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APPENDICES

APPENDIX A

SAMPLING DATA

A1. Great Argus (*Argusianus argus argus*) data from Sampling site and date collection at other sources.

Number	Sex	Sampling site	Region	Code	Date of collection
1	M	Hala Bala wildlife sanctuary	S	AAM_HLBL1	February 2005
2	F	Hala Bala wildlife sanctuary	S	AAF_HLBL2	February 2005
3	M	Hala Bala wildlife sanctuary	S	AAM_HLBL3	February 2005
4	UI	Khao Pratabcharng wildlife research and breeding station	W	AAUI_PTC1	26-01-2005
5	UI	Khao Pratabcharng wildlife research and breeding station	W	AAUI_PTC2	26-01-2005
6	UI	Khao Pratabcharng wildlife research and breeding station	W	AAUI_PTC3	26-01-2005
7	M	Khao Soi Dao wildlife research and breeding station	E	AAM_SD1	08-11-2003
8	M	Khao Soi Dao wildlife research and breeding station	E	AAM_SD2	08-11-2003
9	F	Khao Soi Dao wildlife research and breeding station	E	AAF_SD3	08-11-2003
10	F	Individual farm in Amphoe Sattaheep, Chonburi Province	E	AAF_STH1	14-08-2004
11	M	Individual farm in Amphoe Sattaheep, Chonburi Province	E	AAM_STH2	14-08-2004

A2. Red Junglefowl (*Gallus gallus spadiceous*) data from Sampling site and date collection at other sources.

Number	Sex	Sampling site	Region	Code	Date of collection
1	M	Huay Kha Kaeng Wildlife Sanctuary	W	GGSM_HKK1	22-08-2004
2	F	Huay Kha Kaeng Wildlife Sanctuary	W	GGSF_HKK2	22-08-2004
3	M	Huay Kha Kaeng Wildlife Sanctuary	W	GGSM_HKK3	22-08-2004
4	F	Huay Yang Parn wildlife research and breeding station	N	GGSF_HYP	22-08-2004
5	M	Huay Kha Kaeng Wildlife Sanctuary	W	GGSM_HKK6	13-02-2005
6	M	Huay Kha Kaeng Wildlife Sanctuary	W	GGSM_HKK7	13-02-2005
7	F	Huay Kha Kaeng Wildlife Sanctuary	W	GGSF_HKK8	13-02-2005
8	M	Phatthalung wildlife research and breeding station	S	GGSM_PTL21	26-01-2005
9	F	Phatthalung wildlife research and breeding station	S	GGSF_PTL24	26-01-2005
10	M	Phatthalung wildlife research and breeding station	S	GGSM_PTL25	26-01-2005
11	M	Satun	S	GGSM_ST1	27-01-2005
12	F	Satun	S	GGSF_ST2	27-01-2005
13	F	Satun	S	GGSF_ST3	27-01-2005

A3. Siamese Fireback (*Lophura diardi*) data from Sampling site and date collection at other sources.

Number	Sex	Sampling site	Region	Code	Date of collection
1	F	Phu Khieu wildlife research and breeding station	NE	LDF_PK1	19-08-2004
2	M	Phu Khieu wildlife research and breeding station	NE	LDM_PK2	19-08-2004
3	M	Phu Khieu wildlife research and breeding station	NE	LDM_PK3	19-08-2004
4	M	Individual farm in Amphoe Sattaheep, Chonburi Province	E	LDM_STH1	14-08-2004
5	F	Individual farm in Amphoe Sattaheep, Chonburi Province	E	LDF_STH2	14-08-2004
6	F	Individual farm in Amphoe Sattaheep, Chonburi Province	E	LDF_STH3	14-08-2004
7	M	Khao Pratabcharng wildlife research and breeding station	W	LDM_PTC1	25-12-2004
8	M	Khao Pratabcharng wildlife research and breeding station	W	LDM_PTC2	25-12-2004
9	M	Khao Pratabcharng wildlife research and breeding station	W	LDM_PTC3	25-12-2004
10	M	Khao Soi Dao wildlife research and breeding station	E	LDM_SD4	29-01-2005
11	F	Khao Soi Dao wildlife research and breeding station	E	LDF_SD5	29-01-2005
12	M	Khao Soi Dao wildlife research and breeding station	E	LDM_SD6	29-01-2005

A4. Green Peafowl (*Pavo muticus imperator*) data from Sampling site and date collection at other sources.

Number	Sex	Sampling site	Region	Code	Date of collection
1	M	Khao Pratabcharng wildlife research and breeding station	W	PMM_PTC1	25-12-2004
2	F	Khao Pratabcharng wildlife research and breeding station	W	PMF_PTC2	25-12-2004
3	F	Khao Pratabcharng wildlife research and breeding station	W	PMF_PTC3	25-12-2004
4	M	Huay Yang Parn wildlife research and breeding station	N	PMM_HYP	19-08-2004
5	M	Pong Wild, Payao province	N	PMM_P	19-08-2004
6	F	Lumpang Wild, Lumpang province	N	PMF_LP	19-08-2004
7	F	Chiang Khong Wild, Chiang Rai province	N	PMF_CK	19-08-2004
8	F	Surin Wild	NE	PMF_SR1	02-08-2004
9	M	Surin Wild	NE	PMM_SR2	02-08-2004
10	M	Surin Wild	NE	PMM_SR3	02-08-2004
11	M	Phu Khieu wildlife research and breeding station	NE	PMM_PK1	19-08-2004
12	F	Phu Khieu wildlife research and breeding station	NE	PMF_PK2	22-08-2004
13	F	Khao Soi Dao wildlife research and breeding station	E	PMF_SD4	29-01-2005

A4. Green Peafowl (*Pavo muticus imperator*) data from Sampling site and date collection at other sources (continued)

Number	Sex	Sampling site	Region	Code	Date of collection
14	M	Khao Soi Dao wildlife research and breeding station	E	PMM_SD5	29-01-2005
15	M	Khao Soi Dao wildlife research and breeding station	E	PMM_SD6	29-01-2005
16	UI	Ping River watershed, Amphoe Li, Lampun province	N	PING1	May 2005
17	UI	Ping River watershed, Amphoe Li, Lampun province	N	PING2	May 2005
18	UI	Ping River watershed, Amphoe Li, Lampun province	N	PING3	May 2005

A5. Creasted Wood Partridge (*Rollulus roulroul*) data from Sampling site and date collection at other sources.

