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APPENDICES

Appendix A

A. Sampling sites, date of collection and code of abalone used in this study

Species	Location	Code of populations	Code of samples	Remark
H. asinina	Angsila Marine Biological Research Station, Angsila, Chon Buri	HASH	A01-A30	Hatchery stock, P_o (Brood stock from Samet Island, Rayong)
	Samet Island, Rayong	HASM	A41-A60	Haemolymp was collected from each specimens
	Phuket Abalone Farm	HACH	A81-A95	Hatchery stock, P_o (Brood stock from Cambodia)
	Cambodia	HACB	A100-A122	
	Talibong Island, Trang	HALB	L01-L28	
	The Philippines	HAPH	P01-P30	Hatchery stock, F_1 (Brood stock from The Philippines)
	Indonesia	-	A61-A80	
H. ovina	Khang Kao Island, Chon Buri	HOSC	O1-O30	
	Samet Island, Rayong	HOSM	O41-O80	
	Chuak Island, Trang	HOTR	T01-T47	
	Similan Island, Phang-nga	HOPG	O81-O96	
H. varia	Aeo Island, Phuket	HVPK	V01-V30	
	Similan Island, Phang-nga	HVPG	V31-V34	

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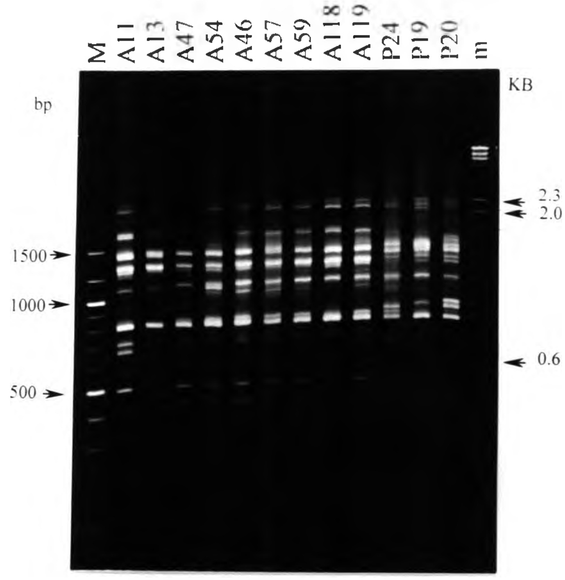
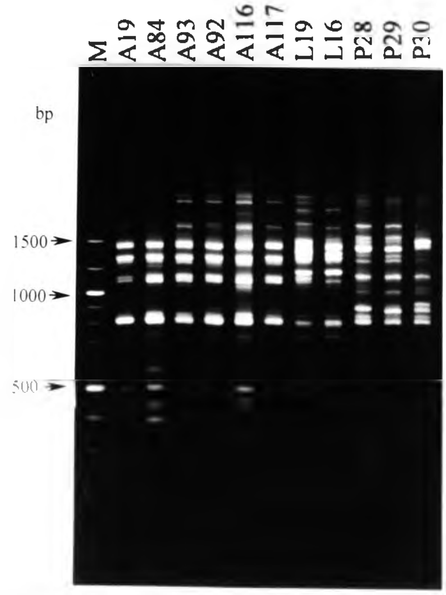
Appendix B

RAPD patterns of all individuals of *Haliotis asinina* (n=99), *H. ovina* (n=95) and *H. varia* (n=33) analyzed by primers OPB11 (B.1), UBC101 (B.2), and *H. asinina* analyzed with UBC195 (B.3), UBC197 (B.4), and UBC271 (B.5). The DNA markers were a 100 bp (Lane M) and λ *Hin*dIII (Lane m), respectively.

B. 1 Primer OPB11





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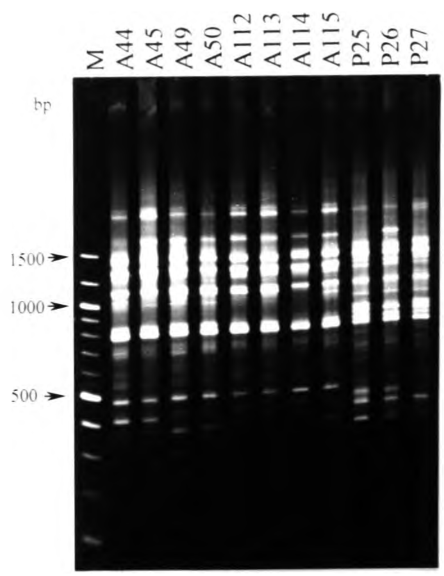

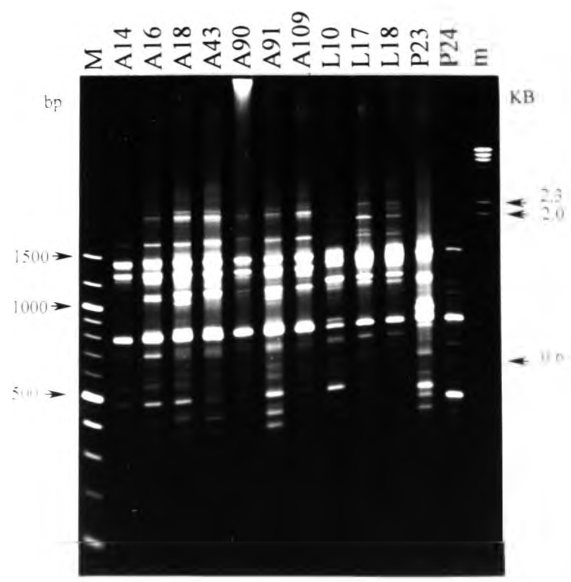

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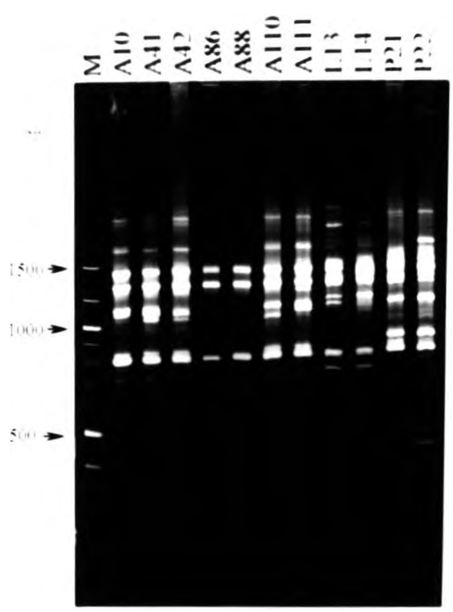

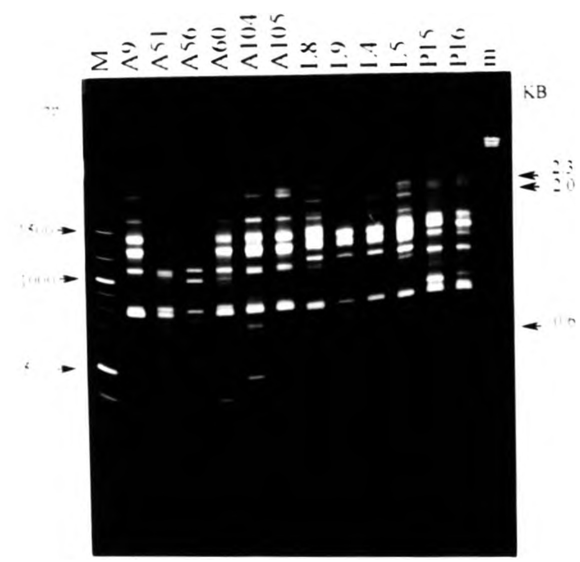

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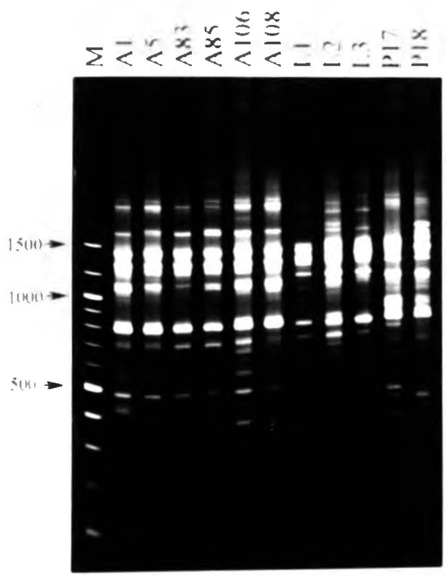

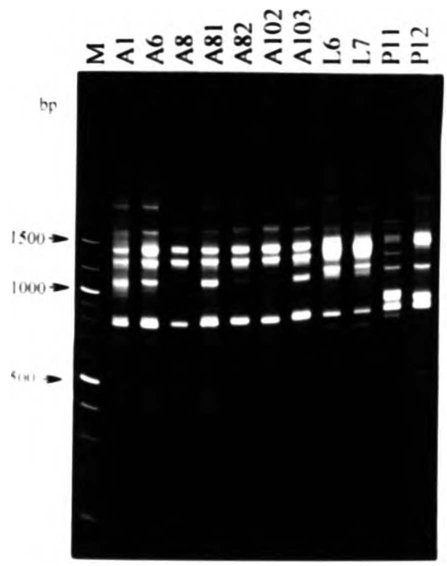

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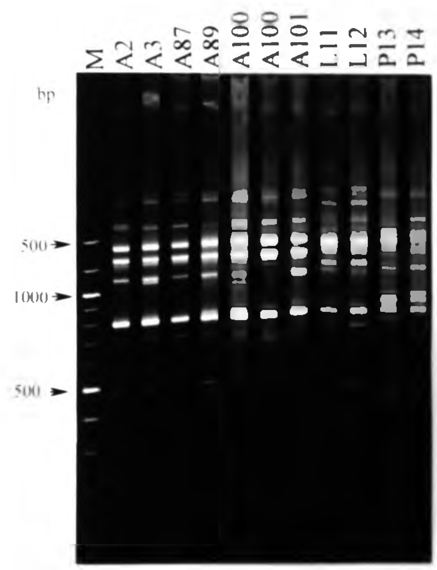

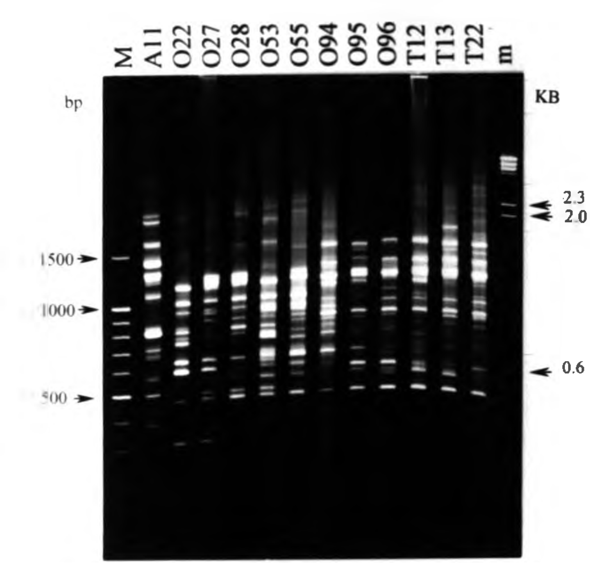

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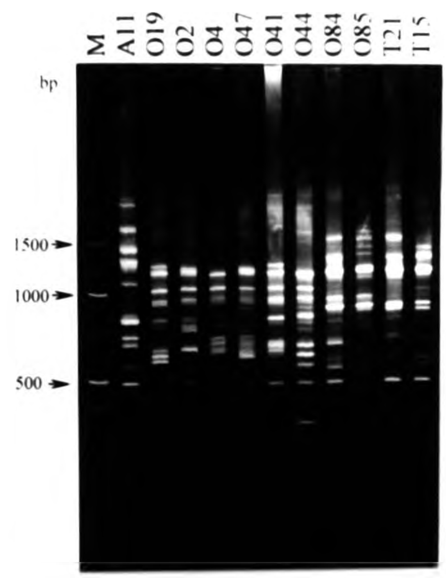

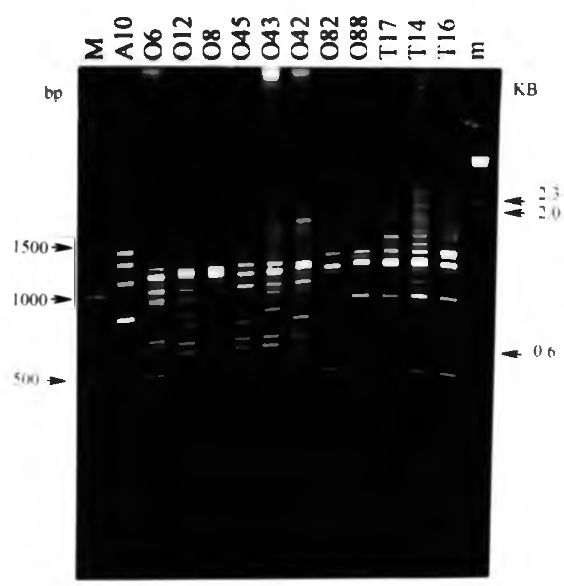

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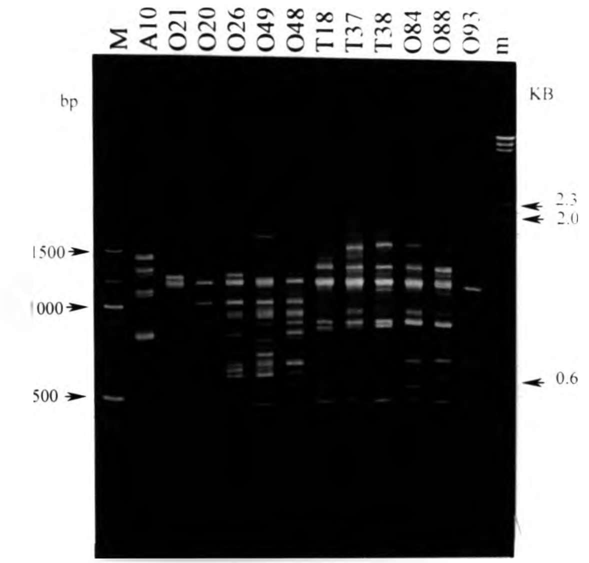

