

Appendix 1

Table A1.1: Oligonucleotides for sequencing and PCR experiments

Name	Sequence	Element	Position & Direction
BCH3	CCCgATGCCATTGAAAGACA	<i>vap</i>	1919 in L31763 ←
BCH7	GCTTGCgTAAATGATAGGC	<i>vap</i>	2168 in L31763 ←
BCH10	GCGCGGAATTGTCTGATTA	<i>pnpA</i>	354 in PVUDS.W →
BCH12	TAGAAGCCACGCATGTACG	<i>askA</i>	412-431 in λGB321 →
BCH15	GCCATCTCATCTTCCTTACG	<i>intD</i>	from pGW46.8 from λGB300 →
BCH16	CACGGAGATAAACGTAAC3C	<i>intD</i>	from pGW204.1 from λGB300 →
BCH17	CACTAGTCGTCATCGTATCG	<i>intD</i>	C305 <i>intD</i> element ←
BCH18	GCAAACGCGCAATGATGATG	<i>intC</i>	C305 <i>intD</i> element →
GB1	ATAACGCTGGCTTTAGGT3A	<i>vap</i>	12535 in L31763 ←
GBSEQ3	AGCGGTTGTCCCACATAAA	<i>intC</i>	end <i>intC</i> , C305, λGB321 ←
G3	GCCACACATAGCCGCACA3G	pDN1	4969 in pDN1 ←
G4	GCTCAGAGGCCAGTGGTT3G	pDN1	4970 in pDN1 →
G5	TGTCAGCAAGCCAACTATG	pDN1	4144 in pDN1 →
G6	AATCAACGCCGAGATCCAAC	pDN1	722 in pDN1 ←
G7	ATGTACGCATCAGCATGGAC	pDN1	4832 in pDN1 →
GWSEQ8	TGGACGTGACGTATGACTAC	pDN1	4375 in pDN1 →
GWSEQ9	CCTCTGCATACCCGATTTCA	pDN1	4619 in pDN1 ←
GWSEQ10	AGGTGTTGGACAGCATCGAA	pDN1	2670 in pDN1 →
GWSEQ11	AGCTCGATAGTCACCCGTTA	pDN1	3232 in pDN1 ←
GWSEQ12	ATCCATCTTGCCCTAACGT	pDN1	1568 in pDN1 →
GWSEQ13	AATAGGCATCAGGAAGCGA	pDN1	2022 in pDN1 ←
GWSEQ14	CCATTGCATGGAGCTAAACC	pDN1	930 in pDN1 →
GWSEQ15	GCTGGAGCGATTTTACGCTT	pDN1	350 in pDN1 →
GWSEQ16	AAGTTGAAAACGGCGAGT3G	pDN1	592 in pDN1 ←

Notes: The approximate position of oligonucleotides are shown elsewhere as follows: those from the sequence of *vap* region 1/3 (GenBank Accession L31763) or left of *vap* region 2 (PVUDS.W) are shown in Appendix A3; those from the *intC* element sequence (λGB321) are shown in Appendix A3; those from the *intD* element are shown in Figure 6.3; whilst those used in the sequencing pDN1 are shown in Figure 3.2.

Table A1.2: Oligonucleotides for construction of pDN2

#	Name	Sequence	Position & Direction
1	pEC1.SEQ1	TTGATGCATCCCCCTGTTTAAACAGTCACG	1-20 in pDN1 →
2	pEC1.SEQ2	CCAGAATATCGATAGGCTTA	3466 in pDN1 →
3	pEC1.SEQ3	TAAGCCTATCGATATTCTGG	3447 in pDN1 ←
4	pEC1.SEQ4	TCAGGATCCGCAIGCGAGCTCAAGCTTCTAGAG GCCTTCAGCCTGCCGCTTGGGCC	38-57 to 5112-5093 in pDN1 ←
5	pEC1.SEQ5	CGTGGATCCAGACGAAAGGGCTCGTGAT	684-703 in pUC18 →
6	pEC1.SEQ6	CGCATGCATTTAT3AGTAAACTTGGTCTGA	1748-1767 in pUC18 ←

Notes: The approximate position of oligonucleotides used in the construction of pDN1 derivative, pDN2 are shown in Figure 3.7.