Number	Sex	Sampling site	Region	Code	Date of collection
1	M	Individual Farm in Bangkok	C	RRM_BKK	26-01-2005
2	F	Khok Mai Rua wildlife research and breeding station	S	RRF_KMR1	26-01-2005
3	M	Khok Mai Rua wildlife research and breeding station	S	RRM_KMR2	26-01-2005
4	M	Amphoe Sattaheep, Chonburi Province	E	RRM_STH1	14-08-2004
5	F	Amphoe Sattaheep, Chonburi Province	E	RRM_STH2	14-08-2004
6	F	Amphoe Sattaheep, Chonburi Province	E	RRM_STH3	14-08-2004
7	M	Khao Pratabcharng wildlife research and breeding station	W	RRM_PTC1	25-12-2004
8	M	Khao Pratabcharng wildlife research and breeding station	W	RRM_PTC2	25-12-2004
9	M	Khao Pratabcharng wildlife research and breeding station	W	RRM_PTC3	25-12-2004

APPENDIX B

B1. Fragment Sharing of RAPD patterns observe in intraspecies of Great Argus (*Argusianus argus argus*) when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

Primer OPA-18

Code	Size (bp)																
	1200	1100	1000	900	850	800	700	600	590	580	550	500	450	410	380	300	280
HLBL1	1	1	2	1	2	1	1	1	2	2	2	1	1	2	1	1	1
HLBL2	1	2	2	2	1	1	1	2	1	2	1	2	1	2	1	1	1
HLBL3	2	1	1	1	2	1	2	1	2	1	2	2	2	2	2	2	2
PTC1	1	2	2	2	1	2	1	1	2	2	2	1	1	1	2	1	1
PTC2	1	2	2	2	1	2	1	1	2	2	2	1	1	1	2	1	1
PTC3	1	2	2	2	1	2	1	1	2	2	2	1	1	2	2	1	1
SD1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
SD2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
SD3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2
STH1	2	2	2	2	2	2	1	2	2	2	2	1	1	2	2	1	2
STH2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2

Primer OPC-02

Code	Size (bp)																
	1300	1200	950	900	880	800	750	720	700	650	550	500	480	450	350	300	250
HLBL1	2	2	2	2	1	2	1	2	2	1	1	2	2	2	2	2	1
HLBL2	2	2	1	2	2	1	2	2	2	1	1	2	1	1	1	2	2
HLBL3	1	1	2	1	2	2	2	1	2	1	1	2	1	1	2	2	2
PTC1	1	1	2	1	1	2	1	2	1	2	1	1	2	2	1	2	2
PTC2	1	1	2	1	2	1	1	2	1	2	1	1	2	2	1	2	2
PTC3	2	2	2	2	2	2	1	2	1	2	1	1	2	2	2	2	2
SD1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
SD2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
SD3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
STH1	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2	2	2
STH2	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2	1	2

Primer OPP-03

Code	Size (bp)													
	1500	1400	800	720	700	650	550	500	480	450	380	340	300	280
HLBL1	2	2	1	1	2	1	1	2	2	2	2	2	2	1
HLBL2	2	2	2	2	1	2	2	1	2	2	1	2	2	1
HLBL3	1	2	2	2	2	2	1	2	1	2	2	1	1	2
PTC1	2	1	2	2	2	2	2	1	2	1	1	2	2	1
PTC2	2	1	2	2	2	2	2	1	2	1	1	2	2	1
PTC3	1	1	2	1	2	2	2	1	2	2	1	2	2	1
SD1	2	2	2	2	2	2	2	1	2	2	2	2	2	1
SD2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
SD3	2	2	2	2	2	2	2	2	2	2	2	2	2	2
STH1	2	2	2	2	2	2	2	2	2	2	2	2	2	2
STH2	2	2	2	2	2	2	2	2	2	2	2	2	2	2

Primer UBC-133

Code	Size (bp)									
	1200	1100	900	850	780	700	690	600	580	450
HLBL1	2	1	2	1	2	2	1	1	1	1
HLBL2	2	1	2	1	1	2	1	1	1	1
HLBL3	1	1	1	2	2	1	2	2	1	2
PTC1	2	1	2	1	1	2	1	2	2	2
PTC2	2	1	2	1	1	2	1	1	2	2
PTC3	1	1	2	1	1	2	1	1	1	2
SD1	2	1	2	1	2	2	1	2	1	1
SD2	2	1	2	2	1	2	2	2	2	1
SD3	2	1	2	1	2	2	2	2	2	1
STH1	2	1	2	1	1	2	1	2	1	1
STH2	2	1	2	1	2	2	1	2	2	1

Primer UBC-135

Code	Size (bp)										
	1200	1000	900	850	800	680	650	500	420	320	250
HLBL1	1	2	1	2	2	2	1	1	1	1	2
HLBL2	2	1	2	2	2	2	2	1	2	1	2
HLBL3	2	2	1	2	2	2	2	1	2	2	2
PTC1	2	2	2	2	2	2	2	1	1	2	2
PTC2	1	1	2	1	1	1	2	1	1	2	2
PTC3	1	2	2	1	2	1	2	1	1	2	2
SD1	2	2	2	2	2	2	2	1	2	2	2
SD2	2	2	2	2	2	2	2	2	2	2	2
SD3	2	2	2	2	2	2	2	1	1	2	1
STH1	2	2	2	2	2	2	2	2	2	2	2
STH2	1	2	2	2	1	2	2	1	1	2	1

B2. Fragment Sharing of RAPD patterns observe in intraspecies of Red Junglefowl (*Gallus gallus spadiceous*) when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

OPA-18

Code	Size (bp)					
	1000	900	800	700	500	400
HKK1	1	1	1	1	1	1
HKK2	1	1	1	1	1	1
HKK3	1	1	1	1	1	1
HYP	2	1	1	1	1	1
HKK6	2	1	1	1	1	1
HKK7	2	1	1	1	1	1
HKK8	1	1	1	1	1	1
PTL21	1	1	1	1	1	1
PTL24	2	1	1	1	1	1
PTL25	1	1	1	1	1	1
ST1	1	1	1	1	1	1
ST2	1	1	1	1	1	1
ST3	1	1	1	1	1	1

OPC-02

Code	Size (bp)					
	1200	1100	900	720	650	500
HKK1	1	2	1	1	1	2
HKK2	1	2	2	1	1	2
HKK3	1	1	2	1	1	2
HYP	1	1	2	1	1	2
HKK6	2	1	2	1	1	2
HKK7	2	1	2	1	1	2
HKK8	1	1	2	1	1	2
PTL21	2	1	2	1	1	1
PTL24	2	1	2	1	1	1
PTL25	2	2	2	1	1	2
ST1	1	1	2	1	1	2
ST2	1	1	1	1	1	1
ST3	2	2	2	1	1	2

OPP-03

Code	Size (bp)							
	1500	1400	1200	1000	900	650	450	400
HKK1	1	2	1	1	2	2	1	1
HKK2	1	1	1	1	2	2	1	1
HKK3	1	1	1	1	2	2	1	1
HYP	1	1	1	1	2	1	1	1
HKK6	1	1	1	1	2	1	1	2
HKK7	2	2	2	1	1	1	1	1
HKK8	1	1	1	1	1	1	1	1
PTL21	1	1	1	1	1	1	1	2
PTL24	1	1	1	1	1	1	1	2
PTL25	1	1	1	1	2	1	1	2
ST1	1	1	1	1	1	1	1	1
ST2	1	1	1	1	1	1	1	1
ST3	1	1	1	1	1	1	1	2