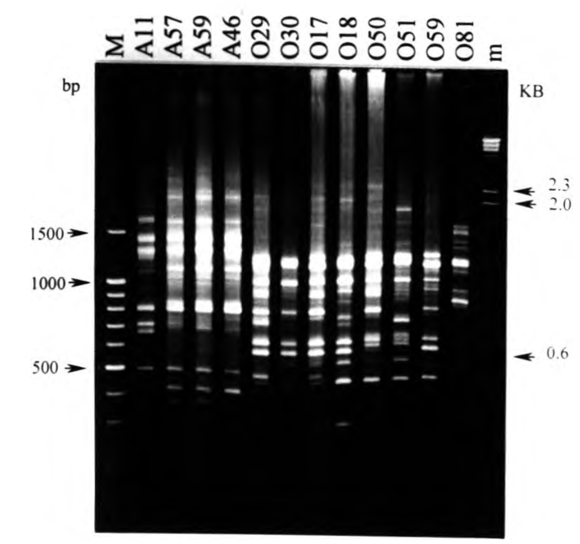

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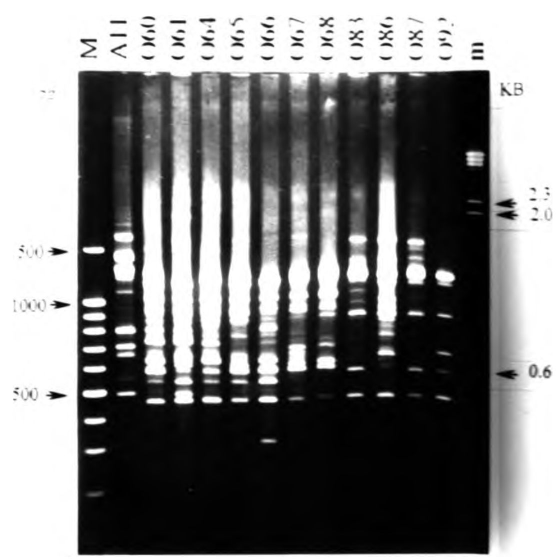

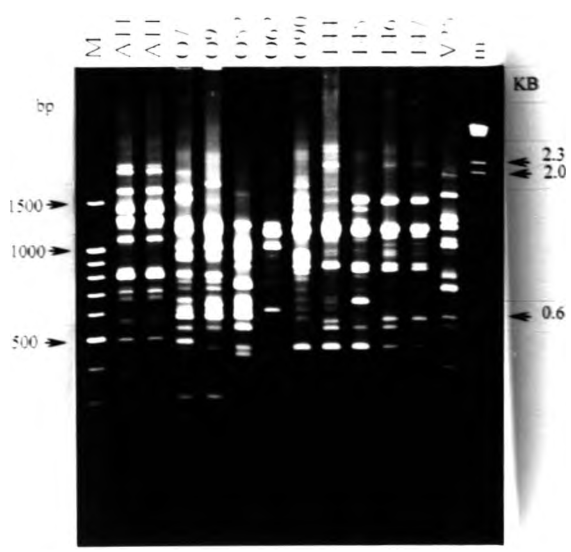

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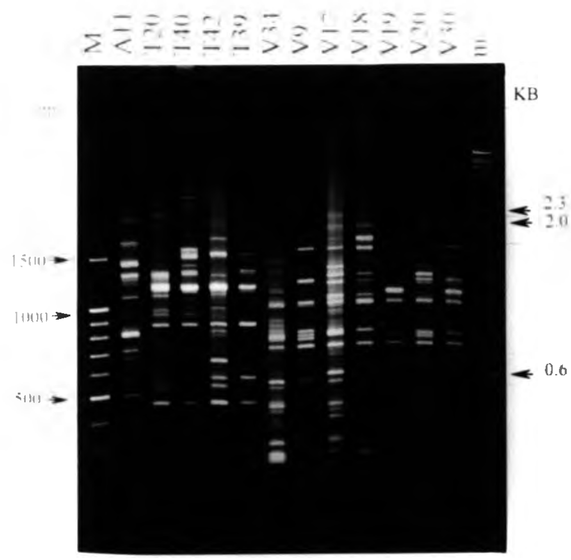

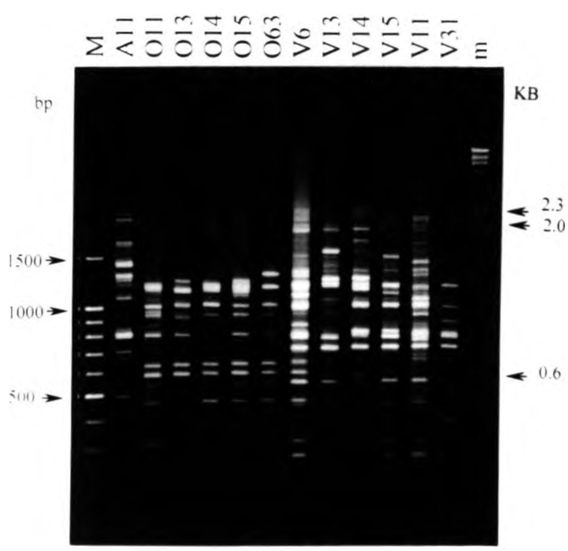

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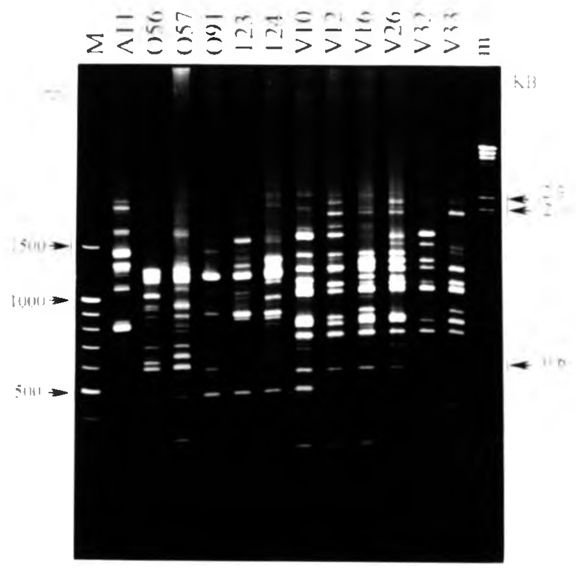

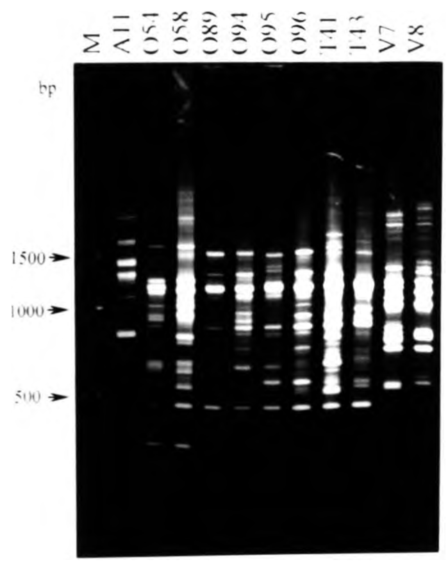

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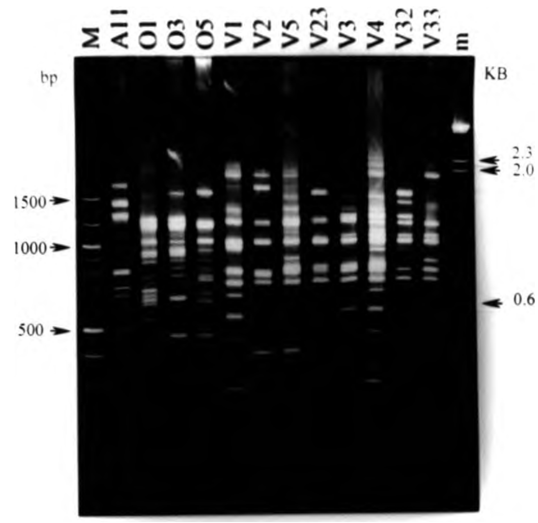

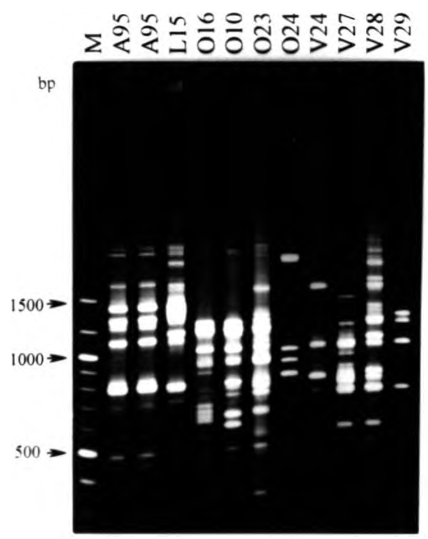

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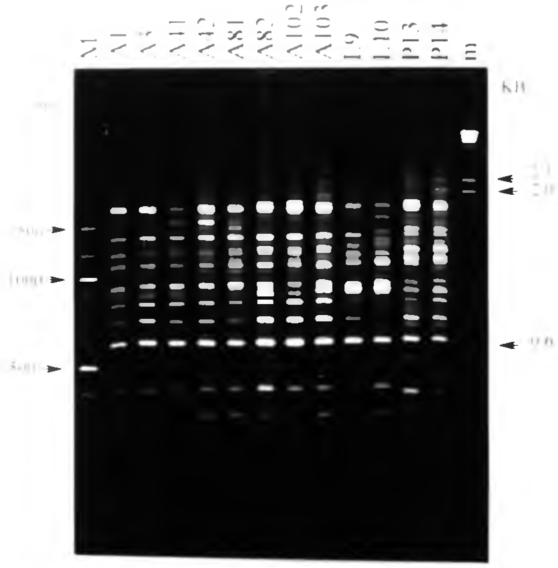

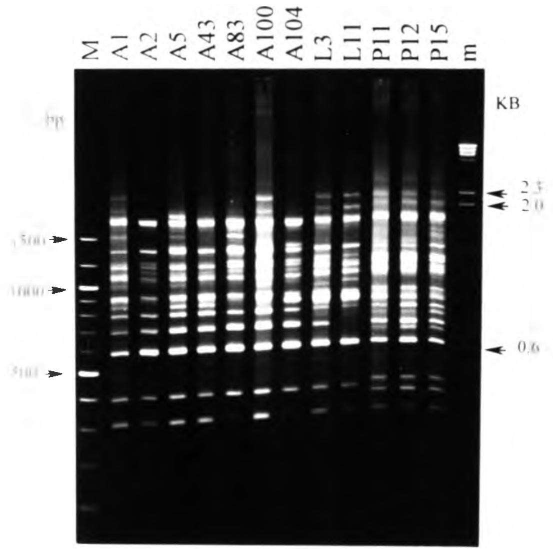

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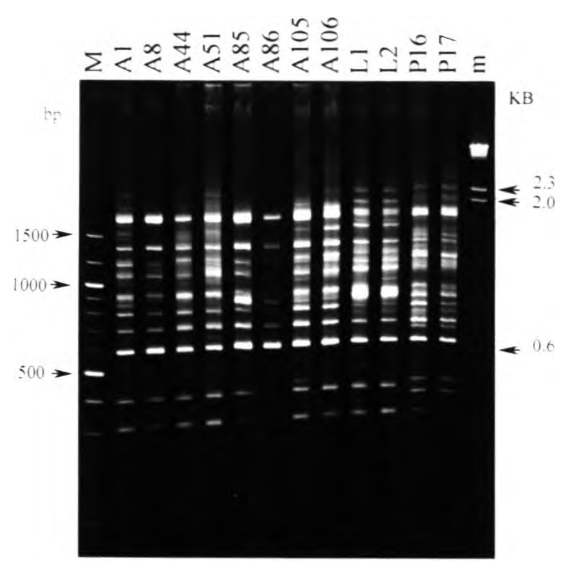

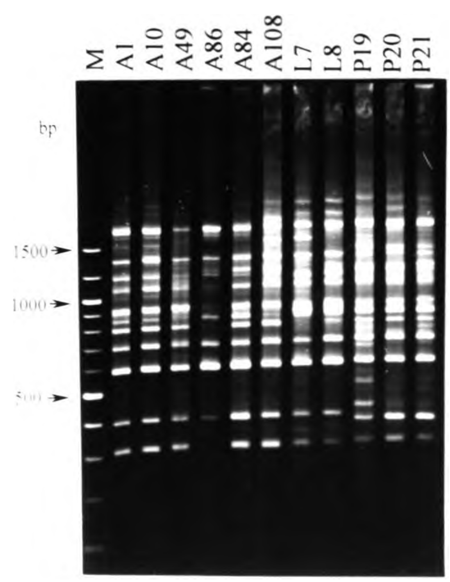

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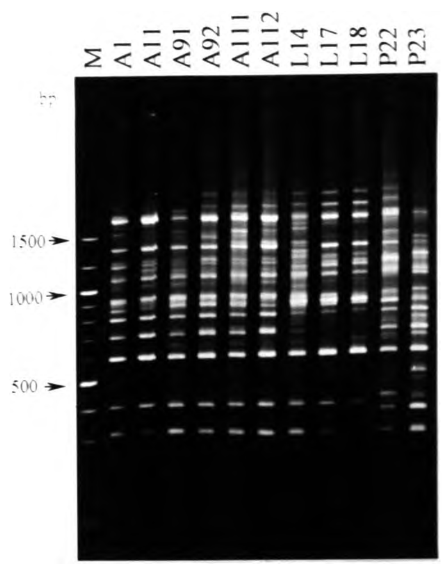

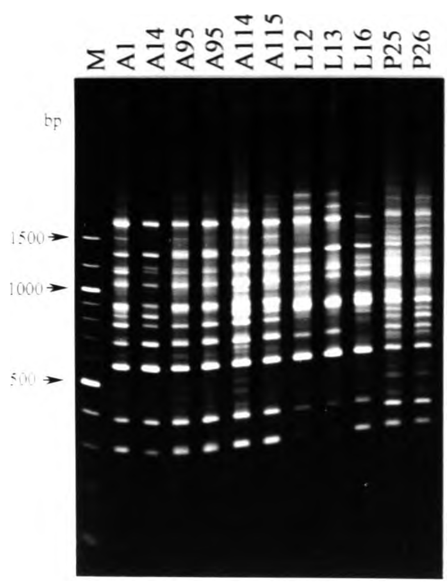

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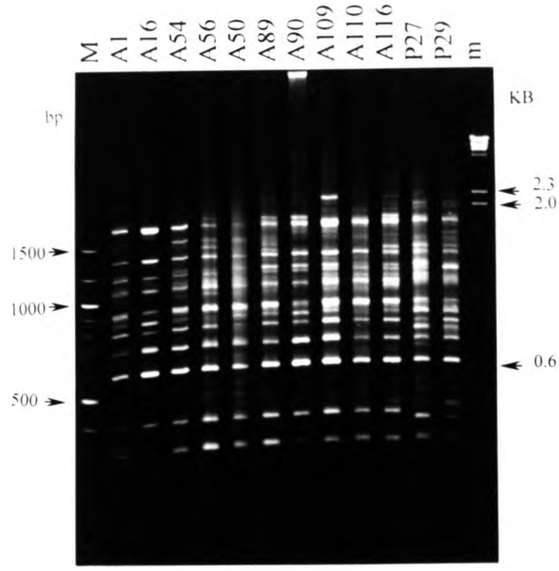