Appendix 2

Table A2.1: Probes used in Southern and northern blot experiments

Probe #	Probe	Subclone name	Insert size (kb)	Restriction fragment
1	<i>askA</i>	pDT17.1	0.67	<i>XbaI/NruI</i>
2	<i>glpA</i>	pGB60.2	0.26	<i>NruI</i>
3	<i>intA</i>	pDT20.10	0.60	<i>RsaI</i>
4	<i>vapHG</i>	pGW34.1	0.36	<i>RsaI/FspI</i>
5	<i>vapE</i>	pDT3.4	1.20	<i>NruI/XbaI</i>
6	<i>vapD</i>	pJIR343	0.20	<i>DraI</i>
7	<i>vapBC</i>	pGW33.1	0.64	<i>KpnI</i>
8	<i>vapA</i>	pJIR412	0.28	<i>DraI/NsiI</i>
9	<i>toxA</i>	pJIR421	0.28	<i>DraI/ClaI</i>
10	<i>vapE'</i>	pGW38.2	0.89	<i>BbuI/EcoRI</i>
11	<i>pnpA</i>	pGW19.2	0.65	<i>PvuII/RsaI</i>
12	<i>intB</i>	pBC121.11	1.20	<i>SacI/HindIII</i>
13	<i>regA</i>	pBC159.1	0.30	<i>SspI/EcoRI</i>
14	<i>gepA</i>	pGB22.2	0.60	<i>SspI</i>
15	<i>gepB</i>	pGB79.4	0.30	<i>TaqI</i>
16	<i>gepC</i>	pGB96.1	0.40	<i>DraI/HindIII</i>
17	<i>gepEFG</i>	pGW226.1	3.00	<i>HindIII</i>
18	5'- <i>gepG</i>	pGW40.1	4.00	<i>EcoRI</i>
19	<i>intC</i>	pGB97.12	0.60	<i>AluI</i>
20	<i>orf242</i>	pGB120.6	0.45	<i>DraI</i>
21	<i>orf171</i>	pGB164.1	0.80	<i>DraI/NsiI</i>
22	IS1253	pGB50.4	0.58	<i>HindIII/SspI</i>
23	<i>dapABC</i>	pGW46.8	1.80	<i>EcoRI/BamHI</i>
24	<i>dapDE</i>	pGW204.1	1.20	<i>BamHI/HindIII</i>
25	102 bp rpts	pGB72.1	0.45	<i>HindIII/SspI</i>
26	<i>orf379</i>	pGB117.1	0.75	<i>SspI/DraI</i>
27	left <i>vrl</i>	pJIR743	3.00	<i>HindIII/EcoRI</i>
28	right <i>vrl</i>	pJIR590	2.00	<i>EcoRI</i>

Notes: The probe numbers correspond to the positions of the above probes on the map in Appendix A3.

