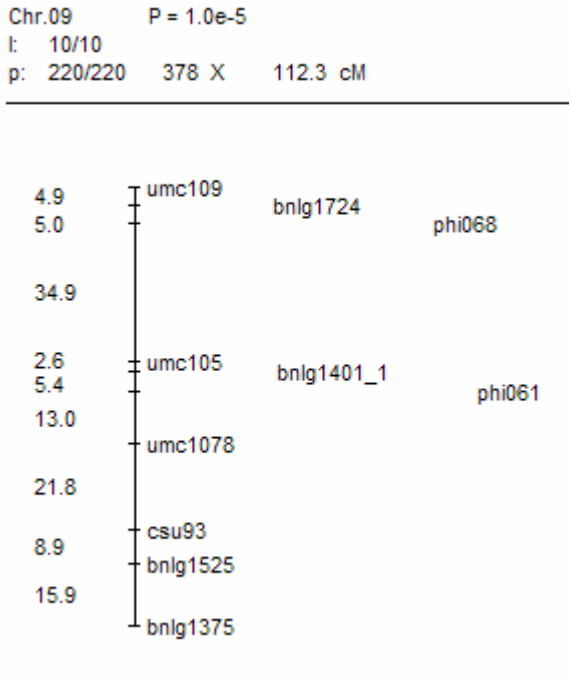


FIGURE 12i. Genetic marker map for chromosome 9

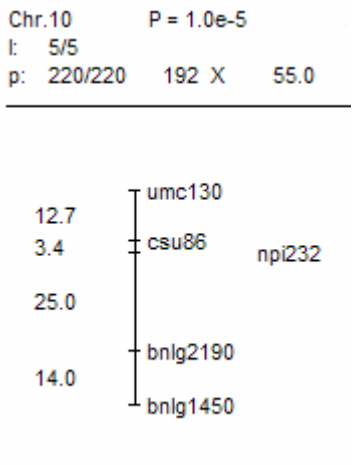


FIGURE 12j. Genetic marker map for chromosome 10

Phenotypic analysis. The 221 $F_{2:3}$ families along with the two parents and controls were tested for sorghum downy mildew resistance. The evaluation was conducted in four locations; two sites in Thailand, Egypt and Corpus Christi, Texas in addition to the greenhouse. Each environment had three replicates except Texas where there was not enough seed, only one replicate was tested. Therefore this set of data was only used for QTL analysis. Because of the loss of DNA sample (DMR P3 x P2)-3.106 during genotyping, only data from 220 $F_{2:3}$ families ware used for statistical analysis and QTL mapping.

The phenotypic data from both field and greenhouse trials was recorded as the percentage of plants showing disease symptoms. The percentage values for local, systemic and total infection ranged from zero to one hundred and would generally be characterized as binomially distributed. Data was transformed using the arcsine transformation (Appendixes E, F, G, H, I, J, K and L) as described by Steel and James (26), and Gomez and Gomez (12). This transformation was intended to make the means and variances independent and normally distributed.

Analyses of variance were conducted on transformed phenotypic data for individual and combined environments using PROC GLM, SAS Institutes. Components of variance for the $F_{2:3}$ families in all locations and across locations were computed considering all effects in the statistical model as random.

Calculated F values for the blocking factor resulting from the analysis of variance are given in Tables 15, 16 and 17 for sites 1 and 2 in Thailand and Egypt. They were, respectively, 1.42 (P=0.1384), 1.39 (P=0.1523), and 1.15 (P=0.3114) which indicated no significant difference among the blocks. Therefore, the block term was eliminated from further analysis models.

Also, analysis of variance of the greenhouse trial showed no significant effect due to blocks, where calculated F values for blocks were 1.66

(P=0.1073), and 0.51 (P=0.85) for local and systemic infection respectively (Table 18 and 19). Furthermore analysis of variance was conducted using only the susceptible control sweetcorn "Golden Bantam" that was included in each of the greenhouse trays, which resembles the blocks in the greenhouse. Calculated F values for trays effect in both local and systemic infection were 0.41 (P=0.8956), and 0.32 (P=0.947) respectively which are not significant and confirm the homogeneity between trays and further indicated that no significant differences resulted from daily inoculum preparation (Table 20 and 21).

Due to non-significance, blocks were eliminated from further analysis models and analyses of variance were repeated again without block term in all models using PROC GLM (Tables 22, 23, 24, 25 and 26). Genotypic components of variance (σ^2_g) were again highly significant for infection in all environments. This is indicative of the presence of genotypic variability in the population.

Parental line means, expressed in transformed values, are presented in Table 27 along with the infection grand mean for the tested $F_{2:3}$ families. The infection grand mean ranged from 36.87% in site 1 to 7.72% in site 2 in Thailand, while was 14.53% in Egypt. For local and systemic infection in the greenhouse, grand means were 26.37 and 23.21% respectively.

Before combining data across environments, Bartlett's test was performed to test the homogeneity between all combinations of field locations and systemic infection in greenhouse. Results in Table 28 indicated that the only homogenous combination was site 1 in Thailand and Egypt. Therefore combined analysis was based only on those two locations.

Heritability (H^2) was calculated for each location and presented along with variance components in Table 27. The heritability value was as high as 93.3 in site 1 in Thailand, while it was 48.0 in site 2. Values were 78.0 and 63.1 in Egypt and the College Station greenhouse, respectively.

Transformed entry means were then used to compute the combined analyses of variance and covariance across environments using only data from site 1 in Thailand and the Egypt locations. Calculated heritability for combined analysis was 58.88. Genotypic components of variance (σ^2_g) were significant for infection in all environments and across environments in the population. This is indicative of the presence of relatively high genetic variance for resistance to sorghum downy mildew. However, a partitioned genotype-by-environment component reduced the H^2 value (Table 27).

TABLE 15. Analysis of variance for site 1 in Thailand

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	394958.4552	1803.4633	14.62	<.0001
Rep	2	1953.1160	976.5580	7.92	0.0004
Block	14	2458.4058	175.6004	1.42	0.1384
Error	424	52310.4733	123.3738		
Corrected Total	659	463902.0707			

TABLE 16. Analysis of variance for site 2 in Thailand

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	32589.49723	148.81049	1.96	<.0001
Rep	2	220.89003	110.44501	1.46	0.2343
Block	14	1479.67053	105.69075	1.39	0.1523
Error	424	32158.20679	75.84483		
Corrected Total	659	66224.91157			

TABLE 17. Analysis of variance for Egypt

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	143873.8709	656.9583	4.46	<.0001
Rep	2	1015.8523	507.9262	3.45	0.0328
Block	14	2375.1103	169.6507	1.15	0.3114
Error	419	61776.5778	147.4381		
Corrected Total	654	212903.2816			

TABLE 18. Analysis of variance for greenhouse local infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	310291.7687	1416.8574	4.12	<.0001
Rep	2	2747.8772	1373.9386	3.99	0.0191
Block	8	4556.9903	569.6238	1.66	0.1073
Error	424	147248.9486	344.0396		
Corrected Total	657	465441.8538			

TABLE 19. Analysis of variance for greenhouse systemic infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	218	253217.1663	1161.5466	2.65	<.0001
Rep	2	5298.5457	2649.2729	6.04	0.0026
Block	8	1784.8116	223.1015	0.51	0.8500
Error	401	175898.1695	438.6488		
Corrected Total	629	438498.0381			

TABLE 20. Analysis of variance for greenhouse control for local infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Rep	2	65.4095407	32.7047704	0.16	0.8520
Block	8	670.7901630	83.8487704	0.41	0.8956
Error	16	3234.863393	202.178962		
Corrected Total	26	3971.063096			

TABLE 21. Analysis of variance for greenhouse control for systemic infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Rep	2	511.6114296	255.8057148	0.93	0.4155
Block	8	703.3445407	87.9180676	0.32	0.9470
Error	16	4408.617237	275.538577		
Corrected Total	26	5623.573207			

TABLE 22. Analysis of variance for site 1 in Thailand

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	407204.6284	1859.3819	14.87	<.0001
Rep	2	1928.5632	964.2816	7.71	0.0005
Error	438	54768.8791	125.0431		
Corrected Total	659	463902.0707			

TABLE 23. Analysis of variance for site 2 in Thailand

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	32361.64864	147.77009	1.92	<.0001
Rep	2	225.38561	112.69281	1.47	0.2317
Error	438	33637.87732	76.79881		
Corrected Total	659	66224.91157			

TABLE 24. Analysis of variance for Egypt

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	147730.2902	674.5675	4.55	<.0001
Rep	2	1033.1206	516.5603	3.49	0.0315
Error	433	64151.6881	148.1563		
Corrected Total	654	212903.2816			

TABLE 25. Analysis of variance for greenhouse local infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	219	310910.3496	1419.6820	4.08	<.0001
Rep	2	2774.4260	1387.2130	3.98	0.0193
Error	436	151805.9390	348.1788		
Corrected Total	657	465441.8538			

TABLE 26. Analysis of variance for greenhouse systemic infection

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Entry	218	256556.0955	1176.8628	2.71	<.0001
Rep	2	5139.9684	2569.9842	5.92	0.0029
Error	409	177682.9811	434.4327		
Corrected Total	629	438498.0381			

TABLE 27. Parent lines means, grand means, genetic variance (σ^2_g), genotypexenvironment (σ^2_{ge}), environment variance (σ^2), and heritability (H^2) of sorghum downy mildew infection (arcsine transformed values) for all tested environments and field combined data.

Environment	P3 Mean	P2 Mean	$F_{2:3}$ grand Mean	Variance components			Heritability
				σ^2_g	σ^2_{ge}	σ^2	H^2
Thai, site1	89.34	6.62	36.87	578.11		125.04	93.28
Thai, Site 2	26.62	0.70	7.72	23.66		76.8	48.03
Egypt	6.75*	9.46	14.53	175.47		148.16	78.04
Greenhouse local infection	76.11	1.28	26.37	357.17		348.18	75.47
Greenhouse systemic infection	53.11	1.28	23.21	247.48		434.43	63.09
Combined	48.06*	8.04	25.74	267.12	327.60	136.53	58.88

* Unexpected value which may be due to unknown error

TABLE 28. Homogeneity test between all possible combinations of environments

Combination	**χ^2**	**Tabular χ^2**	
		.05	**0.01**
Thai 1 + Thai 2	25.74	3.84	6.63
Thai 1 + Egypt	3.13	3.84	6.63
Thai 2 + Egypt	46.19	3.84	6.63
Thai 1 + Greenhouse	156.26	3.84	6.63
Thai 2 + Greenhouse	288.90	3.84	6.63
Egypt + Greenhouse	117.24	3.84	6.63
Thai 1 + Thai 2 + Egypt	47.90	5.99	9.21
Thai 1 + Thai 2 + Greenhouse	351.96	5.99	9.21
Thai 1 + Egypt + Greenhouse	206.59	5.99	9.21
Thai 2 + Egypt + Greenhouse	325.37	5.99	9.21
Thai 1 + Thai 2 + Egypt + Greenhouse	369.10	7.81	11.34

QTL analysis. Transformed values of the percentage of infection were used to get the mean of replicates for each $F_{2:3}$ family within each environment and across environments. Means for each $F_{2:3}$ family were subtracted from 100 to express the results in terms of resistance. Percentage of resistance was more realistic for QTL analysis. Map Manager QTXb17 for Windows™ (21) was used to conduct the QTL analysis on transformed data

means. Markers dupssr12 and bnlg2123 in addition to bnlg1867 and bnlg249 from chromosomes one and six as well as bnlg1721 from chromosome two were eliminated as duplicated and very close markers to avoid failure of regression and only 128 linked markers out of 133 in ten groups were used for QTL analysis.

Marker regression analysis revealed only one chromosome that is significantly associated between segregating markers and sorghum downy mildew resistance as a quantitative trait using a threshold of $P<0.00001$. Analysis for each individual environment and combined data was in agreement, all identifying a single QTL at bin 9 of chromosome two that was significantly associated with variation in resistance to sorghum downy mildew (Figures 13a-13c). More than one marker in this specific region significantly associated with the phenotypic measurement, but only the marker most strongly associated with the QTL was used. The likelihood ratio statistic (LRS) was used as indication for the significance of association of the trait with the locus (13). Also, LRS can be interpreted as a χ^2 statistic or as a LOD score, but the LOD differs from conventional base-10 LOD scores by a factor of 4.6. The likelihood ratio statistic needed for significance is about 20 for an F_2 cross as mentioned by Lander and Kruglyak (18). The LRS for locus bnlg1893 varied from 262.1 using combined data to 89.2 in Corpus Christi systemic infection data. In site 2 Thailand, the adjacent locus ums36, which is 3.1 cM downstream of bnlg1893, had the highest LRS value of 47.4 (Table 29). The total trait variance explained by the QTL at locus bnlg1893 was as high as 70% in both site 1 in Thailand and combined data and as low as 34% in Corpus Christi systemic infection (Table 29). Meanwhile, locus umc36 explained only 22% of the phenotypic variance in site 2 in Thailand. Also, the P value for the association confirmed the high significance of this specific QTL in all data sites. Confidence interval values for locus bnlg1893 were 3 and 4 for combined data and site 1 in Thailand, and 7 at Corpus

Christi for the systemic infection data. For Thailand site 2, the confidence interval value was 13.

The interval mapping procedure was used to fit a regression equation for the effect of the hypothetical QTL at the position of each marker locus and at regular intervals between the marker loci. This procedure also provided the resulting regression coefficient and a likelihood ratio statistic (LRS) that measures the significance of the coefficient(s). Because the population is an intercross population, a "free" model was used to fit coefficients for both additive and dominance effects. The permutation test described by Churchill and Doerge (7) was used to establish the significance of the LRSs generated by the interval mapping procedures which estimate an empirical genome-wide probability for observing a given LRS score by chance (Table 30).

Composite interval mapping (3) was also applied by removing the effects of the highly significant QTL on chromosome 2 in an attempt to detect other QTLs with lower effects using individual data sets. While interval mapping analyses were not capable of detecting any additional QTLs using any set of data, composite interval mapping analysis revealed two additional significant QTLs. One QTL was identified in association with locus phi073 at chromosome 3 bin 5, which explained 4% of the phenotypic variance in data only from Corpus Christi local (LRS=19.1) and total (LRS=22.1) infection. The same QTL was detected with the adjacent locus bnlg1035 but was not significant in greenhouse local (LRS=15.4) and systemic (LRS=11.8) infection data and explained 4% and 3% of the trait variance respectively. Composite interval mapping analyses for site 1 Thailand, Corpus Christi total infection, and combined data detected a second QTL that is associated with locus umc105 at chromosome 9 bin 2 that explained 3% of the phenotypic variance with significant LRS values of 17.2, 16.1 and 19.7 respectively. The second QTL was detected in Corpus Christi local infection and greenhouse

local infection data, but LRS values were not significant at 11.4 and 16.0 respectively, and explained only 2% and 4% of the trait variance.

TABLE 29. Marker regression analysis in Chromosome (Chr.), Bin number (Bin), Locus name, likelihood ratio statistic (Stat), total trait variance explained by QTL at this locus (%), the probability of an association this strong happening by chance (P), an estimate of the size of a 95% confidence interval for QTL of this strength (CI), and the additive regression coefficient for association (Add)

Data set	Chr.	Bin	Locus	Stat	%	P	CI	Add
Thailand, site 1	2	9	bnlg1893	258.9	70	0.00000	4	27.94
Thailand, site 2	2	10	umc36	47.4	22	0.00000	13	4.26
Egypt	2	9	bnlg1893	143.1	48	0.00000	5	13.55
Corpus Christi Local infection	2	9	bnlg1893	163.8	53	0.00000	5	25.41
Corpus Christi systemic infection	2	9	bnlg1893	89.2	34	0.00000	7	7.75
Corpus Christi total infection	2	9	bnlg1893	215.6	63	0.00000	4	31.06
Greenhouse local infection	2	9	bnlg1893	122.6	43	0.00000	6	19.38
Greenhouse systemic infection	2	9	bnlg1893	133.9	46	0.00000	5	18.57
Combined	2	9	bnlg1893	262.1	70	0.00000	3	20.75

TABLE 30. Significance levels of LRS that resulted from permutation test

Data set	Suggestive LRS	Significant LRS	Highly Significant LRS
Thailand, site 1	9.3	16.1	21.1
Thailand, site 2	9.5	16.2	21.5
Egypt	9.5	16.6	22.9
Corpus Christi Local infection	9.4	15.7	22.1
Corpus Christi systemic infection	9.5	15.8	20.8
Corpus Christi total infection	9.4	15.9	22.3
Greenhouse local infection	9.7	16.8	22.3
Greenhouse systemic infection	9.5	16.5	24.3
Combined	9.4	16.3	25.1