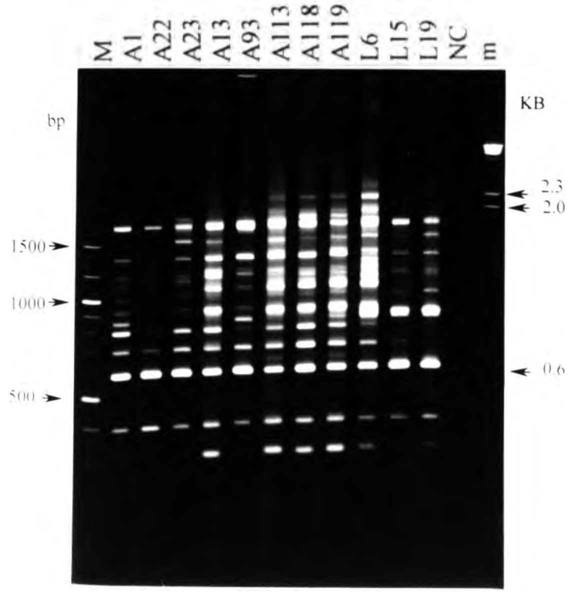

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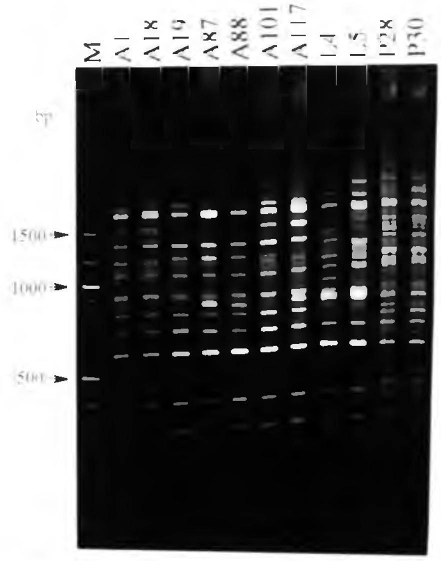

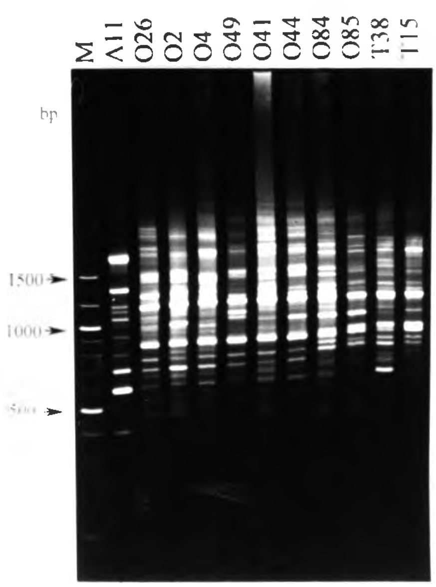

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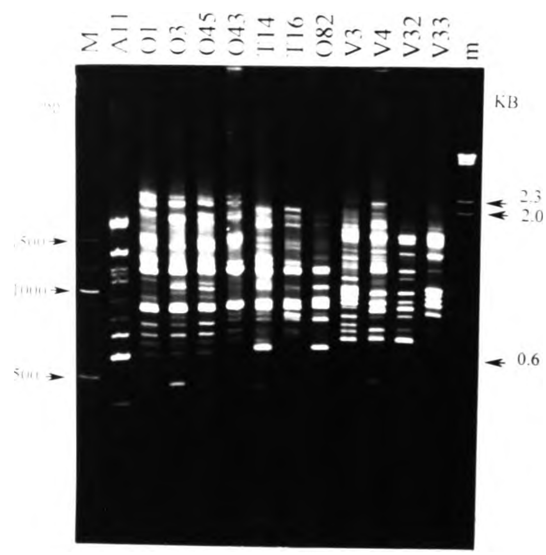
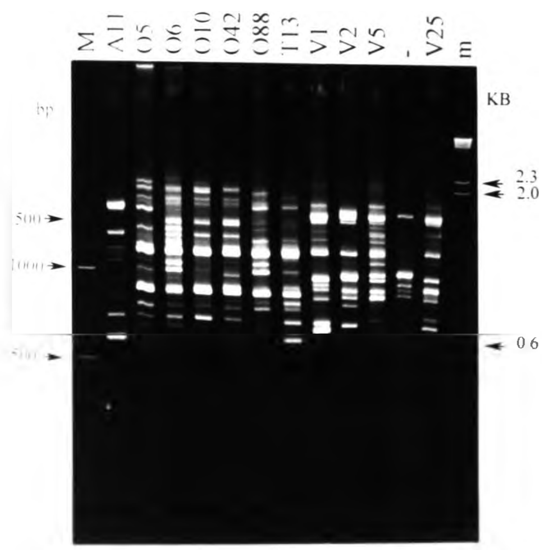
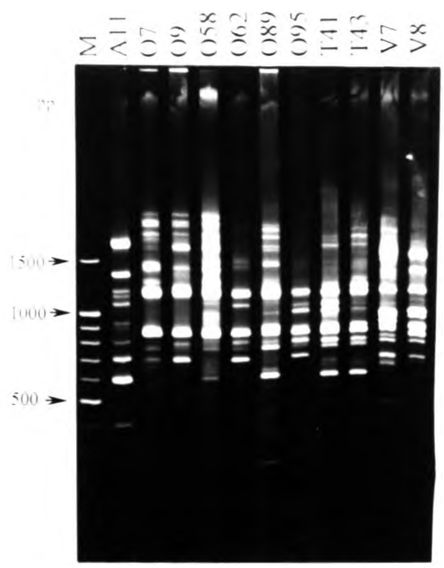
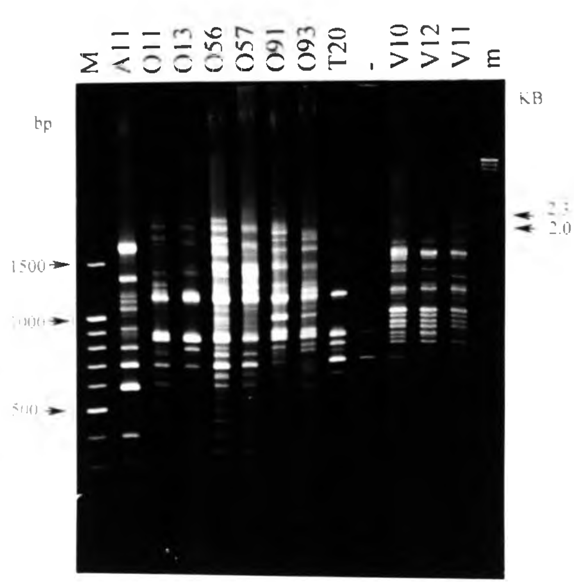


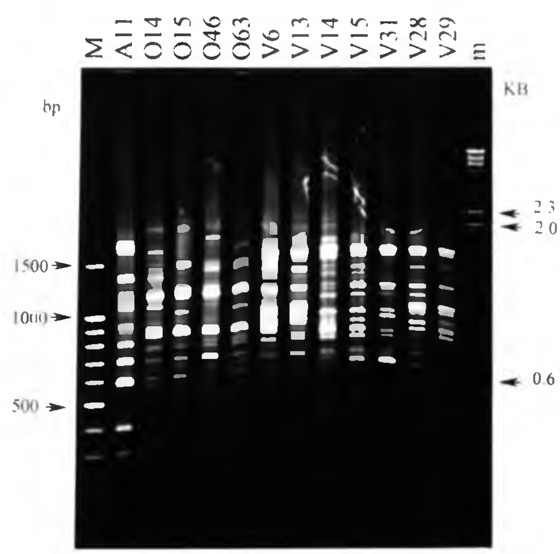


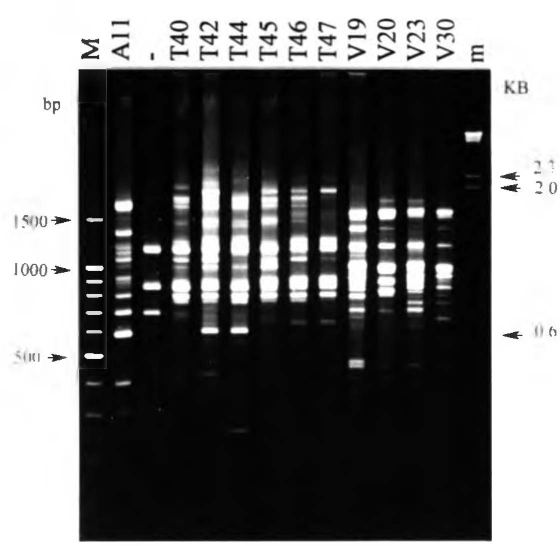
B. 2 Primer UBC101 (continued)



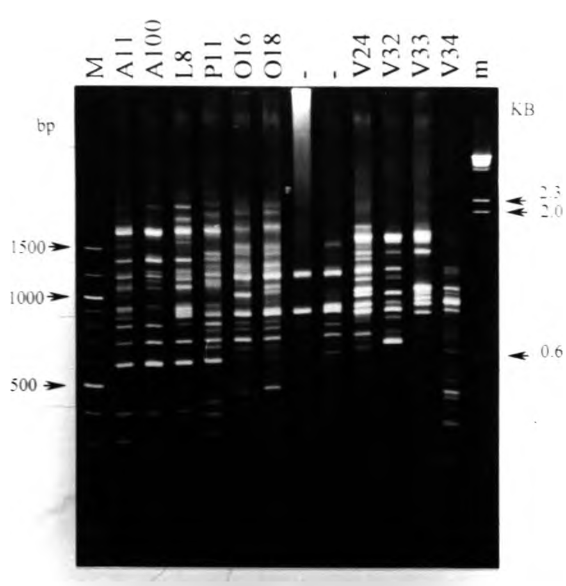


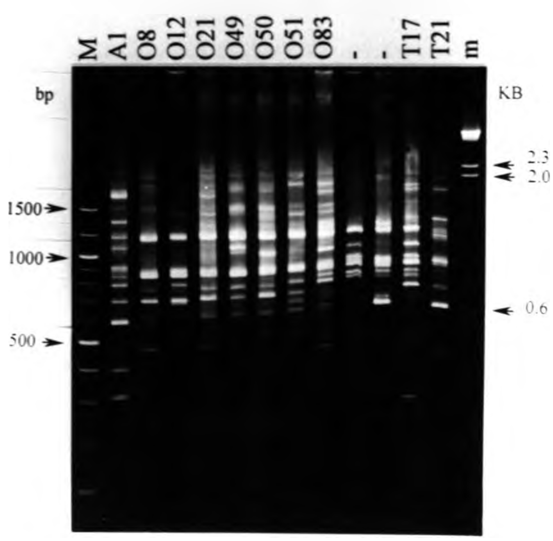
B. 2 Primer UBC101 (continued)



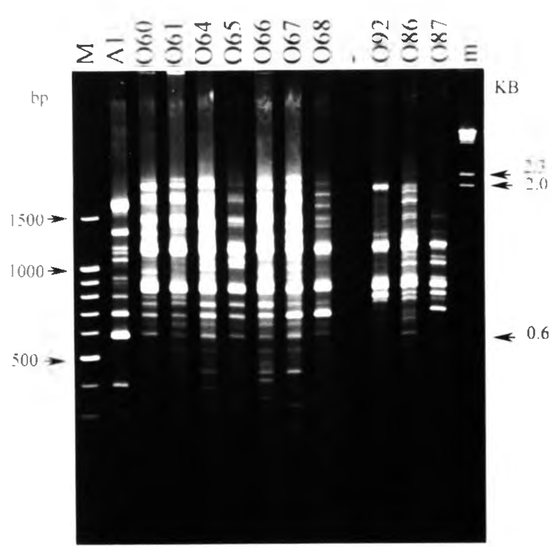


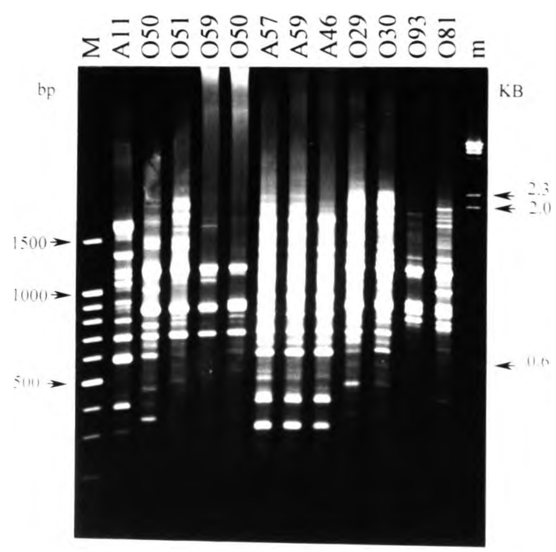
B. 2 Primer UBC101 (continued)



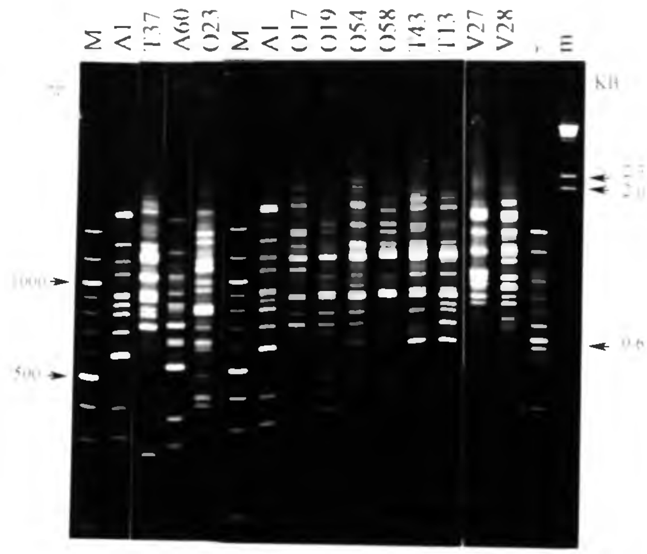


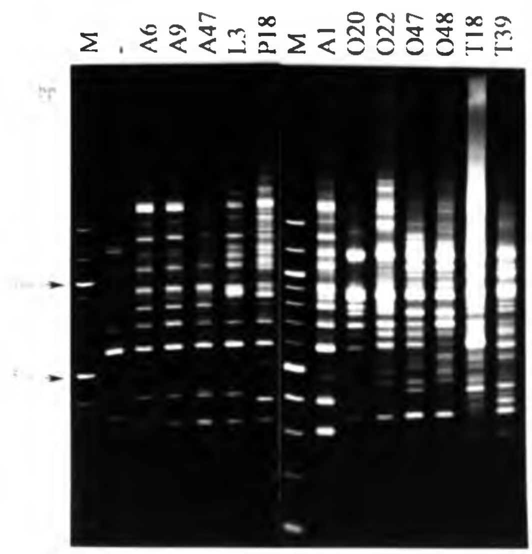
B. 2 Primer UBC101 (continued)