Appendix 3

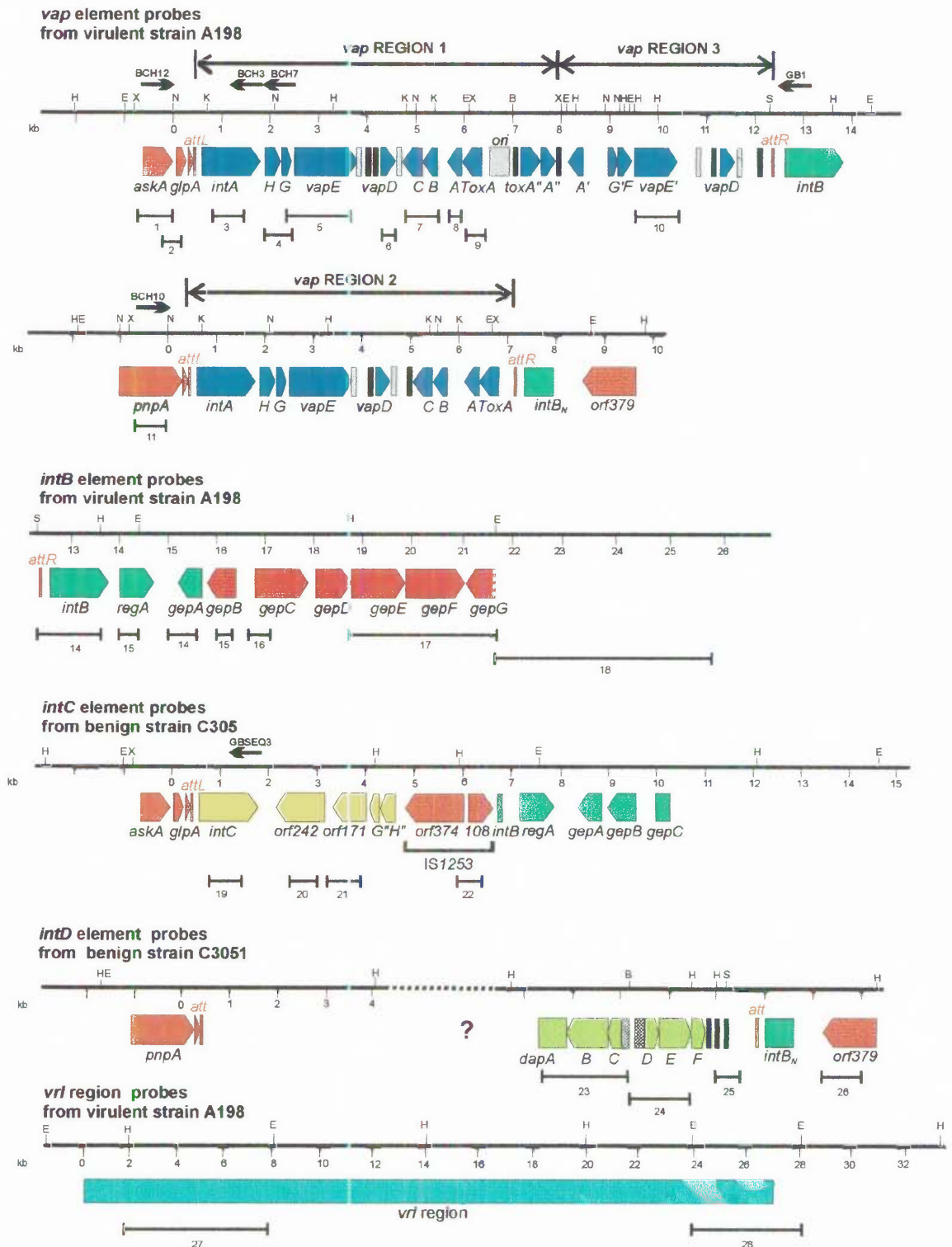


Figure A3.1: Map of probes used in Southern and northern blot experiments. The probes are indicated below the corresponding sequences and the numbers correspond to those shown in Table A2.1 (Appendix 2). The approximate positions of oligonucleotides (Table A1.1, Appendix 1) BCH12, BCH3, GB1, BCH10 and GBSEQ3 are also shown.

Appendix 4

Table A4: Restriction fragment sizes from Southern blot analyses of the *vap* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	<i>intA - pOT20(10)</i>			<i>vapA-D - pJR318</i>			<i>vapE - pGW38(2)</i>			<i>vapHG - pGW34(1)</i>			Kpnl
	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	
A198	8.7 ¹ , 7.4 ¹	6.2 ¹ , 5.2 ¹	5.2 ¹ , 4.7 ¹	7.4 ¹ , 6.7 ¹ , 4.4 ¹	6.4 ¹ , 4.4 ¹ , 3.2 ³	3.5 ³ , 3.2 ¹ , 2.6 ¹ , 1.95 ³		3.6 ² , 1.1 ¹	3.7 ² , 1.1 ¹	8.5 ² , 7.4 ¹ , 1.2 ²	6.0 ¹ , 5.3 ² , 1.0 ³	5.3 ³ , 5.4 ¹ , 1.7 ²	4.7 ¹ , 4.1 ¹
C3052	-	-	-	-	-	-	n/a	-	-	8.5 ²	8.7 ³ , 6.9 ²	6.0 ²	4.3 ⁴
1311	8.4 ¹	5.2 ¹	5.2 ¹	8.1 ¹ , 2.0 ¹	6.4 ¹	3.1 ¹ , 1.95 ³	n/a	-	-	13.8 ² , 8.5 ²	10.5 ² , 6.9 ³ , 5.1 ³	6.0 ² , 5.4 ²	4.7 ¹
1311A	8.4 ¹	5.2 ¹	5.2 ¹	8.1 ¹ , 2.0 ¹	6.4 ¹	3.1 ¹ , 1.95 ³	n/a	-	-	8.5 ²	6.9 ² , 5.1 ¹	5.4 ²	
AC3577	10.9 ¹	13.2 ² , 5.2 ¹ , 4.1 ²	5.2 ¹ , 4.0 ²	9.7 ¹ , 8.5 ² , 6.9 ³	9.9 ³ , 4.8 ¹	2.7 ¹ , 2.3 ³	n/a	-	-	10.0 ¹ , 8.5 ² , 9.0 ²	13.2 ¹ , 8.2 ⁴ , 6.9 ³ , 5.1 ⁴ , 4.1 ²	9.8 ⁴ , 7.3 ² , 5.4 ⁴ , 4.2 ¹	>23.1 ¹ , 4.3 ¹
B1006	10.9 ¹	5.2 ¹	5.2 ¹	10.0, 3.8	8.7 ¹	3.8, 2.8	n/a	-	-	14.6 ² , 10.0 ¹	13.2 ² , 9.5 ¹ , 6.9 ³ , 5.1 ³	9.4 ¹ , 5.4 ³ , 3.0 ⁴ , 1.4 ⁴	4.3 ¹
G1220	10.9 ¹	5.2 ¹	5.2 ¹	9.8, 4.8	8.3 ¹	4.8, 2.8	n/a	8.2 ⁵	7.9 ⁵ , 5.0 ⁵	10.0 ¹	6.9 ⁵ , 5.1 ¹	7.5 ⁵ , 5.4 ¹	4.7 ¹
H1204	10.9 ¹	5.2 ¹	5.2 ¹	9.7	8.3 ¹	2.85	n/a	8.2 ⁵	7.9 ⁵ , 5.0 ⁵	10.0 ¹	6.9 ⁵ , 5.1 ¹	7.5 ⁵ , 5.4 ¹	4.8 ¹
H1215	5.7 ¹	4.9 ¹ , 4.2 ¹	4.3 ¹	4.1	12.3 ² , 9.5 ¹	3.55	n/a	13.2 ⁴ , 9.2 ¹ , 4.5 ² , 1.1 ¹	7.9 ⁵ , 5.0 ⁵ , 4.0 ⁴ , 3.4 ² , 1.2 ¹	10.0 ⁴ , 5.4 ¹	4.8 ² , 4.2 ¹	8.0 ⁴ , 6.3 ⁴ , 4.4 ¹	4.7 ¹
819	-	-	-	n/a	-	n/a	n/a	-	-	8.4 ²	8.7 ³ , 6.7 ²	6.0 ²	
1169	-	-	-	n/a	-	n/a	n/a	-	-	-	-	-	
2483	-	-	-	n/a	-	n/a	n/a	-	-	6.3 ²	8.7 ³ , 6.7 ²	6.0 ²	
1493	-	-	-	n/a	-	n/a	n/a	-	-	14.6 ²	6.7 ¹	6.0 ²	
3138	-	-	-	n/a	-	n/a	n/a	-	-	7.4 ² , 2.3 ²	6.9 ¹	6.0 ² , 2.8 ¹	
1469	-	-	-	n/a	-	n/a	n/a	-	-	7.4 ²	6.9 ³	6.0 ²	
AC390 (JIR1212)	11.3 ¹ , 6.5 ¹	2.8 ¹	2.8 ¹	10.2 ¹ , 7.1 ¹ , 4.6 ¹	10.5 ² , 7.1 ² , 5.9 ¹	3.5 ² , 3.1 ¹ , 2.5 ¹	4.6 ¹	1.3 ² , 1.1 ¹	1.3 ² , 1.1 ¹				
D1172 (JIR1214)	8.9 ¹	4.9 ¹	4.9 ¹	9.6 ¹ , 2.1 ²	10.2 ² , 6.8 ¹	3.3 ¹ , 2.1 ³	-	-	-				
lab book reference	6.81, 7.168, 7.219	6.64, 7.168, 7.219	6.108, 7.168, 7.219	4.11, 7.174, 7.202	4.11, 7.174, 7.202	4.68, 4.73, 7.174, 7.202	8.14	6.120, 6.137, 8.14	6.140, 8.14	6.124	6.92	6.62	3.339