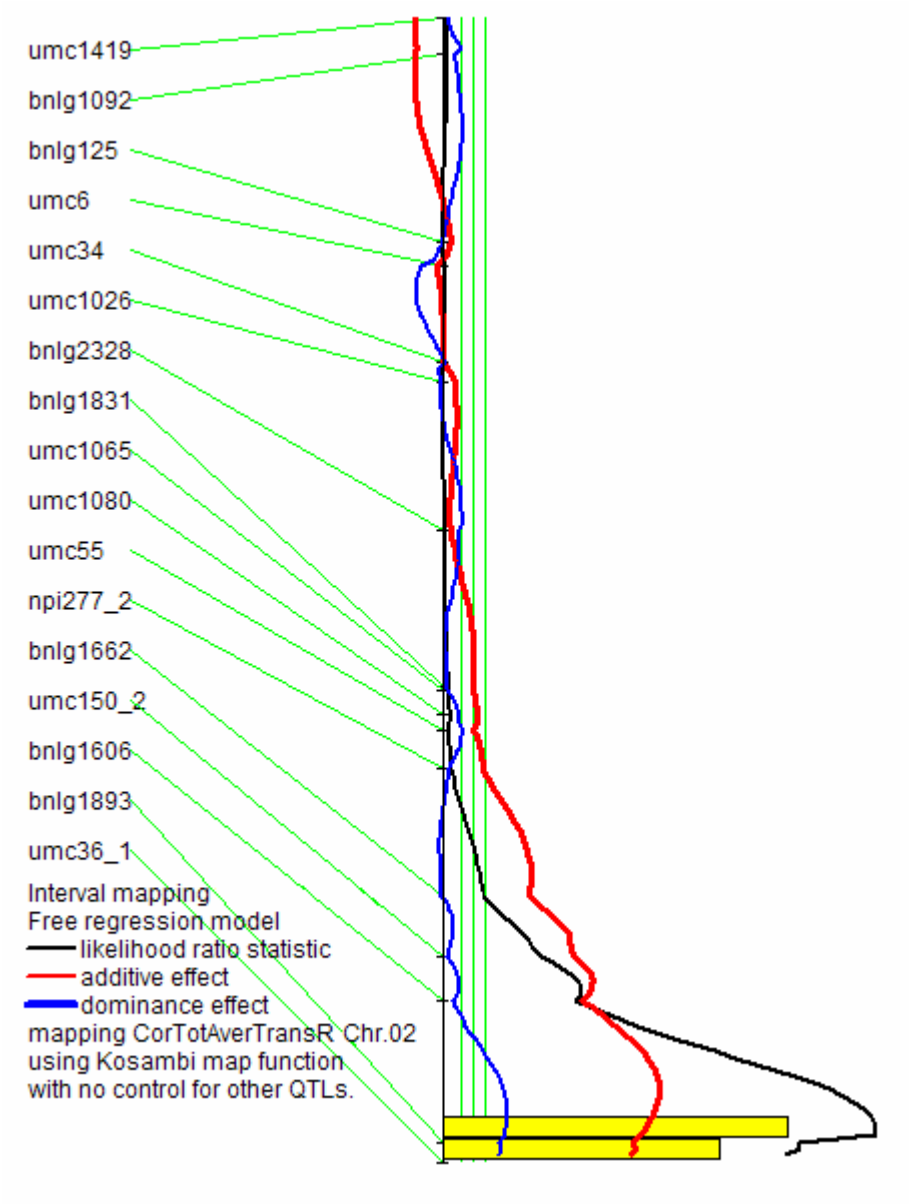


FIGURE 13a. QTL map for chromosome 2

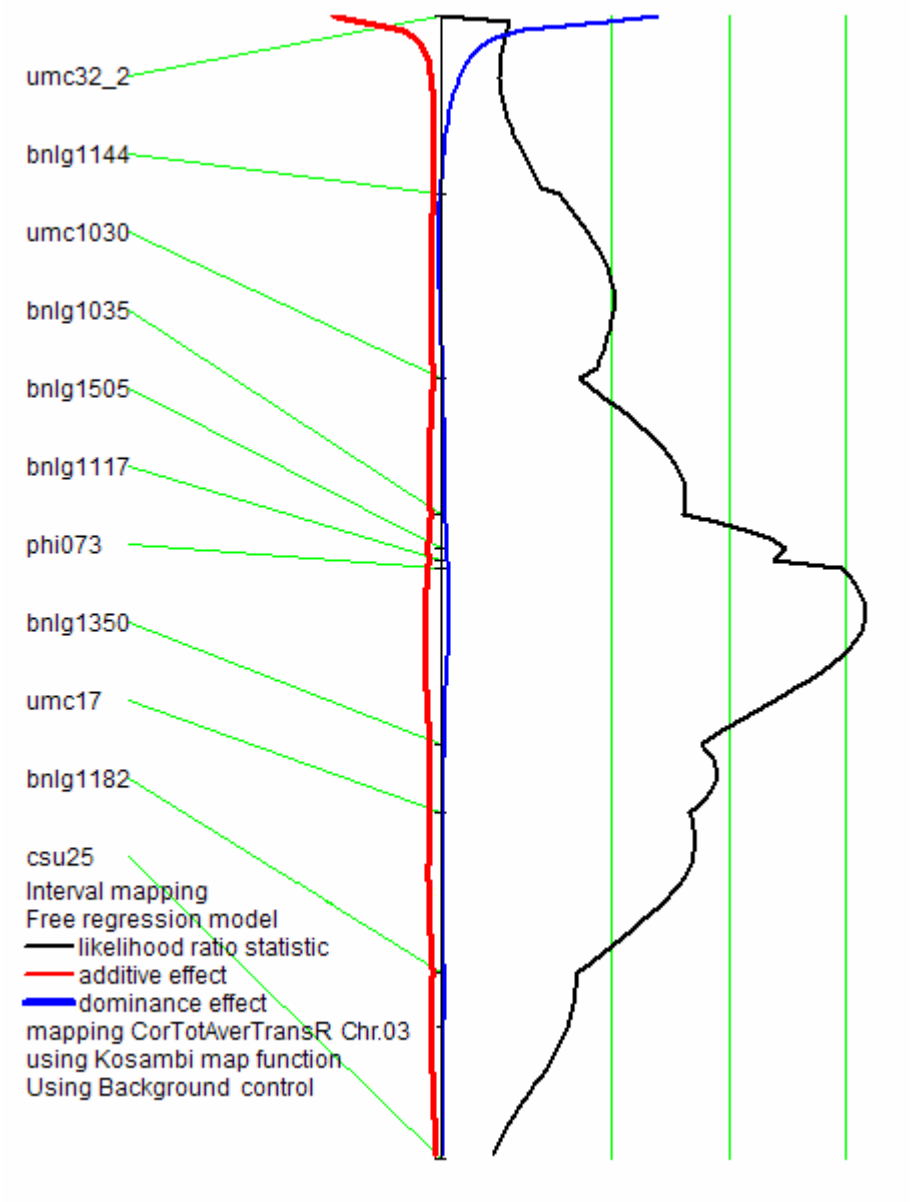


FIGURE 13b. QTL map for chromosome 3

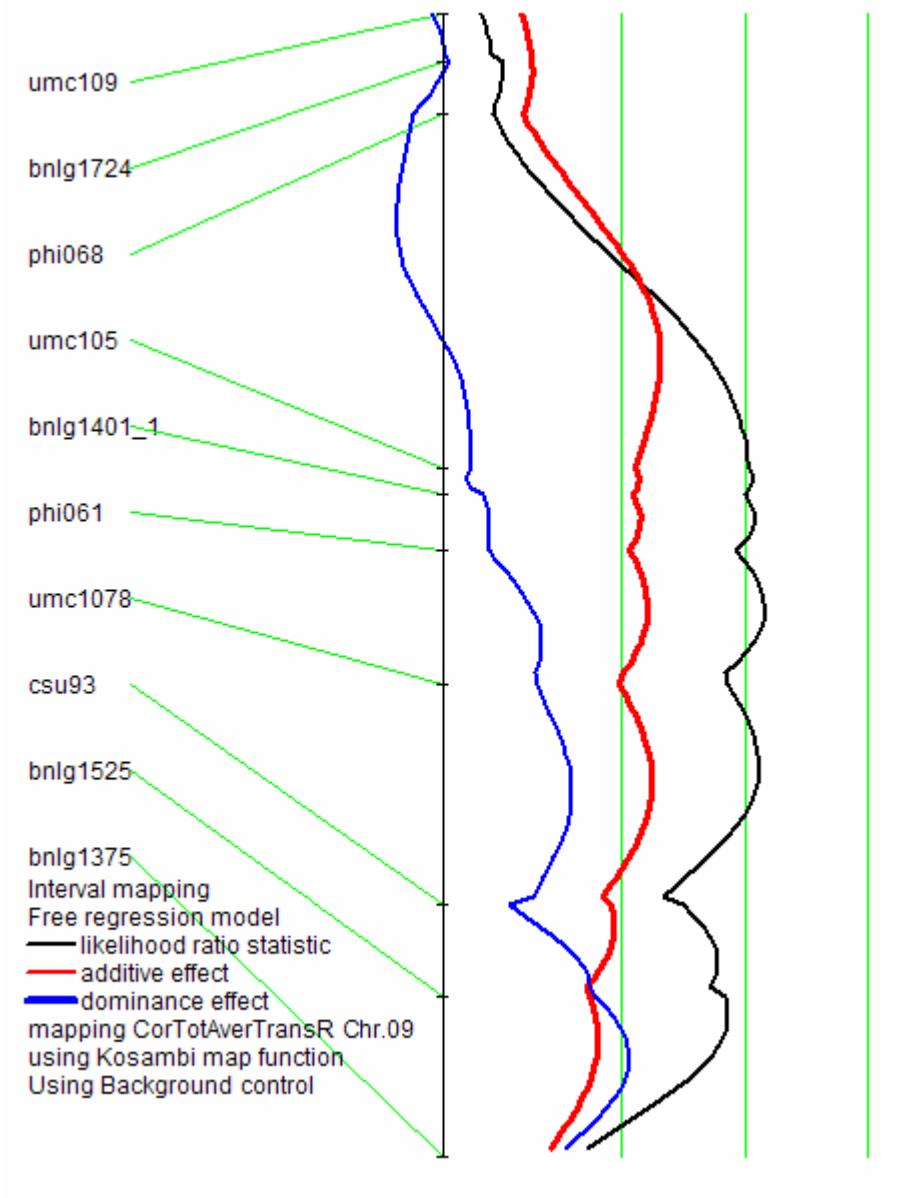


FIGURE 13c. QTL map for chromosome 9

DISCUSSION AND CONCLUSIONS

The development of a reliable method for evaluating maize plants for the expression of sorghum downy mildew resistance was crucial to the success of this study. Consistent heavy disease pressure is required to assess accurately the potential of plant genotypes to resist sorghum downy mildew and to accurately determine the magnitude of the effect of genetic factors that contribute to resistance. The heavy disease pressure expected in field plots and the greenhouse, combined with replicated disease evaluation in five environments was meant to make sure that this assay was sufficiently sensitive to detect all possible QTLs that contributed to sorghum downy mildew resistance in the $F_{2:3}$ families. On the other hand, those five locations covered a wide range of distinct environments that provided the opportunity to explore the expression of the QTL in different environments and enhanced the prospects for discovering QTL by environment interactions. In addition to the differences between environments, the five locations provided at least four different pathogen populations. In Egypt, the causal agent of sorghum downy mildew was verified to be *P. sorgi* using the species-specific primers developed by Yao et.al. (29), while the pathotypes present were primarily pathotype 1, with a lesser occurrence of pathotype 2, using sorghum differential trials. *P. sorghi*, pathotype 3 was used in the greenhouse trial, while pathotype 1 was predominant in Corpus Christi. Although not confirmed experimentally, it is very likely that *P. zeae* was predominant in Thailand.

The two parent lines SC-TEP5-19-1-3-1-4-1-1 (white, P3) and P345C4S2B46-2-2-1-2-B-B-B (yellow, P2) which were used to develop the segregating $F_{2:3}$ families exhibited the most extreme phenotypes to sorghum downy mildew. The parent line P3 had been identified as being highly susceptible and the inbred P2 was highly resistant to sorghum downy mildew.

Initial surveys also showed sufficient diversity in DNA based markers between these lines to permit mapping, another important consideration in the choice of parents.

While RFLP analysis required relatively large quantities of high quality DNA, the SSR technique was useful when less DNA was available. Combining both RFLP and SSR techniques made it possible to verify marker positions within the genetic map generated in this study by comparison to core marker positions in published maps.

Map Manager QTXb17 for Windows™ platform provided a reliable stable application for marker linkage and QTL analyses (21). Genotype frequencies among the 220 F_2 plants satisfied the expected Mendelian segregation ratios for all markers. When combined, the RFLP and SSR markers formed ten linkage groups very similar to the majority of published maps. Dominant markers were initially scored, but their inclusion in the map made it impossible to establish an unambiguous order of markers within some linkage groups. These markers also led to the detection of insignificant QTLs, therefore all dominant markers were eliminated except for three that closed significant gaps in the map and that also matched previously reported chromosomal locations. All markers were linked to the map with LOD scores exceeding 4.9. The map covered about 1265 cM with 133 markers distributed over all chromosomal regions and classified into ten linkage groups with an average interval length of 9.5 cM. About 90% of the genome was located within a 10 cM distance to the nearest marker. The spacing of marker loci affects the confidence interval less crucially and there is little to be gaind by having marker loci spaced more closely together than 20 cM. Even with a strong QTL and large sample population, the confidence interval is unlikely to be less than 10 cM (21). Also, Varvasi and Soller mentioned that there is little point in having markers that are closer together than 10 cM for QTL analyses using data from single-generation crosses. In addition, markers

which are not separated by any recombinations may cause the regression to fail (9). The map is largely in agreement with the most recently published RFLP and SSR maps and database established for temperate maize by "Maize DB".

Data transformation was used to normalize the distribution of binomially distributed phenotypic data (12, 20, 26). Using an "all random effects" model, statistical analyses proved the insignificance of blocking effect, therefore it was eliminated from further models. Likewise, homogeneity among greenhouse treatments was shown to be a valid assumption. The significance of genotypic components of variance in all environments confirmed our expectation of genotypic variability within the population sample.

The infection grand mean of $F_{2:3}$ families in contrast to parental line means for each environment indicated that a larger portion of the population tends to show resistance to sorghum downy mildew. Meanwhile, differences among means indicated that disease pressure varied between locations. Site 1 in Thailand and the greenhouse had the highest disease pressure and therefore were considered to be the most informative environments.

Bartlett's test for homogeneity among the results from different sites indicated that the only homogenous combination was site 1 in Thailand and Egypt. Therefore these were the only two environments to be combined. Usually combined data is needed when multiple small-effect QTLs are detected and the most significant QTL(s) are yet to be identified, but in this study it was obviously clear from the analyses of each environment that one QTL had most of the effect on sorghum downy mildew resistance in this population. Therefore combined data did not provide significantly different information.

Different disease pressure between environments affected the calculation of heritability. Values vary from 93.3 in Thailand site 1 to 48.0 in site 2. The

high heritability values in Thailand site 1, Egypt, and the greenhouse trails is in agreement with detecting one locus that has a large effect on sorghum downy mildew resistance, essentially behaving as a major gene for resistance. Lower heritability may result when there is low disease pressure, so that susceptible plants are misclassified.

While marker regression and interval mapping analyses revealed only one QTL that significantly controlled resistance to sorghum downy mildew in this population, composite interval mapping analysis revealed two additional QTLs with less effect. The QTL showing large and consistent effect on sorghum downy mildew resistance in all data sets was detected on chromosome 2 bin 9 (Figure 13). The agreement among the QTL detected in all environments provides evidence for the consistency of QTL mapping results across environments. Also, the high LRS of the detected QTL across all traits suggesting that it may will effectively control SDM in a variety of environments. It proved to be effective against *P. sorghi* pathotypes 1 and 3 in addition to *P. zeae*.

The other two QTLs at chromosome 3 bin 5 and chromosome 9 bin 2 had minor effects and were not constant in all environments. Both QTLs are not linked to the major QTL being mapped and seems to interact with environmental factors.

The finding that sorghum downy mildew resistance is determined by a relatively small number of QTLs agrees with the study of Agrama et al., (1) who reported that the inheritance of sorghum downy mildew resistance in maize is governed by two QTLs on chromosome 1 and a third QTL on chromosome 9 which is in a similar position to a minor QTL identified in the resistant parent of this study. Also, earlier studies on the inheritance of Philippine downy mildew resistance indicated that only a few genes controlled the reaction and resistance was partially dominant (11). The additivity effect of the QTLs detected in our study in consistent with results

from previous studies. However, other studies have demonstrated that such an assumption might not be valid in all cases. The results of Borges, Handoo et al., and Singburaudom and Renfro indicated that both additive and non-additive gene actions were important in the control of resistance. Moreover the additive gene action was more prominent (5, 15, 25).

While our conclusions are in agreement with Agrama et al. on the position and the contribution of a QTL on chromosome 9 in addition to the low number of QTLs, their major QTLs mapped to chromosome 1 but ours were on chromosome 2. The difference can easily be explained by the use of different resistant line sources, and suggest the possibility that a cross between the two resistant lines could be used to pyramid resistance. However, the results of Lambert et al. suggested that disease or insect resistance genes or QTLs occur in clusters spread across the ten chromosomes of maize, and that chromosome 2 had the most mapped fragments in comparison to chromosome 9.

The QTL on chromosome 3 seems to correspond to an environmental factor(s) that is present in Corpus Christi Texas, and in the greenhouse trials so could reflect a difference in the pathogen population. On the other hand, the QTL on chromosome 9 may correspond either to local infection or higher disease pressure. The main effect QTL on chromosome 2 was responsible for resistance against both pathotypes of *P. sorghi*, 1 in Egypt and Corpus Christi, and 3 in the greenhouse, as well as *P. zeae* in Thailand (28). These results suggest that the resistance effect of the major QTL on chromosome 2 does not distinguish between pathogen populations indicating the power of utilizing such a factor in any sorghum downy mildew resistance breeding program.

These results revealed one major gene and two minor genes that control sorghum downy mildew resistance. These markers should be very useful in breeding programs in facilitating the introgression of the resistance genes

into commercial varieties. DNA markers in genomic regions of interest enable breeders to select on the basis of genotype rather than phenotype, which can be especially helpful if a target trait is time-consuming to score. Marker based breeding will revolutionize the process of cultivar development (31). Another interesting application of these results would be the use of these linked markers as a starting point for molecular approaches, such as chromosome walking, to clone the resistance genes (2). Marker-assisted selection for these loci should be productive for enhancing the expression of SDM resistance genes in maize across environments.

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APPENDIX A

LIST OF THE 221 F_2 INDIVIDUALS FORMED FROM THE CROSS (P3XP2)

No.	Pedigree
1	(DMR P3 x P2)-3.2
2	(DMR P3 x P2)-3.3
3	(DMR P3 x P2)-3.4
4	(DMR P3 x P2)-3.5
5	(DMR P3 x P2)-3.6
6	(DMR P3 x P2)-3.7
7	(DMR P3 x P2)-3.8
8	(DMR P3 x P2)-3.10
9	(DMR P3 x P2)-3.11
10	(DMR P3 x P2)-3.12
11	(DMR P3 x P2)-3.14
12	(DMR P3 x P2)-3.15
13	(DMR P3 x P2)-3.19
14	(DMR P3 x P2)-3.20
15	(DMR P3 x P2)-3.23
16	(DMR P3 x P2)-3.25
17	(DMR P3 x P2)-3.28
18	(DMR P3 x P2)-3.30
19	(DMR P3 x P2)-3.32
20	(DMR P3 x P2)-3.33
21	(DMR P3 x P2)-3.34
22	(DMR P3 x P2)-3.36
23	(DMR P3 x P2)-3.37
24	(DMR P3 x P2)-3.38
25	(DMR P3 x P2)-3.39
26	(DMR P3 x P2)-3.41
27	(DMR P3 x P2)-3.42
28	(DMR P3 x P2)-3.47
29	(DMR P3 x P2)-3.48
30	(DMR P3 x P2)-3.51
31	(DMR P3 x P2)-3.53
32	(DMR P3 x P2)-3.54
33	(DMR P3 x P2)-3.55
34	(DMR P3 x P2)-3.56
35	(DMR P3 x P2)-3.57
36	(DMR P3 x P2)-3.62
37	(DMR P3 x P2)-3.63
38	(DMR P3 x P2)-3.64
39	(DMR P3 x P2)-3.65
40	(DMR P3 x P2)-3.67
41	(DMR P3 x P2)-3.68

No.	Pedigree
75	(DMR P3 x P2)-3.132
76	(DMR P3 x P2)-3.137
77	(DMR P3 x P2)-3.138
78	(DMR P3 x P2)-3.139
79	(DMR P3 x P2)-3.140
80	(DMR P3 x P2)-3.142
81	(DMR P3 x P2)-3.144
82	(DMR P3 x P2)-3.145
83	(DMR P3 x P2)-3.146
84	(DMR P3 x P2)-3.148
85	(DMR P3 x P2)-3.151
86	(DMR P3 x P2)-3.152
87	(DMR P3 x P2)-3.153
88	(DMR P3 x P2)-3.154
89	(DMR P3 x P2)-3.155
90	(DMR P3 x P2)-3.159
91	(DMR P3 x P2)-4.1
92	(DMR P3 x P2)-4.2
93	(DMR P3 x P2)-4.3
94	(DMR P3 x P2)-4.4
95	(DMR P3 x P2)-4.6
96	(DMR P3 x P2)-4.7
97	(DMR P3 x P2)-4.8
98	(DMR P3 x P2)-4.9
99	(DMR P3 x P2)-4.10
100	(DMR P3 x P2)-4.11
101	(DMR P3 x P2)-4.12
102	(DMR P3 x P2)-4.13
103	(DMR P3 x P2)-4.15
104	(DMR P3 x P2)-4.16
105	(DMR P3 x P2)-4.17
106	(DMR P3 x P2)-4.18
107	(DMR P3 x P2)-4.19
108	(DMR P3 x P2)-4.20
109	(DMR P3 x P2)-4.21
110	(DMR P3 x P2)-4.22
111	(DMR P3 x P2)-4.24
112	(DMR P3 x P2)-4.27
113	(DMR P3 x P2)-4.28
114	(DMR P3 x P2)-4.29
115	(DMR P3 x P2)-4.30

No.	Pedigree
149	(DMR P3 x P2)-4.81
150	(DMR P3 x P2)-4.84
151	(DMR P3 x P2)-4.85
152	(DMR P3 x P2)-4.87
153	(DMR P3 x P2)-4.88
154	(DMR P3 x P2)-4.89
155	(DMR P3 x P2)-4.90
156	(DMR P3 x P2)-4.93
157	(DMR P3 x P2)-4.97
158	(DMR P3 x P2)-4.99
159	(DMR P3 x P2)-4.100
160	(DMR P3 x P2)-4.102
161	(DMR P3 x P2)-4.104
162	(DMR P3 x P2)-4.106
163	(DMR P3 x P2)-4.108
164	(DMR P3 x P2)-4.110
165	(DMR P3 x P2)-4.112
166	(DMR P3 x P2)-4.114
167	(DMR P3 x P2)-4.115
168	(DMR P3 x P2)-4.116
169	(DMR P3 x P2)-4.117
170	(DMR P3 x P2)-4.118
171	(DMR P3 x P2)-4.119
172	(DMR P3 x P2)-4.120
173	(DMR P3 x P2)-4.122
174	(DMR P3 x P2)-4.125
175	(DMR P3 x P2)-4.126
176	(DMR P3 x P2)-4.127
177	(DMR P3 x P2)-4.129
178	(DMR P3 x P2)-4.131
179	(DMR P3 x P2)-4.132
180	(DMR P3 x P2)-4.133
181	(DMR P3 x P2)-4.135
182	(DMR P3 x P2)-4.137
183	(DMR P3 x P2)-4.138
184	(DMR P3 x P2)-4.139
185	(DMR P3 x P2)-4.141
186	(DMR P3 x P2)-4.142
187	(DMR P3 x P2)-4.144
188	(DMR P3 x P2)-4.146
189	(DMR P3 x P2)-4.147