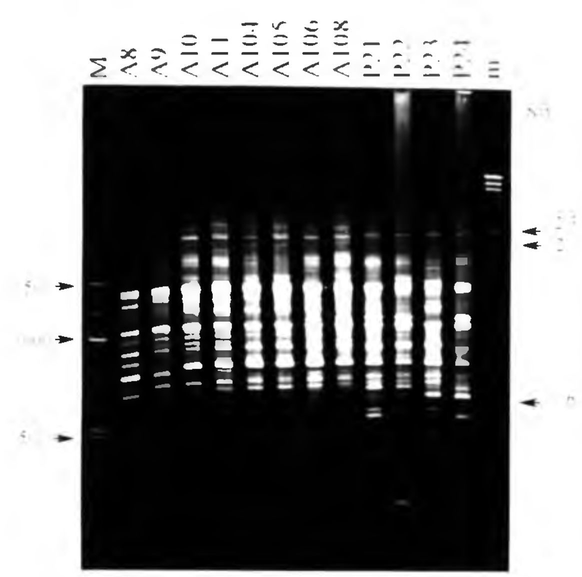


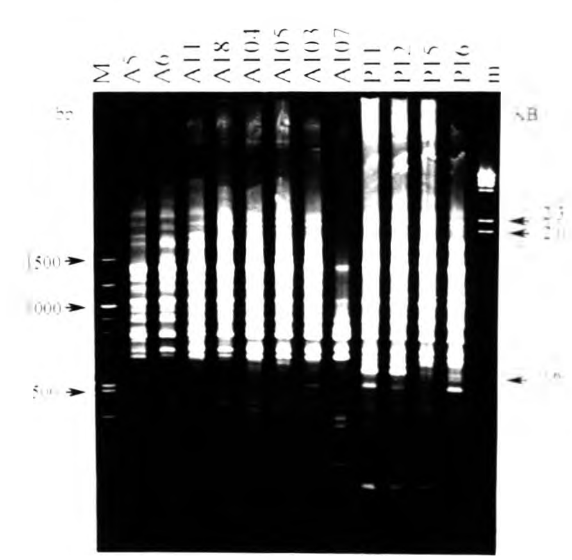
B. 2 Primer UBC101 (continued)



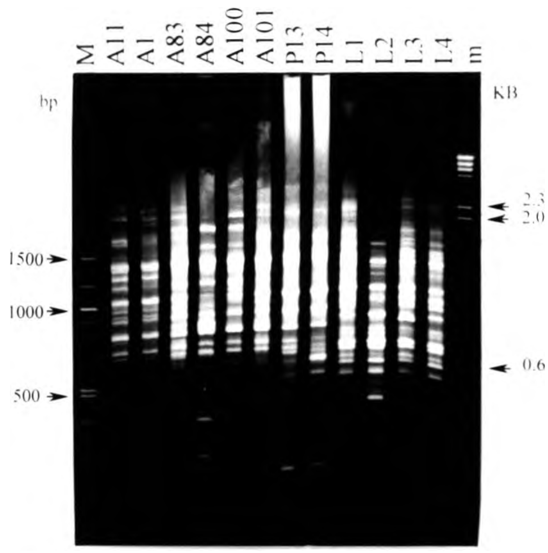


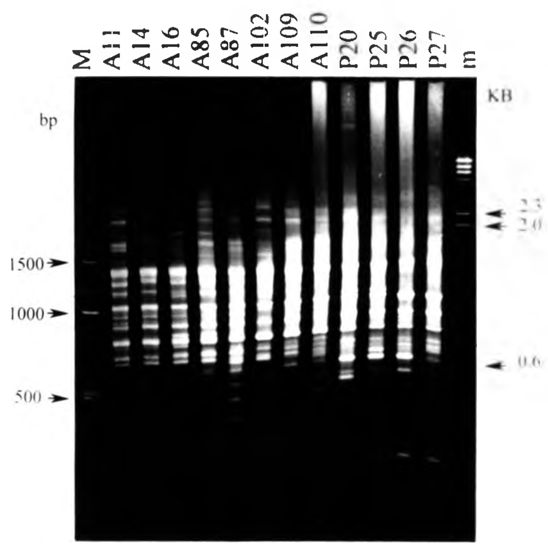
B.3 Primer UBC195



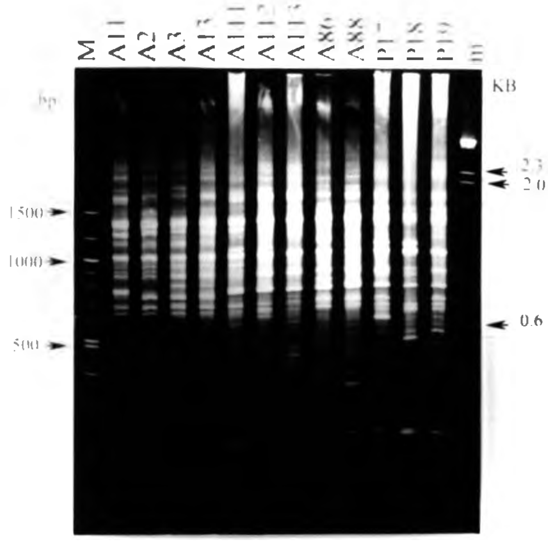


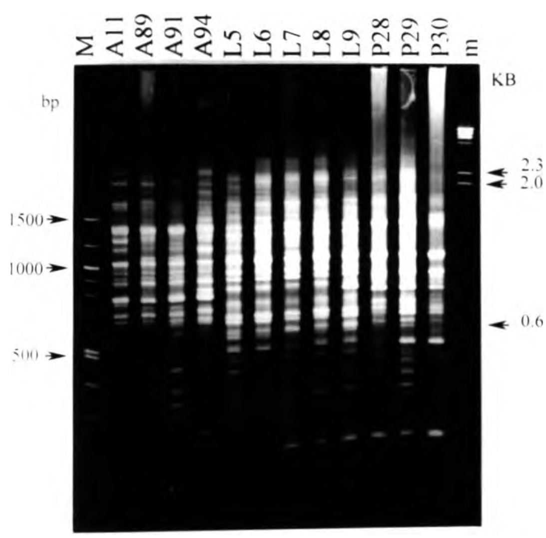
B.3 Primer UBC195 (continued)



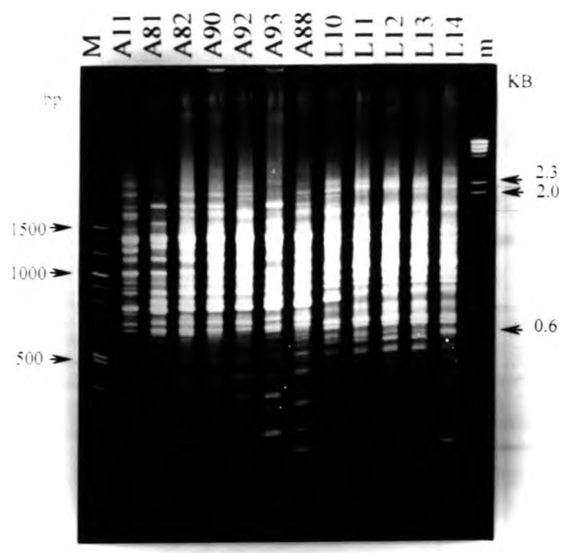


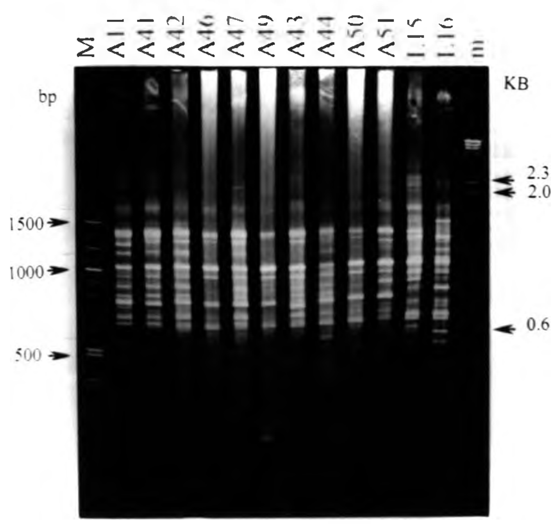
B.3 Primer UBC195 (continued)



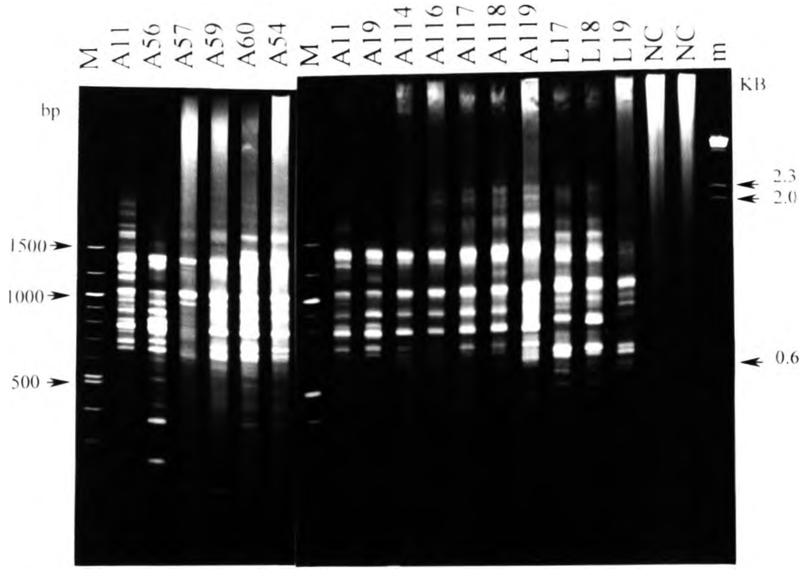


B.3 Primer UBC195 (continued)

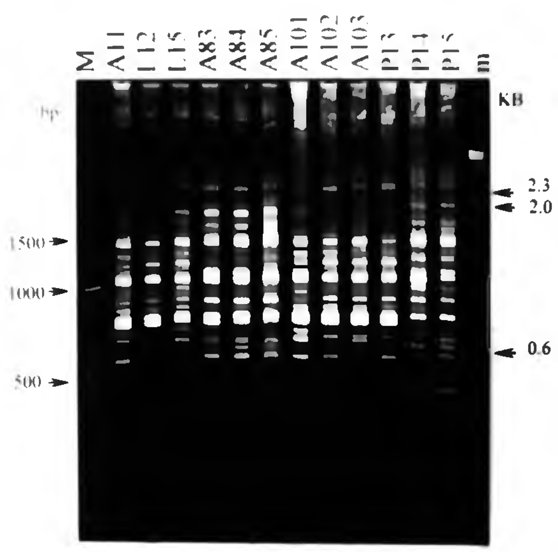


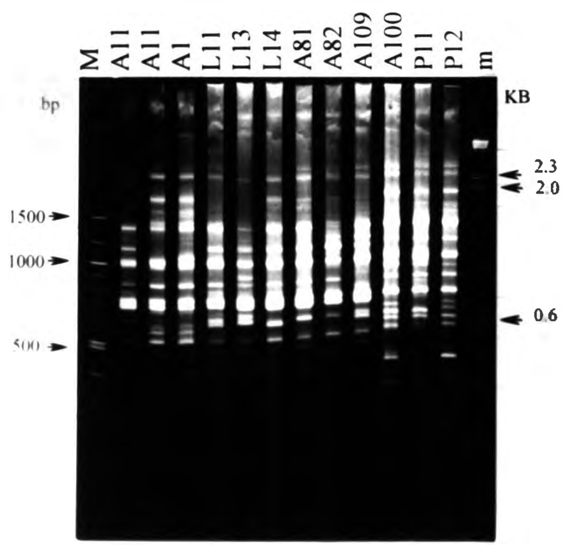


B.3 Primer UBC195 (continued)

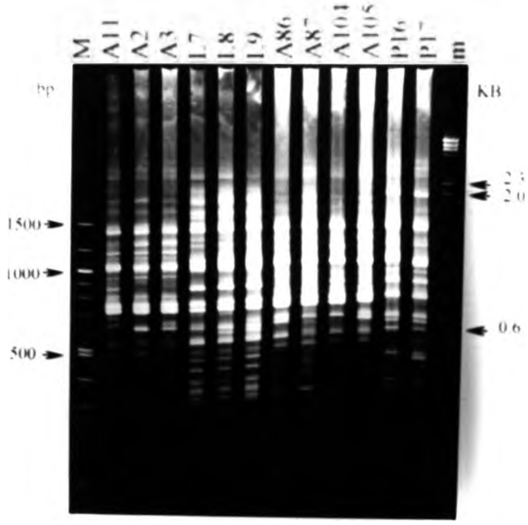


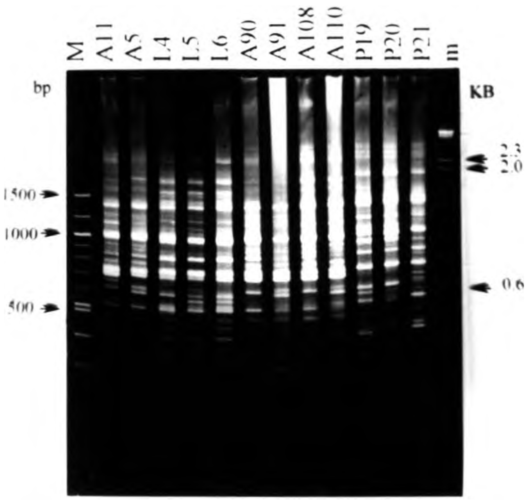
B.4 Primer UBC197



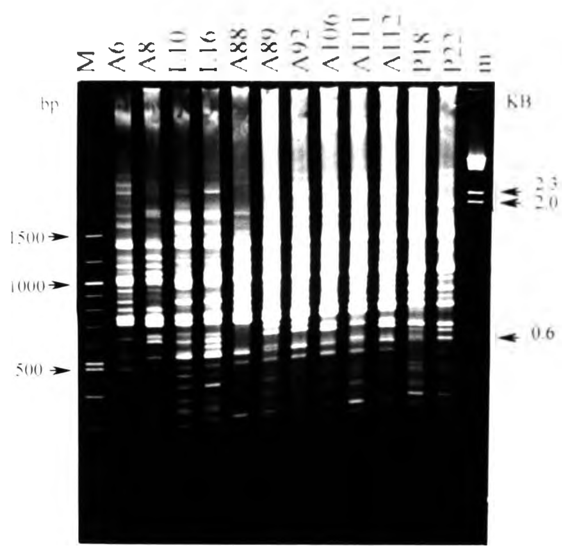


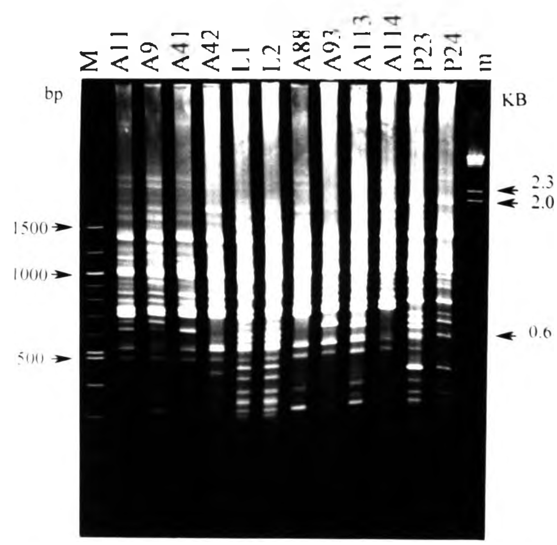
B.4 Primer UBC197 (continued)