Table A4 (continued): Restriction fragment sizes from Southern blot analyses of the *vap* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	<i>vapA</i> - pJIR412		<i>vapD</i> - pJIR343		<i>vapE</i> - pDT3(4)		<i>vapA</i> - pJIR421					
	EcoRI	EcoRI/HindIII	EcoRI	HindIII	EcoRI	HindIII	EcoRI	HindIII				
A198	10.0	8.3	8.7, 7.6 ¹ 5.2 ¹	6.6 ² , 5.3 ¹ 3.7 ¹	8.8 ¹ , 7.0 ¹	5.6 ¹ , 5.0 ¹	5.2 ¹ , 4.7 ¹	8.8 ¹ , 7.0 ¹ 1.95 ¹ , 1.8 ¹	8.6, 6.4, 5.0	3.1 ¹ , 2.6 ¹ 2.1 ¹	8.1 ¹	5.6 ¹ , 3.3 ¹
C3052	-	-	-	-	-	-	-	-	-	-	-	-
13111	-	-	9.0 ¹	6.8 ¹	8.8 ¹	5.0 ¹	5.2 ¹	8.6 ¹ , 1.95 ¹	8.6 ¹ , 6.4 ¹	3.1 ¹ , 2.1 ²	17.9 ¹	8.6 ¹ , 5.9 ¹
1311A	-	-	9.0 ¹	6.8 ¹	8.8 ¹	5.0 ¹	5.2 ¹	-	-	-	-	-
AC3577	-	-	10.2 ¹ 10.0 ²	5.8 ¹	11.2 ¹ , 9.3 ²	5.0 ¹ , 3.9 ²	5.2 ¹ , 4.0 ²	10.1 ¹ , 6.8 ²	5.2 ¹ , 5.2 ¹	2.8 ¹ , 2.3 ²	10.2 ¹ 10.2 ¹	3.2 ¹
EN006	10.0	8.3	10.0, 3.8	6.3, 11.0	9.8	4.8	-	10.1 ¹ , 3.9 ¹	10.1 ¹ , 7.8 ¹	3.9 ¹ , 2.8 ¹	10.2 ¹	3.2 ¹
G1220	9.8	7.9	9.8, 4.1 2.8	7.9, 4.8	9.8	4.8	-	8.6 ¹ , 1.95 ¹	8.6 ¹ , 6.4 ¹	3.1 ² , 2.1 ¹	17.9 ¹	8.3 ¹ , 5.9 ¹
H1204	9.7	7.3	9.7	7.7	9.7	4.9	-	9.4 ¹	9.4 ¹ , 7.9 ²	4.9 ¹ , 2.6 ¹	10.2 ¹	3.2 ¹
H1215	4.1	8.4	4.1	8.4	-	-	-	10.1 ¹ , 3.9 ¹	11.0 ² , 8.6 ¹	4.8 ² , 3.3 ¹	10.2 ¹	3.8 ¹
819	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1169	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
2483	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1493	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
3138	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
1469	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
AC390	4.6 ¹	10.2 ³ , 6.9 ² 5.7 ¹	12.3 ² , 7.4 ¹	5.9 ¹ , 3.4 ²	3.4 ² , 2.7 ¹	-	-	-	-	-	-	-
(JIR1212)	-	-	9.4 ¹	9.9 ² , 6.6 ¹	3.2 ¹	5.2 ¹	5.2 ¹	-	-	-	-	-
D1172	9.1 ¹	9.4 ⁴ , 6.6 ¹	3.2 ¹	9.4 ¹	9.6 ¹	5.2 ¹	5.2 ¹	-	-	-	-	-
(JIR1214)	-	-	4.65, 8.16	4.65, 8.16	4.68, 4.71, 8.16	4.45, 4.47, 8.72, 8.76	8.72, 8.76	3.336	3.337	4.124 4.131	4.118	4.117
lab book reference	8.72, 8.76	8.72, 8.76	8.72, 8.76	8.72, 8.76	4.65, 8.16	4.65, 8.16	4.65, 8.16	4.65, 8.16	4.65, 8.16	4.65, 8.16	4.65, 8.16	4.65, 8.16