UBC-133

Code	Size (bp)							
	1400	1200	1000	850	700	600	550	400
HKK1	1	1	2	1	1	1	1	1
HKK2	1	1	2	1	1	1	1	1
HKK3	1	1	2	1	1	1	1	1
HYP	2	2	1	1	1	1	1	1
HKK6	1	1	2	1	1	1	1	2
HKK7	2	1	2	1	1	1	1	2
HKK8	1	1	2	1	1	1	1	1
PTL21	1	1	1	1	1	1	1	1
PTL24	1	1	1	1	1	1	1	1
PTL25	2	1	1	1	1	1	1	1
ST1	1	1	1	1	1	1	1	1
ST2	2	1	1	1	1	1	1	1
ST3	1	1	1	1	1	1	1	1

UBC-135

Code	Size (bp)								
	1300	1100	950	900	700	600	500	420	300
HKK1	2	1	1	2	1	2	2	1	2
HKK2	2	1	1	2	1	2	2	1	2
HKK3	2	1	1	2	1	2	2	1	2
HYP	2	1	1	1	1	2	1	1	2
HKK6	2	1	1	1	1	2	2	1	2
HKK7	2	2	2	2	1	2	1	1	2
HKK8	2	1	1	1	1	2	1	1	1
PTL21	1	1	1	1	1	1	2	1	2
PTL24	2	1	1	2	1	2	2	1	2
PTL25	2	2	2	2	1	2	2	1	2
ST1	1	1	2	1	1	1	2	1	2
ST2	1	1	1	1	1	1	2	1	2
ST3	1	1	1	1	1	1	2	1	2

B3. Fragment Sharing of RAPD patterns observe in intraspecies of Siamese Fireback (*Lophura diardi*) when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

OPA-18

Code	Size (bp)									
	850	750	700	650	580	500	420	350	300	280
PK1	1	1	1	1	1	2	1	1	1	1
PK2	1	1	1	1	1	2	1	1	1	2
PK3	2	1	2	1	1	2	1	1	1	2
STH1	1	1	1	1	1	2	1	1	1	2
STH2	2	2	2	2	1	2	1	1	1	2
STH3	2	1	2	2	1	1	1	1	1	1
PTC1	1	2	1	1	1	1	1	1	1	1
PTC2	1	2	1	1	1	2	1	1	1	1
PTC3	1	1	2	1	1	2	1	2	1	1
SD4	1	2	1	1	1	1	1	2	1	1
SD5	1	2	1	1	1	2	1	2	1	1
SD6	1	1	1	1	1	2	1	1	1	2

OPC-02

Code	Size (bp)						
	800	650	600	550	500	400	300
PK1	2	1	1	1	1	1	1
PK2	2	1	2	1	1	1	2
PK3	2	2	2	2	1	1	2
STH1	2	1	1	1	1	1	1
STH2	2	1	2	1	1	1	2
STH3	2	1	2	1	1	1	2
PTC1	1	1	1	1	1	1	2
PTC2	2	1	1	1	1	1	2
PTC3	2	1	2	1	1	1	1
SD4	2	1	2	1	1	1	2
SD5	2	1	2	1	1	1	2
SD6	2	2	2	2	1	1	2

OPP-03

Code	Size (bp)					
	1500	1300	1200	900	800	650
PK1	2	2	2	2	2	2
PK2	2	1	1	1	2	2
PK3	2	1	1	2	2	2
STH1	2	2	2	2	2	2
STH2	2	1	1	1	2	2
STH3	2	1	1	1	2	2
PTC1	1	1	1	1	2	2
PTC2	1	1	1	2	2	1
PTC3	1	1	1	1	2	2
SD4	1	1	1	2	2	1
SD5	1	1	1	2	2	1
SD6	1	1	1	2	1	1

UBC-133

Code	Size (bp)			
	900	700	550	400
PK1	2	2	1	1
PK2	2	1	2	1
PK3	2	2	2	1
STH1	1	1	1	1
STH2	2	2	1	1
STH3	2	2	1	1
PTC1	1	2	1	1
PTC2	1	2	1	1
PTC3	2	2	1	1
SD4	1	1	1	1
SD5	1	1	1	1
SD6	1	1	1	1

UBC-135

Code	Size (bp)						
	1100	900	800	700	550	500	400
PK1	1	1	1	2	2	2	2
PK2	1	1	1	2	2	1	1
PK3	2	1	1	2	2	1	1
STH1	1	1	1	2	2	2	2
STH2	2	1	1	2	2	1	1
STH3	1	1	1	2	2	1	1
PTC1	1	1	1	1	1	2	1
PTC2	1	1	1	1	1	2	1
PTC3	1	1	1	1	1	2	1
SD4	1	1	1	1	1	2	1
SD5	1	1	1	1	1	2	1
SD6	1	1	1	1	1	1	1

B4. Fragment Sharing of RAPD patterns observe in intraspecies of Green Peafowl (*Pavo muticus imperator*) when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

OPA-18

Code	Size (bp)										
	1400	1300	1000	750	700	650	600	550	500	480	350
PTC1	1	2	2	2	2	1	2	2	1	2	2
PTC2	1	2	2	2	2	1	2	2	1	2	2
PTC3	1	2	2	2	2	1	2	2	1	2	2
HYP	2	2	2	2	2	1	2	2	1	2	2
P	2	2	2	1	2	1	2	2	1	2	2
LP	2	2	2	1	2	1	2	2	1	2	2
CK	1	2	2	1	2	1	2	2	1	2	2
SR1	1	2	2	2	2	1	2	2	1	2	2
SR2	1	1	2	2	2	1	2	2	1	2	2
SR3	1	2	2	2	2	1	2	2	1	2	2
PK1	2	2	2	1	2	1	2	2	1	2	2
PK2	2	2	2	1	2	1	2	2	1	2	2
SD4	1	2	2	1	2	1	2	2	1	2	2
SD5	2	2	2	2	2	1	2	2	1	2	2
SD6	2	2	2	2	2	1	2	2	1	2	2
PING1	2	2	1	2	2	1	2	2	2	2	2