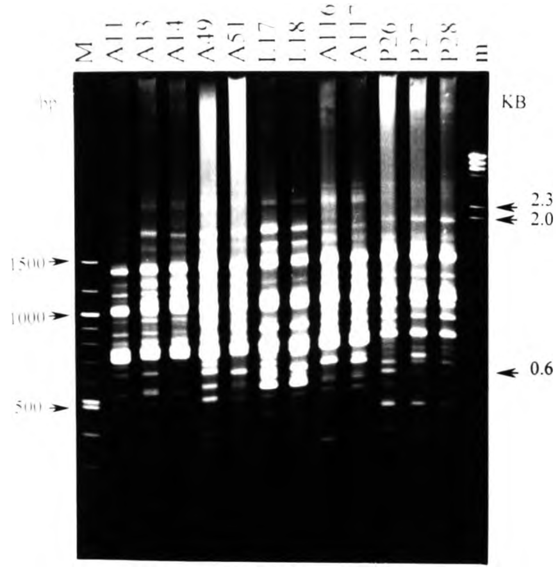


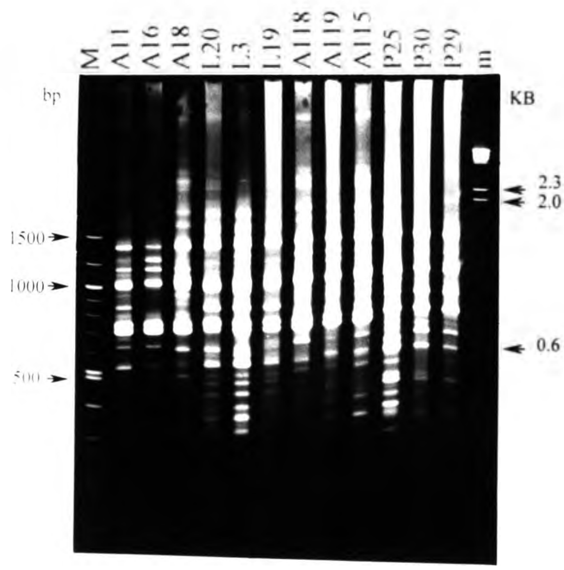
B.4 Primer UBC197 (continued)



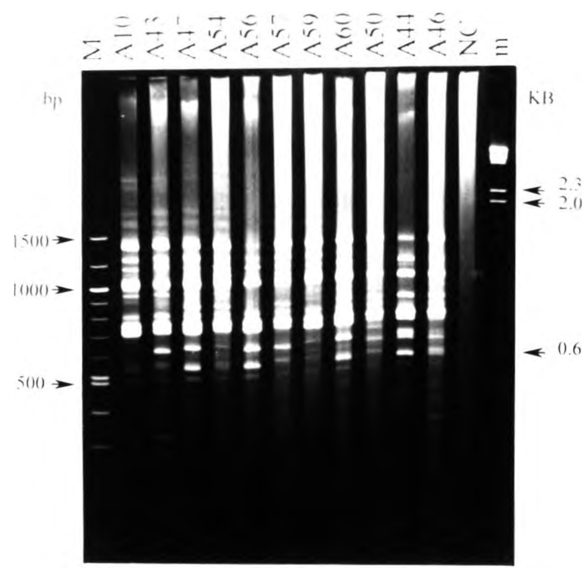


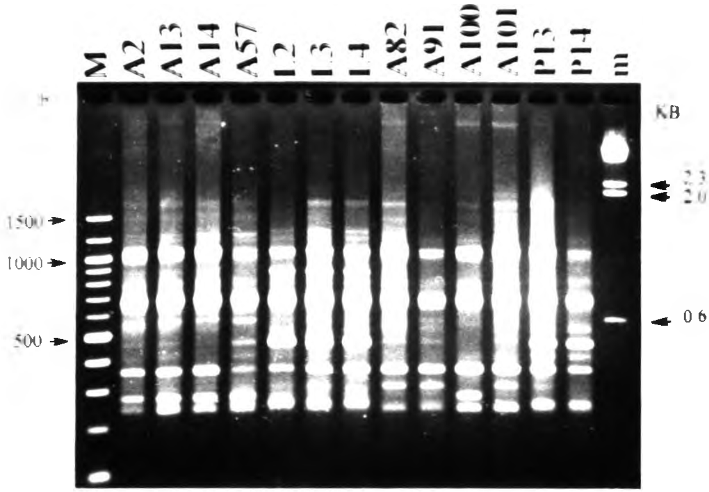
B.4 Primer UBC197 (continued)

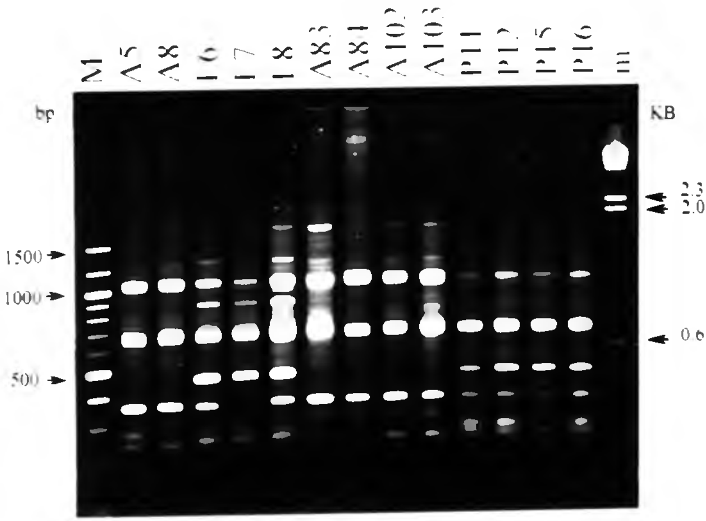




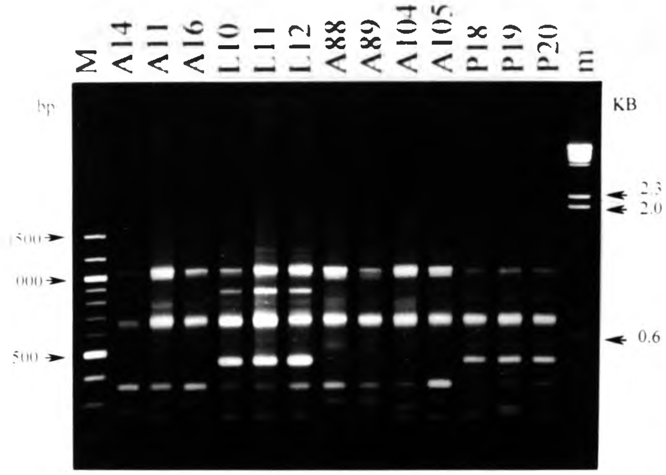
B.4 Primer UBC197 (continued)

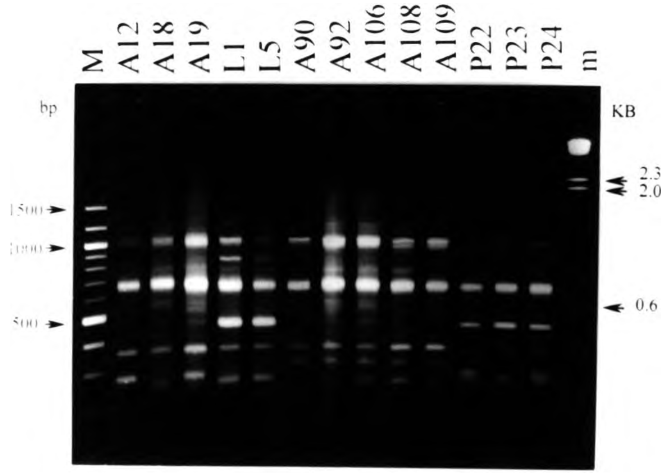



M
A2
A13
A14
A57
L2
L3
L4
A82
A91
A100
A101
P13
P14
m
1500
1000
500
KB
2.3
2.0
0.6

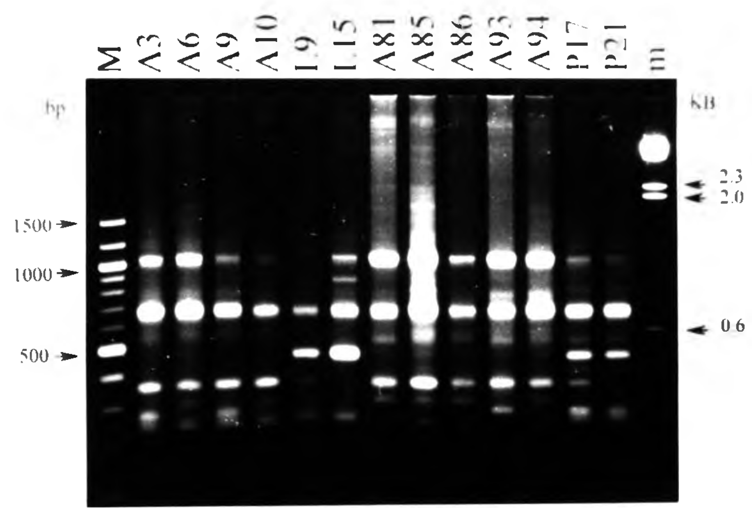

M
A5
A8
L6
L7
L8
A83
A84
A102
A103
P11
P12
P15
P16
m
bp
1500
1000
500
KB
2.3
2.0
0.6

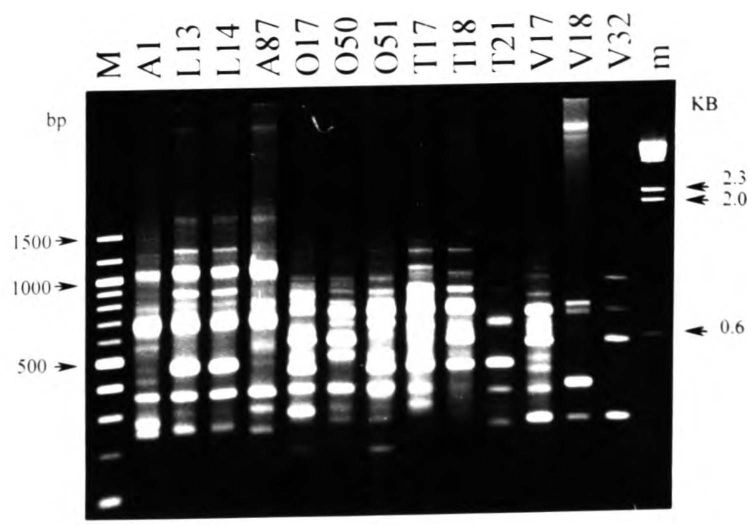
B.5 Primer UBC271 (continued)



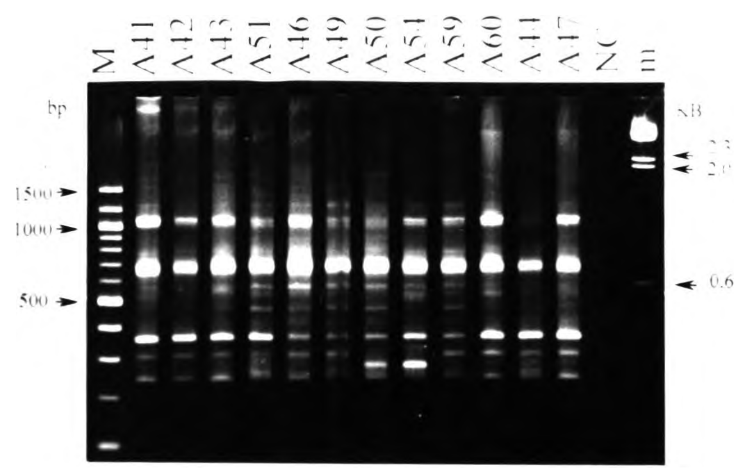


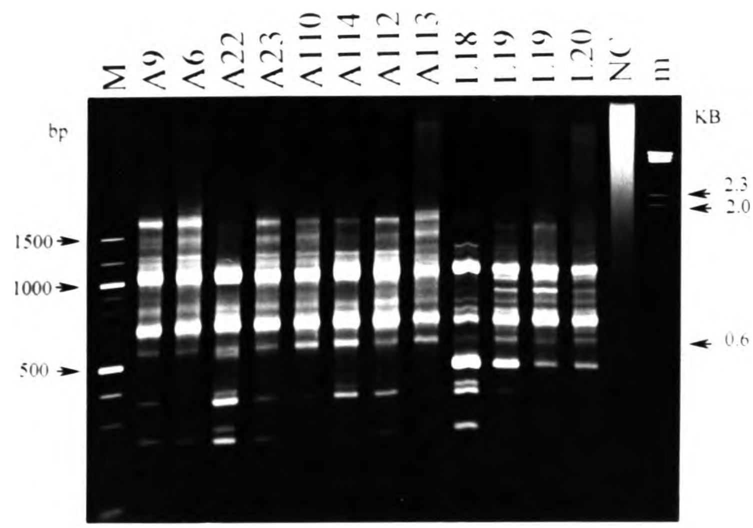
B.5 Primer UBC271 (continued)



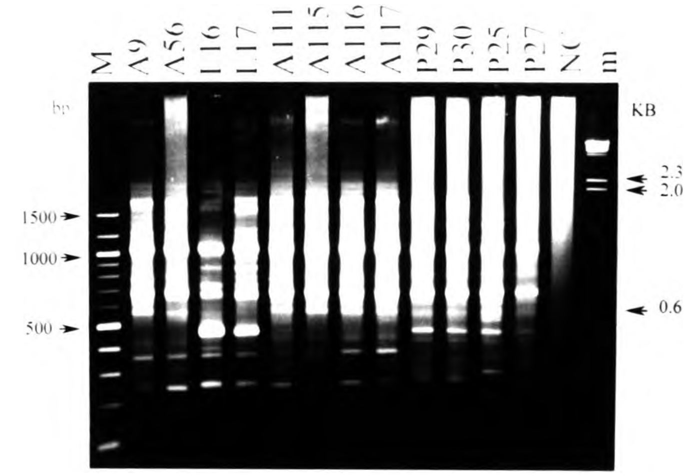


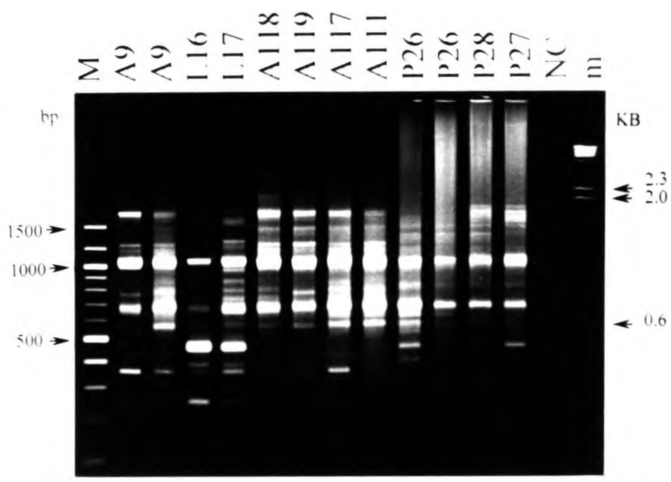
B.5 Primer UBC271 (continued)