No.	Pedigree
42	(DMR P3 x P2)-3.69
43	(DMR P3 x P2)-3.71
44	(DMR P3 x P2)-3.74
45	(DMR P3 x P2)-3.76
46	(DMR P3 x P2)-3.77
47	(DMR P3 x P2)-3.78
48	(DMR P3 x P2)-3.79
49	(DMR P3 x P2)-3.80
50	(DMR P3 x P2)-3.81
51	(DMR P3 x P2)-3.82
52	(DMR P3 x P2)-3.83
53	(DMR P3 x P2)-3.84
54	(DMR P3 x P2)-3.85
55	(DMR P3 x P2)-3.87
56	(DMR P3 x P2)-3.89
57	(DMR P3 x P2)-3.91
58	(DMR P3 x P2)-3.92
59	(DMR P3 x P2)-3.93
60	(DMR P3 x P2)-3.94
61	(DMR P3 x P2)-3.96
62	(DMR P3 x P2)-3.99
63	(DMR P3 x P2)-3.102
64	(DMR P3 x P2)-3.103
65	(DMR P3 x P2)-3.106
66	(DMR P3 x P2)-3.107
67	(DMR P3 x P2)-3.112
68	(DMR P3 x P2)-3.114
69	(DMR P3 x P2)-3.117
70	(DMR P3 x P2)-3.118
71	(DMR P3 x P2)-3.125
72	(DMR P3 x P2)-3.128
73	(DMR P3 x P2)-3.129
74	(DMR P3 x P2)-3.131

No.	Pedigree
116	(DMR P3 x P2)-4.32
117	(DMR P3 x P2)-4.33
118	(DMR P3 x P2)-4.34
119	(DMR P3 x P2)-4.36
120	(DMR P3 x P2)-4.38
121	(DMR P3 x P2)-4.39
122	(DMR P3 x P2)-4.40
123	(DMR P3 x P2)-4.41
124	(DMR P3 x P2)-4.42
125	(DMR P3 x P2)-4.43
126	(DMR P3 x P2)-4.44
127	(DMR P3 x P2)-4.45
128	(DMR P3 x P2)-4.47
129	(DMR P3 x P2)-4.48
130	(DMR P3 x P2)-4.52
131	(DMR P3 x P2)-4.54
132	(DMR P3 x P2)-4.55
133	(DMR P3 x P2)-4.56
134	(DMR P3 x P2)-4.57
135	(DMR P3 x P2)-4.58
136	(DMR P3 x P2)-4.59
137	(DMR P3 x P2)-4.60
138	(DMR P3 x P2)-4.61
139	(DMR P3 x P2)-4.64
140	(DMR P3 x P2)-4.66
141	(DMR P3 x P2)-4.70
142	(DMR P3 x P2)-4.71
143	(DMR P3 x P2)-4.72
144	(DMR P3 x P2)-4.74
145	(DMR P3 x P2)-4.75
146	(DMR P3 x P2)-4.76
147	(DMR P3 x P2)-4.77
148	(DMR P3 x P2)-4.78

No.	Pedigree
190	(DMR P3 x P2)-4.149
191	(DMR P3 x P2)-4.150
192	(DMR P3 x P2)-4.151
193	(DMR P3 x P2)-4.152
194	(DMR P3 x P2)-4.153
195	(DMR P3 x P2)-4.155
196	(DMR P3 x P2)-4.156
197	(DMR P3 x P2)-4.157
198	(DMR P3 x P2)-4.158
199	(DMR P3 x P2)-4.161
200	(DMR P3 x P2)-4.164
201	(DMR P3 x P2)-4.165
202	(DMR P3 x P2)-4.166
203	(DMR P3 x P2)-4.167
204	(DMR P3 x P2)-4.168
205	(DMR P3 x P2)-4.171
206	(DMR P3 x P2)-4.172
207	(DMR P3 x P2)-4.173
208	(DMR P3 x P2)-4.174
209	(DMR P3 x P2)-4.176
210	(DMR P3 x P2)-4.178
211	(DMR P3 x P2)-4.179
212	(DMR P3 x P2)-4.180
213	(DMR P3 x P2)-4.181
214	(DMR P3 x P2)-4.183
215	(DMR P3 x P2)-4.184
216	(DMR P3 x P2)-4.188
217	(DMR P3 x P2)-4.189
218	(DMR P3 x P2)-4.191
219	(DMR P3 x P2)-4.192
220	(DMR P3 x P2)-4.193
221	(DMR P3 x P2)-4.194

APPENDIX B

LIST OF RFLP PROBES USED FOR PARENTAL SCREENING

No.	Probe ID
1	umc161
2	umc164
3	umc167
4	umc14
5	npi239
6	umc36
7	umc55
8	umc6
9	csu25
10	umc10
11	umc3
12	umc121
13	umc123
14	umc156
15	umc90
16	umc38
17	umc65
18	umc85
19	csu8
20	csu129
21	umc168
22	csu142
23	umc8
24	umc7
25	umc103
26	csu54
27	umc109
28	umc153
29	umc130
30	umc163
31	csu136
32	csu46
33	umc107
34	umc157
35	umc86
36	umc122
37	umc135
38	umc53
39	umc17
40	umc60

No.	Probe ID
41	umc63
42	umc154
43	umc133
44	umc19
45	umc42
46	umc87
47	csu173
48	umc104
49	umc54
50	umc147
51	csu60
52	umc132
53	umc177
54	umc21
55	umc151
56	npi110
57	umc12
58	csu110
59	csu155
60	csu93
61	umc113
62	umc81
63	umc44
64	npi290
65	umc8
66	umc128
67	csu61
68	csu40
69	csu4
70	umc171
71	umc32
72	npi249
73	umc39
74	umc24
75	csu100
76	npi409
77	umc166
78	npi237
79	bnl5.71
80	umc59

No.	Probe ID
81	umc173
82	umc62
83	asg52
84	umc149
85	npi278
86	umc89
87	umc150
88	umc105
89	bnl14.28
90	npi285
91	csu86
92	npi232
93	bnl5.62
94	csu154
95	umc23
96	umc83
97	umc106
98	npi238
99	npi414
100	bnl6.32
101	bnl8.45
102	csu133
103	csu148
104	umc92
105	umc165
106	umc16
107	umc15
108	csu39
109	bnl8.33
110	umc68
111	csu56
112	umc150
113	php20581
114	umc45
115	php1106
116	csu11
117	umc93
118	umc102
119	umc1860
120	csu110

No.	Probe ID
121	umc20
122	umc64
123	umc2
124	umc34
125	php3853
126	umc176
127	umc29
128	bnl8.23
129	umc8
130	umc67
131	umc119
132	umc140
133	umc84
134	umc139
135	umc88
136	umc111
137	umc43
138	umc40
139	umc70
140	umc120
141	umc127
142	npi287
143	npi235
144	npi277
145	npi438
146	php4233
147	php20725
148	php20608
149	bnl5.46
150	bnl10.06
151	bnl15.4
152	bnl14.07
153	bnl8.17
154	bnl7.49
155	csu26
156	csu12
157	csu48
158	asg8
159	umc71
160	bnl3.04

APPENDIX C

LIST OF SSR PRIMERS USED FOR PARENTAL SCREENING

No.	SSR ID
1	mmc0092
2	umc1041
3	bnlg1014
4	bnlg1112
5	bnlg1124
6	bnlg1179
7	umc1071
8	bnlg1007
9	bnlg1178
10	bnlg1429
11	bnlg1614
12	bnlg1627
13	bnlg1803
14	umc1070
15	bnlg182
16	bnlg1203
17	bnlg1458
18	bnlg1953
19	bnlg2180
20	bnlg2204
21	umc1044
22	bnlg1016
23	bnlg1811
24	bnlg2238
25	bnlg652
26	bnlg1832
27	bnlg1886
28	bnlg2086
29	umc1076
30	bnlg1041
31	bnlg1273
32	bnlg1598
33	bnlg1908
34	mmc0011
35	mmc0031
36	bnlg1025
37	bnlg1044
38	bnlg1629
39	bnlg1643
40	bnlg2228

No.	SSR ID
125	phi127
126	mmc0022
127	phi049
128	umc1057
129	bnlg1520
130	bnlg1144
131	bnlg1019
132	bnlg1447
133	bnlg1452
134	bnlg1628
135	bnlg1638
136	bnlg1647
137	bnlg1904
138	bnlg2047
139	bnlg2136
140	phi029
141	umc1025
142	bnlg1030
143	bnlg1022
144	bnlg1035
145	bnlg1113
146	bnlg1117
147	bnlg1246
148	bnlg1399
149	bnlg1505
150	bnlg1957
151	bnlg1601
152	dupssr17
153	dupssr23
154	umc1027
155	bnlg197
156	bnlg1160
157	bnlg1605
158	bnlg1779
159	bnlg1931
160	bnlg1108
161	bnlg1350
162	bnlg2243
163	bnlg1182
164	bnlg1257

No.	SSR ID
249	bnlg1188
250	bnlg1422
251	bnlg1432
252	bnlg1433
253	bnlg1538
254	bnlg1641
255	bnlg1753
256	bnlg1867
257	mmc0071
258	mmc0001
259	bnlg490
260	nc005
261	mmc0321
262	mmc0081
263	bnlg2097
264	bnlg2191
265	phi077
266	umc1018
267	bnlg1371
268	bnlg2151
269	y1SSR
270	bnlg480
271	nc009
272	nc010
273	phi031
274	bnlg1443
275	bnlg1617
276	bnlg1702
277	bnlg1732
278	bnlg1922
279	bnlg2249
280	mmc0241
281	nc012
282	nc013
283	phi025
284	phi129
285	umc1087
286	bnlg345
287	phi070
288	bnlg1136

No.	SSR ID
373	bnlg1082
374	bnlg1372
375	bnlg1401
376	bnlg1913
377	phi017
378	umc1033
379	umc1037
380	bnlg127
381	bnlg430
382	bnlg1687
383	bnlg1730
384	mmc0051
385	nc134
386	phi027
387	phi061
388	phi065
389	phi016
390	phi032
391	bnlg1012
392	bnlg1091
393	bnlg1129
394	bnlg1209
395	bnlg1270
396	bnlg1884
397	bnlg128
398	bnlg279
399	bnlg619
400	bnlg1191
401	bnlg1375
402	bnlg1506
403	bnlg1525
404	bnlg1588
405	dupssr29
406	phi117
407	phi118
408	umc1045
409	bnlg1451
410	phi052
411	bnlg210
412	bnlg640

No.	SSR ID
41	dupssr12
42	mmc0041
43	bnlg400
44	bnlg1331
45	bnlg1502
46	bnlg1597
47	bnlg1720
48	phi055
49	bnlg1347
50	bnlg1671
51	bnlg131
52	bnlg504
53	bnlg2123
54	phi064
55	umc1064
56	mmc0063
57	bnlg1092
58	bnlg1338
59	bnlg469
60	bnlg1017
61	bnlg1302
62	bnlg1327
63	bnlg2042
64	phi098
65	bnlg381
66	bnlg1064
67	bnlg1537
68	bnlg1621
69	umc1026
70	bnlg108
71	bnlg166
72	bnlg1018
73	bnlg1175
74	bnlg1613
75	phi083
76	umc1003
77	umc1024
78	bnlg180
79	bnlg371
80	bnlg1036

No.	SSR ID
165	bnlg1536
166	bnlg1754
167	umc1052
168	umc1062
169	bnlg1098
170	bnlg372
171	bnlg1370
172	umc1008
173	bnlg1241
174	bnlg1318
175	bnlg1434
176	umc1017
177	umc1022
178	bnlg1126
179	bnlg1162
180	umc1067
181	umc1088
182	bnlg667
183	bnlg1217
184	bnlg1265
185	bnlg1729
186	bnlg1755
187	umc1031
188	bnlg1741
189	bnlg1137
190	bnlg1784
191	bnlg1927
192	bnlg2291
193	dupssr34
194	bnlg1444
195	bnlg2162
196	dupssr28
197	phi093
198	umc1086
199	bnlg1019
200	bnlg1565
201	bnlg1917
202	bnlg589
203	bnlg1337
204	bnlg1890

No.	SSR ID
289	bnlg1521
290	bnlg1740
291	bnlg1759
292	phi123
293	umc1063
294	bnlg1367
295	bnlg1686
296	mmc0171
297	bnlg1200
298	bnlg1292
299	bnlg2160
300	phi057
301	bnlg398
302	bnlg657
303	bnlg1003
304	bnlg1094
305	bnlg1164
306	bnlg1247
307	bnlg1380
308	bnlg1792
309	bnlg1808
310	bnlg2203
311	bnlg2233
312	phi114
313	umc1016
314	umc1036
315	bnlg339
316	bnlg434
317	bnlg572
318	bnlg1070
319	bnlg1305
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485	umc1078
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No.	SSR ID
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371	umc1040
372	bnlg244