PING2	2	2	2	2	1	2	1	1	2	1	1
PING3	2	2	2	2	2	2	2	2	2	1	2

OPC-02

Code	Size (bp)									
	1000	950	800	700	500	450	420	400	350	320
PTC1	1	1	1	1	1	1	2	2	2	2
PTC2	1	1	1	1	1	1	2	2	2	2
PTC3	1	1	1	1	1	1	2	2	2	2
HYP	2	2	2	2	2	1	2	2	2	2
P	2	2	2	2	2	1	2	2	2	2
LP	2	2	1	2	2	1	2	2	2	2
CK	1	1	1	1	1	1	2	2	2	2
SR1	2	1	1	2	2	1	2	2	2	2
SR2	2	1	1	1	1	1	2	2	2	2
SR3	2	2	1	1	1	1	2	2	2	2
PK1	2	2	1	1	2	1	2	2	2	2
PK2	2	2	1	2	2	1	2	2	2	2
SD4	2	2	1	1	1	1	2	2	2	2
SD5	2	2	1	1	1	1	2	2	2	2
SD6	2	2	2	2	2	1	2	2	2	2
PING1	2	1	1	1	2	1	1	1	2	1
PING2	2	1	2	1	1	2	1	2	1	2
PING3	2	2	2	1	1	1	2	1	2	2

OPP-03

Code	Size (bp)									
	1100	950	900	850	700	650	600	500	450	400
PTC1	1	1	2	2	2	2	2	2	1	2
PTC2	1	1	2	2	2	1	2	2	1	2
PTC3	1	1	2	2	2	1	2	2	1	2
HYP	2	1	2	2	2	2	2	2	1	2
P	2	2	2	2	2	2	2	2	1	2
LP	1	1	2	2	1	2	2	2	1	2
CK	1	1	2	2	1	2	2	2	1	2
SR1	2	2	2	2	2	2	2	2	1	2
SR2	2	2	2	2	2	2	2	2	2	2
SR3	1	1	2	2	2	1	2	2	1	2
PK1	1	1	2	2	1	1	2	2	1	2
PK2	2	2	2	2	2	2	2	2	2	2

SD4	1	1	2	2	2	1	2	2	1	2
SD5	1	2	2	2	2	1	2	2	1	2
SD6	2	2	2	2	2	2	2	2	1	2
PING1	2	1	1	1	2	1	1	2	1	2
PING2	1	2	2	2	1	1	1	1	1	1
PING3	2	2	2	2	2	2	2	1	2	2

UBC-133

Code	Size (bp)								
	1300	1100	900	800	700	650	500	450	400
PTC1	1	1	1	2	2	1	2	1	1
PTC2	1	1	1	2	2	1	2	1	1
PTC3	1	1	1	2	2	1	2	1	2
HYP	1	1	2	2	2	1	2	1	2
P	2	1	2	2	2	1	2	1	2
LP	1	1	1	1	2	1	1	2	2
CK	1	1	1	1	2	1	2	1	2
SR1	1	1	2	1	2	1	2	1	2
SR2	1	1	1	1	2	1	2	1	1
SR3	1	1	1	1	2	1	2	1	1
PK1	1	1	2	1	2	1	2	1	2
PK2	1	1	2	1	2	1	2	2	2
SD4	1	1	1	1	2	1	1	2	2
SD5	1	1	1	2	2	1	1	2	2
SD6	2	2	2	2	2	1	2	2	1
PING1	1	2	1	2	1	2	1	2	2
PING2	1	1	1	1	1	2	2	2	2
PING3	2	2	2	2	1	2	2	2	2

UBC-135

Code	Size (bp)								
	1200	950	680	600	550	500	450	400	350
PTC1	1	1	1	1	2	2	1	1	2
PTC2	1	1	1	1	2	2	1	1	2
PTC3	1	1	1	1	2	2	1	1	2
HYP	2	1	1	1	2	2	2	2	2
P	2	1	1	1	2	2	2	2	2
LP	1	1	1	1	2	2	2	2	2
CK	1	1	1	1	2	2	2	2	2
SR1	2	1	1	1	2	2	2	2	2
SR2	1	1	1	1	2	2	1	2	2
SR3	1	1	1	1	2	2	1	2	2
PK1	2	1	1	1	2	2	2	2	2
PK2	1	1	1	1	2	2	1	1	2
SD4	1	1	1	1	2	2	1	1	2
SD5	2	1	1	1	2	2	2	1	2
SD6	2	1	1	1	2	2	2	2	2
PING1	2	2	2	1	2	1	2	2	1
PING2	2	2	2	1	1	2	2	2	2
PING3	2	2	2	2	1	1	2	2	1

B5. Fragment Sharing of RAPD patterns observe in intraspecies of Creasted Wood Partridge (*Rollulus roulroul*) when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

OPA-18

Code	Size (bp)								
	800	700	650	550	500	480	450	420	380
BKK	2	2	2	2	2	1	2	2	2
KMR1	2	1	2	1	2	2	1	2	2
KMR2	2	1	2	1	1	1	2	2	1
STH1	1	1	1	1	2	1	2	1	1
STH2	2	2	2	2	2	2	2	2	2
STH3	1	1	1	1	2	1	2	1	1
PTC1	2	1	1	1	2	1	2	1	1
PTC2	1	1	1	1	2	2	2	2	1
PTC3	2	1	1	1	2	2	2	2	2

OPC-02

Code	Size (bp)								
	650	600	550	500	480	450	340	280	250
BKK	2	2	2	1	1	2	1	2	2
KMR1	1	2	2	1	1	2	1	2	2
KMR2	2	2	1	1	1	2	1	2	2
STH1	2	2	2	2	2	2	2	2	2
STH2	2	2	1	1	1	2	1	2	1
STH3	2	1	1	1	1	1	1	2	2
PTC1	2	2	1	1	1	2	1	2	1
PTC2	1	2	2	1	1	2	1	2	1
PTC3	2	1	1	2	1	2	1	1	1

OPP-03

Code	Size (bp)			
	1200	980	950	550
BKK	2	1	1	1
KMR1	2	1	1	1
KMR2	2	1	1	2
STH1	2	1	1	1
STH2	2	1	1	1
STH3	2	1	1	1
PTC1	1	2	2	1
PTC2	1	1	1	1
PTC3	1	1	1	1

UBC-133

Code	Size (bp)											
	1100	900	800	700	600	550	500	450	420	400	350	300
BKK	1	1	1	1	1	1	2	1	2	1	2	2
KMR1	1	1	1	1	1	2	2	2	2	2	2	2
KMR2	1	1	1	1	1	2	2	2	1	2	2	2
STH1	2	2	2	1	1	2	1	1	1	2	2	1
STH2	2	2	1	1	2	2	2	1	2	1	2	1
STH3	1	2	1	1	2	2	2	2	2	1	2	1
PTC1	1	1	1	1	1	1	2	2	2	1	2	1
PTC2	1	1	1	1	1	1	2	1	2	2	1	2
PTC3	1	1	1	1	1	1	1	2	1	2	1	2

UBC-135

Code	Size (bp)									
	800	700	650	600	500	450	420	410	370	300
BKK	2	1	2	1	2	2	1	1	1	2
KMR1	1	1	2	1	1	1	2	1	1	2
KMR2	1	1	2	1	1	1	2	1	2	2
STH1	2	2	2	1	2	2	2	2	2	1
STH2	2	2	2	1	2	2	2	2	2	1
STH3	1	1	2	1	2	2	2	1	2	2
PTC1	2	1	2	1	2	2	2	1	2	1
PTC2	1	2	1	1	2	1	2	2	2	1
PTC3	2	2	2	1	2	2	2	2	2	2

B6. Fragment Sharing of RAPD patterns observe in interspecies of gallopheasants and partridge when analyzed by primer OPA-18, OPC-02, OPP-03, UBC-133 and UBC-135.