B.5 Primer UBC271 (continued)





Appendix C

C. 1 Frequencies of each amplified RAPD band within each investigated samples of *H. asinina, H. ovina* and *H. varia* generated from primer UBC101

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
1850	-	-	-	-	-	-	17	17	12	11	3	-
%	-	-	-	-	-	-	58.62	62.96	75.00	47.83	10.71	-
1800	1	3	4	6	-	-	18	15	4	11	11	-
%	7.14	21.43	30.77	31.58	-	-	62.07	55.56	25.00	47.83	39.29	-
1750	6	1	4	10	4	20	9	8	14	18	19	2
%	42.86	7.14	30.77	52.63	21.05	100.00	31.03	29.63	87.50	78.26	67.86	50.00
1700	14	14	13	19	19	19	-	-	-	-	-	-
%	100.00	100.00	100.00	100.00	100.00	95.00	-	-	-	-	-	-
1650	-	-	-	-	-	1	10	7	4	10	6	1
%	-	-	-	-	-	5.00	34.48	25.93	25.00	43.48	21.43	25.00
1600	-	-	-	-	-	-	-	-	-	2	28	3
%	-	-	-	-	-	-	-	-	-	8.70	100.00	75.00
1540	11	10	5	15	10	10	-	-	-	-	24	2
%	78.57	71.43	38.46	78.95	52.63	50.00	-	-	-	-	85.71	50.00

C. 1 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
1490	-	-	-	-	-	1	14	21	10	10	-	-
%	-	-	-	-	-	5.00	48.28	77.78	62.50	43.48	-	-
1480	-	3	4	1	-	10	9	13	5	13	-	-
%	-	21.43	30.77	5.26	-	50.00	31.03	48.15	31.25	56.52	-	-
1450	1	-	1	7	4	18	23	17	6	10	26	2
%	7.14	-	7.69	36.84	21.05	90.00	79.31	62.96	37.50	43.48	92.86	50.00
1350	14	14	13	19	18	20	3	1	-	3	15	-
%	100.00	100.00	100.00	100.00	94.74	100.00	10.34	3.70	-	13.04	53.57	-
1300	-	-	-	-	4	2	-	-	-	-	-	-
%	-	-	-	-	21.05	10.00	-	-	-	-	-	-
1260	-	-	-	-	14	4	19	14	13	17	-	-
%	-	-	-	-	73.68	20.00	65.52	51.85	81.25	73.91	-	-
1220	10	12	12	19	2	17	18	21	11	21	-	-
%	71.43	85.71	92.31	100.00	10.53	85.00	62.07	77.78	68.75	91.30	-	-
1190	14	13	13	19	17	15	-	-	-	-	-	-
%	100.00	92.86	100.00	100.00	89.47	75.00	-	-	-	-	-	-

C. 1 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
1170	1	3	-	-	17	-	29	27	16	23	27	4
%	7.14	21.43	-	-	89.47	-	100.00	100.00	100.00	100.00	96.43	100.00
1150	3	8	5	11	-	9	-	-	-	-	-	-
%	21.43	57.14	38.46	57.89	-	45.00	-	-	-	-	-	-
1100	14	14	13	19	17	19	16	17	12	8	11	2
%	100.00	100.00	100.00	100.00	89.47	95.00	55.17	62.96	75.00	34.78	39.29	50.00
1040	-	-	-	-	-	1	11	7	1	8	14	3
%	-	-	-	-	-	5.00	37.93	25.93	6.25	34.78	50.00	75.00
1000	-	-	-	-	-	-	19	19	15	19	18	2
%	-	-	-	-	-	-	65.52	70.37	93.75	82.61	64.29	50.00
980	-	-	-	-	-	-	-	-	-	-	28	4
%	-	-	-	-	-	-	-	-	-	-	100.00	100.00
920	14	14	13	19	6	19	-	-	-	-	-	-
%	100.00	100.00	100.00	100.00	31.58	95.00	-	-	-	-	-	-
900	2	5	-	3	18	-	-	-	-	-	18	4
%	14.29	35.71	-	15.79	94.74	-	-	-	-	-	64.29	100.00

C. 1 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
870	-	-	-	-	-	-	20	15	15	23	4	-
%	-	-	-	-	-	-	68.97	55.56	93.75	100.00	14.29	-
850	9	10	11	12	19	18	29	27	16	23	22	2
%	64.29	71.43	84.62	63.16	100.00	90.00	100.00	100.00	100.00	100.00	78.57	50.00
820	-	-	-	-	1	-	-	-	-	-	21	1
%	-	-	-	-	5.26	-	-	-	-	-	75.00	25.00
800	14	14	13	19	16	20	21	15	16	23	23	2
%	100.00	100.00	100.00	100.00	84.21	100.00	72.41	55.56	100.00	100.00	82.14	50.00
750	-	1	-	-	4	18	29	26	16	22	17	2
%	-	7.14	-	-	21.05	90.00	100.00	96.30	100.00	95.65	60.71	50.00
700	14	14	13	19	13	20	29	26	6	11	27	3
%	100.00	100.00	100.00	100.00	68.42	100.00	100.00	96.30	37.50	47.83	96.43	75.00
680	-	-	-	1	1	17	-	-	-	-	-	-
%	-	-	-	5.26	5.26	85.00	-	-	-	-	-	-
650	2	10	3	10	5	5	28	23	9	14	17	2
%	14.29	71.43	23.08	52.63	26.32	25.00	96.55	85.19	56.25	60.87	60.71	50.00

C. 1 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
600	14	14	13	19	19	20	22	26	10	13	-	-
%	100.00	100.00	100.00	100.00	100.00	100.00	75.86	96.30	62.50	56.52	-	-
440	-	-	1	3	-	14	11	15	3	7	7	2
%	-	-	7.69	15.79	-	70.00	37.93	55.56	18.75	30.43	25.00	50.00
400	14	14	13	19	19	3	5	5	3	3	-	1
%	100.00	100.00	100.00	100.00	100.00	15.00	17.24	18.52	18.75	13.04	-	25.00
380	-	-	-	-	-	19	-	-	-	-	-	-
%	-	-	-	-	-	95.00	-	-	-	-	-	-
350	-	-	-	-	-	2	11	18	3	1	1	1
%	-	-	-	-	-	10.00	37.93	66.67	18.75	4.35	3.57	25.00
320	14	14	13	19	19	19	-	-	-	1	-	-
%	100.00	100.00	100.00	100.00	100.00	95.00	-	-	-	4.35	-	-

C. 2 Frequencies of each amplified RAPD band within each investigated samples of *H. asinina, H. ovina* and *H. varia* generated from primer OPB11

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
2300	9	12	7	17	13	15	-	4	-	6	6	-
%	64.29	85.71	53.85	89.47	68.42	75.00	-	14.81	-	26.09	21.43	-
2150	12	10	11	19	12	17	4	2	1	7	12	-
%	85.71	71.43	84.62	100.00	63.16	85.00	13.79	7.41	6.25	30.43	42.86	-
1700	14	10	13	19	18	7	3	5	1	5	8	-
%	100.00	71.43	100.00	100.00	94.74	35.00	10.34	18.52	6.25	21.74	28.57	-
1480	-	-	-	-	12	18	-	-	1	4	2	-
%	-	-	-	-	63.16	90.00	-	-	6.25	17.39	7.14	-
1450	14	13	13	19	-	-	-	-	2	4	6	2
%	100.00	92.86	100.00	100.00	-	-	-	-	12.50	17.39	21.43	50.00
1420	-	-	-	-	19	19	-	-	3	4	7	2
%	-	-	-	-	100	95	-	-	18.75	17.39	25.00	50.00
1350	-	-	-	-	19	-	-	2	6	8	12	1
%	-	-	-	-	100.00	-	-	7.41	37.50	34.78	42.86	25.00
1300	14	12	13	19	19	19	1	1	7	14	11	1
%	100.00	85.71	100.00	100.00	100.00	95.00	3.45	3.70	43.75	60.87	39.29	25.00

C. 2 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
1220	6	2	4	8	1	11	18	18	1	6	12	2
%	42.86	14.29	30.77	42.11	5.26	55.00	62.07	66.67	6.25	26.09	42.86	50.00
1190	-	-	-	-	-	-	13	11	9	9	13	1
%	-	-	-	-	-	-	44.83	40.74	56.25	39.13	46.43	25.00
1180	-	-	-	-	19	-	25	20	9	20	13	1
%	-	-	-	-	100.00	-	86.21	74.07	56.25	86.96	46.43	25.00
1100	13	14	11	17	15	20	1	2	10	9	10	1
%	92.86	100.00	84.62	89.47	78.95	100.00	3.45	7.41	62.50	39.13	35.71	25.00
1080	6	6	6	10	7	-	-	-	-	-	-	-
%	42.86	42.86	46.15	52.63	36.84	-	-	-	-	-	-	-
1050	-	-	-	-	-	-	1	2	-	-	18	3
%	-	-	-	-	-	-	3.45	7.41	-	-	64.29	75.00
1000	-	-	-	-	-	-	28	26	3	1	27	4
%	-	-	-	-	-	-	96.55	96.30	18.75	4.35	96.43	100.00
950	-	-	-	-	-	-	23	24	8	13	4	-
%	-	-	-	-	-	-	79.31	88.89	50.00	56.52	14.29	-

C. 2 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
920	-	-	-	-	-	-	22	24	2	10	6	-
%	-	-	-	-	-	-	75.86	88.89	12.50	43.48	21.43	-
900	-	-	-	-	-	9	-	-	-	-	-	-
%	-	-	-	-	-	45.00	-	-	-	-	-	-
880	-	-	-	-	-	19	10	23	15	23	2	3
%	-	-	-	-	-	95.00	34.48	85.19	93.75	100.00	7.14	75.00
840	4	12	5	8	4	14	6	3	3	13	6	1
%	28.57	85.71	38.46	42.11	21.05	70.00	20.69	11.11	18.75	56.52	21.43	25.00
800	14	14	13	19	19	20	19	15	4	2	18	3
%	100.00	100.00	100.00	100.00	100.00	100.00	65.52	55.56	25.00	8.70	64.29	75.00
760	-	-	-	-	-	-	23	20	3	5	17	2
%	-	-	-	-	-	-	79.31	74.07	18.75	21.74	60.71	50.00
740	-	-	-	-	-	-	19	16	4	1	5	1
%	-	-	-	-	-	-	65.52	59.26	25.00	4.35	17.86	25.00
700	-	-	-	-	-	-	-	3	3	-	16	4
%	-	-	-	-	-	-	-	11.11	18.75	-	57.14	100.00

C. 2 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
660	-	-	-	-	-	-	4	8	4	10	3	1
%	-	-	-	-	-	-	13.79	29.63	25.00	43.48	10.71	25.00
650	-	-	-	-	-	-	27	24	3	6	6	1
%	-	-	-	-	-	-	93.10	88.89	18.75	26.09	21.43	25.00
620	-	-	-	-	-	-	9	16	5	3	1	-
%	-	-	-	-	-	-	31.03	59.26	31.25	13.04	3.57	-
590	-	-	-	-	-	-	22	23	5	4	2	-
%	-	-	-	-	-	-	75.86	85.19	31.25	17.39	7.14	-
570	3	2	1	4	-	-	1	2	4	13	3	-
%	21.43	14.29	7.69	21.05	-	-	3.45	7.41	25.00	56.52	10.71	-
550	-	-	-	-	-	-	20	19	7	15	20	3
%	-	-	-	-	-	-	68.97	70.37	43.75	65.22	71.43	75.00
540	-	-	-	-	1	-	2	2	2	9	4	-
%	-	-	-	-	5.26	-	6.90	7.41	12.50	39.13	14.29	-
500	14	13	13	19	3	5	14	2	-	-	4	-
%	100.00	92.86	100.00	100.00	15.79	25.00	48.28	7.41	-	-	14.29	-

C. 2 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
470	-	-	-	-	-	-	18	26	16	23	15	3
%	-	-	-	-	-	-	62.07	96.30	100.00	100.00	53.57	75.00
440	10	9	3	12	2	20	-	-	-	-	2	1
%	71.43	64.29	23.08	63.16	10.53	100.00	-	-	-	-	7.14	25.00
390	3	11	4	11	2	11	-	-	-	-	1	-
%	21.43	78.57	30.77	57.89	10.53	55.00	-	-	-	-	3.57	-

C. 3 Frequencies of each amplified RAPD band within each conspecific population of *H. asinina* generated from primer UBC195

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)
1480	-	-	1	-	-	9
%	-	-	7.69	-	-	45.00
1450	14	8	12	19	11	16
%	100.00	57.14	92.31	100.00	57.89	80.00
1300	14	14	13	18	18	18
%	100.00	100.00	100.00	94.74	94.74	90.00
1280	8	5	11	9	15	-
%	57.14	35.71	84.62	47.37	78.95	-
1250	13	8	6	14	18	-
%	92.86	57.14	46.15	73.68	94.74	-
1200	2	-	6	5	6	7
%	14.29	-	46.15	26.32	31.58	35
1160	13	5	13	14	16	9
%	92.86	35.71	100.00	73.68	84.21	45.00
1150	5	1	2	3	-	-
%	35.71	7.14	15.38	15.79	-	-
1080	-	-	6	5	13	9
%	-	-	46.15	26.32	68.42	45.00
1030	14	14	13	19	19	20
%	100.00	100.00	100.00	100.00	100.00	100.00
1000	-	-	1	4	-	-
%	-	-	7.69	21.05	-	-
970	13	14	13	14	19	10
%	92.86	100.00	100.00	73.68	100.00	50.00
910	9	9	6	15	-	1
%	64.29	64.29	46.15	78.95	-	5.00
890	14	10	13	19	18	20
%	100.00	71.43	100.00	100.00	94.74	100.00

C. 3 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)
850	-	-	-	-	-	12
%	-	-	-	-	-	60.00
810	5	7	11	7	17	12
%	35.71	50.00	84.62	36.84	89.47	60.00
790	14	13	13	19	4	20
%	100.00	92.86	100.00	100.00	21.05	100.00
750	4	5	-	1	-	-
%	28.57	35.71	-	5.26	-	-
720	-	5	5	5	19	-
%	-	35.71	38.46	26.32	100.00	-
690	14	11	13	19	7	18
%	100.00	78.57	100.00	100.00	36.84	90.00
650	14	14	13	19	19	20
%	100.00	100.00	100.00	100.00	100.00	100.00
620	-	-	5	7	19	17
%	-	-	38.46	36.84	100.00	85.00
600	-	-	4	10	18	19
%	-	-	30.77	52.63	94.74	95.00
570	-	4	3	-	15	16
%	-	28.57	23.08	-	78.95	80.00
520	1	6	9	1	18	9
%	7.14	42.86	69.23	5.26	94.74	45.00