No.	SSR ID
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APPENDIX D

GENOTYPIC DATA FOR THE 220 F_2 INDIVIDUALS

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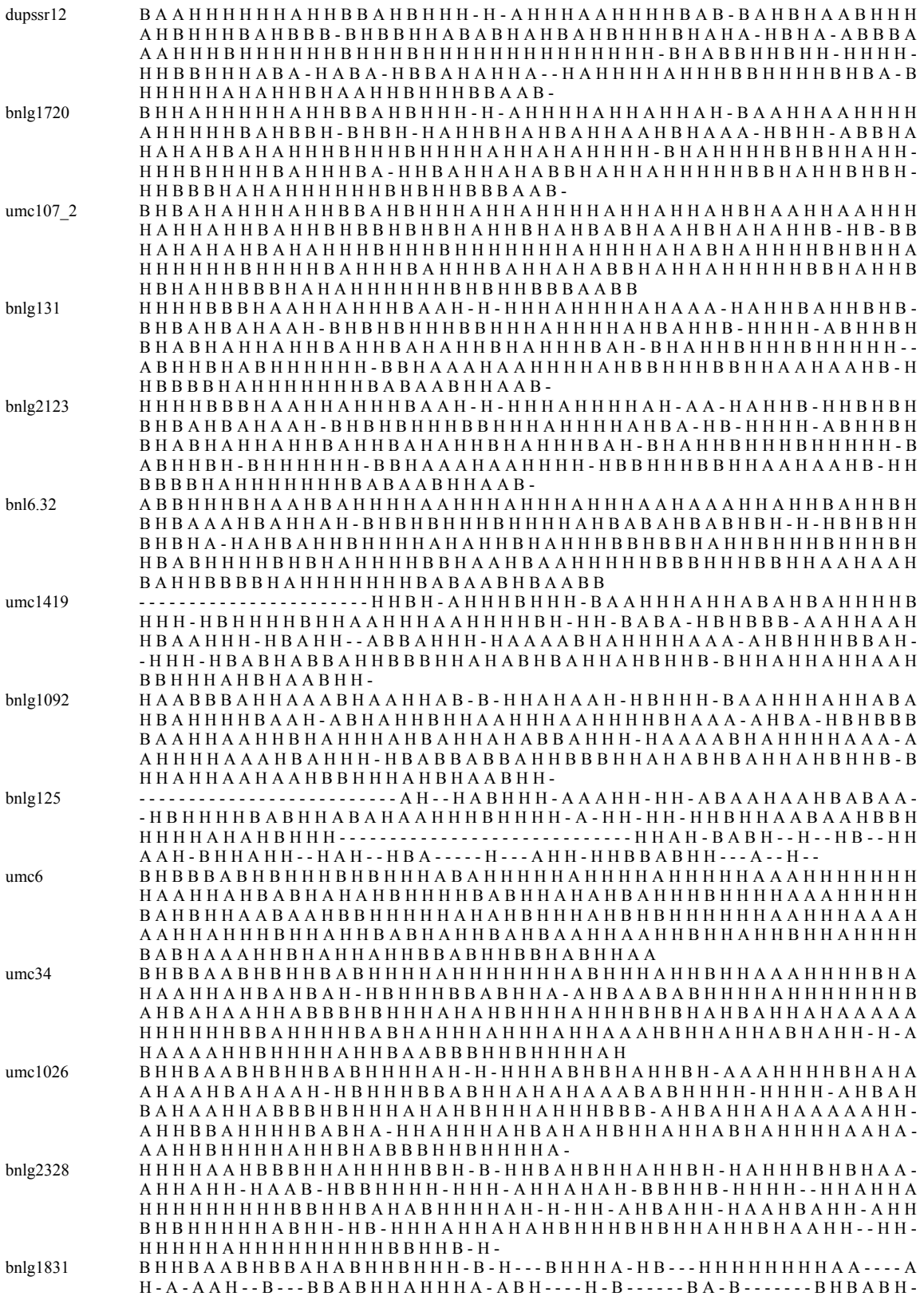
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bnlg1831
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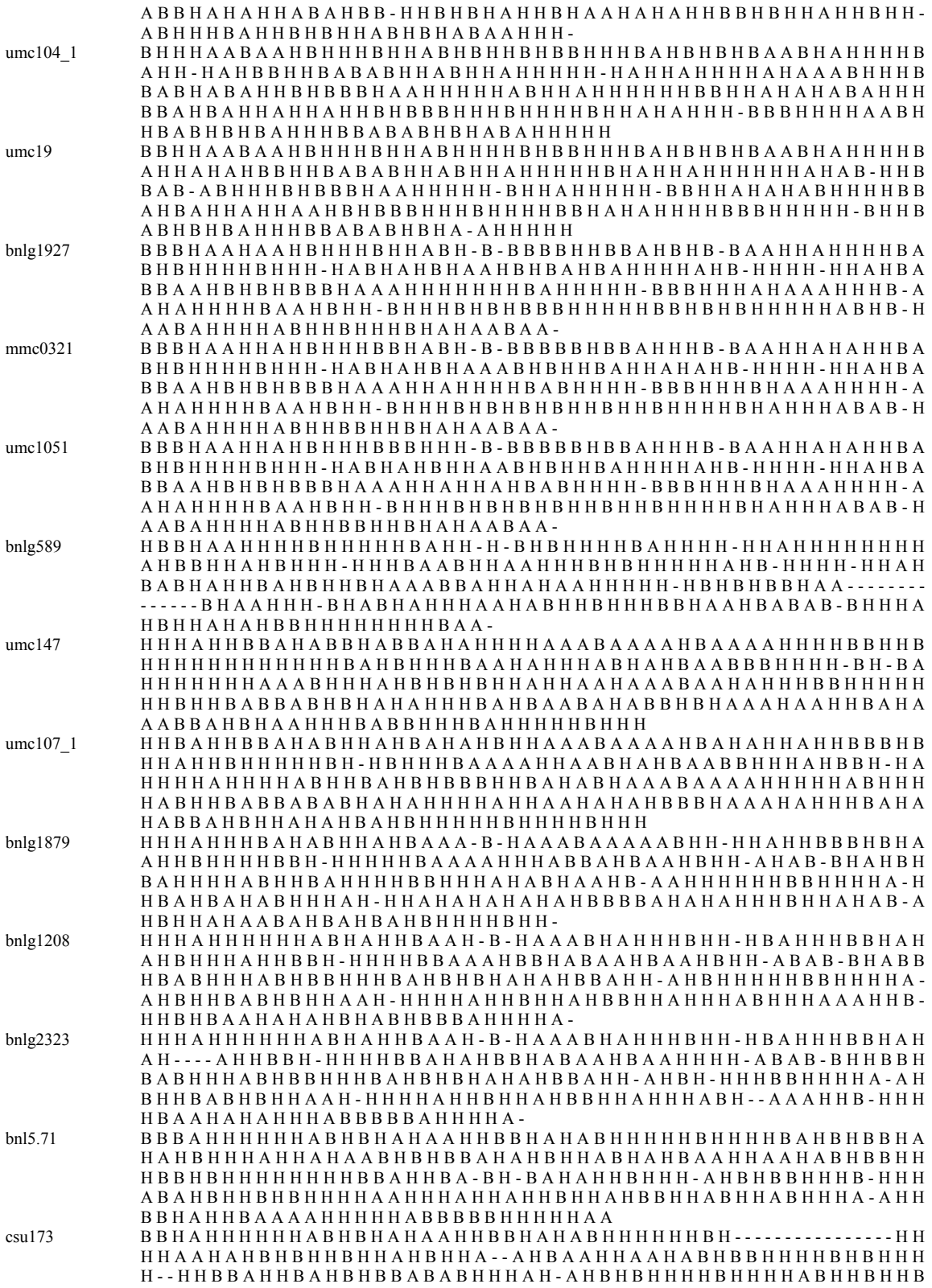
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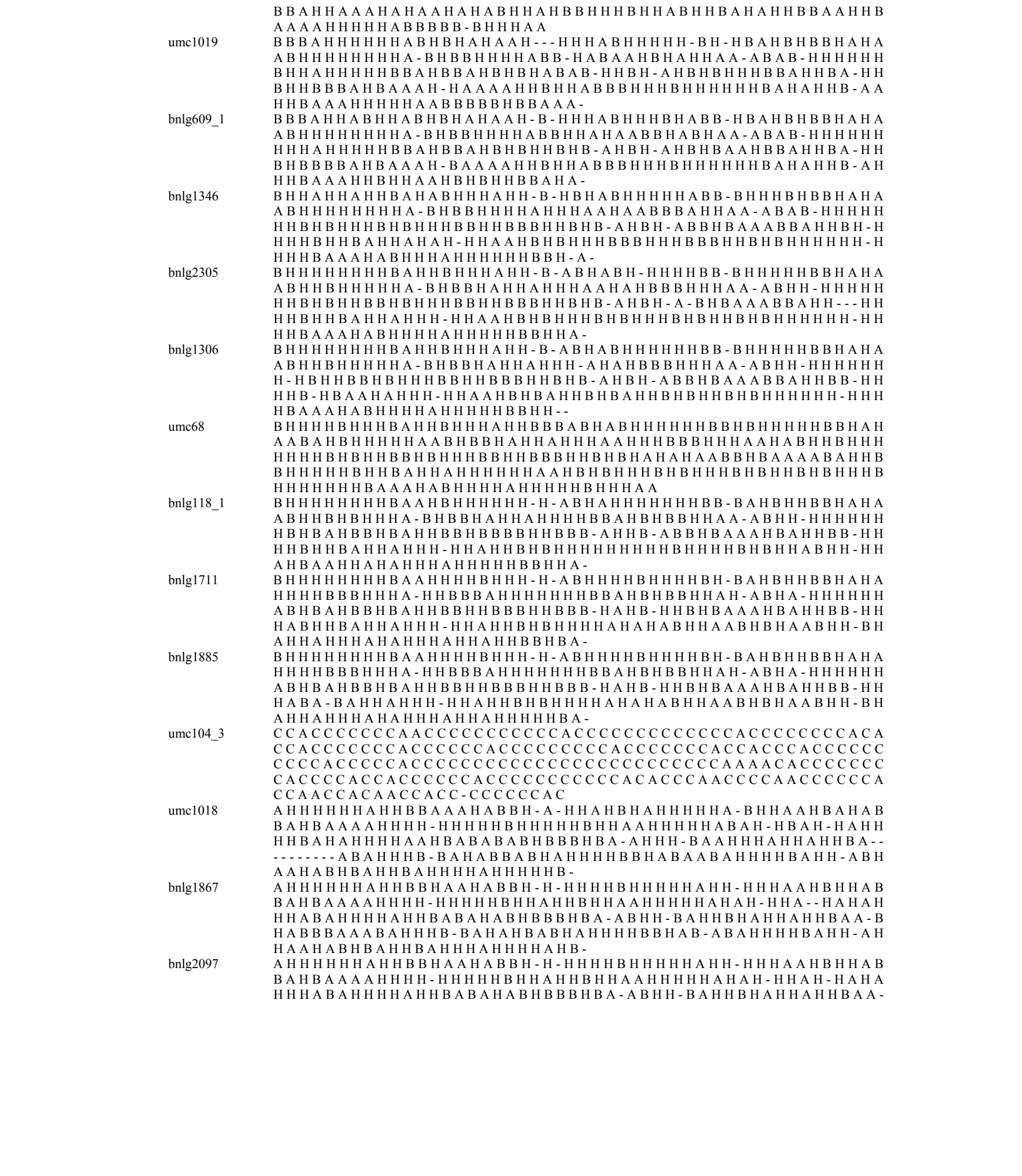
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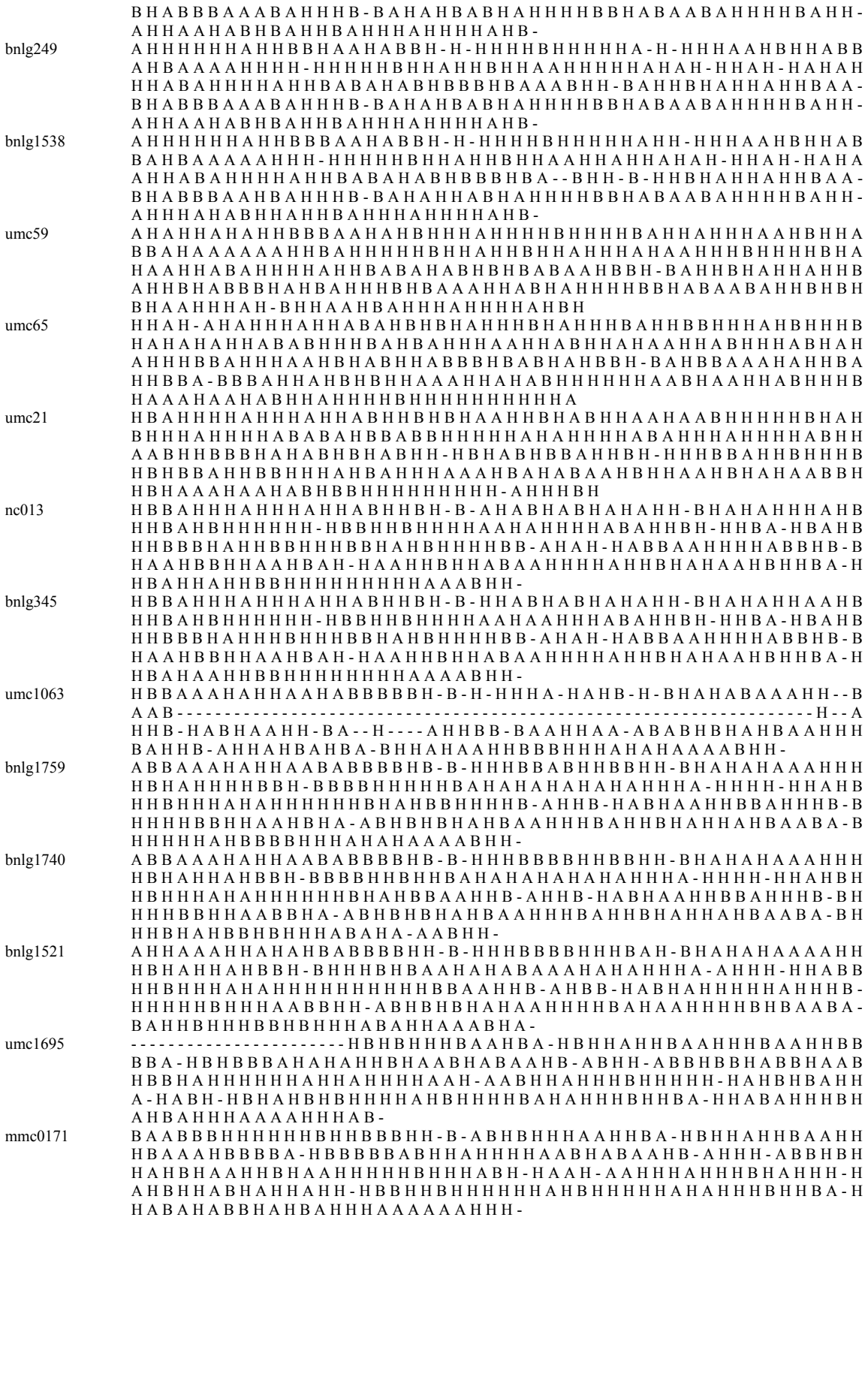
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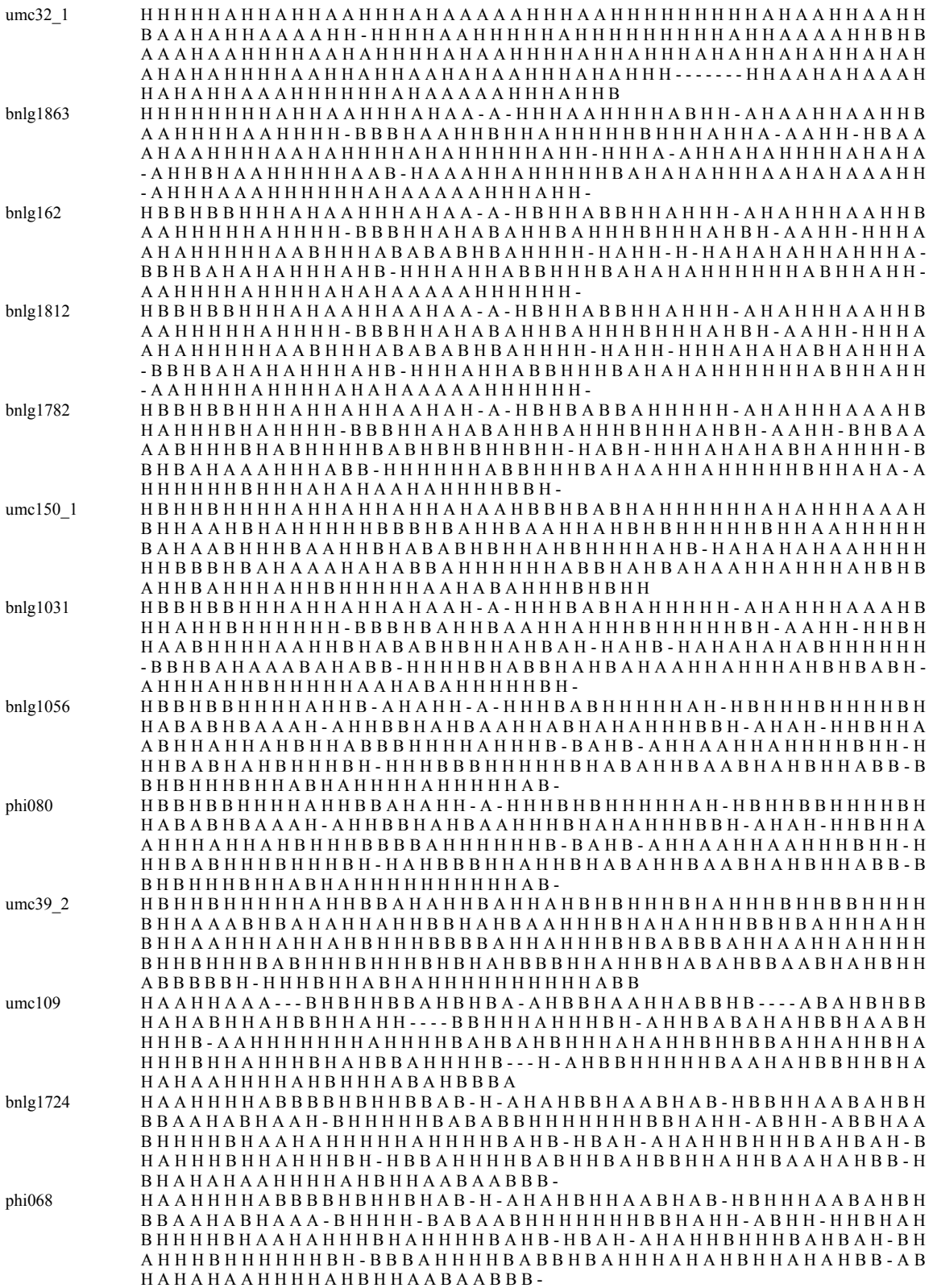
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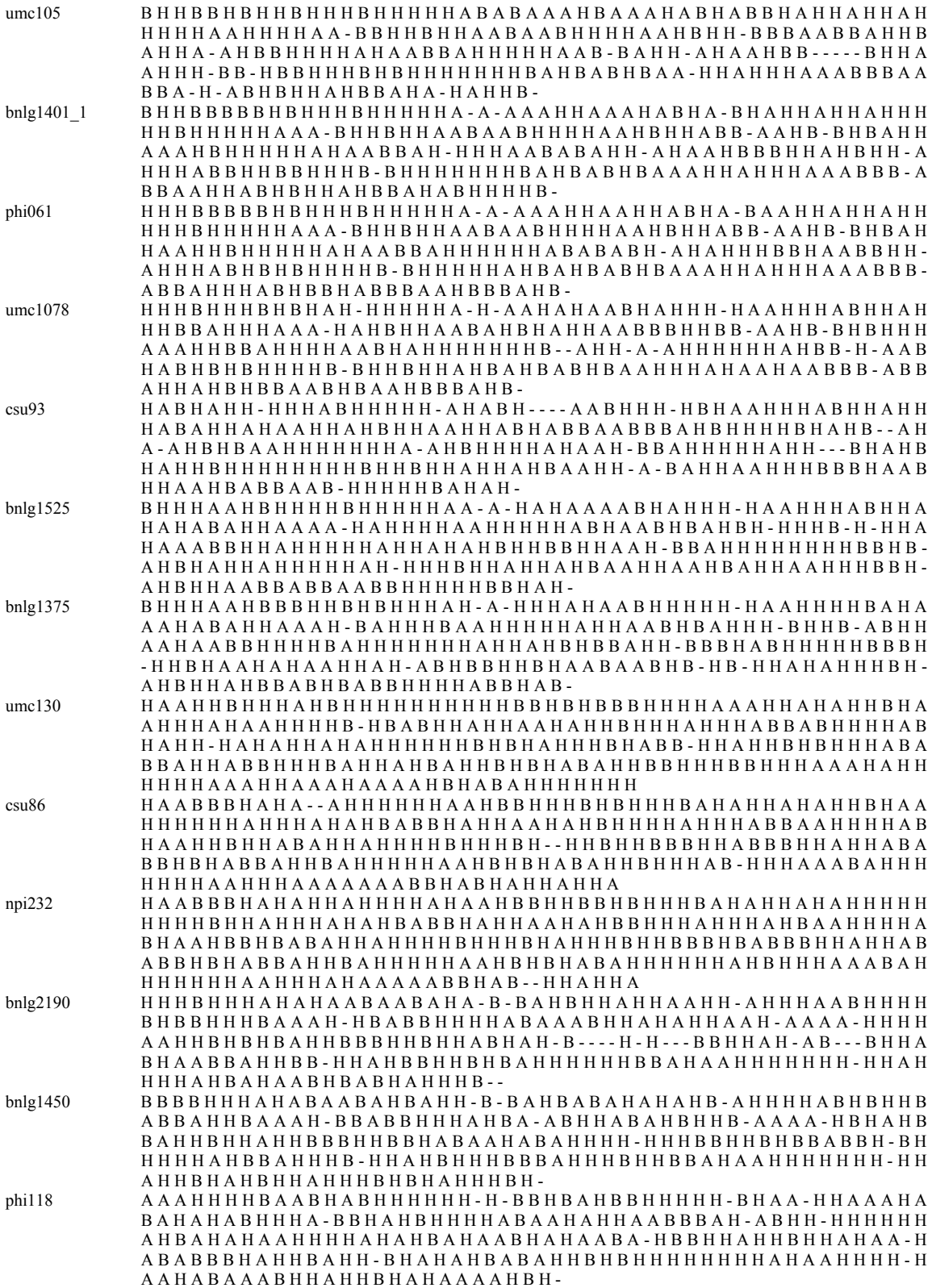
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APPENDIX E

TRANSFORMED PHENOTYPIC DATA FOR SIT 1 THAILAND

Pedigree	%
(DMR P3 x P2)-3.2	13.64
(DMR P3 x P2)-3.3	26.88
(DMR P3 x P2)-3.4	24.46
(DMR P3 x P2)-3.5	60.05
(DMR P3 x P2)-3.6	33.46
(DMR P3 x P2)-3.7	35.21
(DMR P3 x P2)-3.8	10.59
(DMR P3 x P2)-3.10	27.57
(DMR P3 x P2)-3.11	28.32
(DMR P3 x P2)-3.12	33.66
(DMR P3 x P2)-3.14	47.61
(DMR P3 x P2)-3.15	15.79
(DMR P3 x P2)-3.19	63.44
(DMR P3 x P2)-3.20	62.34
(DMR P3 x P2)-3.23	41.25
(DMR P3 x P2)-3.25	34.16
(DMR P3 x P2)-3.28	0.70
(DMR P3 x P2)-3.30	10.77
(DMR P3 x P2)-3.32	58.65
(DMR P3 x P2)-3.33	10.65
(DMR P3 x P2)-3.34	30.60
(DMR P3 x P2)-3.36	29.31
(DMR P3 x P2)-3.37	33.37
(DMR P3 x P2)-3.38	82.44
(DMR P3 x P2)-3.39	85.03
(DMR P3 x P2)-3.41	73.31
(DMR P3 x P2)-3.42	19.02
(DMR P3 x P2)-3.47	6.06
(DMR P3 x P2)-3.48	47.99
(DMR P3 x P2)-3.51	0.70
(DMR P3 x P2)-3.53	5.84
(DMR P3 x P2)-3.54	52.16
(DMR P3 x P2)-3.55	25.08
(DMR P3 x P2)-3.56	53.03
(DMR P3 x P2)-3.57	27.09
(DMR P3 x P2)-3.62	85.27
(DMR P3 x P2)-3.63	78.33
(DMR P3 x P2)-3.64	6.62
(DMR P3 x P2)-3.65	14.58
(DMR P3 x P2)-3.67	33.14

Pedigree	%
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(DMR P3 x P2)-3.138	31.95
(DMR P3 x P2)-3.139	44.20
(DMR P3 x P2)-3.140	65.44
(DMR P3 x P2)-3.142	89.34
(DMR P3 x P2)-3.144	11.55
(DMR P3 x P2)-3.145	0.70
(DMR P3 x P2)-3.146	0.70
(DMR P3 x P2)-3.148	0.70
(DMR P3 x P2)-3.151	39.91
(DMR P3 x P2)-3.152	17.16
(DMR P3 x P2)-3.153	0.70
(DMR P3 x P2)-3.154	18.23
(DMR P3 x P2)-3.155	36.42
(DMR P3 x P2)-3.159	77.24
(DMR P3 x P2)-4.1	78.25
(DMR P3 x P2)-4.2	52.75
(DMR P3 x P2)-4.3	51.94
(DMR P3 x P2)-4.4	40.53
(DMR P3 x P2)-4.6	30.20
(DMR P3 x P2)-4.7	4.89
(DMR P3 x P2)-4.8	38.44
(DMR P3 x P2)-4.9	0.70
(DMR P3 x P2)-4.10	77.68
(DMR P3 x P2)-4.11	15.17
(DMR P3 x P2)-4.12	35.68
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(DMR P3 x P2)-4.30	27.40