OPA-18

Code	Size (bp)															
	1500	1400	850	800	750	720	700	680	650	580	540	520	500	450	380	320
Gallus_HKK1	2	2	2	2	1	1	2	2	2	1	2	2	2	2	2	2
Gallus_HYP	2	2	1	2	1	1	2	2	1	1	2	2	2	2	2	2
Gallus_ST1	2	2	1	2	2	1	2	2	2	1	1	2	2	1	2	2
Argusianus_HLBL3	1	1	2	2	2	2	2	2	2	1	2	2	2	2	2	2
Argusianus_PTC1	2	2	2	2	2	1	2	2	1	2	2	2	2	2	2	1
Argusianus_STH1	2	2	2	2	2	1	2	2	1	2	2	2	2	2	2	1
Rollulus_KMR1	1	2	2	2	1	2	2	2	2	1	2	2	2	1	2	2
Rollulus_STH3	2	2	2	2	1	2	1	2	2	1	2	2	2	2	2	2
Rollulus_PTC2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2
Lophura_PK1	2	2	2	2	2	1	2	2	1	2	2	2	2	2	1	2
Lophura_STH1	2	2	2	2	2	1	2	2	1	2	2	2	1	2	1	2
Lophura_PTC1	2	1	1	1	2	1	2	2	1	2	2	2	2	2	1	2
Pavo_PTC1	2	2	2	2	2	2	2	1	2	2	2	1	2	2	2	2
Pavo_LP	2	2	2	2	2	2	2	1	2	2	2	1	2	2	2	2
Pavo_SD4	2	2	2	2	2	2	2	1	2	2	2	1	2	2	2	2

OPC-02

Code	Size (bp)															
	1300	1000	850	820	800	750	720	700	620	580	550	500	420	320	300	250
Gallus_HKK1	1	2	2	2	1	2	1	2	1	2	2	2	2	2	2	2
Gallus_HYP	1	2	2	2	2	2	1	2	1	2	2	2	2	2	2	2
Gallus_ST1	2	2	2	2	2	2	1	2	1	2	2	2	2	2	2	2
Argusianus_HLBL3	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Argusianus_PTC1	2	2	2	1	2	2	2	1	2	1	2	2	2	2	2	2
Argusianus_STH1	2	2	2	1	2	1	2	1	2	1	2	2	2	2	2	2
Rollulus_KMR1	2	2	2	2	1	2	1	2	2	2	1	2	2	2	1	1
Rollulus_STH3	2	2	2	2	2	2	1	2	2	2	1	1	2	2	1	1
Rollulus_PTC2	2	2	2	2	2	2	1	2	2	2	2	1	2	1	2	1
Lophura_PK1	2	1	2	1	2	2	2	2	2	1	2	2	2	2	2	2
Lophura_STH1	2	2	2	1	2	2	2	2	2	1	2	2	2	2	2	2
Lophura_PTC1	2	2	2	1	2	2	2	2	1	1	2	2	2	2	2	2
Pavo_PTC1	2	2	1	2	2	2	2	2	2	2	2	1	1	2	2	2
Pavo_LP	2	2	1	2	2	2	2	2	2	2	2	1	1	2	2	2
Pavo_SD4	2	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2

OPP-03

Code	Size (bp)																						
	1200	980	950	850	780	720	700	680	650	620	600	580	550	520	500	450	420	400	380	350	300	280	250
Gallus_HKK1	2	2	1	2	2	2	2	2	2	1	2	2	2	2	2	1	2	2	1	2	2	1	2
Gallus_HYP	2	2	1	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	1	2	2	1	2
Gallus_ST1	2	2	1	2	2	2	2	1	2	1	2	2	2	2	2	2	2	2	1	2	2	1	2
Argusianus_HLBL3	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2	1	2	2	2	2	1	2	2
Argusianus_PTC1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2	1	2	2	2	2	1	2
Argusianus_STH1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	2	1	2	2	2	2	2	2
Rollulus_KMR1	2	1	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2
Rollulus_STH3	2	1	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2
Rollulus_PTC2	2	1	2	2	2	2	1	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2
Lophura_PK1	1	2	2	1	2	1	2	2	1	2	1	1	2	2	2	2	2	2	2	2	2	2	2
Lophura_STH1	1	2	2	2	2	1	2	2	2	2	1	1	2	2	2	1	2	2	2	2	2	2	2
Lophura_PTC1	2	2	2	1	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Pavo_PTC1	2	2	2	2	2	2	2	2	2	1	2	2	2	2	2	2	1	1	2	1	2	2	1
Pavo_LP	2	2	2	2	1	2	2	2	2	1	2	2	2	2	2	2	1	1	2	1	2	2	1
Pavo_SD4	2	2	2	2	2	2	2	2	2	1	2	2	2	2	2	2	1	1	2	1	2	2	1

UBC-133

Code	Size (bp)																					
	1500	1400	1300	1200	1100	1050	1000	950	920	900	820	800	750	680	650	600	550	500	450	400	380	350
Gallus_HKK1	2	1	2	1	2	2	1	2	2	2	1	2	2	2	2	1	2	2	1	2	2	1
Gallus_HYP	2	1	2	2	2	2	1	2	2	2	1	2	2	2	2	1	2	2	1	2	2	1
Gallus_ST1	2	1	2	1	2	2	1	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2
Argusianus_HLBL3	1	2	2	2	1	2	2	2	2	2	2	2	2	1	2	2	2	1	2	2	1	2
Argusianus_PTC1	1	2	2	2	1	2	1	2	2	2	2	1	1	1	2	2	2	2	1	2	2	2
Argusianus_STH1	1	2	2	2	1	2	1	2	2	2	2	1	1	1	2	2	2	2	1	2	2	2
Rollulus_KMR1	2	2	1	2	1	2	1	2	1	2	2	2	2	2	1	2	2	1	1	1	2	2
Rollulus_STH3	2	2	1	1	2	2	2	2	1	2	2	2	2	2	1	2	2	1	1	1	2	2
Rollulus_PTC2	2	2	1	1	2	2	2	2	1	2	2	2	2	2	1	2	2	2	1	2	2	2
Lophura_PK1	1	2	2	1	2	2	2	1	2	2	1	2	2	2	2	2	1	2	1	2	2	2
Lophura_STH1	2	2	2	2	2	1	2	1	2	1	2	2	2	2	2	2	1	2	1	2	2	2
Lophura_PTC1	1	2	2	2	2	2	2	1	2	2	1	2	2	2	2	2	1	2	1	2	2	2
Pavo_PTC1	2	2	2	2	2	1	2	1	2	2	2	2	1	2	2	2	2	2	1	2	2	2
Pavo_LP	2	2	2	2	2	1	2	1	2	2	2	2	1	2	2	2	2	2	1	2	2	2
Pavo_SD4	2	2	2	2	2	1	2	1	2	2	2	2	1	2	2	2	2	2	1	2	2	2