C. 4 Frequencies of each amplified RAPD band within each conspecific population of *H. asinina* generated from primer UBC197

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)
1480	12	6	12	18	19	18
%	85.71	42.86	92.31	94.74	100.00	90.00
1450	14	14	13	19	19	20
%	100.00	100.00	100.00	100.00	100.00	100.00
1250	13	11	12	17	5	3
%	92.86	78.57	92.31	89.47	26.32	15.00
1210	-	-	-	-	-	4
%	-	-	-	-	-	20.00
1200	-	-	-	-	18	19
%	-	-	-	-	94.74	95.00
1180	14	12	13	19	-	-
%	100	85.71	100	100	-	-
1170	2	1	-	-	9	-
%	14.29	7.14	-	-	47.37	-
1150	11	7	1	5	15	13
%	78.57	50.00	7.69	26.32	78.95	65.00
1050	12	14	13	19	19	20
%	85.71	100.00	100.00	100.00	100.00	100.00
980	-	-	-	-	10	-
%	-	-	-	-	52.63	-
920	13	9	7	14	-	19
%	92.86	64.29	53.85	73.68	-	95.00
900	11	2	10	12	14	6
%	78.57	14.29	76.92	63.16	73.68	30.00
850	8	11	13	13	17	20
%	57.14	78.57	100.00	68.42	89.47	100.00
800	14	13	13	18	1	6
%	100.00	92.86	100.00	94.74	5.26	30.00

C. 4 (Continued)

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)
750	14	14	13	19	19	20
%	100.00	100.00	100.00	100.00	100.00	100.00
700	14	14	13	19	19	0
%	100.00	100.00	100.00	100.00	100.00	0.00
680	4	1	4	-	4	13
%	28.57	7.14	30.77	-	21.05	65.00
650	0	3	1	8	7	4
%	0.00	21.43	7.69	42.11	36.84	20.00
620	10	13	10	15	7	17
%	71.43	92.86	76.92	78.95	36.84	85.00
600	5	-	5	-	17	13
%	35.71	-	38.46	-	89.47	65.00
570	-	1	-	1	14	11
%	-	7.14	-	5.26	73.68	55.00
520	14	13	13	19	19	13
%	100.00	92.86	100.00	100.00	100.00	65.00
500	14	12	13	18	19	12
%	100.00	85.71	100.00	94.74	100.00	60.00

C. 5 Frequencies of each amplified RAPD band within each conspecific population of *H. asinina* generated from primer UBC271

Size (bp) %	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)
1020	14	13	13	19	19	20
%	100.00	92.86	100.00	100.00	100.00	100.00
1000	3	5	5	13	3	1
%	21.43	35.71	38.46	68.42	15.79	5.00
880	-	-	-	-	19	-
%	-	-	-	-	100.00	-
680	14	14	13	19	19	20
%	100.00	100.00	100.00	100.00	100.00	100.00
480	-	-	-	-	19	20
%	-	-	-	-	100.00	100.00
475	6	6	7	5	-	-
%	42.86	42.86	53.85	26.32	-	-
470	3	5	-	5	2	14
%	21.43	35.71	-	26.32	10.53	70.00
370	14	14	13	19	17	14
%	100.00	100.00	100.00	100.00	89.47	70.00
320	5	10	12	7	6	1
%	35.71	71.43	92.31	36.84	31.58	5.00
280	7	3	1	2	-	11
%	50.00	21.43	7.69	10.53	-	55.00
270	-	-	-	-	19	19
%	-	-	-	-	100.00	95.00
250	14	14	10	19	-	-
%	100.00	100.00	76.92	100.00	-	-

Appendix D

D. 1 Pairwise comparisons of inter - and intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina, H. ovina* and *H. varia* samples using primers UBC101

Dij/Sij	HASH (N=14)	HASM (N=14)	HACH (N=13)	HACB (N=19)	HALB (N=19)	HAPH (N=20)	HOSC (N=29)	HOSM (N=27)	HOPG (N=16)	HOTR (N=23)	HVPK (N=28)	HVPG (N=4)
HASH	-	0.8531	0.8668	0.8613	0.7354	0.6953	0.3448	0.3501	0.3380	0.3287	0.3284	0.2603
HASM	0.1469	-	0.8494	0.8511	0.7277	0.6749	0.3892	0.3927	0.3528	0.3547	0.3395	0.2801
HACH	0.1332	0.1506	-	0.8540	0.7068	0.7027	0.3802	0.3900	0.3615	0.3657	0.3045	0.2326
HACB	0.1387	0.1489	0.1460	-	0.6998	0.7177	0.3860	0.3876	0.3576	0.3613	0.3509	0.2728
HALB	0.2646	0.2723	0.2932	0.3002	-	0.5886	0.4133	0.4030	0.4113	0.3866	0.3940	0.3663
HAPH	0.3047	0.3251	0.2973	0.2823	0.4114	-	0.4520	0.4552	0.4358	0.4420	0.3892	0.2987
HOSC	0.6552	0.6108	0.6198	0.6140	0.5867	0.5480	-	0.6989	0.6685	0.6657	0.4863	0.4173
HOSM	0.6499	0.6073	0.6100	0.6124	0.5970	0.5448	0.3011	-	0.6627	0.6491	0.4450	0.3973
HOPG	0.6620	0.6472	0.6385	0.6424	0.5887	0.5642	0.3315	0.3373	-	0.7115	0.4448	0.3806
HOTR	0.6713	0.6453	0.6343	0.6387	0.6134	0.5580	0.3343	0.3509	0.2885	-	0.4588	0.3862
HVPU	0.6716	0.6605	0.6955	0.6491	0.6060	0.6108	0.5137	0.5550	0.5552	0.5412	-	0.6377
HVPG	0.7397	0.7199	0.7674	0.7272	0.6337	0.7013	0.5827	0.6027	0.6194	0.6138	0.3623	-

D. 2 Pairwise comparisons of inter - and intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina, H. ovina* and *H. varia* samples using primers OPB11

Dij/Sij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)	HOSC (*N*=29)	HOSM (*N*=27)	HOPG (*N*=16)	HOTR (*N*=23)	HVPK (*N*=28)	HVPG (*N*=4)
HASH	-	0.7604	0.8023	0.8232	0.5253	0.5583	0.1607	0.1217	0.1731	0.2118	0.2630	0.2268
HASM	0.2396	-	0.7476	0.7959	0.4967	0.5815	0.1471	0.1058	0.1724	0.2197	0.2438	0.2127
HACH	0.1977	0.2524	-	0.8064	0.5276	0.5159	0.1609	0.1169	0.1705	0.2073	0.2605	0.2180
HACB	0.1768	0.2041	0.1936	-	0.5366	0.5839	0.1591	0.1230	0.1663	0.2201	0.2653	0.2173
HALB	0.4747	0.5033	0.4724	0.4634	-	0.5699	0.1804	0.1630	0.2655	0.3116	0.3075	0.2358
HAPH	0.4417	0.4185	0.4841	0.4161	0.4301	-	0.1556	0.7194	0.2619	0.3053	0.2472	0.2903
HOSC	0.8393	0.8529	0.8391	0.8409	0.8196	0.8444	-	0.6493	0.3661	0.3745	0.3913	0.3788
HOSM	0.8783	0.8942	0.8831	0.8770	0.8370	0.2806	0.3507	-	0.4408	0.4437	0.3968	0.4229
HOPG	0.8269	0.8276	0.8295	0.8337	0.7345	0.7381	0.6339	0.5592	-	0.4751	0.3073	0.3562
HOTR	0.7882	0.7803	0.7927	0.7799	0.6884	0.6947	0.6255	0.5563	0.5249	-	0.3018	0.3253
HVPU	0.7370	0.7562	0.7395	0.7347	0.6925	0.7528	0.6087	0.6032	0.6927	0.6982	-	0.5034
HVPG	0.7732	0.7873	0.7820	0.7827	0.7642	0.7097	0.6212	0.5771	0.6438	0.6747	0.4966	-

D. 3 Pairwise comparisons of intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina* using primer UBC101

Daij /Saij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)
HASH	-	0.9840	0.9919	0.9887	0.8875	0.8351
HASM	0.0160	-	0.9865	0.9905	0.8919	0.8268
HACH	0.0081	0.0135	-	0.9877	0.8652	0.8488
HACB	0.0113	0.0095	0.0123	-	0.8605	0.8661
HALB	0.1125	0.1081	0.1348	0.1395	-	0.7617
HAPH	0.1649	0.1732	0.1512	0.1339	0.2383	-

D. 4 Pairwise comparisons of intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina* using primer OPB11

Daij/Saij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)
HASH	-	0.9632	0.998	0.997	0.7131	0.7455
HASM	0.0368	-	0.9574	0.9838	0.6985	0.7828
HACH	0.0020	0.0426	-	0.9872	0.7223	0.7101
HACB	0.0030	0.0162	0.0128	-	0.7094	0.7562
HALB	0.2869	0.3015	0.2777	0.2906	-	0.7561
HAPH	0.2545	0.2172	0.2899	0.2438	0.2439	-

D. 5 Pairwise comparisons of intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina* using primer UBC195

Daij/Saij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)
HASH	-	0.9565	0.9417	0.9766	0.7548	0.7926
HASM	0.0435	-	0.9405	0.9494	0.8152	0.8373
HACH	0.0583	0.0595	-	0.9652	0.9003	0.8881
HACB	0.0234	0.0506	0.0348	-	0.8289	0.8782
HALB	0.2452	0.1848	0.0997	0.1711	-	0.839
HAPH	0.2074	0.1627	0.1119	0.1218	0.1610	-

D. 6 Pairwise comparisons of intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina* using primer UBC197

Daij/Saij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)
HASH	-	0.9678	0.9767	0.9834	0.8084	0.8098
HASM	0.0322	-	0.9658	0.982	0.7898	0.8102
HACH	0.0233	0.0342	-	0.9908	0.8092	0.8008
HACB	0.0166	0.0180	0.0092	-	0.8028	0.7976
HALB	0.1916	0.2102	0.1908	0.1972	-	0.8785
HAPH	0.1902	0.1898	0.1992	0.2024	0.1215	-

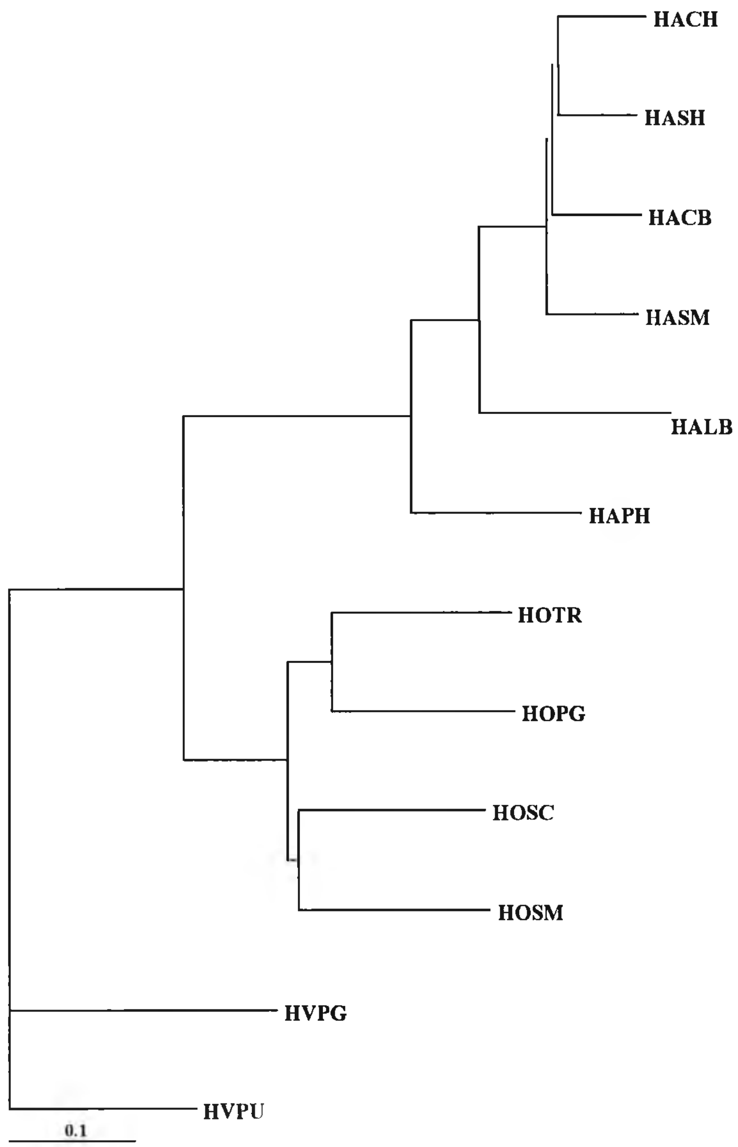
D. 7 Pairwise comparisons of intraspecific similarity indices (above diagonal) and genetic distances (below diagonal) of *H. asinina* using primer UBC271

Daij/Saij	HASH (*N*=14)	HASM (*N*=14)	HACH (*N*=13)	HACB (*N*=19)	HALB (*N*=19)	HAPH (*N*=20)
HASH	-	0.9935	0.9604	0.9763	0.6458	0.7073
HASM	0.0065	-	0.9915	0.9847	0.6476	0.6784
HACH	0.0396	0.0085	-	0.9523	0.6551	0.6344
HACB	0.0237	0.0153	0.0477	-	0.6437	0.6683
HALB	0.3542	0.3524	0.3449	0.3563	-	0.8661
HAPH	0.2927	0.3216	0.3656	0.3317	0.1339	-

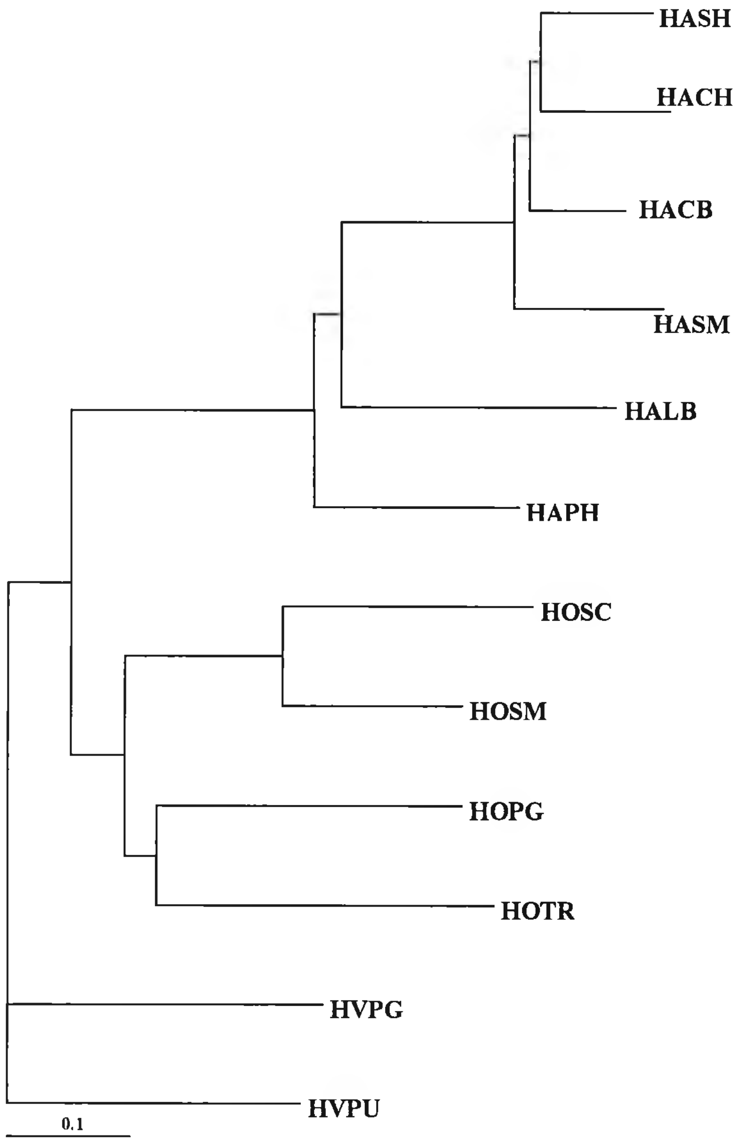
Appendix E

Neighbor - joining trees illustrating genetic relationships of 3 tropical abalone found in Thailand, *Haliotis asinina*, *H. ovina*, and *H. varia*, base on genetic distances resulted from RAPD analysis using primer UBC101 (E. 1), OPB11 (E. 2). Detailed information and abbreviations of sample sites are shown in Appendix A.