Notes regarding tabulated data:

- (i) Restriction fragments hybridising to the probe sequence are ranked according to the intensity of the band, the band intensity is indicated by superscripted numbers, 1 being most intense and 5 being least intense;
- (ii) Dashes (-) indicate that no hybridisation to the probe was observed, whilst blank squares indicate the experiments which have not yet been done;
- (iii) Lab book page reference numbers for autoradiograph are provided at the bottom of the appropriate columns;
- (iv) For some of the probed sequences (*IS1253*, *inIB*, *vapHG*, 102 bp repeats) in some strains there are more bands hybridising to the probe than might be predicted from the maps constructed for each strain (Appendix 11). To determine whether these bands constitute extra copies of the genes/sequences in question or correspond to a related gene or whether they are the result of restriction fragment length polymorphisms within the probed sequence in certain strains *D. nodosus* requires a more comprehensive study, utilising a larger variety of restriction enzymes;
- (v) Shaded cells indicate experiments in which fragment sizes were determined in experiments prior to this work (Bloomfield *et al.*, 1997), whilst all unshaded data were determined in this work;
- (vi) n/a indicates where no hybridisation is expected due to lack of hybridisation to the pJIR318 probe which incorporates corresponding probe sequences;
- (vii) Note that a viable stock of the original laboratory strain of C305 (C3051) is not available, however some genomic DNA from this strain had previously been fixed to a nylon membrane, which was as a result available for reprobing, and these results are distinguished (*) from those results generated using the genomic DNA from the current laboratory strain of C305 (C3052).

Appendix 5

Table A5: Restriction fragment sizes from Southern blot analyses of the *intB* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	<i>intB</i> - pBC121(11)			<i>regA</i> - pBC159(1)			<i>gcpA</i> - pGB22(2)			<i>gcpC</i> - pGB96(1)		
	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII
A198	5.1 ¹ , 2.2 ²	9.7 ³ , 6.7 ² 3.8 ¹	3.8 ¹ , 2.2 ²	4.3 ¹	4.7 ¹	0.9 ¹	7.3 ¹	5.0 ¹	4.3 ¹	7.3 ¹	5.1 ¹	4.5 ¹
C3052	13.8 ¹ , 8.8 ²	7.0 ² , 5.8 ³ 4.3 ¹	7.2 ² , 4.3 ² 1.9 ³	8.5 ¹	5.7 ¹	1.6 ¹	7.3 ¹	6.1 ¹	4.3 ¹	7.3 ¹	6.0 ¹	4.5 ¹
1311	2.5 ¹ , 2.2 ²	10.2 ¹ , 6.7 ²	2.2 ² , 1.9 ¹	2.5 ¹ , 2.8 ²	6.4 ² , 4.9 ¹	2.8 ² , 0.9 ¹	7.3 ¹	5.0 ¹	4.3 ¹	7.3 ¹	5.1 ¹	4.5 ¹
1311A	3.3 ¹ , 2.2 ²	6.7 ² , 3.6 ¹	2.7 ¹ , 2.2 ²	2.8 ² , 3.2 ¹	6.4 ² , 4.9 ¹	2.8 ² , 0.9 ¹	7.3 ¹	5.0 ¹	4.3 ¹	7.3 ¹	5.1 ¹	4.5 ¹
AC3577	13.4 ² , 11.0 ² 7.4 ² , 3.3 ² 2.5 ¹	9.5 ¹ , 6.7 ¹ 4.9 ² , 3.6 ²	7.2 ¹ , 2.7 ³ 2.0 ¹	3.2 ² , 2.6 ¹	4.9 ¹	0.9 ¹	7.3 ¹	5.0 ¹	4.3 ¹	7.3 ¹	5.1 ¹	4.5 ¹
B1006	4.0 ²	8.7 ²	4.2 ²	2.8 ¹	6.7 ¹	2.8 ¹	-	-	-	7.7 ¹	3.7 ¹	4.0 ¹
G1220	4.0 ²	7.9 ²	4.2 ²	2.0 ¹	6.7 ¹	1.9 ¹	-	-	-	5.4 ¹	3.7 ¹	4.0 ¹
H1204	16.9 ² , 11.3 ¹ 3.3 ¹	11.1 ² , 8.3 ² 3.5 ¹ , 2.1 ²	8.6 ³ , 5.2 ² 2.7 ¹ , 2.3 ²	3.2 ¹	1.9 ¹	0.9 ¹	-	-	-	5.4 ¹	3.7 ¹	3.1 ¹
H1215	16.9 ² , 11.3 ¹ 3.3 ¹	11.8 ² , 8.7 ² 3.5 ¹ , 2.1 ²	8.6 ² , 5.2 ² 2.7 ¹ , 2.3 ²	2.8 ¹	21.5 ⁴ , 6.7 ¹ 5.4 ² , 1.9 ³	2.8 ¹ , 0.9 ¹	-	-	-	5.4 ¹	3.7 ¹	3.1 ¹
319	16.9 ² , 8.8 ¹	5.8 ² , 5.6 ¹	6.1 ¹ , 1.9 ²	8.3 ¹	5.8 ¹	1.6 ¹	7.3 ¹	6.1 ¹	4.3 ¹	7.3 ¹	6.0 ¹	4.6 ¹
1169	13.8 ² , 3.3 ¹	4.1 ² , 3.4 ¹	7.5 ² , 4.3 ¹ 2.7 ¹	3.2 ¹	1.9 ³	0.9 ¹	-	-	-	7.7 ¹	3.5 ¹	3.9 ¹
2483	12.9 ¹ , 2.5 ²	4.1 ¹ , 2.5 ²	7.4 ² , 4.3 ¹ 1.9 ²	2.5 ¹	2.5 ¹	1.6 ¹	-	-	-	5.4 ¹	3.7 ¹	3.1 ¹
1493	15.0 ² , 12.9 ¹	5.8 ² , 4.1 ¹	7.4 ² , 6.4 ² 4.3 ¹	14.9 ¹	6.1 ¹	6.1 ¹	>23.1 ¹	6.1 ¹	6.4 ¹	17.1 ¹	6.0 ¹	5.6 ¹
3138	8.8 ¹ , >23.1 ²	5.2 ² , 3.2 ¹	6.1 ² , 3.4 ¹ 1.2 ²	8.5 ¹	5.2 ¹	-	7.3 ¹	5.2 ¹	4.3 ¹	7.3 ¹	4.9 ¹	-
1469	8.8 ¹ , >23.1 ²	5.8 ¹ , 4.1 ¹	4.3 ¹ , 1.9 ²	-	5.9 ¹	-	7.3 ¹	6.1 ¹	4.3 ¹	7.3 ¹	6.0 ¹	-
AC390 (JIR1212)	18.5 ¹ , 9.6 ² 5.3 ¹	9.6 ³ , 6.8 ² 3.6 ¹ , 2.2 ¹	3.3 ² , 2.6 ¹ 2.2 ¹	-	6.6 ¹ , 1.8 ¹	1.9 ¹ , 1.8 ¹	-	-	-	5.7 ¹	3.6 ¹	2.8 ¹
CH72	10.8 ¹ , 2.2 ²	9.6 ¹ , 6.8 ²	2.2 ² , 1.9 ¹	10.1 ¹ , 2.8 ¹	6.6 ¹ , 4.8 ¹	4.7 ¹ , 2.7 ¹	9.3 ¹	5.0 ¹	4.8 ¹	11.6 ¹	4.9 ¹	4.8 ¹
(JIR1214)												
lab book reference	5.297 5.304 7.172	5.269 5.280 7.172	5.281 5.287 7.172	5.263 5.274 5.278	5.155	5.123 5.138	6.122 6.148 6.142	6.94 6.100	6.138	6.196 6.200	6.4 6.19	5.201 5.214