Pedigree	%
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(DMR P3 x P2)-4.102	36.81
(DMR P3 x P2)-4.104	33.52
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(DMR P3 x P2)-4.108	41.35
(DMR P3 x P2)-4.110	73.59
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Pedigree	%
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(DMR P3 x P2)-3.77	77.35
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(DMR P3 x P2)-3.81	36.58
(DMR P3 x P2)-3.82	13.52
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(DMR P3 x P2)-3.107	0.70
(DMR P3 x P2)-3.112	62.23
(DMR P3 x P2)-3.114	70.99
(DMR P3 x P2)-3.117	79.57
(DMR P3 x P2)-3.118	36.97
(DMR P3 x P2)-3.125	33.94
(DMR P3 x P2)-3.128	20.91
(DMR P3 x P2)-3.129	79.67
(DMR P3 x P2)-3.131	36.44
(DMR P3 x P2)-3.132	33.36

Pedigree	%
(DMR P3 x P2)-4.32	31.18
(DMR P3 x P2)-4.33	26.08
(DMR P3 x P2)-4.34	83.98
(DMR P3 x P2)-4.36	7.87
(DMR P3 x P2)-4.38	89.34
(DMR P3 x P2)-4.39	89.34
(DMR P3 x P2)-4.40	81.98
(DMR P3 x P2)-4.41	37.63
(DMR P3 x P2)-4.42	0.70
(DMR P3 x P2)-4.43	8.97
(DMR P3 x P2)-4.44	46.98
(DMR P3 x P2)-4.45	55.82
(DMR P3 x P2)-4.47	29.17
(DMR P3 x P2)-4.48	22.20
(DMR P3 x P2)-4.52	89.34
(DMR P3 x P2)-4.54	34.12
(DMR P3 x P2)-4.55	39.19
(DMR P3 x P2)-4.56	68.57
(DMR P3 x P2)-4.57	27.08
(DMR P3 x P2)-4.58	5.84
(DMR P3 x P2)-4.59	53.01
(DMR P3 x P2)-4.60	19.36
(DMR P3 x P2)-4.61	47.13
(DMR P3 x P2)-4.64	70.75
(DMR P3 x P2)-4.66	29.66
(DMR P3 x P2)-4.70	32.42
(DMR P3 x P2)-4.71	14.74
(DMR P3 x P2)-4.72	28.34
(DMR P3 x P2)-4.74	12.55
(DMR P3 x P2)-4.75	0.70
(DMR P3 x P2)-4.76	64.91
(DMR P3 x P2)-4.77	48.25
(DMR P3 x P2)-4.78	83.43
(DMR P3 x P2)-4.81	0.70

Pedigree	%
(DMR P3 x P2)-4.149	31.70
(DMR P3 x P2)-4.150	17.34
(DMR P3 x P2)-4.151	68.86
(DMR P3 x P2)-4.152	29.89
(DMR P3 x P2)-4.153	0.70
(DMR P3 x P2)-4.155	40.25
(DMR P3 x P2)-4.156	29.09
(DMR P3 x P2)-4.157	28.00
(DMR P3 x P2)-4.158	26.05
(DMR P3 x P2)-4.161	39.45
(DMR P3 x P2)-4.164	27.55
(DMR P3 x P2)-4.165	40.81
(DMR P3 x P2)-4.166	80.47
(DMR P3 x P2)-4.167	33.43
(DMR P3 x P2)-4.168	6.32
(DMR P3 x P2)-4.171	31.15
(DMR P3 x P2)-4.172	10.57
(DMR P3 x P2)-4.173	0.70
(DMR P3 x P2)-4.174	36.99
(DMR P3 x P2)-4.176	28.92
(DMR P3 x P2)-4.178	27.23
(DMR P3 x P2)-4.179	8.07
(DMR P3 x P2)-4.180	27.11
(DMR P3 x P2)-4.181	7.87
(DMR P3 x P2)-4.183	5.01
(DMR P3 x P2)-4.184	73.06
(DMR P3 x P2)-4.188	30.71
(DMR P3 x P2)-4.189	49.53
(DMR P3 x P2)-4.191	22.64
(DMR P3 x P2)-4.192	84.90
(DMR P3 x P2)-4.193	35.58
(DMR P3 x P2)-4.194	36.42

APPENDIX F

TRANSFORMED PHENOTYPIC DATA FOR SIT 2 THAILAND

Pedigree	%
(DMR P3 x P2)-3.2	0.70
(DMR P3 x P2)-3.3	4.89
(DMR P3 x P2)-3.4	5.15
(DMR P3 x P2)-3.5	17.94
(DMR P3 x P2)-3.6	5.46
(DMR P3 x P2)-3.7	20.95
(DMR P3 x P2)-3.8	0.70
(DMR P3 x P2)-3.10	0.70
(DMR P3 x P2)-3.11	9.20
(DMR P3 x P2)-3.12	9.17
(DMR P3 x P2)-3.14	0.70
(DMR P3 x P2)-3.15	0.70
(DMR P3 x P2)-3.19	10.39
(DMR P3 x P2)-3.20	0.70
(DMR P3 x P2)-3.23	10.05
(DMR P3 x P2)-3.25	5.01
(DMR P3 x P2)-3.28	0.70
(DMR P3 x P2)-3.30	15.41
(DMR P3 x P2)-3.32	12.23
(DMR P3 x P2)-3.33	0.70
(DMR P3 x P2)-3.34	9.33
(DMR P3 x P2)-3.36	5.84
(DMR P3 x P2)-3.37	16.31
(DMR P3 x P2)-3.38	11.38
(DMR P3 x P2)-3.39	28.12
(DMR P3 x P2)-3.41	13.29
(DMR P3 x P2)-3.42	8.17
(DMR P3 x P2)-3.47	0.70
(DMR P3 x P2)-3.48	12.82
(DMR P3 x P2)-3.51	0.70
(DMR P3 x P2)-3.53	0.70
(DMR P3 x P2)-3.54	21.91
(DMR P3 x P2)-3.55	14.04
(DMR P3 x P2)-3.56	5.64
(DMR P3 x P2)-3.57	9.20
(DMR P3 x P2)-3.62	18.33
(DMR P3 x P2)-3.63	8.28
(DMR P3 x P2)-3.64	0.70
(DMR P3 x P2)-3.65	0.70
(DMR P3 x P2)-3.67	0.70

Pedigree	%
(DMR P3 x P2)-3.137	0.70
(DMR P3 x P2)-3.138	4.89
(DMR P3 x P2)-3.139	4.89
(DMR P3 x P2)-3.140	13.64
(DMR P3 x P2)-3.142	25.05
(DMR P3 x P2)-3.144	5.46
(DMR P3 x P2)-3.145	0.70
(DMR P3 x P2)-3.146	0.70
(DMR P3 x P2)-3.148	0.70
(DMR P3 x P2)-3.151	10.69
(DMR P3 x P2)-3.152	16.30
(DMR P3 x P2)-3.153	12.93
(DMR P3 x P2)-3.154	0.70
(DMR P3 x P2)-3.155	0.70
(DMR P3 x P2)-3.159	9.33
(DMR P3 x P2)-4.1	15.76
(DMR P3 x P2)-4.2	22.16
(DMR P3 x P2)-4.3	20.13
(DMR P3 x P2)-4.4	0.70
(DMR P3 x P2)-4.6	7.87
(DMR P3 x P2)-4.7	0.70
(DMR P3 x P2)-4.8	0.70
(DMR P3 x P2)-4.9	0.70
(DMR P3 x P2)-4.10	22.54
(DMR P3 x P2)-4.11	0.70
(DMR P3 x P2)-4.12	0.70
(DMR P3 x P2)-4.13	26.18
(DMR P3 x P2)-4.15	0.70
(DMR P3 x P2)-4.16	9.33
(DMR P3 x P2)-4.17	0.70
(DMR P3 x P2)-4.18	7.37
(DMR P3 x P2)-4.19	9.66
(DMR P3 x P2)-4.20	5.84
(DMR P3 x P2)-4.21	5.64
(DMR P3 x P2)-4.22	0.70
(DMR P3 x P2)-4.24	0.70
(DMR P3 x P2)-4.27	0.70
(DMR P3 x P2)-4.28	7.61
(DMR P3 x P2)-4.29	9.37
(DMR P3 x P2)-4.30	0.70

Pedigree	%
(DMR P3 x P2)-4.84	0.70
(DMR P3 x P2)-4.85	11.98
(DMR P3 x P2)-4.87	6.96
(DMR P3 x P2)-4.88	6.78
(DMR P3 x P2)-4.89	10.57
(DMR P3 x P2)-4.90	9.09
(DMR P3 x P2)-4.93	4.89
(DMR P3 x P2)-4.97	0.70
(DMR P3 x P2)-4.99	10.81
(DMR P3 x P2)-4.100	0.70
(DMR P3 x P2)-4.102	4.78
(DMR P3 x P2)-4.104	0.70
(DMR P3 x P2)-4.106	11.41
(DMR P3 x P2)-4.108	7.87
(DMR P3 x P2)-4.110	5.46
(DMR P3 x P2)-4.112	4.89
(DMR P3 x P2)-4.114	18.34
(DMR P3 x P2)-4.115	15.41
(DMR P3 x P2)-4.116	5.46
(DMR P3 x P2)-4.117	7.87
(DMR P3 x P2)-4.118	15.61
(DMR P3 x P2)-4.119	4.89
(DMR P3 x P2)-4.120	0.70
(DMR P3 x P2)-4.122	0.70
(DMR P3 x P2)-4.125	16.48
(DMR P3 x P2)-4.126	16.22
(DMR P3 x P2)-4.127	0.70
(DMR P3 x P2)-4.129	0.70
(DMR P3 x P2)-4.131	0.70
(DMR P3 x P2)-4.132	5.30
(DMR P3 x P2)-4.133	0.70
(DMR P3 x P2)-4.135	12.86
(DMR P3 x P2)-4.137	0.70
(DMR P3 x P2)-4.138	20.65
(DMR P3 x P2)-4.139	0.70
(DMR P3 x P2)-4.141	0.70
(DMR P3 x P2)-4.142	5.46
(DMR P3 x P2)-4.144	0.70
(DMR P3 x P2)-4.146	0.70
(DMR P3 x P2)-4.147	0.70

Pedigree	%
(DMR P3 x P2)-3.68	0.70
(DMR P3 x P2)-3.71	18.97
(DMR P3 x P2)-3.74	4.89
(DMR P3 x P2)-3.76	0.70
(DMR P3 x P2)-3.77	5.15
(DMR P3 x P2)-3.78	7.16
(DMR P3 x P2)-3.79	5.01
(DMR P3 x P2)-3.80	7.37
(DMR P3 x P2)-3.81	6.62
(DMR P3 x P2)-3.82	12.70
(DMR P3 x P2)-3.83	8.17
(DMR P3 x P2)-3.84	15.38
(DMR P3 x P2)-3.85	17.68
(DMR P3 x P2)-3.87	0.70
(DMR P3 x P2)-3.89	0.70
(DMR P3 x P2)-3.91	18.34
(DMR P3 x P2)-3.92	21.70
(DMR P3 x P2)-3.93	18.61
(DMR P3 x P2)-3.94	11.47
(DMR P3 x P2)-3.96	0.70
(DMR P3 x P2)-3.99	11.24
(DMR P3 x P2)-3.102	0.70
(DMR P3 x P2)-3.103	9.58
(DMR P3 x P2)-3.106	0.70
(DMR P3 x P2)-3.107	4.89
(DMR P3 x P2)-3.112	4.78
(DMR P3 x P2)-3.114	16.18
(DMR P3 x P2)-3.117	13.24
(DMR P3 x P2)-3.118	4.89
(DMR P3 x P2)-3.125	8.97
(DMR P3 x P2)-3.128	7.87
(DMR P3 x P2)-3.129	9.20
(DMR P3 x P2)-3.131	19.91
(DMR P3 x P2)-3.132	5.64

Pedigree	%
(DMR P3 x P2)-4.32	5.46
(DMR P3 x P2)-4.33	0.70
(DMR P3 x P2)-4.34	9.66
(DMR P3 x P2)-4.36	0.70
(DMR P3 x P2)-4.38	17.38
(DMR P3 x P2)-4.39	26.00
(DMR P3 x P2)-4.40	11.27
(DMR P3 x P2)-4.41	15.01
(DMR P3 x P2)-4.42	4.89
(DMR P3 x P2)-4.43	0.70
(DMR P3 x P2)-4.44	22.33
(DMR P3 x P2)-4.45	6.06
(DMR P3 x P2)-4.47	4.57
(DMR P3 x P2)-4.48	8.89
(DMR P3 x P2)-4.52	34.42
(DMR P3 x P2)-4.54	5.15
(DMR P3 x P2)-4.55	14.97
(DMR P3 x P2)-4.56	9.58
(DMR P3 x P2)-4.57	0.70
(DMR P3 x P2)-4.58	0.70
(DMR P3 x P2)-4.59	0.70
(DMR P3 x P2)-4.60	12.63
(DMR P3 x P2)-4.61	9.03
(DMR P3 x P2)-4.64	0.70
(DMR P3 x P2)-4.66	0.70
(DMR P3 x P2)-4.70	5.01
(DMR P3 x P2)-4.71	6.62
(DMR P3 x P2)-4.72	10.81
(DMR P3 x P2)-4.74	7.61
(DMR P3 x P2)-4.75	14.14
(DMR P3 x P2)-4.76	8.28
(DMR P3 x P2)-4.77	8.28
(DMR P3 x P2)-4.78	17.11
(DMR P3 x P2)-4.81	0.70

Pedigree	%
(DMR P3 x P2)-4.149	5.01
(DMR P3 x P2)-4.150	0.70
(DMR P3 x P2)-4.151	19.27
(DMR P3 x P2)-4.152	6.62
(DMR P3 x P2)-4.153	0.70
(DMR P3 x P2)-4.155	17.21
(DMR P3 x P2)-4.156	15.61
(DMR P3 x P2)-4.157	0.70
(DMR P3 x P2)-4.158	5.15
(DMR P3 x P2)-4.161	9.53
(DMR P3 x P2)-4.164	13.22
(DMR P3 x P2)-4.165	9.33
(DMR P3 x P2)-4.166	10.15
(DMR P3 x P2)-4.167	13.29
(DMR P3 x P2)-4.168	5.84
(DMR P3 x P2)-4.171	11.70
(DMR P3 x P2)-4.172	0.70
(DMR P3 x P2)-4.173	0.70
(DMR P3 x P2)-4.174	7.87
(DMR P3 x P2)-4.176	4.78
(DMR P3 x P2)-4.178	0.70
(DMR P3 x P2)-4.179	0.70
(DMR P3 x P2)-4.180	0.70
(DMR P3 x P2)-4.181	0.70
(DMR P3 x P2)-4.183	0.70
(DMR P3 x P2)-4.184	12.06
(DMR P3 x P2)-4.188	21.68
(DMR P3 x P2)-4.189	12.55
(DMR P3 x P2)-4.191	0.70
(DMR P3 x P2)-4.192	16.94
(DMR P3 x P2)-4.193	16.12
(DMR P3 x P2)-4.194	0.70

APPENDIX G

TRANSFORMED PHENOTYPIC DATA FOR EGYPT

Pedigree	%
(DMR P3 x P2)-3.2	0.91
(DMR P3 x P2)-3.3	9.46
(DMR P3 x P2)-3.4	11.68
(DMR P3 x P2)-3.5	27.91
(DMR P3 x P2)-3.6	23.87
(DMR P3 x P2)-3.7	6.75
(DMR P3 x P2)-3.8	9.46
(DMR P3 x P2)-3.10	6.75
(DMR P3 x P2)-3.11	12.60
(DMR P3 x P2)-3.12	23.87
(DMR P3 x P2)-3.14	6.75
(DMR P3 x P2)-3.15	0.91
(DMR P3 x P2)-3.19	40.88
(DMR P3 x P2)-3.20	54.10
(DMR P3 x P2)-3.23	6.75
(DMR P3 x P2)-3.25	0.91
(DMR P3 x P2)-3.28	0.91
(DMR P3 x P2)-3.30	0.91
(DMR P3 x P2)-3.32	0.91
(DMR P3 x P2)-3.33	0.91
(DMR P3 x P2)-3.34	6.75
(DMR P3 x P2)-3.36	24.17
(DMR P3 x P2)-3.37	0.91
(DMR P3 x P2)-3.38	43.10
(DMR P3 x P2)-3.39	70.51
(DMR P3 x P2)-3.41	42.72
(DMR P3 x P2)-3.42	9.98
(DMR P3 x P2)-3.47	0.91
(DMR P3 x P2)-3.48	24.62
(DMR P3 x P2)-3.51	0.91
(DMR P3 x P2)-3.53	0.91
(DMR P3 x P2)-3.54	28.06
(DMR P3 x P2)-3.55	31.01
(DMR P3 x P2)-3.56	36.57
(DMR P3 x P2)-3.57	20.24
(DMR P3 x P2)-3.62	20.24
(DMR P3 x P2)-3.63	26.77
(DMR P3 x P2)-3.64	0.91
(DMR P3 x P2)-3.65	0.91
(DMR P3 x P2)-3.67	15.83

Pedigree	%
(DMR P3 x P2)-3.137	6.75
(DMR P3 x P2)-3.138	6.75
(DMR P3 x P2)-3.139	35.03
(DMR P3 x P2)-3.140	59.03
(DMR P3 x P2)-3.142	49.95
(DMR P3 x P2)-3.144	6.75
(DMR P3 x P2)-3.145	0.91
(DMR P3 x P2)-3.146	7.51
(DMR P3 x P2)-3.148	0.91
(DMR P3 x P2)-3.151	12.60
(DMR P3 x P2)-3.152	0.91
(DMR P3 x P2)-3.153	0.91
(DMR P3 x P2)-3.154	0.91
(DMR P3 x P2)-3.155	0.91
(DMR P3 x P2)-3.159	20.24
(DMR P3 x P2)-4.1	15.31
(DMR P3 x P2)-4.2	21.16
(DMR P3 x P2)-4.3	22.15
(DMR P3 x P2)-4.4	23.37
(DMR P3 x P2)-4.6	6.75
(DMR P3 x P2)-4.7	0.91
(DMR P3 x P2)-4.8	17.53
(DMR P3 x P2)-4.9	0.91
(DMR P3 x P2)-4.10	37.16
(DMR P3 x P2)-4.11	0.91
(DMR P3 x P2)-4.12	18.54
(DMR P3 x P2)-4.13	9.46
(DMR P3 x P2)-4.15	0.91
(DMR P3 x P2)-4.16	6.75
(DMR P3 x P2)-4.17	0.91
(DMR P3 x P2)-4.18	0.91
(DMR P3 x P2)-4.19	9.46
(DMR P3 x P2)-4.20	46.83
(DMR P3 x P2)-4.21	6.75
(DMR P3 x P2)-4.22	6.75
(DMR P3 x P2)-4.24	6.75
(DMR P3 x P2)-4.27	6.75
(DMR P3 x P2)-4.28	15.31
(DMR P3 x P2)-4.29	9.46
(DMR P3 x P2)-4.30	0.91

Pedigree	%
(DMR P3 x P2)-4.84	47.27
(DMR P3 x P2)-4.85	15.11
(DMR P3 x P2)-4.87	21.76
(DMR P3 x P2)-4.88	15.31
(DMR P3 x P2)-4.89	25.38
(DMR P3 x P2)-4.90	17.53
(DMR P3 x P2)-4.93	7.51
(DMR P3 x P2)-4.97	23.87
(DMR P3 x P2)-4.99	15.61
(DMR P3 x P2)-4.100	0.91
(DMR P3 x P2)-4.102	15.31
(DMR P3 x P2)-4.104	0.91
(DMR P3 x P2)-4.106	9.46
(DMR P3 x P2)-4.108	0.91
(DMR P3 x P2)-4.110	28.10
(DMR P3 x P2)-4.112	30.31
(DMR P3 x P2)-4.114	46.95
(DMR P3 x P2)-4.115	22.52
(DMR P3 x P2)-4.116	0.91
(DMR P3 x P2)-4.117	37.37
(DMR P3 x P2)-4.118	23.76
(DMR P3 x P2)-4.119	12.60
(DMR P3 x P2)-4.120	42.02
(DMR P3 x P2)-4.122	0.91
(DMR P3 x P2)-4.125	24.06
(DMR P3 x P2)-4.126	17.53
(DMR P3 x P2)-4.127	6.75
(DMR P3 x P2)-4.129	0.91
(DMR P3 x P2)-4.131	0.91
(DMR P3 x P2)-4.132	7.10
(DMR P3 x P2)-4.133	6.75
(DMR P3 x P2)-4.135	0.91
(DMR P3 x P2)-4.137	0.91
(DMR P3 x P2)-4.138	14.49
(DMR P3 x P2)-4.139	0.91
(DMR P3 x P2)-4.141	0.91
(DMR P3 x P2)-4.142	18.02
(DMR P3 x P2)-4.144	12.37
(DMR P3 x P2)-4.146	0.91
(DMR P3 x P2)-4.147	0.91