UBC-135

Code	Size (bp)																				
	1400	1300	1200	1000	950	900	820	800	750	700	650	620	600	580	520	500	480	420	400	390	380
Gallus_HKK1	2	2	1	1	2	1	2	1	2	2	1	2	2	2	2	1	2	2	1	2	2
Gallus_HYP	2	2	1	1	2	2	1	1	1	2	1	2	2	2	2	1	2	2	1	2	2
Gallus_ST1	2	2	1	1	2	2	1	1	1	2	1	2	1	2	2	1	2	2	1	2	2
Argusianus_HLBL3	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	1	2	2	2	2
Argusianus_PTC1	2	2	1	2	2	2	2	1	2	2	1	2	2	2	2	1	2	1	2	2	2
Argusianus_STH1	2	2	1	2	2	2	2	1	2	2	1	2	2	2	2	1	2	1	2	2	2
Rollulus_KMR1	1	2	2	2	2	1	2	2	1	2	2	2	2	1	2	1	2	2	1	2	2
Rollulus_STH3	2	2	2	2	2	2	2	2	1	1 ·	2	2	2	1	2	1	2	2	2	2	2
Rollulus_PTC2	1	2	2	2	2	1	2	2	1	2	1	2	2	1	2	2	1	2	2	2	2
Lophura_PK1	2	2	2	1	2	2	1	2	1	2	1	2	2	2	2	1	1	2	2	2	1
Lophura_STH1	2	2	2	1	2	2	1	2	1	2	1	2	2	2	2	1	1	2	2	2	1
Lophura_PTC1	2	2	2	1	2	2	1	2	1	2	1	2	2	2	1	1	1	2	2	2	1
Pavo_PTC1	2	1	1	2	1	1	2	2	2	2	2	1	2	1	2	1	1	1	2	1	2
Pavo_LP	2	1	1	2	1	1	2	2	2	2	2	1	2	1	2	1	1	1	2	1	2
Pavo_SD4	2	2	2	2	1	1	2	2	2	2	2	1	2	1	2	1	1	1	2	1	2

Interspecies

5 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

 Neighbor-joining method

 Negative branch lengths allowed


```
      +------Rol
    +-3
  +-2 +-----------Pav
  ! !
  ! +---Arg
  !
  1-------Lop
  !
  +--------Gal
```


remember: this is an unrooted tree!

Between	And	Length
1	2	0.02619
2	3	0.02084
3	Rol	0.12719
3	Pav	0.22211
2	Arg	0.07896
1	Lop	0.12827
1	Gal	0.14323

(((Rol:0.12719,Pav:0.22211):0.02084,Arg:0.07896):0.02619,
Lop:0.12827,Gal:0.14323);

Intraspecies of Great Argus (*Argusianus argus agus*)

4 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

 Neighbor-joining method

 Negative branch lengths allowed


```
      +-------PTC
  +----1
  !       +------STH
  !
  2SD
  !
  +---HLBL
```

```
remember: this is an unrooted tree!

Between          And          Length
-------          ---          ------
   2               1          0.07838
   1             PTC          0.13343
   1             STH          0.12607
   2              SD          0.00757
   2            HLBL          0.06302
```

((PTC:0.13343,STH:0.12607):0.07838,SD:0.00757,HLBL:0.06302);

Intraspecies of Red Junglefowl (*Gallus gallus spadiceous*)

4 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

Neighbor-joining method

Negative branch lengths allowed


```
   +PTL
 +-2
 ! +----ST
 !
 1-------HYP
 !
 +---HKK
```


remember: this is an unrooted tree!

```
Between          And          Length
-------          ---          ------
   1               2          0.03065
   2             PTL          0.00830
   2              ST          0.08060
   1             HYP          0.13555
   1             HKK          0.07045
```

((PTL:0.00830,ST:0.08060):0.03065,HYP:0.13555,HKK:0.07045);

Intraspecies of Siamese Fireback (*Lophura diardi*)

4 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

Neighbor-joining method

Negative branch lengths allowed

```
                  +PTC
   +-----------2
   !              +---------SD
   !
   1-STH
   !
   +--PK
```

remember: this is an unrooted tree!

Between	And	Length
1	2	0.22300
2	PTC	-0.00970
2	SD	0.17230
1	STH	0.03775
1	PK	0.04235

((PTC:-0.00970,SD:0.17230):0.22300,STH:0.03775,PK:0.04235);

        Intraspecies of Green Peafowl (*Pavo muticus imperator*)

   9 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

 Neighbor-joining method

 Negative branch lengths allowed

     +SR
     !
     !   +----LP
     !   +-4
   +--5   ! +PK
   ! ! +-7
   ! ! ! !   +----------------PING
   ! ! ! +---1
   ! +-6   +SD
   !   !
   !   ! +HYP
   !   +--3
   !   +---P
   !
   2-CK
   !
   +----PTC
```

remember: this is an unrooted tree!

| Between | And | Length |
| --- | --- | --- |
| 2 | 5 | 0.05677 |
| 5 | SR | 0.01798 |
| 5 | 6 | 0.02036 |
| 6 | 7 | 0.01670 |
| 7 | 4 | 0.04167 |
| 4 | LP | 0.08203 |
| 4 | PK | 0.00247 |
| 7 | 1 | 0.06743 |
| 1 | PING | 0.30910 |
| 1 | SD | -0.02100 |
| 6 | 3 | 0.06139 |
| 3 | HYP | 0.01756 |
| 3 | P | 0.05343 |
| 2 | CK | 0.03497 |
| 2 | PTC | 0.08473 |

((SR:0.01798,(((LP:0.08203,PK:0.00247):0.04167,(PING:0.30910,
SD:-
0.02100):0.06743):0.01670,(HYP:0.01756,P:0.05343):0.06139):0.02036):0
.05677,
CK:0.03497,PTC:0.08473);


Intraspecies of Creasted Wood Partridge (*Rollulus roulroul*)


4 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1


Neighbor-joining method

Negative branch lengths allowed


```
      +-----KMR
  +---1
  !   +-------PTC
  !
  2---------STH
  !
  +-------BKK
```


remember: this is an unrooted tree!

Between	And	Length
2	1	0.07218
1	KMR	0.09353
1	PTC	0.14407
2	STH	0.18317
2	BKK	0.14043

((KMR:0.09353,PTC:0.14407):0.07218,STH:0.18317,BKK:0.14043);

```
2/9/2005 7:17:34 PM
Analysis of C:\TFPGA\ARG\OPA18.TXT
Data set contains genotypes of individuals sampled from populations.
Organism Type: Diploid
Marker Type: Dominant
H-W Equilibrium Assumed.
Allele frequencies estimated based on Lynch and
Milligan's (1994) Taylor expansion estimate.