Table A5 (continued):
Restriction fragment sizes from Southern blot analyses of the *iniB* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	gcpB - pGB79(4)		- pGW225(t)		- pGW40(1)		pGBT17(1) - ori379	
	EcoRI	HindIII	EcoRI	EcoRI/HindIII	EcoRI	HindIII	EcoRI	HindIII
A198	7.3'	5.3'	7.0'	2.4'	>23.1'	17.7'	6.6'	7.4'
C0052	7.3'	6.3'	7.0'	2.4'	>23.1'	17.7'	15.6'	4.5'
1311	7.3'	5.3'	7.0'	2.4'	>23.1'	17.7'	6.6'	7.4'
1311A	7.3'	5.3'	7.0'	2.4'	>23.1'	17.7'	6.6'	7.4'
AC9577	7.3'	5.3'	7.0'	2.4'	>23.1'	17.7'	14.9'	
BH006	8.1'	3.8'	7.6'	2.4'	>23.1'	17.7'	6.6'	
G1220	5.5'	3.8'	5.4'	2.4'	>23.1'	17.7'	12.6'	
H1204	5.5'	3.8'	5.4'	2.4'	>23.1'	17.7'	12.6'	
H1215	5.9'	3.8'	5.4'	2.4'	>23.1'	17.7'	12.6'	
819	7.7'	6.3'	7.4'	2.4'	>23.1'	17.7'	21.5'	
1169	8.1'	3.8'	8.0'	2.4'	>23.1'	17.7'	15.6'	
2461	5.7'	3.8'	5.4'	2.4'	>23.1'	17.7'	15.6'	
1493	>23.1'	6.3'	>23.1'	2.4'	>23.1'	17.7'	15.6'	
3138	7.7'	5.3'	7.4'	2.4'	>23.1'	17.7'	-	
1489	7.7'	6.3'		2.4'	>23.1'	17.7'	15.6'	
AC390 (JIR1212)	5.7'	3.8'		2.4'	>23.1'			
D1172 (JIR1214)	11.6'	4.8'			>23.1'			
lab book reference	8.96 8.103	8.70 8.78	8.149	8.145 8.134	8.146	8.147 8.136	6.286 6.294 6.296	