Pedigree	%
(DMR P3 x P2)-3.68	6.75
(DMR P3 x P2)-3.71	36.16
(DMR P3 x P2)-3.74	0.91
(DMR P3 x P2)-3.76	0.91
(DMR P3 x P2)-3.77	36.87
(DMR P3 x P2)-3.78	32.23
(DMR P3 x P2)-3.79	37.16
(DMR P3 x P2)-3.80	9.46
(DMR P3 x P2)-3.81	18.86
(DMR P3 x P2)-3.82	6.75
(DMR P3 x P2)-3.83	15.31
(DMR P3 x P2)-3.84	28.79
(DMR P3 x P2)-3.85	6.75
(DMR P3 x P2)-3.87	0.91
(DMR P3 x P2)-3.89	6.75
(DMR P3 x P2)-3.91	17.53
(DMR P3 x P2)-3.92	53.18
(DMR P3 x P2)-3.93	22.45
(DMR P3 x P2)-3.94	18.02
(DMR P3 x P2)-3.96	6.75
(DMR P3 x P2)-3.99	28.85
(DMR P3 x P2)-3.102	12.60
(DMR P3 x P2)-3.103	36.16
(DMR P3 x P2)-3.106	0.91
(DMR P3 x P2)-3.107	0.91
(DMR P3 x P2)-3.112	33.02
(DMR P3 x P2)-3.114	17.23
(DMR P3 x P2)-3.117	83.29
(DMR P3 x P2)-3.118	18.21
(DMR P3 x P2)-3.125	0.91
(DMR P3 x P2)-3.128	0.91
(DMR P3 x P2)-3.129	36.87
(DMR P3 x P2)-3.131	6.75
(DMR P3 x P2)-3.132	12.60

Pedigree	%
(DMR P3 x P2)-4.32	24.17
(DMR P3 x P2)-4.33	6.75
(DMR P3 x P2)-4.34	27.65
(DMR P3 x P2)-4.36	0.91
(DMR P3 x P2)-4.38	0.91
(DMR P3 x P2)-4.39	35.03
(DMR P3 x P2)-4.40	59.73
(DMR P3 x P2)-4.41	13.69
(DMR P3 x P2)-4.42	6.75
(DMR P3 x P2)-4.43	0.91
(DMR P3 x P2)-4.44	0.91
(DMR P3 x P2)-4.45	8.64
(DMR P3 x P2)-4.47	23.37
(DMR P3 x P2)-4.48	24.62
(DMR P3 x P2)-4.52	20.10
(DMR P3 x P2)-4.54	0.91
(DMR P3 x P2)-4.55	15.31
(DMR P3 x P2)-4.56	46.09
(DMR P3 x P2)-4.57	0.91
(DMR P3 x P2)-4.58	0.91
(DMR P3 x P2)-4.59	17.53
(DMR P3 x P2)-4.60	6.75
(DMR P3 x P2)-4.61	15.61
(DMR P3 x P2)-4.64	18.02
(DMR P3 x P2)-4.66	0.91
(DMR P3 x P2)-4.70	20.24
(DMR P3 x P2)-4.71	6.75
(DMR P3 x P2)-4.72	6.75
(DMR P3 x P2)-4.74	9.46
(DMR P3 x P2)-4.75	0.91
(DMR P3 x P2)-4.76	27.97
(DMR P3 x P2)-4.77	15.31
(DMR P3 x P2)-4.78	41.09
(DMR P3 x P2)-4.81	0.91

Pedigree	%
(DMR P3 x P2)-4.149	18.02
(DMR P3 x P2)-4.150	0.91
(DMR P3 x P2)-4.151	20.24
(DMR P3 x P2)-4.152	6.75
(DMR P3 x P2)-4.153	0.91
(DMR P3 x P2)-4.155	9.46
(DMR P3 x P2)-4.156	0.91
(DMR P3 x P2)-4.157	0.91
(DMR P3 x P2)-4.158	0.91
(DMR P3 x P2)-4.161	6.75
(DMR P3 x P2)-4.164	18.02
(DMR P3 x P2)-4.165	11.68
(DMR P3 x P2)-4.166	44.24
(DMR P3 x P2)-4.167	0.91
(DMR P3 x P2)-4.168	0.91
(DMR P3 x P2)-4.171	12.60
(DMR P3 x P2)-4.172	0.91
(DMR P3 x P2)-4.173	0.91
(DMR P3 x P2)-4.174	9.46
(DMR P3 x P2)-4.176	0.91
(DMR P3 x P2)-4.178	11.68
(DMR P3 x P2)-4.179	0.91
(DMR P3 x P2)-4.180	18.02
(DMR P3 x P2)-4.181	6.75
(DMR P3 x P2)-4.183	0.91
(DMR P3 x P2)-4.184	18.02
(DMR P3 x P2)-4.188	9.46
(DMR P3 x P2)-4.189	10.61
(DMR P3 x P2)-4.191	0.91
(DMR P3 x P2)-4.192	26.08
(DMR P3 x P2)-4.193	9.46
(DMR P3 x P2)-4.194	12.60

APPENDIX H

TRANSFORMED PHENOTYPIC DATA FOR GREENHOUSE LOCAL INFECTION

Pedigree	%
(DMR P3 x P2)-3.2	13.94
(DMR P3 x P2)-3.3	22.37
(DMR P3 x P2)-3.4	13.94
(DMR P3 x P2)-3.5	30.44
(DMR P3 x P2)-3.6	15.86
(DMR P3 x P2)-3.7	20.44
(DMR P3 x P2)-3.8	1.28
(DMR P3 x P2)-3.10	30.44
(DMR P3 x P2)-3.11	13.94
(DMR P3 x P2)-3.12	26.59
(DMR P3 x P2)-3.14	20.44
(DMR P3 x P2)-3.15	1.28
(DMR P3 x P2)-3.19	34.65
(DMR P3 x P2)-3.20	48.87
(DMR P3 x P2)-3.23	38.51
(DMR P3 x P2)-3.25	1.28
(DMR P3 x P2)-3.28	1.28
(DMR P3 x P2)-3.30	1.28
(DMR P3 x P2)-3.32	19.11
(DMR P3 x P2)-3.33	18.15
(DMR P3 x P2)-3.34	9.71
(DMR P3 x P2)-3.36	13.94
(DMR P3 x P2)-3.37	12.62
(DMR P3 x P2)-3.38	51.17
(DMR P3 x P2)-3.39	55.38
(DMR P3 x P2)-3.41	50.03
(DMR P3 x P2)-3.42	21.55
(DMR P3 x P2)-3.47	1.28
(DMR P3 x P2)-3.48	42.72
(DMR P3 x P2)-3.51	1.28
(DMR P3 x P2)-3.53	1.28
(DMR P3 x P2)-3.54	26.22
(DMR P3 x P2)-3.55	43.10
(DMR P3 x P2)-3.56	50.03
(DMR P3 x P2)-3.57	28.44
(DMR P3 x P2)-3.62	43.10
(DMR P3 x P2)-3.63	50.03
(DMR P3 x P2)-3.64	1.28
(DMR P3 x P2)-3.65	1.28
(DMR P3 x P2)-3.67	15.86

Pedigree	%
(DMR P3 x P2)-3.137	1.28
(DMR P3 x P2)-3.138	59.60
(DMR P3 x P2)-3.139	26.22
(DMR P3 x P2)-3.140	46.95
(DMR P3 x P2)-3.142	40.80
(DMR P3 x P2)-3.144	9.71
(DMR P3 x P2)-3.145	26.22
(DMR P3 x P2)-3.146	9.71
(DMR P3 x P2)-3.148	9.71
(DMR P3 x P2)-3.151	27.72
(DMR P3 x P2)-3.152	23.52
(DMR P3 x P2)-3.153	1.28
(DMR P3 x P2)-3.154	1.28
(DMR P3 x P2)-3.155	26.59
(DMR P3 x P2)-3.159	57.68
(DMR P3 x P2)-4.1	63.83
(DMR P3 x P2)-4.2	88.76
(DMR P3 x P2)-4.3	38.10
(DMR P3 x P2)-4.4	42.74
(DMR P3 x P2)-4.6	19.29
(DMR P3 x P2)-4.7	9.71
(DMR P3 x P2)-4.8	10.86
(DMR P3 x P2)-4.9	1.28
(DMR P3 x P2)-4.10	55.40
(DMR P3 x P2)-4.11	9.71
(DMR P3 x P2)-4.12	50.19
(DMR P3 x P2)-4.13	46.95
(DMR P3 x P2)-4.15	1.28
(DMR P3 x P2)-4.16	1.28
(DMR P3 x P2)-4.17	1.28
(DMR P3 x P2)-4.18	17.79
(DMR P3 x P2)-4.19	18.15
(DMR P3 x P2)-4.20	62.68
(DMR P3 x P2)-4.21	27.36
(DMR P3 x P2)-4.22	34.29
(DMR P3 x P2)-4.24	35.03
(DMR P3 x P2)-4.27	51.17
(DMR P3 x P2)-4.28	23.52
(DMR P3 x P2)-4.29	26.58
(DMR P3 x P2)-4.30	1.28

Pedigree	%
(DMR P3 x P2)-4.84	46.95
(DMR P3 x P2)-4.85	1.28
(DMR P3 x P2)-4.87	48.87
(DMR P3 x P2)-4.88	30.44
(DMR P3 x P2)-4.89	30.44
(DMR P3 x P2)-4.90	13.94
(DMR P3 x P2)-4.93	80.33
(DMR P3 x P2)-4.97	30.44
(DMR P3 x P2)-4.99	18.15
(DMR P3 x P2)-4.100	9.71
(DMR P3 x P2)-4.102	27.72
(DMR P3 x P2)-4.104	17.79
(DMR P3 x P2)-4.106	26.59
(DMR P3 x P2)-4.108	1.28
(DMR P3 x P2)-4.110	10.86
(DMR P3 x P2)-4.112	35.03
(DMR P3 x P2)-4.114	46.18
(DMR P3 x P2)-4.115	45.02
(DMR P3 x P2)-4.116	1.28
(DMR P3 x P2)-4.117	76.11
(DMR P3 x P2)-4.118	12.62
(DMR P3 x P2)-4.119	34.29
(DMR P3 x P2)-4.120	49.25
(DMR P3 x P2)-4.122	1.28
(DMR P3 x P2)-4.125	22.37
(DMR P3 x P2)-4.126	62.68
(DMR P3 x P2)-4.127	18.15
(DMR P3 x P2)-4.129	30.80
(DMR P3 x P2)-4.131	1.28
(DMR P3 x P2)-4.132	63.83
(DMR P3 x P2)-4.133	13.94
(DMR P3 x P2)-4.135	26.59
(DMR P3 x P2)-4.137	35.02
(DMR P3 x P2)-4.138	18.15
(DMR P3 x P2)-4.139	9.71
(DMR P3 x P2)-4.141	28.52
(DMR P3 x P2)-4.142	41.78
(DMR P3 x P2)-4.144	1.28
(DMR P3 x P2)-4.146	1.28
(DMR P3 x P2)-4.147	18.15

Pedigree	%
(DMR P3 x P2)-3.68	22.37
(DMR P3 x P2)-3.71	22.37
(DMR P3 x P2)-3.74	22.37
(DMR P3 x P2)-3.76	9.71
(DMR P3 x P2)-3.77	59.60
(DMR P3 x P2)-3.78	59.60
(DMR P3 x P2)-3.79	59.24
(DMR P3 x P2)-3.80	25.44
(DMR P3 x P2)-3.81	27.20
(DMR P3 x P2)-3.82	35.80
(DMR P3 x P2)-3.83	71.90
(DMR P3 x P2)-3.84	88.76
(DMR P3 x P2)-3.85	23.52
(DMR P3 x P2)-3.87	1.28
(DMR P3 x P2)-3.89	18.15
(DMR P3 x P2)-3.91	26.58
(DMR P3 x P2)-3.92	76.11
(DMR P3 x P2)-3.93	59.60
(DMR P3 x P2)-3.94	55.02
(DMR P3 x P2)-3.96	19.29
(DMR P3 x P2)-3.99	13.94
(DMR P3 x P2)-3.102	1.28
(DMR P3 x P2)-3.103	40.02
(DMR P3 x P2)-3.106	1.28
(DMR P3 x P2)-3.107	9.71
(DMR P3 x P2)-3.112	1.28
(DMR P3 x P2)-3.114	48.27
(DMR P3 x P2)-3.117	88.76
(DMR P3 x P2)-3.118	48.87
(DMR P3 x P2)-3.125	1.28
(DMR P3 x P2)-3.128	13.94
(DMR P3 x P2)-3.129	51.17
(DMR P3 x P2)-3.131	26.22
(DMR P3 x P2)-3.132	13.94

Pedigree	%
(DMR P3 x P2)-4.32	50.79
(DMR P3 x P2)-4.33	9.71
(DMR P3 x P2)-4.34	59.60
(DMR P3 x P2)-4.36	1.28
(DMR P3 x P2)-4.38	54.60
(DMR P3 x P2)-4.39	88.76
(DMR P3 x P2)-4.40	17.79
(DMR P3 x P2)-4.41	19.11
(DMR P3 x P2)-4.42	1.28
(DMR P3 x P2)-4.43	18.15
(DMR P3 x P2)-4.44	12.62
(DMR P3 x P2)-4.45	56.36
(DMR P3 x P2)-4.47	13.94
(DMR P3 x P2)-4.48	9.71
(DMR P3 x P2)-4.52	50.03
(DMR P3 x P2)-4.54	23.52
(DMR P3 x P2)-4.55	10.86
(DMR P3 x P2)-4.56	56.52
(DMR P3 x P2)-4.57	13.94
(DMR P3 x P2)-4.58	1.28
(DMR P3 x P2)-4.59	46.95
(DMR P3 x P2)-4.60	1.28
(DMR P3 x P2)-4.61	27.36
(DMR P3 x P2)-4.64	39.25
(DMR P3 x P2)-4.66	9.71
(DMR P3 x P2)-4.70	38.87
(DMR P3 x P2)-4.71	38.87
(DMR P3 x P2)-4.72	1.28
(DMR P3 x P2)-4.74	13.94
(DMR P3 x P2)-4.75	1.28
(DMR P3 x P2)-4.76	48.27
(DMR P3 x P2)-4.77	13.94
(DMR P3 x P2)-4.78	71.90
(DMR P3 x P2)-4.81	1.28

Pedigree	%
(DMR P3 x P2)-4.149	31.95
(DMR P3 x P2)-4.150	1.28
(DMR P3 x P2)-4.151	1.28
(DMR P3 x P2)-4.152	17.79
(DMR P3 x P2)-4.153	9.71
(DMR P3 x P2)-4.155	43.10
(DMR P3 x P2)-4.156	30.44
(DMR P3 x P2)-4.157	1.28
(DMR P3 x P2)-4.158	1.28
(DMR P3 x P2)-4.161	41.95
(DMR P3 x P2)-4.164	9.71
(DMR P3 x P2)-4.165	28.52
(DMR P3 x P2)-4.166	67.68
(DMR P3 x P2)-4.167	30.44
(DMR P3 x P2)-4.168	1.28
(DMR P3 x P2)-4.171	10.86
(DMR P3 x P2)-4.172	1.28
(DMR P3 x P2)-4.173	1.28
(DMR P3 x P2)-4.174	1.28
(DMR P3 x P2)-4.176	1.28
(DMR P3 x P2)-4.178	19.29
(DMR P3 x P2)-4.179	22.37
(DMR P3 x P2)-4.180	22.37
(DMR P3 x P2)-4.181	9.71
(DMR P3 x P2)-4.183	30.44
(DMR P3 x P2)-4.184	55.38
(DMR P3 x P2)-4.188	38.87
(DMR P3 x P2)-4.189	9.71
(DMR P3 x P2)-4.191	1.28
(DMR P3 x P2)-4.192	60.75
(DMR P3 x P2)-4.193	1.28
(DMR P3 x P2)-4.194	22.37

APPENDIX I

TRANSFORMED PHENOTYPIC DATA FOR GREENHOUSE SYSTEMIC INFECTION

Pedigree	%
(DMR P3 x P2)-3.2	12.62
(DMR P3 x P2)-3.3	25.44
(DMR P3 x P2)-3.4	9.71
(DMR P3 x P2)-3.5	45.02
(DMR P3 x P2)-3.6	24.29
(DMR P3 x P2)-3.7	1.28
(DMR P3 x P2)-3.8	13.93
(DMR P3 x P2)-3.10	13.94
(DMR P3 x P2)-3.11	9.71
(DMR P3 x P2)-3.12	1.28
(DMR P3 x P2)-3.14	18.28
(DMR P3 x P2)-3.15	1.28
(DMR P3 x P2)-3.19	24.29
(DMR P3 x P2)-3.20	67.68
(DMR P3 x P2)-3.23	19.29
(DMR P3 x P2)-3.25	33.87
(DMR P3 x P2)-3.28	1.28
(DMR P3 x P2)-3.30	1.28
(DMR P3 x P2)-3.32	30.44
(DMR P3 x P2)-3.33	1.28
(DMR P3 x P2)-3.34	13.94
(DMR P3 x P2)-3.36	29.48
(DMR P3 x P2)-3.37	23.95
(DMR P3 x P2)-3.38	48.27
(DMR P3 x P2)-3.39	48.45
(DMR P3 x P2)-3.41	40.02
(DMR P3 x P2)-3.42	26.22
(DMR P3 x P2)-3.47	1.28
(DMR P3 x P2)-3.48	18.15
(DMR P3 x P2)-3.51	1.28
(DMR P3 x P2)-3.53	1.28
(DMR P3 x P2)-3.54	24.29
(DMR P3 x P2)-3.55	50.03
(DMR P3 x P2)-3.56	74.40
(DMR P3 x P2)-3.57	30.02
(DMR P3 x P2)-3.62	29.12
(DMR P3 x P2)-3.63	45.02
(DMR P3 x P2)-3.64	1.28
(DMR P3 x P2)-3.65	1.28
(DMR P3 x P2)-3.67	1.28

Pedigree	%
(DMR P3 x P2)-3.137	1.28
(DMR P3 x P2)-3.138	28.87
(DMR P3 x P2)-3.139	21.05
(DMR P3 x P2)-3.140	57.68
(DMR P3 x P2)-3.142	33.87
(DMR P3 x P2)-3.144	1.28
(DMR P3 x P2)-3.145	13.94
(DMR P3 x P2)-3.146	1.28
(DMR P3 x P2)-3.148	18.15
(DMR P3 x P2)-3.151	22.37
(DMR P3 x P2)-3.152	19.29
(DMR P3 x P2)-3.153	1.28
(DMR P3 x P2)-3.154	1.28
(DMR P3 x P2)-3.155	35.03
(DMR P3 x P2)-3.159	88.76
(DMR P3 x P2)-4.1	1.28
(DMR P3 x P2)-4.2	42.74
(DMR P3 x P2)-4.3	55.20
(DMR P3 x P2)-4.4	45.02
(DMR P3 x P2)-4.6	15.65
(DMR P3 x P2)-4.7	1.28
(DMR P3 x P2)-4.8	10.86
(DMR P3 x P2)-4.9	1.28
(DMR P3 x P2)-4.10	70.94
(DMR P3 x P2)-4.11	1.28
(DMR P3 x P2)-4.12	1.28
(DMR P3 x P2)-4.13	43.27
(DMR P3 x P2)-4.15	9.71
(DMR P3 x P2)-4.16	1.28
(DMR P3 x P2)-4.17	1.28
(DMR P3 x P2)-4.18	17.79
(DMR P3 x P2)-4.19	34.65
(DMR P3 x P2)-4.20	47.12
(DMR P3 x P2)-4.21	1.28
(DMR P3 x P2)-4.22	28.87
(DMR P3 x P2)-4.24	36.94
(DMR P3 x P2)-4.27	10.86
(DMR P3 x P2)-4.28	28.02
(DMR P3 x P2)-4.29	9.71
(DMR P3 x P2)-4.30	26.59