Exact tests for population differentiation (Raymond and Rousset 1995)
# of dememorization steps: 1000
# of batches: 10
# of permutations per batch: 2000


Pairwise analysis of all populations

Matrix of combined probabilities for each pairwise comparison


           1          2          3
1          *****
2          0.9969     *****
3          1.0000     0.9999     *****

Analysis of C:\TFPGA\ARG\OPC02.TXT
Matrix of combined probabilities for each pairwise comparison


           1          2          3
1          *****
2          0.9794     *****
3          1.0000     0.9999     *****

Analysis of C:\TFPGA\ARG\OPP03.TXT
Matrix of combined probabilities for each pairwise comparison


           1          2          3
1          *****
2          0.9962     *****
3          1.0000     1.0000     *****

Analysis of C:\TFPGA\ARG\UBC133.TXT
Matrix of combined probabilities for each pairwise comparison


           1          2          3          4
1          *****
2          0.9994     *****
3          1.0000     0.9650     *****
4          1.0000     0.9896     1.0000     *****

Analysis of C:\TFPGA\ARG\UBC135.TXT
Matrix of combined probabilities for each pairwise comparison


           1          2          3          4
1          *****
2          0.9926     *****
3          0.9999     0.9927     *****
4          0.9999     1.0000     1.0000     *****