Notes regarding tabulated data as per appendix 4

Appendix 6

Table A6 : Restriction fragment sizes from Southern Blot analyses of the *intD* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	- pGW46(8)				102 bp repeats - pGB72(1)				- pGW204.1				
	EcoRI	HindIII	EcoRI/HindIII	BamHI/EcoRI	BamHI/HindIII	FspI/HindIII	FspI/EcoRI	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII
A198	-	-	-	-	-	-	-	9.0 ¹ , 7.9 ¹ , 4.9 ⁴	9.5 ⁵ , 6.7 ² , 5.1 ² , 3.8 ⁶	4.0 ² , 3.2 ¹ , 3.0 ¹	-	-	-
C3052	-	-	-	-	-	-	-	-	-	-	-	-	-
1911	10.1 ¹	9.9 ¹	7.3 ¹	4.2 ¹	2.7 ¹	8.9 ¹	8.4 ² , 6.8 ¹	9.0 ¹ , 6.9 ⁴ , 5.9 ⁴	10.0 ¹ , 6.7 ²	7.3 ¹ , 3.2 ¹	-	-	-
1311A	-	-	-	-	-	-	-	9.0 ¹ , 6.9 ⁴	6.7 ²	3.2 ¹	-	-	-
AC3577	8.3 ¹	14.5 ³ , 9.3 ¹	5.9 ¹	4.2 ¹	2.7 ¹	11.1 ² , 8.5 ¹	-	12.5 ¹ , 10.1 ¹ , 7.7 ⁴ , 6.7 ¹	10.5 ³ , 9.3 ¹ , 6.7 ² , 5.2 ² , 4.7 ⁵ , 4.0 ⁵	5.9 ¹ , 4.6 ³ , 4.2 ⁴ , 2.8 ⁵ , 1.9 ¹	-	-	-
B1006	8.3 ¹	10.4 ¹	5.9 ¹	4.2 ¹	2.7 ¹	9.4 ¹	6.3 ¹	12.5 ¹ , 4.0 ⁴	10.5 ¹ , 8.7 ²	5.9 ¹ , 4.6 ⁵ , 2.8 ⁵	-	-	-
G1220	-	-	-	-	-	-	-	12.5 ¹ , 3.9 ⁴	7.0 ¹	7.6 ³ , 4.8 ⁵ , 2.7 ¹	-	-	-
H1204	-	-	-	-	-	-	-	12.5 ¹	7.0 ¹	2.7 ³	-	-	-
H1215	-	-	-	-	-	-	-	12.5 ¹	18.9 ² , 9.5 ¹	12.4 ⁵ , 7.6 ¹ , 4.8 ⁵	-	-	-
819	>23.1 ¹	3.7 ¹	3.5 ¹	-	-	-	-	>23.1 ¹ , 11.6 ¹	5.7 ¹ , 4.8 ³ , 3.7 ²	5.3 ¹ , 3.5 ⁴ , 2.8 ⁴	14.9	3.6	3.6
1169	-	-	-	-	-	-	-	-	-	-	-	-	-
2483	-	-	-	-	-	-	-	-	-	-	-	-	-
1493	-	-	-	-	-	-	-	-	-	-	-	-	-
3138	>23.1 ¹	3.7 ¹	3.5 ¹	-	-	-	-	>23.1 ¹	6.0 ⁵ , 3.8 ² , 3.2 ¹	5.0 ³ , 3.4 ² , 3.0 ¹	14.9	3.6	3.6
1469	-	-	-	-	-	-	-	-	-	-	-	-	-
1383	-	-	-	-	-	-	-	-	-	-	-	-	-
1136	-	-	-	-	-	-	-	-	-	-	-	-	-
AC390 (1212)	-	-	-	-	-	-	-	-	-	-	-	-	-
D1172 (1214)	8.3 ¹	10.0 ¹	5.5 ¹	-	-	-	-	9.8 ¹	10.0 ¹ , 6.8 ²	5.5 ³ , 2.9 ⁵	-	-	-
page reference	6.272, 6.279, 7.56, 7.74, 7.82	7.54, 7.42	6.284, 6.293, 7.60, 7.62	7.130, 7.142	7.130, 7.142	7.130, 7.142	7.130, 7.142	7.66	7.78	7.2, 7.80	8.68, 8.77, 8.82, 8.95	8.102, 8.98	7.176