E. 1 UBC101



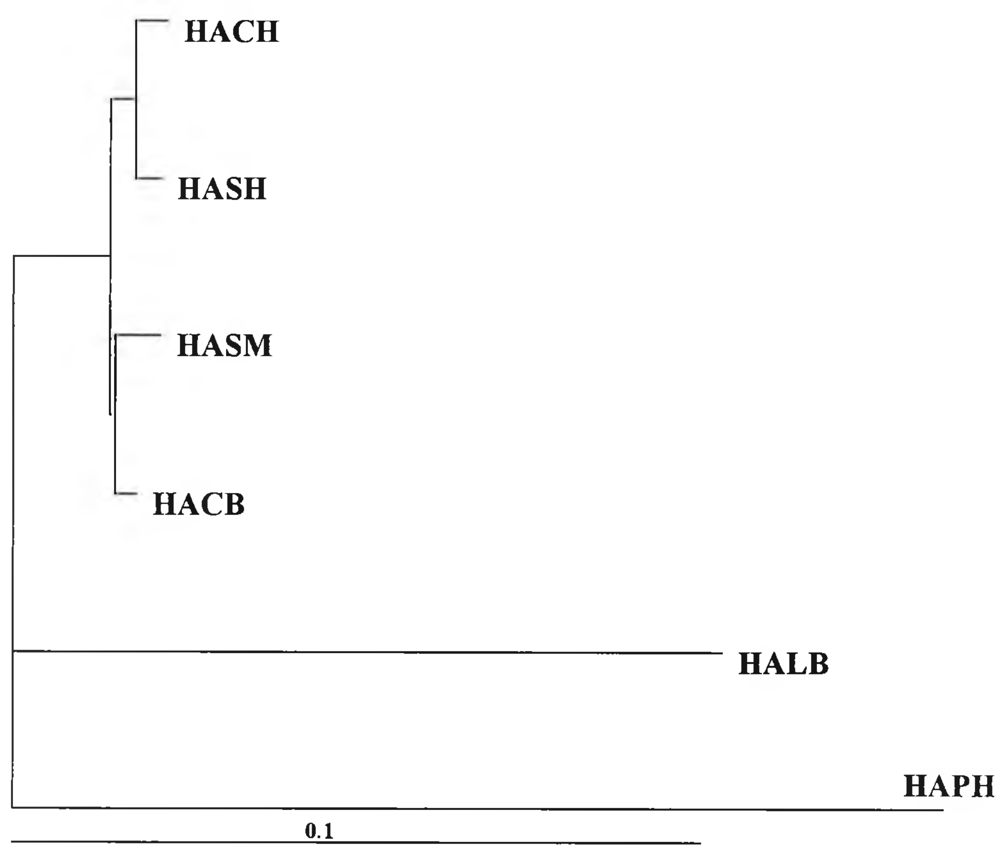
E. 2 OPB11


HASH
HACH
HACB
HASM
HALB
HAPH
HOSC
HOSM
HOPG
HOTR
HVPG
HVPU
0.1

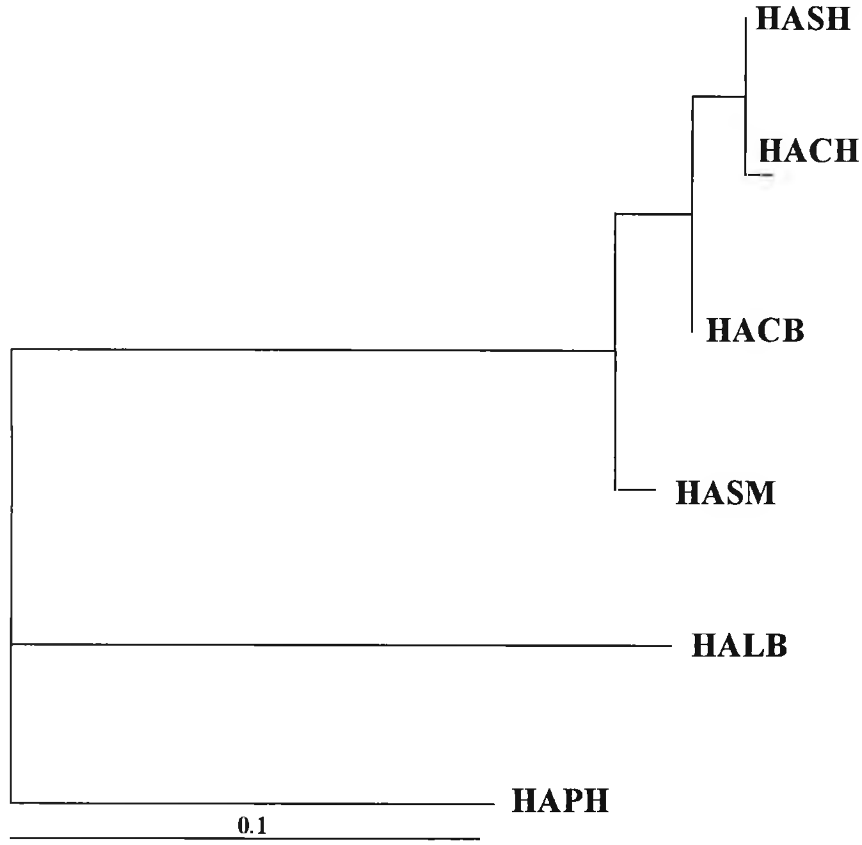
Appendix F

Neighbor - joining trees illustrating genetic relationships of 6 populations of *Haliotis asinina*, base on genetic distances resulted from RAPD analysis using primer UBC101 (F. 1), OPB11 (F. 2), UBC195 (F. 3), UBC197 (F. 4), and UBC271 (F. 5). Detailed information and abbreviations of sample sites are shown in Appendix A.

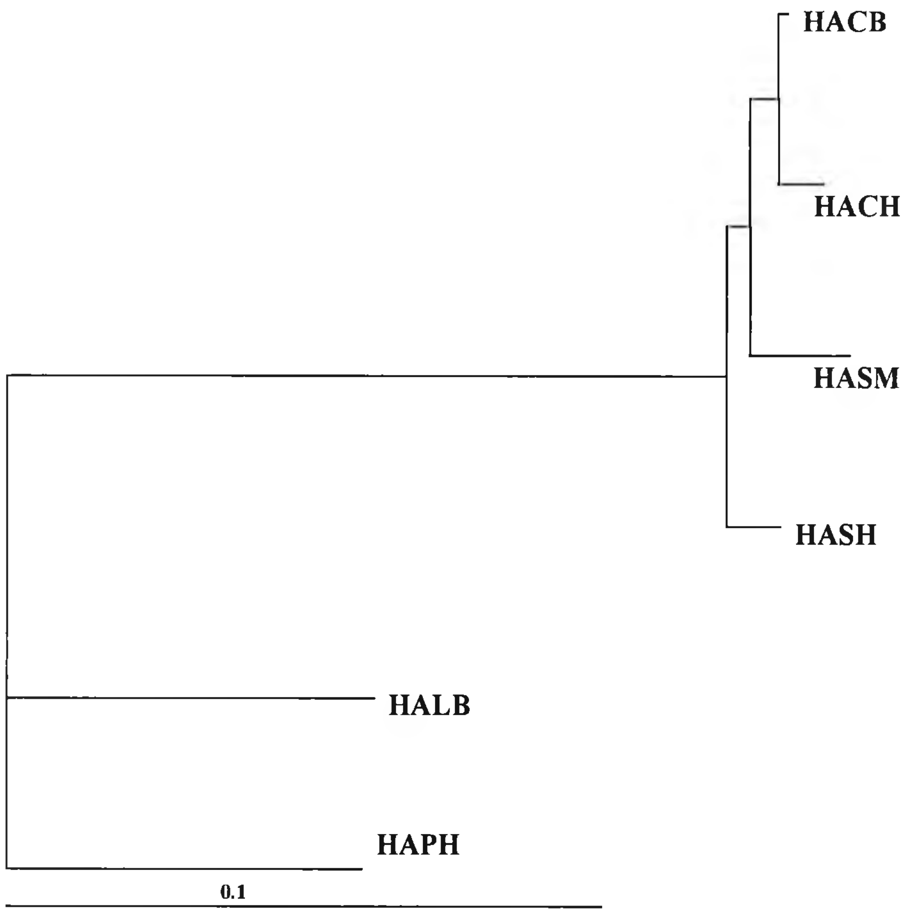
F. 1 UBC101



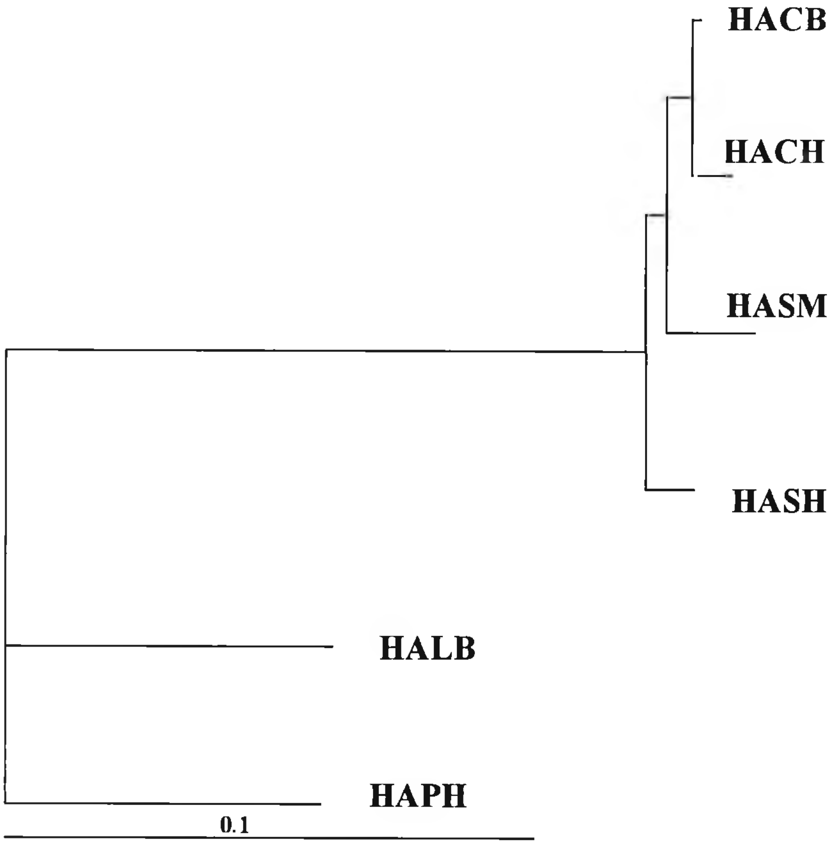
F. 2 OPB11



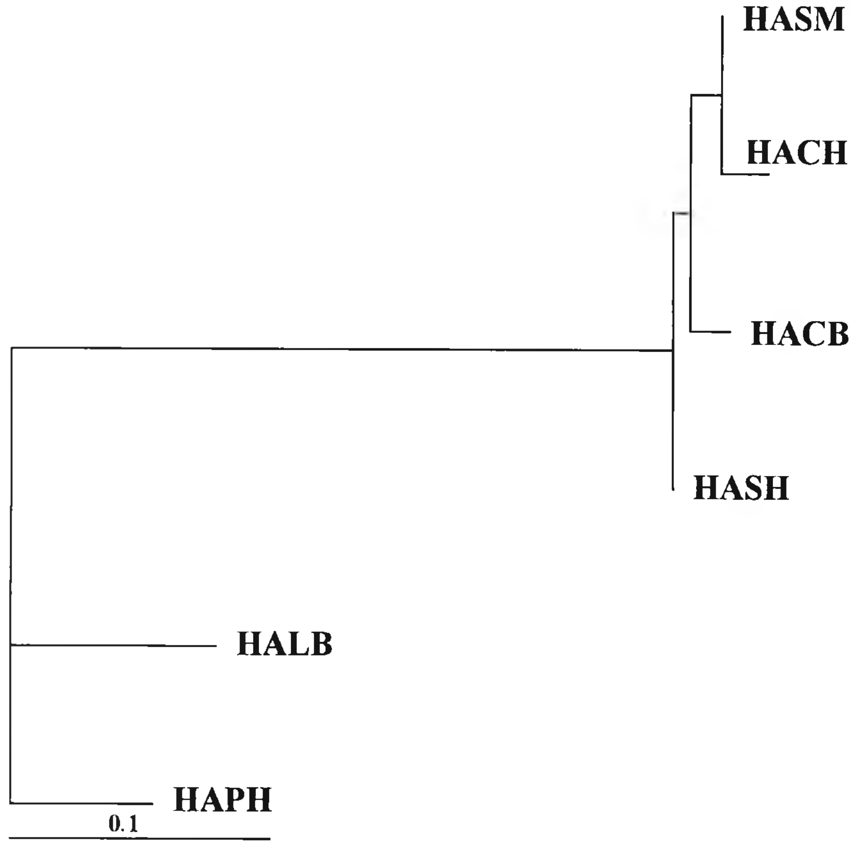
F. 3 UBC195



F. 4 UBC197



F. 5 UBC271



BIOGRAPHY

Miss Aporn Popongviwat was born on June 16, 1974 in Kanchanaburi, Thailand. She graduated with the Bachelor of Science degree in Marine Science from Department of Marine Science, Faculty of Science, Chulalongkorn University in 1995.