4/9/2005 1:16:21 PM
```

Analysis of C:\TFPGA\GALHKK\OPA18.TXT
Data set contains genotypes of individuals sampled from populations.
Organism Type: Diploid
Marker Type: Dominant
H-W Equilibrium Assumed.
Allele frequencies estimated based on Lynch and
Milligan's (1994) Taylor expansion estimate.

Exact tests for population differentiation (Raymond and Rousset 1995)
# of dememorization steps: 1000
# of batches: 10
# of permutations per batch: 2000

Pairwise analysis of all populations
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.9998	*****		
3	1.0000	1.0000	*****	
4	0.9999	0.9971	1.0000	*****

Analysis of C:\TFPGA\GALHKK\OPC02.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	0.7415	0.9969	*****	
4	0.9990	1.0000	0.9996	*****

Analysis of C:\TFPGA\GALHKK\OPP03.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	0.8400	0.9999	*****	
4	0.9812	0.9999	1.0000	*****

Analysis of C:\TFPGA\GALHKK\UBC133.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.8592	*****		
3	0.8551	0.9999	*****	
4	0.8637	0.9999	1.0000	*****

Analysis of C:\TFPGA\GALHKK\UBC135.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.9999	*****		
3	0.9970	1.0000	*****	
4	0.2027	0.9745	0.9978	*****

2/9/2005 7:41:25 PM
Analysis of C:\TFPGA\LOP\OPA18.TXT

Data set contains genotypes of individuals sampled from populations.
Organism Type: Diploid
Marker Type: Dominant
H-W Equilibrium Assumed.
Allele frequencies estimated based on Lynch and
Milligan's (1994) Taylor expansion estimate.

Exact tests for population differentiation (Raymond and Rousset 1995)
# of dememorization steps: 1000
# of batches: 10
# of permutations per batch: 2000

Pairwise analysis of all populations

	1	2	3	4
1	*****			
2	1.0000	*****		
3	1.0000	0.9994	*****	
4	1.0000	0.9955	1.0000	*****

Analysis of C:\TFPGA\LOP\OPC02.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	1.0000	1.0000	*****	
4	1.0000	1.0000	0.9999	*****

Analysis of C:\TFPGA\LOP\OPP03.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	0.9707	0.9706	*****	
4	0.5451	0.3035	0.9887	*****

Analysis of C:\TFPGA\LOP\UBC133.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.9853	*****		
3	0.6982	1.0000	*****	
4	0.4013	0.8849	0.7886	*****

Analysis of C:\TFPGA\LOP\UBC135.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	0.6790	0.6854	*****	
4	0.8058	0.8227	1.0000	*****

Organism Type: Diploid
Marker Type: Dominant
H-W Equilibrium Assumed.
Allele frequencies estimated based on Lynch and
Milligan's (1994) Taylor expansion estimate.

Exact tests for population differentiation (Raymond and Rousset 1995)
# of dememorization steps: 1000
# of batches: 10
# of permutations per batch: 2000

Pairwise analysis of all populations
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4	5	6	7	8	9
1	•••••								
2	1.0000	•••••							
3	0.9999	1.0000	•••••						
4	0.9998	1.0000	1.0000	•••••					
5	1.0000	1.0000	1.0000	1.0000	•••••				
6	1.0000	1.0000	0.9999	0.9998	1.0000	•••••			
7	0.9929	1.0000	1.0000	1.0000	1.0000	0.9922	•••••		
8	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	•••••	
9	0.4456	1.0000	1.0000	1.0000	0.9993	0.4636	1.0000	0.7413	•••••

Analysis of C:\TFPGA\PAV\OPC02.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4	5	6	7
1	•••••						
2	0.9452	•••••					
3	1.0000	1.0000	•••••				
4	0.9999	1.0000	1.0000	•••••			
5	0.7449	1.0000	0.9977	1.0000	•••••		
6	0.9783	0.9999	0.9999	1.0000	1.0000	•••••	
7	0.9643	1.0000	1.0000	0.9994	0.9472	0.9956	•••••

Analysis of C:\TFPGA\PAV\OPP03.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4	5	6	7	8
1	•••••							
2	1.0000	•••••						
3	1.0000	1.0000	•••••					
4	1.0000	1.0000	1.0000	•••••				
5	1.0000	1.0000	1.0000	1.0000	•••••			
6	1.0000	1.0000	1.0000	1.0000	1.0000	•••••		
7	1.0000	0.9999	0.9999	0.9999	1.0000	1.0000	•••••	
8	0.6274	0.9999	0.9999	0.9999	1.0000	1.0000	1.0000	•••••

Analysis of C:\TFPGA\PAV\UBC133.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4	5	6	7	8	9
1	•••••								
2	1.0000	•••••							
3	0.9977	1.0000	•••••						
4	0.9740	1.0000	1.0000	•••••					
5	1.0000	1.0000	1.0000	1.0000	•••••				
6	0.9994	1.0000	0.9978	0.9978	1.0000	•••••			
7	0.7929	1.0000	0.9995	0.9995	1.0000	0.9978	•••••		
8	0.9941	1.0000	1.0000	1.0000	1.0000	0.9752	0.9873	•••••	
9	0.2781	0.9633	0.8923	0.9996	0.9930	0.2829	0.9933	0.9542	•••••

Analysis of C:\TFPGA\PAV\UBC135.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4	5	6	7	8	9
1	•••••								
2	0.9720	•••••							
3	0.9749	1.0000	•••••						
4	0.9978	1.0000	1.0000	•••••					
5	0.9979	1.0000	1.0000	1.0000	•••••				
6	0.9994	1.0000	1.0000	1.0000	1.0000	•••••			
7	0.9978	1.0000	1.0000	1.0000	1.0000	1.0000	•••••		
8	0.9999	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	•••••	
9	0.0575	0.9979	0.9978	0.9739	0.9745	0.4333	0.3180	0.5584	•••••

2/9/2005 8:07:35 PM
Analysis of C:\TFPGA\ROL\OPA18.TXT

Data set contains genotypes of individuals sampled from populations.
Organism Type: Diploid
Marker Type: Dominant
H-W Equilibrium Assumed.
Allele frequencies estimated based on Lynch and
Milligan's (1994) Taylor expansion estimate.

Exact tests for population differentiation (Raymond and Rousset 1995)
# of dememorization steps: 1000
# of batches: 10
# of permutations per batch: 2000

Pairwise analysis of all populations
Matrix of combined probabilities for each pairwise comparison

	1	2	3
1	*****		
2	0.9936	*****	
3	0.9736	0.9979	*****

Analysis of C:\TFPGA\ROL\OPC02.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	1.0000	1.0000	*****	
4	1.0000	0.9993	0.9999	*****

Analysis of C:\TFPGA\ROL\OPP03.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	1.0000	*****		
3	1.0000	0.9862	*****	
4	0.9461	0.6059	0.7931	*****

Analysis of C:\TFPGA\ROL\UBC133.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.9998	*****		
3	0.9986	0.8641	*****	
4	1.0000	0.9999	0.8634	*****

Analysis of C:\TFPGA\ROL\UBC135.TXT
Matrix of combined probabilities for each pairwise comparison

	1	2	3	4
1	*****			
2	0.9861	*****		
3	0.9994	0.5605	*****	
4	0.9979	0.9999	1.0000	*****

APPENDIX C

DNA EXTRACTION PROTOCOL

QIAGEN extraction

1. Place 3 punched-out circles from a dried blood spot into a sterile labeled 1.5 ml microcentrifuge tube and add 180 µl of Buffer ATL.

2. Incubate at 85 ^{0}C for 10 min. Briefly centrifuge to remove drops from inside the lid.

3. Add 20 µl Proteinase K stock, mix by vortexing, and incubate at 37 ^{0}C for 1 hr. Briefly centrifuge to remove drops from inside the lid.

4. Add 200 µl Buffer AL to the sample, mix thoroughly by vortexing, and incubate at 70^{0}C for 10 min. Briefly centrifuge to remove drops from inside the lid.

5. Add 200 µl ethanol (96-100%) to the sample, and mix thoroughly by vortexing. Briefly centrifuge to remove drops from inside the lid.

6. Carefully apply the mixture from step 5 to the QIAamp Spin Column (in a 2 ml collection tube) without wetting the rim. Close the cap, and centrifuge at 6000 x g (8000 rpm) for 1 min. Place the QIAamp Spin Column in a clean 2 ml collection tube, and discard the tube containing the filtrate.

7. Carefully open the QIAamp Spin Column and add 500 µl Buffer AW1 without wetting the rim. Close the cap and centrifuge at 6000 x g (8000 rpm) for 1 min. Place the QIAamp Spin Column in a clean 2 ml collection tube, and discard the collection tube containing the filtrate.

8. Carefully open the column and add 500 µl Buffer AW2 without wetting the rim. Close the cap and centrifuge at full speed (20,000 x g; 14,000 rpm) for 3 min. Continued directly with step 9, or to eliminate any chance of possible Buffer AW2 carryover, perform step 8a, and then continue with step 9.

8a (Optional): Place the QIAamp Spin Column in a new 2 ml collection tube and discard the collection tube with the filtrate. Centrifuge at full speed for 1 min.

9. Place the QIAamp Spin Column in a clean 1.5 ml microcentrifuge tube and discard the collection tube containing the filtrate. Carefully open the QIAamp Spin Column and add 150 µl Buffer AE or distilled water. Incubate at room temperature for 1 ml, and then centrifuge at 6000 x g (8000 rpm) for 1 min.

APPENDIX D

REAGENT PREPARATION PROTOCOL

1. Agarose

1.1) 0.8% Agarose

An enough amount of ingredients for a 100 ml gel composed of:

- Agarose	0.8	gm
- 1 X TBE buffer	100.0	ml

1.2) 1.8% Agarose

Preparing 1.8% agarose is like 0.8% agarose but 1.8 gram of agarose is used to dissolve in 100 ml 1xTBE buffer.

How to apply the description previously is used follow:

1. For 0.8% Agarose, agarose powder about 0.8 gm is mixed into 1X TBE buffer 100 ml.

   For 1.8% Agarose, agarose powder about 1.8 gm is mixed into 1X TBE buffer 100 ml.

2. The agarose solution is solubilized by heating in a microwave oven.

3. The solubilized agarose allow for cool to 50-60 ^{0}C before pour into a gel mould.

4. Prepare gel mould for set the gel. When time is finished, the dissolved gel is transferred about 25-50 ml

5. The soluble gel is poured into the gel mould which the comb is already inserted to the gel mould.

6. When the gel has completely setting. The comb was removed.

7. The gel is transferred into a gel chamber containing an enough of 1X TBE buffer that covered the gel to about 1-2 mm depth.

2. 10X Tris Boric EDTA buffer (10X TBE)

An enough amount of ingredients for a 1000 ml composed of:

- Tris aminomethane   108.0   gm
- Boric acid   50.4   gm
- EDTA   7.44   gm

The solution is prepared as follow:

1. Tris, Boric and EDTA are mixed into volumetric flask 1000 ml.

2. Double distilled water is added up 1000 ml.

3. Solutions stirred until completely dissolve.

4. Store in room temperature and use 1X TBE for running electrophoresis.

BIOGRAPHY

Mr. Sathit Malawong was born on September 10, 1977 in Suphanburi Province. He graduated from bachelor's degree of Science in Agriculture in 1999 from Department of Soil Science, Faculty of Agriculture, Kasetsart University. He has studied for the degree of Master of Science at the program of Biotechnology, Chulalongkorn University since 2002.