Pedigree	%
(DMR P3 x P2)-4.84	56.36
(DMR P3 x P2)-4.85	1.28
(DMR P3 x P2)-4.87	79.19
(DMR P3 x P2)-4.88	13.94
(DMR P3 x P2)-4.89	45.02
(DMR P3 x P2)-4.90	43.10
(DMR P3 x P2)-4.93	80.33
(DMR P3 x P2)-4.97	35.45
(DMR P3 x P2)-4.99	9.71
(DMR P3 x P2)-4.100	1.28
(DMR P3 x P2)-4.102	27.72
(DMR P3 x P2)-4.104	26.22
(DMR P3 x P2)-4.106	12.62
(DMR P3 x P2)-4.108	1.28
(DMR P3 x P2)-4.110	62.85
(DMR P3 x P2)-4.112	39.25
(DMR P3 x P2)-4.114	66.53
(DMR P3 x P2)-4.115	59.60
(DMR P3 x P2)-4.116	1.28
(DMR P3 x P2)-4.117	70.94
(DMR P3 x P2)-4.118	12.62
(DMR P3 x P2)-4.119	34.65
(DMR P3 x P2)-4.120	62.50
(DMR P3 x P2)-4.122	1.28
(DMR P3 x P2)-4.125	23.15
(DMR P3 x P2)-4.126	45.02
(DMR P3 x P2)-4.127	23.52
(DMR P3 x P2)-4.129	9.71
(DMR P3 x P2)-4.131	9.71
(DMR P3 x P2)-4.132	21.05
(DMR P3 x P2)-4.133	12.62
(DMR P3 x P2)-4.135	17.79
(DMR P3 x P2)-4.137	25.44
(DMR P3 x P2)-4.138	18.15
(DMR P3 x P2)-4.139	1.28
(DMR P3 x P2)-4.141	24.29
(DMR P3 x P2)-4.142	1.28
(DMR P3 x P2)-4.144	66.89
(DMR P3 x P2)-4.146	1.28
(DMR P3 x P2)-4.147	15.86

Pedigree	%
(DMR P3 x P2)-3.68	9.71
(DMR P3 x P2)-3.71	24.29
(DMR P3 x P2)-3.74	1.28
(DMR P3 x P2)-3.76	1.28
(DMR P3 x P2)-3.77	33.52
(DMR P3 x P2)-3.78	37.37
(DMR P3 x P2)-3.79	22.01
(DMR P3 x P2)-3.80	22.19
(DMR P3 x P2)-3.81	1.28
(DMR P3 x P2)-3.82	28.52
(DMR P3 x P2)-3.83	59.60
(DMR P3 x P2)-3.84	41.78
(DMR P3 x P2)-3.85	27.36
(DMR P3 x P2)-3.87	1.28
(DMR P3 x P2)-3.89	1.28
(DMR P3 x P2)-3.91	22.37
(DMR P3 x P2)-3.92	56.52
(DMR P3 x P2)-3.93	71.90
(DMR P3 x P2)-3.94	27.54
(DMR P3 x P2)-3.96	10.86
(DMR P3 x P2)-3.99	17.79
(DMR P3 x P2)-3.102	1.28
(DMR P3 x P2)-3.103	45.19
(DMR P3 x P2)-3.106	1.28
(DMR P3 x P2)-3.107	1.28
(DMR P3 x P2)-3.112	41.94
(DMR P3 x P2)-3.114	48.27
(DMR P3 x P2)-3.117	38.69
(DMR P3 x P2)-3.118	26.59
(DMR P3 x P2)-3.125	1.28
(DMR P3 x P2)-3.128	1.28
(DMR P3 x P2)-3.129	30.44
(DMR P3 x P2)-3.131	19.29
(DMR P3 x P2)-3.132	13.93

Pedigree	%
(DMR P3 x P2)-4.32	26.22
(DMR P3 x P2)-4.33	22.37
(DMR P3 x P2)-4.34	47.12
(DMR P3 x P2)-4.36	1.28
(DMR P3 x P2)-4.38	30.44
(DMR P3 x P2)-4.39	74.18
(DMR P3 x P2)-4.40	45.02
(DMR P3 x P2)-4.41	19.11
(DMR P3 x P2)-4.42	1.28
(DMR P3 x P2)-4.43	1.28
(DMR P3 x P2)-4.44	15.86
(DMR P3 x P2)-4.45	15.86
(DMR P3 x P2)-4.47	25.27
(DMR P3 x P2)-4.48	1.28
(DMR P3 x P2)-4.52	40.15
(DMR P3 x P2)-4.54	9.71
(DMR P3 x P2)-4.55	35.45
(DMR P3 x P2)-4.56	53.27
(DMR P3 x P2)-4.57	22.37
(DMR P3 x P2)-4.58	1.28
(DMR P3 x P2)-4.59	38.87
(DMR P3 x P2)-4.60	1.28
(DMR P3 x P2)-4.61	1.28
(DMR P3 x P2)-4.64	12.62
(DMR P3 x P2)-4.66	12.62
(DMR P3 x P2)-4.70	13.93
(DMR P3 x P2)-4.71	28.52
(DMR P3 x P2)-4.72	28.52
(DMR P3 x P2)-4.74	1.28
(DMR P3 x P2)-4.75	1.28
(DMR P3 x P2)-4.76	41.94
(DMR P3 x P2)-4.77	36.94
(DMR P3 x P2)-4.78	27.72
(DMR P3 x P2)-4.81	1.28

Pedigree	%
(DMR P3 x P2)-4.149	45.02
(DMR P3 x P2)-4.150	10.86
(DMR P3 x P2)-4.151	15.86
(DMR P3 x P2)-4.152	19.29
(DMR P3 x P2)-4.153	1.28
(DMR P3 x P2)-4.155	38.87
(DMR P3 x P2)-4.156	50.21
(DMR P3 x P2)-4.157	1.28
(DMR P3 x P2)-4.158	15.86
(DMR P3 x P2)-4.161	32.73
(DMR P3 x P2)-4.164	1.28
(DMR P3 x P2)-4.165	26.04
(DMR P3 x P2)-4.166	60.57
(DMR P3 x P2)-4.167	9.71
(DMR P3 x P2)-4.168	1.28
(DMR P3 x P2)-4.171	10.86
(DMR P3 x P2)-4.172	1.28
(DMR P3 x P2)-4.173	1.28
(DMR P3 x P2)-4.174	x
(DMR P3 x P2)-4.176	10.86
(DMR P3 x P2)-4.178	23.52
(DMR P3 x P2)-4.179	22.37
(DMR P3 x P2)-4.180	9.71
(DMR P3 x P2)-4.181	1.28
(DMR P3 x P2)-4.183	15.86
(DMR P3 x P2)-4.184	30.44
(DMR P3 x P2)-4.188	33.87
(DMR P3 x P2)-4.189	23.52
(DMR P3 x P2)-4.191	1.28
(DMR P3 x P2)-4.192	43.88
(DMR P3 x P2)-4.193	1.28
(DMR P3 x P2)-4.194	30.44

APPENDIX J

TRANSFORMED PHENOTYPIC DATA FOR CORPUS CHRISTI LOCAL INFECTION

Pedigree	%
(DMR P3 x P2)-3.2	0.51
(DMR P3 x P2)-3.3	30.02
(DMR P3 x P2)-3.4	26.58
(DMR P3 x P2)-3.5	60.70
(DMR P3 x P2)-3.6	44.25
(DMR P3 x P2)-3.7	27.81
(DMR P3 x P2)-3.8	0.51
(DMR P3 x P2)-3.10	47.63
(DMR P3 x P2)-3.11	0.51
(DMR P3 x P2)-3.12	34.21
(DMR P3 x P2)-3.14	33.00
(DMR P3 x P2)-3.15	11.32
(DMR P3 x P2)-3.19	74.81
(DMR P3 x P2)-3.20	80.31
(DMR P3 x P2)-3.23	25.50
(DMR P3 x P2)-3.25	22.22
(DMR P3 x P2)-3.28	0.51
(DMR P3 x P2)-3.30	16.79
(DMR P3 x P2)-3.32	28.14
(DMR P3 x P2)-3.33	0.51
(DMR P3 x P2)-3.34	22.22
(DMR P3 x P2)-3.36	28.14
(DMR P3 x P2)-3.37	14.97
(DMR P3 x P2)-3.38	54.76
(DMR P3 x P2)-3.39	76.21
(DMR P3 x P2)-3.41	79.52
(DMR P3 x P2)-3.42	20.38
(DMR P3 x P2)-3.47	0.51
(DMR P3 x P2)-3.48	16.11
(DMR P3 x P2)-3.51	0.51
(DMR P3 x P2)-3.53	0.51
(DMR P3 x P2)-3.54	26.18
(DMR P3 x P2)-3.55	22.22
(DMR P3 x P2)-3.56	89.53
(DMR P3 x P2)-3.57	30.44
(DMR P3 x P2)-3.62	57.43
(DMR P3 x P2)-3.63	89.53
(DMR P3 x P2)-3.64	0.51
(DMR P3 x P2)-3.65	0.51
(DMR P3 x P2)-3.67	10.03

Pedigree	%
(DMR P3 x P2)-3.137	0.51
(DMR P3 x P2)-3.138	14.26
(DMR P3 x P2)-3.139	48.21
(DMR P3 x P2)-3.140	72.76
(DMR P3 x P2)-3.142	89.53
(DMR P3 x P2)-3.144	18.77
(DMR P3 x P2)-3.145	9.60
(DMR P3 x P2)-3.146	21.68
(DMR P3 x P2)-3.148	0.51
(DMR P3 x P2)-3.151	33.71
(DMR P3 x P2)-3.152	21.06
(DMR P3 x P2)-3.153	0.51
(DMR P3 x P2)-3.154	23.11
(DMR P3 x P2)-3.155	29.14
(DMR P3 x P2)-3.159	62.46
(DMR P3 x P2)-4.1	59.42
(DMR P3 x P2)-4.2	80.02
(DMR P3 x P2)-4.3	61.56
(DMR P3 x P2)-4.4	44.25
(DMR P3 x P2)-4.6	20.28
(DMR P3 x P2)-4.7	10.53
(DMR P3 x P2)-4.8	39.68
(DMR P3 x P2)-4.9	0.51
(DMR P3 x P2)-4.10	47.23
(DMR P3 x P2)-4.11	13.64
(DMR P3 x P2)-4.12	31.50
(DMR P3 x P2)-4.13	40.60
(DMR P3 x P2)-4.15	10.19
(DMR P3 x P2)-4.16	10.71
(DMR P3 x P2)-4.17	0.51
(DMR P3 x P2)-4.18	17.84
(DMR P3 x P2)-4.19	16.44
(DMR P3 x P2)-4.20	52.27
(DMR P3 x P2)-4.21	31.96
(DMR P3 x P2)-4.22	51.45
(DMR P3 x P2)-4.24	15.51
(DMR P3 x P2)-4.27	26.02
(DMR P3 x P2)-4.28	24.66
(DMR P3 x P2)-4.29	32.62
(DMR P3 x P2)-4.30	22.56

Pedigree	%
(DMR P3 x P2)-4.84	76.78
(DMR P3 x P2)-4.85	14.48
(DMR P3 x P2)-4.87	45.76
(DMR P3 x P2)-4.88	27.00
(DMR P3 x P2)-4.89	49.45
(DMR P3 x P2)-4.90	0.51
(DMR P3 x P2)-4.93	61.91
(DMR P3 x P2)-4.97	30.55
(DMR P3 x P2)-4.99	9.88
(DMR P3 x P2)-4.100	0.51
(DMR P3 x P2)-4.102	26.18
(DMR P3 x P2)-4.104	11.78
(DMR P3 x P2)-4.106	32.86
(DMR P3 x P2)-4.108	26.58
(DMR P3 x P2)-4.110	77.43
(DMR P3 x P2)-4.112	58.55
(DMR P3 x P2)-4.114	62.61
(DMR P3 x P2)-4.115	69.33
(DMR P3 x P2)-4.116	53.89
(DMR P3 x P2)-4.117	77.43
(DMR P3 x P2)-4.118	49.82
(DMR P3 x P2)-4.119	0.51
(DMR P3 x P2)-4.120	45.02
(DMR P3 x P2)-4.122	9.34
(DMR P3 x P2)-4.125	40.91
(DMR P3 x P2)-4.126	52.27
(DMR P3 x P2)-4.127	27.90
(DMR P3 x P2)-4.129	22.65
(DMR P3 x P2)-4.131	0.51
(DMR P3 x P2)-4.132	37.78
(DMR P3 x P2)-4.133	0.51
(DMR P3 x P2)-4.135	23.69
(DMR P3 x P2)-4.137	32.33
(DMR P3 x P2)-4.138	24.47
(DMR P3 x P2)-4.139	0.51
(DMR P3 x P2)-4.141	19.87
(DMR P3 x P2)-4.142	39.78
(DMR P3 x P2)-4.144	45.02
(DMR P3 x P2)-4.146	0.51
(DMR P3 x P2)-4.147	17.29

Pedigree	%
(DMR P3 x P2)-3.68	9.88
(DMR P3 x P2)-3.71	33.57
(DMR P3 x P2)-3.74	25.01
(DMR P3 x P2)-3.76	43.34
(DMR P3 x P2)-3.77	73.01
(DMR P3 x P2)-3.78	79.69
(DMR P3 x P2)-3.79	89.53
(DMR P3 x P2)-3.80	27.72
(DMR P3 x P2)-3.81	46.53
(DMR P3 x P2)-3.82	32.33
(DMR P3 x P2)-3.83	71.60
(DMR P3 x P2)-3.84	70.18
(DMR P3 x P2)-3.85	19.87
(DMR P3 x P2)-3.87	12.04
(DMR P3 x P2)-3.89	23.76
(DMR P3 x P2)-3.91	30.02
(DMR P3 x P2)-3.92	67.48
(DMR P3 x P2)-3.93	80.31
(DMR P3 x P2)-3.94	72.21
(DMR P3 x P2)-3.96	29.03
(DMR P3 x P2)-3.99	27.17
(DMR P3 x P2)-3.102	22.65
(DMR P3 x P2)-3.103	75.32
(DMR P3 x P2)-3.106	0.51
(DMR P3 x P2)-3.107	0.51
(DMR P3 x P2)-3.112	59.50
(DMR P3 x P2)-3.114	89.53
(DMR P3 x P2)-3.117	77.43
(DMR P3 x P2)-3.118	34.21
(DMR P3 x P2)-3.125	0.51
(DMR P3 x P2)-3.128	0.51
(DMR P3 x P2)-3.129	46.39
(DMR P3 x P2)-3.131	39.78
(DMR P3 x P2)-3.132	20.07

Pedigree	%
(DMR P3 x P2)-4.32	63.47
(DMR P3 x P2)-4.33	52.27
(DMR P3 x P2)-4.34	58.94
(DMR P3 x P2)-4.36	11.54
(DMR P3 x P2)-4.38	76.41
(DMR P3 x P2)-4.39	57.34
(DMR P3 x P2)-4.40	73.61
(DMR P3 x P2)-4.41	70.56
(DMR P3 x P2)-4.42	9.60
(DMR P3 x P2)-4.43	0.51
(DMR P3 x P2)-4.44	10.03
(DMR P3 x P2)-4.45	89.53
(DMR P3 x P2)-4.47	29.51
(DMR P3 x P2)-4.48	37.51
(DMR P3 x P2)-4.52	65.94
(DMR P3 x P2)-4.54	43.43
(DMR P3 x P2)-4.55	31.50
(DMR P3 x P2)-4.56	54.76
(DMR P3 x P2)-4.57	32.57
(DMR P3 x P2)-4.58	15.80
(DMR P3 x P2)-4.59	45.80
(DMR P3 x P2)-4.60	0.51
(DMR P3 x P2)-4.61	14.04
(DMR P3 x P2)-4.64	67.48
(DMR P3 x P2)-4.66	29.14
(DMR P3 x P2)-4.70	63.87
(DMR P3 x P2)-4.71	44.25
(DMR P3 x P2)-4.72	13.10
(DMR P3 x P2)-4.74	0.51
(DMR P3 x P2)-4.75	0.51
(DMR P3 x P2)-4.76	89.53
(DMR P3 x P2)-4.77	39.57
(DMR P3 x P2)-4.78	50.48
(DMR P3 x P2)-4.81	0.51

Pedigree	%
(DMR P3 x P2)-4.149	27.07
(DMR P3 x P2)-4.150	0.51
(DMR P3 x P2)-4.151	71.91
(DMR P3 x P2)-4.152	22.56
(DMR P3 x P2)-4.153	0.51
(DMR P3 x P2)-4.155	52.27
(DMR P3 x P2)-4.156	48.21
(DMR P3 x P2)-4.157	46.39
(DMR P3 x P2)-4.158	17.29
(DMR P3 x P2)-4.161	35.28
(DMR P3 x P2)-4.164	26.11
(DMR P3 x P2)-4.165	54.76
(DMR P3 x P2)-4.166	67.13
(DMR P3 x P2)-4.167	0.51
(DMR P3 x P2)-4.168	15.80
(DMR P3 x P2)-4.171	23.11
(DMR P3 x P2)-4.172	12.93
(DMR P3 x P2)-4.173	0.51
(DMR P3 x P2)-4.174	89.53
(DMR P3 x P2)-4.176	25.43
(DMR P3 x P2)-4.178	20.72
(DMR P3 x P2)-4.179	0.51
(DMR P3 x P2)-4.180	20.28
(DMR P3 x P2)-4.181	10.53
(DMR P3 x P2)-4.183	0.51
(DMR P3 x P2)-4.184	46.01
(DMR P3 x P2)-4.188	17.03
(DMR P3 x P2)-4.189	15.80
(DMR P3 x P2)-4.191	34.21
(DMR P3 x P2)-4.192	54.76
(DMR P3 x P2)-4.193	23.30
(DMR P3 x P2)-4.194	16.55

APPENDIX K

TRANSFORMED PHENOTYPIC DATA FOR CORPUS CHRISTI SYSTEMIC INFECTION

Pedigree	%
(DMR P3 x P2)-3.2	0.51
(DMR P3 x P2)-3.3	14.48
(DMR P3 x P2)-3.4	0.51
(DMR P3 x P2)-3.5	20.28
(DMR P3 x P2)-3.6	0.51
(DMR P3 x P2)-3.7	0.51
(DMR P3 x P2)-3.8	0.51
(DMR P3 x P2)-3.10	14.26
(DMR P3 x P2)-3.11	0.51
(DMR P3 x P2)-3.12	9.34
(DMR P3 x P2)-3.14	0.51
(DMR P3 x P2)-3.15	0.51
(DMR P3 x P2)-3.19	0.51
(DMR P3 x P2)-3.20	0.51
(DMR P3 x P2)-3.23	11.10
(DMR P3 x P2)-3.25	9.74
(DMR P3 x P2)-3.28	0.51
(DMR P3 x P2)-3.30	0.51
(DMR P3 x P2)-3.32	0.51
(DMR P3 x P2)-3.33	0.51
(DMR P3 x P2)-3.34	10.90
(DMR P3 x P2)-3.36	26.18
(DMR P3 x P2)-3.37	0.51
(DMR P3 x P2)-3.38	35.28
(DMR P3 x P2)-3.39	9.74
(DMR P3 x P2)-3.41	0.51
(DMR P3 x P2)-3.42	10.03
(DMR P3 x P2)-3.47	0.51
(DMR P3 x P2)-3.48	9.22
(DMR P3 x P2)-3.51	0.51
(DMR P3 x P2)-3.53	0.51
(DMR P3 x P2)-3.54	0.51
(DMR P3 x P2)-3.55	0.51
(DMR P3 x P2)-3.56	0.51
(DMR P3 x P2)-3.57	9.22
(DMR P3 x P2)-3.62	23.69
(DMR P3 x P2)-3.63	0.51
(DMR P3 x P2)-3.64	0.51
(DMR P3 x P2)-3.65	0.51
(DMR P3 x P2)-3.67	0.51

Pedigree	%
(DMR P3 x P2)-3.137	0.51
(DMR P3 x P2)-3.138	10.03
(DMR P3 x P2)-3.139	9.60
(DMR P3 x P2)-3.140	17.29
(DMR P3 x P2)-3.142	0.51
(DMR P3 x P2)-3.144	0.51
(DMR P3 x P2)-3.145	0.51
(DMR P3 x P2)-3.146	0.51
(DMR P3 x P2)-3.148	0.51
(DMR P3 x P2)-3.151	0.51
(DMR P3 x P2)-3.152	10.35
(DMR P3 x P2)-3.153	0.51
(DMR P3 x P2)-3.154	0.51
(DMR P3 x P2)-3.155	0.51
(DMR P3 x P2)-3.159	22.22
(DMR P3 x P2)-4.1	28.14
(DMR P3 x P2)-4.2	0.51
(DMR P3 x P2)-4.3	25.25
(DMR P3 x P2)-4.4	16.55
(DMR P3 x P2)-4.6	0.51
(DMR P3 x P2)-4.7	0.51
(DMR P3 x P2)-4.8	0.51
(DMR P3 x P2)-4.9	0.51
(DMR P3 x P2)-4.10	30.44
(DMR P3 x P2)-4.11	0.51
(DMR P3 x P2)-4.12	14.26
(DMR P3 x P2)-4.13	45.02
(DMR P3 x P2)-4.15	0.51
(DMR P3 x P2)-4.16	0.51
(DMR P3 x P2)-4.17	0.51
(DMR P3 x P2)-4.18	0.51
(DMR P3 x P2)-4.19	0.51
(DMR P3 x P2)-4.20	37.78
(DMR P3 x P2)-4.21	11.54
(DMR P3 x P2)-4.22	13.64
(DMR P3 x P2)-4.24	0.51
(DMR P3 x P2)-4.27	0.51
(DMR P3 x P2)-4.28	21.18
(DMR P3 x P2)-4.29	14.72
(DMR P3 x P2)-4.30	9.88

Pedigree	%
(DMR P3 x P2)-4.84	13.27
(DMR P3 x P2)-4.85	0.51
(DMR P3 x P2)-4.87	26.94
(DMR P3 x P2)-4.88	0.51
(DMR P3 x P2)-4.89	31.27
(DMR P3 x P2)-4.90	27.44
(DMR P3 x P2)-4.93	28.14
(DMR P3 x P2)-4.97	0.51
(DMR P3 x P2)-4.99	0.51
(DMR P3 x P2)-4.100	0.51
(DMR P3 x P2)-4.102	19.48
(DMR P3 x P2)-4.104	11.78
(DMR P3 x P2)-4.106	20.07
(DMR P3 x P2)-4.108	0.51
(DMR P3 x P2)-4.110	12.61
(DMR P3 x P2)-4.112	20.38
(DMR P3 x P2)-4.114	17.56
(DMR P3 x P2)-4.115	14.48
(DMR P3 x P2)-4.116	0.51
(DMR P3 x P2)-4.117	12.61
(DMR P3 x P2)-4.118	0.51
(DMR P3 x P2)-4.119	22.22
(DMR P3 x P2)-4.120	45.02
(DMR P3 x P2)-4.122	0.51
(DMR P3 x P2)-4.125	12.61
(DMR P3 x P2)-4.126	37.78
(DMR P3 x P2)-4.127	14.48
(DMR P3 x P2)-4.129	0.51
(DMR P3 x P2)-4.131	0.51
(DMR P3 x P2)-4.132	11.78
(DMR P3 x P2)-4.133	0.51
(DMR P3 x P2)-4.135	0.51
(DMR P3 x P2)-4.137	0.51
(DMR P3 x P2)-4.138	0.51
(DMR P3 x P2)-4.139	0.51
(DMR P3 x P2)-4.141	11.32
(DMR P3 x P2)-4.142	0.51
(DMR P3 x P2)-4.144	0.51
(DMR P3 x P2)-4.146	0.51
(DMR P3 x P2)-4.147	0.51

Pedigree	%
(DMR P3 x P2)-3.68	0.51
(DMR P3 x P2)-3.71	9.60
(DMR P3 x P2)-3.74	0.51
(DMR P3 x P2)-3.76	0.51
(DMR P3 x P2)-3.77	13.84
(DMR P3 x P2)-3.78	10.35
(DMR P3 x P2)-3.79	0.51
(DMR P3 x P2)-3.80	9.47
(DMR P3 x P2)-3.81	0.51
(DMR P3 x P2)-3.82	0.51
(DMR P3 x P2)-3.83	0.51
(DMR P3 x P2)-3.84	0.51
(DMR P3 x P2)-3.85	0.51
(DMR P3 x P2)-3.87	0.51
(DMR P3 x P2)-3.89	0.51
(DMR P3 x P2)-3.91	10.19
(DMR P3 x P2)-3.92	22.56
(DMR P3 x P2)-3.93	0.51
(DMR P3 x P2)-3.94	17.84
(DMR P3 x P2)-3.96	14.04
(DMR P3 x P2)-3.99	0.51
(DMR P3 x P2)-3.102	0.51
(DMR P3 x P2)-3.103	14.72
(DMR P3 x P2)-3.106	0.51
(DMR P3 x P2)-3.107	0.51
(DMR P3 x P2)-3.112	0.51
(DMR P3 x P2)-3.114	0.51
(DMR P3 x P2)-3.117	0.51
(DMR P3 x P2)-3.118	0.51
(DMR P3 x P2)-3.125	0.51
(DMR P3 x P2)-3.128	0.51
(DMR P3 x P2)-3.129	12.61
(DMR P3 x P2)-3.131	0.51
(DMR P3 x P2)-3.132	14.04

Pedigree	%
(DMR P3 x P2)-4.32	0.51
(DMR P3 x P2)-4.33	14.48
(DMR P3 x P2)-4.34	21.43
(DMR P3 x P2)-4.36	0.51
(DMR P3 x P2)-4.38	0.51
(DMR P3 x P2)-4.39	27.17
(DMR P3 x P2)-4.40	16.44
(DMR P3 x P2)-4.41	0.51
(DMR P3 x P2)-4.42	0.51
(DMR P3 x P2)-4.43	0.51
(DMR P3 x P2)-4.44	22.92
(DMR P3 x P2)-4.45	0.51
(DMR P3 x P2)-4.47	14.26
(DMR P3 x P2)-4.48	11.10
(DMR P3 x P2)-4.52	11.78
(DMR P3 x P2)-4.54	0.51
(DMR P3 x P2)-4.55	0.51
(DMR P3 x P2)-4.56	35.28
(DMR P3 x P2)-4.57	9.34
(DMR P3 x P2)-4.58	0.51
(DMR P3 x P2)-4.59	13.45
(DMR P3 x P2)-4.60	0.51
(DMR P3 x P2)-4.61	14.04
(DMR P3 x P2)-4.64	17.29
(DMR P3 x P2)-4.66	0.51
(DMR P3 x P2)-4.70	9.60
(DMR P3 x P2)-4.71	13.45
(DMR P3 x P2)-4.72	0.51
(DMR P3 x P2)-4.74	0.51
(DMR P3 x P2)-4.75	0.51
(DMR P3 x P2)-4.76	0.51
(DMR P3 x P2)-4.77	0.51
(DMR P3 x P2)-4.78	29.57
(DMR P3 x P2)-4.81	0.51

Pedigree	%
(DMR P3 x P2)-4.149	10.71
(DMR P3 x P2)-4.150	0.51
(DMR P3 x P2)-4.151	0.51
(DMR P3 x P2)-4.152	0.51
(DMR P3 x P2)-4.153	0.51
(DMR P3 x P2)-4.155	0.51
(DMR P3 x P2)-4.156	0.51
(DMR P3 x P2)-4.157	0.51
(DMR P3 x P2)-4.158	0.51
(DMR P3 x P2)-4.161	0.51
(DMR P3 x P2)-4.164	14.72
(DMR P3 x P2)-4.165	10.53
(DMR P3 x P2)-4.166	22.92
(DMR P3 x P2)-4.167	0.51
(DMR P3 x P2)-4.168	0.51
(DMR P3 x P2)-4.171	0.51
(DMR P3 x P2)-4.172	0.51
(DMR P3 x P2)-4.173	0.51
(DMR P3 x P2)-4.174	0.51
(DMR P3 x P2)-4.176	0.51
(DMR P3 x P2)-4.178	9.10
(DMR P3 x P2)-4.179	0.51
(DMR P3 x P2)-4.180	0.51
(DMR P3 x P2)-4.181	0.51
(DMR P3 x P2)-4.183	0.51
(DMR P3 x P2)-4.184	18.77
(DMR P3 x P2)-4.188	9.74
(DMR P3 x P2)-4.189	0.51
(DMR P3 x P2)-4.191	0.51
(DMR P3 x P2)-4.192	33.57
(DMR P3 x P2)-4.193	0.51
(DMR P3 x P2)-4.194	0.51

APPENDIX L

TRANSFORMED PHENOTYPIC DATA FOR CORPUS CHRISTI TOTAL INFECTION

Pedigree	%
(DMR P3 x P2)-3.2	0.51
(DMR P3 x P2)-3.3	34.01
(DMR P3 x P2)-3.4	26.58
(DMR P3 x P2)-3.5	69.77
(DMR P3 x P2)-3.6	44.25
(DMR P3 x P2)-3.7	27.81
(DMR P3 x P2)-3.8	0.51
(DMR P3 x P2)-3.10	51.15
(DMR P3 x P2)-3.11	0.51
(DMR P3 x P2)-3.12	35.81
(DMR P3 x P2)-3.14	33.00
(DMR P3 x P2)-3.15	11.32
(DMR P3 x P2)-3.19	74.81
(DMR P3 x P2)-3.20	80.31
(DMR P3 x P2)-3.23	28.14
(DMR P3 x P2)-3.25	24.47
(DMR P3 x P2)-3.28	0.51
(DMR P3 x P2)-3.30	16.79
(DMR P3 x P2)-3.32	28.14
(DMR P3 x P2)-3.33	0.51
(DMR P3 x P2)-3.34	25.01
(DMR P3 x P2)-3.36	40.22
(DMR P3 x P2)-3.37	14.97
(DMR P3 x P2)-3.38	89.53
(DMR P3 x P2)-3.39	80.31
(DMR P3 x P2)-3.41	79.52
(DMR P3 x P2)-3.42	22.92
(DMR P3 x P2)-3.47	0.51
(DMR P3 x P2)-3.48	18.69
(DMR P3 x P2)-3.51	0.51
(DMR P3 x P2)-3.53	0.51
(DMR P3 x P2)-3.54	26.18
(DMR P3 x P2)-3.55	22.22
(DMR P3 x P2)-3.56	89.53
(DMR P3 x P2)-3.57	32.10
(DMR P3 x P2)-3.62	68.98
(DMR P3 x P2)-3.63	89.53
(DMR P3 x P2)-3.64	0.51
(DMR P3 x P2)-3.65	0.51
(DMR P3 x P2)-3.67	10.03

Pedigree	%
(DMR P3 x P2)-3.137	0.51
(DMR P3 x P2)-3.138	17.56
(DMR P3 x P2)-3.139	49.82
(DMR P3 x P2)-3.140	89.53
(DMR P3 x P2)-3.142	89.53
(DMR P3 x P2)-3.144	18.77
(DMR P3 x P2)-3.145	9.60
(DMR P3 x P2)-3.146	21.68
(DMR P3 x P2)-3.148	0.51
(DMR P3 x P2)-3.151	33.71
(DMR P3 x P2)-3.152	23.69
(DMR P3 x P2)-3.153	0.51
(DMR P3 x P2)-3.154	23.11
(DMR P3 x P2)-3.155	29.14
(DMR P3 x P2)-3.159	74.54
(DMR P3 x P2)-4.1	78.94
(DMR P3 x P2)-4.2	80.02
(DMR P3 x P2)-4.3	77.73
(DMR P3 x P2)-4.4	48.91
(DMR P3 x P2)-4.6	20.28
(DMR P3 x P2)-4.7	10.53
(DMR P3 x P2)-4.8	39.68
(DMR P3 x P2)-4.9	0.51
(DMR P3 x P2)-4.10	63.10
(DMR P3 x P2)-4.11	13.64
(DMR P3 x P2)-4.12	35.28
(DMR P3 x P2)-4.13	73.94
(DMR P3 x P2)-4.15	10.19
(DMR P3 x P2)-4.16	10.71
(DMR P3 x P2)-4.17	0.51
(DMR P3 x P2)-4.18	17.84
(DMR P3 x P2)-4.19	16.44
(DMR P3 x P2)-4.20	89.53
(DMR P3 x P2)-4.21	34.47
(DMR P3 x P2)-4.22	54.76
(DMR P3 x P2)-4.24	15.51
(DMR P3 x P2)-4.27	26.02
(DMR P3 x P2)-4.28	33.50
(DMR P3 x P2)-4.29	36.58
(DMR P3 x P2)-4.30	24.85

Pedigree	%
(DMR P3 x P2)-4.84	89.53
(DMR P3 x P2)-4.85	14.48
(DMR P3 x P2)-4.87	57.95
(DMR P3 x P2)-4.88	27.00
(DMR P3 x P2)-4.89	66.94
(DMR P3 x P2)-4.90	27.44
(DMR P3 x P2)-4.93	89.53
(DMR P3 x P2)-4.97	30.55
(DMR P3 x P2)-4.99	9.88
(DMR P3 x P2)-4.100	0.51
(DMR P3 x P2)-4.102	33.57
(DMR P3 x P2)-4.104	16.79
(DMR P3 x P2)-4.106	39.94
(DMR P3 x P2)-4.108	26.58
(DMR P3 x P2)-4.110	89.53
(DMR P3 x P2)-4.112	67.13
(DMR P3 x P2)-4.114	69.66
(DMR P3 x P2)-4.115	75.56
(DMR P3 x P2)-4.116	53.89
(DMR P3 x P2)-4.117	89.53
(DMR P3 x P2)-4.118	49.82
(DMR P3 x P2)-4.119	22.22
(DMR P3 x P2)-4.120	89.53
(DMR P3 x P2)-4.122	9.34
(DMR P3 x P2)-4.125	43.66
(DMR P3 x P2)-4.126	89.53
(DMR P3 x P2)-4.127	32.04
(DMR P3 x P2)-4.129	22.65
(DMR P3 x P2)-4.131	0.51
(DMR P3 x P2)-4.132	40.22
(DMR P3 x P2)-4.133	0.51
(DMR P3 x P2)-4.135	23.69
(DMR P3 x P2)-4.137	32.33
(DMR P3 x P2)-4.138	24.47
(DMR P3 x P2)-4.139	0.51
(DMR P3 x P2)-4.141	23.11
(DMR P3 x P2)-4.142	39.78
(DMR P3 x P2)-4.144	45.02
(DMR P3 x P2)-4.146	0.51
(DMR P3 x P2)-4.147	17.29

Pedigree	%
(DMR P3 x P2)-3.68	9.88
(DMR P3 x P2)-3.71	35.28
(DMR P3 x P2)-3.74	25.01
(DMR P3 x P2)-3.76	43.34
(DMR P3 x P2)-3.77	80.31
(DMR P3 x P2)-3.78	89.53
(DMR P3 x P2)-3.79	89.53
(DMR P3 x P2)-3.80	29.57
(DMR P3 x P2)-3.81	46.53
(DMR P3 x P2)-3.82	32.33
(DMR P3 x P2)-3.83	71.60
(DMR P3 x P2)-3.84	70.18
(DMR P3 x P2)-3.85	19.87
(DMR P3 x P2)-3.87	12.04
(DMR P3 x P2)-3.89	23.76
(DMR P3 x P2)-3.91	32.04
(DMR P3 x P2)-3.92	89.53
(DMR P3 x P2)-3.93	80.31
(DMR P3 x P2)-3.94	89.53
(DMR P3 x P2)-3.96	32.86
(DMR P3 x P2)-3.99	27.17
(DMR P3 x P2)-3.102	22.65
(DMR P3 x P2)-3.103	89.53
(DMR P3 x P2)-3.106	0.51
(DMR P3 x P2)-3.107	0.51
(DMR P3 x P2)-3.112	59.50
(DMR P3 x P2)-3.114	89.53
(DMR P3 x P2)-3.117	77.43
(DMR P3 x P2)-3.118	34.21
(DMR P3 x P2)-3.125	0.51
(DMR P3 x P2)-3.128	0.51
(DMR P3 x P2)-3.129	49.13
(DMR P3 x P2)-3.131	39.78
(DMR P3 x P2)-3.132	24.85

Pedigree	%
(DMR P3 x P2)-4.32	63.47
(DMR P3 x P2)-4.33	56.04
(DMR P3 x P2)-4.34	68.62
(DMR P3 x P2)-4.36	11.54
(DMR P3 x P2)-4.38	76.41
(DMR P3 x P2)-4.39	73.26
(DMR P3 x P2)-4.40	89.53
(DMR P3 x P2)-4.41	70.56
(DMR P3 x P2)-4.42	9.60
(DMR P3 x P2)-4.43	0.51
(DMR P3 x P2)-4.44	25.25
(DMR P3 x P2)-4.45	89.53
(DMR P3 x P2)-4.47	33.42
(DMR P3 x P2)-4.48	39.68
(DMR P3 x P2)-4.52	69.33
(DMR P3 x P2)-4.54	43.43
(DMR P3 x P2)-4.55	31.50
(DMR P3 x P2)-4.56	89.53
(DMR P3 x P2)-4.57	34.21
(DMR P3 x P2)-4.58	15.80
(DMR P3 x P2)-4.59	48.91
(DMR P3 x P2)-4.60	0.51
(DMR P3 x P2)-4.61	20.07
(DMR P3 x P2)-4.64	76.00
(DMR P3 x P2)-4.66	29.14
(DMR P3 x P2)-4.70	65.94
(DMR P3 x P2)-4.71	47.35
(DMR P3 x P2)-4.72	13.10
(DMR P3 x P2)-4.74	0.51
(DMR P3 x P2)-4.75	0.51
(DMR P3 x P2)-4.76	89.53
(DMR P3 x P2)-4.77	39.57
(DMR P3 x P2)-4.78	66.29
(DMR P3 x P2)-4.81	0.51

Pedigree	%
(DMR P3 x P2)-4.149	29.44
(DMR P3 x P2)-4.150	0.51
(DMR P3 x P2)-4.151	71.91
(DMR P3 x P2)-4.152	22.56
(DMR P3 x P2)-4.153	0.51
(DMR P3 x P2)-4.155	52.27
(DMR P3 x P2)-4.156	48.21
(DMR P3 x P2)-4.157	46.39
(DMR P3 x P2)-4.158	17.29
(DMR P3 x P2)-4.161	35.28
(DMR P3 x P2)-4.164	30.55
(DMR P3 x P2)-4.165	56.82
(DMR P3 x P2)-4.166	89.53
(DMR P3 x P2)-4.167	0.51
(DMR P3 x P2)-4.168	15.80
(DMR P3 x P2)-4.171	23.11
(DMR P3 x P2)-4.172	12.93
(DMR P3 x P2)-4.173	0.51
(DMR P3 x P2)-4.174	89.53
(DMR P3 x P2)-4.176	25.43
(DMR P3 x P2)-4.178	22.80
(DMR P3 x P2)-4.179	0.51
(DMR P3 x P2)-4.180	20.28
(DMR P3 x P2)-4.181	10.53
(DMR P3 x P2)-4.183	0.51
(DMR P3 x P2)-4.184	52.01
(DMR P3 x P2)-4.188	19.77
(DMR P3 x P2)-4.189	15.80
(DMR P3 x P2)-4.191	34.21
(DMR P3 x P2)-4.192	80.45
(DMR P3 x P2)-4.193	23.30
(DMR P3 x P2)-4.194	16.55

VITA

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