Notes regarding tabulated data as per appendix 4

Appendix 7

Table A7: Restriction fragment sizes from Southern blot analyses of the *intC* element in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	<i>intC</i> - pGB97(12)			<i>orf242</i> - pGB120(6)			<i>orf171</i> - pGB164(f)			IS1253 - pGB50(4)				
	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	EcoRI	HindIII	EcoRI/HindIII	XhoI	
A198	-	-	-	-	-	-	-	-	-	>23.1 ¹	18.6 ¹ , 1.5 ¹	>23.1 ³ , 1.6 ¹	10.5 ¹	
C3051*	8.5 ¹	6.6 ¹												
C3052	8.5 ¹	6.6 ¹	5.6 ¹	8.6 ¹	6.6 ¹	5.8 ¹	34.1 ¹	8.9 ¹	1.8 ¹ , 1.2 ¹				34.1 ¹ , 10.5 ¹	
1311	14.0 ¹	6.6 ¹	5.7 ¹	13.0 ¹	6.6 ¹	6.0 ¹	19.6 ¹	>23.1 ¹ , 15.2 ¹ , 8.9 ¹	10.1 ¹ , 7.3 ¹ , 3.5 ¹				19.6 ¹ , 19.6 ¹	
1311A	-	-	-	-	-	-	-	>23.1 ¹	10.5 ²			10.1 ¹	10.5 ¹	
AC3577	18.1 ¹	14.8 ³ 7.5 ¹	6.6 ¹ 5.4 ³	15.5 ¹	14.3 ³ 7.9 ¹	6.6 ¹ , 5.4 ³	14.4 ¹	13.7 ³ , 7.6 ¹	9.8 ¹ , 7.0 ¹ , 1.1 ¹	6.4 ³ , 4.6 ³ , 3.8 ³ , 2.5 ³ , 1.3 ¹			13.7 ¹ , 27.3 ¹	
B1006	18.1 ¹	9.0 ¹	8.1 ¹	15.5 ¹	9.3 ¹	8.1 ¹	14.4 ¹	8.9 ¹	11.3 ² , 1.1 ¹	1.4 ¹ , 1.3 ¹			34.0 ¹ , 10.5 ¹	
G1220		9.0 ¹	8.1 ¹	7.7 ¹	9.3 ¹	8.1 ¹	7.7 ¹	8.9 ¹	12.2 ²	>23.1 ³ , 8.4 ³ , 3.6 ³ , 2.1 ¹ , 1.3 ¹			34.0 ¹ , 10.5 ¹ , 8.5 ¹	
H1204	>23.1 ¹	12.1 ¹	4.6 ¹	-	-	-	-	-	12.2 ²	8.9 ³ , 2.1 ¹ , 1.3 ¹			34.1 ¹ , 10.5 ¹ , 8.5 ¹	
H1215	>23.1 ¹	12.1 ¹ 2.9 ³	4.6 ¹ 2.9 ³	2.8 ¹	3.5 ¹	2.9 ¹	-	-	2.7 ¹	3.6 ³ , 2.5 ¹ , 2.1 ¹ , 1.9 ¹ , 1.3 ¹			34.1 ¹ , 15.3 ¹ , 10.5 ¹ , 8.5 ¹	
819	8.5 ¹	7.9 ³ 6.6 ¹	5.6 ¹ 7.9 ³	8.5 ¹	9.3 ³ 6.7 ¹	7.3 ³ , 5.6 ¹	8.3 ¹	7.6 ³ , 6.6 ¹	1.6 ²	3.5 ³ , 1.8 ¹ , 1.6 ¹			34.1 ¹ , 10.5 ¹	
1169	>23.1 ¹	12.1 ¹	3.9 ¹	15.5 ¹	12.0 ¹	3.9 ¹	-	-	2.0 ²	6.9 ³ , 4.2 ² , 1.3 ¹			34.1 ¹	
2483	8.0 ¹	6.6 ¹	5.6 ¹	7.4 ¹	6.7 ¹	5.6 ¹	7.4 ¹	6.6 ¹	2.7 ²	1.8 ¹ , 1.6 ³ , 1.3 ²			34.1 ¹	
1483	17.0 ¹	6.6 ¹	5.6 ¹	15.5 ¹	6.7 ¹	5.6 ¹	15.5 ¹	6.6 ¹	1.6 ²	5.5 ¹ , 1.9 ³ , 1.6 ¹			34.1 ¹ , 10.5 ¹	
3138	8.9 ¹	9.3 ³ 6.6 ¹		8.5 ¹	10.8 ³ 6.7 ¹		8.3 ¹	8.9 ³ , 6.6 ¹	2.6 ³ , 2.1 ³	2.3 ¹ , 1.8 ¹			34.1 ¹ , 10.5 ¹	
1469	8.9 ¹	6.6 ¹		9.9 ¹	7.3 ¹	5.8 ¹		6.6 ¹	13.2 ³ , 6.4 ³	13.4 ³ , 9.2 ¹ , 1.8 ¹			34.1 ¹ , 15.3 ¹ , 10.5 ¹	
AC390 (JIR1212)	>23.1 ¹	12.5 ¹	4.2 ¹	-	-	-	-	-	>23.1 ¹ , 5.4 ¹	3.3 ¹ , 2.4 ¹ , 2.1 ¹ , 1.9 ¹			15.3 ¹	
D1172 (JIR1214)	14.6 ¹	7.1 ¹	5.8 ¹	17.3 ¹	8.3 ¹	6.6 ¹	14.6 ¹	8.3 ¹	17.0 ¹	1.3 ¹			10.5 ¹	
lab book reference	6.90 6.101 6.205 6.209 7.211 7.307*	5.121 5.137 7.211 7.218 7.218 7.307*	5.156 7.211 7.218	5.124 5.154 5.136	5.317 5.317	5.275 5.288	6.6	5.203 5.216 5.299	7.136 7.143	6.212	7.46 7.144			8.220

Notes regarding tabulated data as per appendix 4

Appendix 8

Table A8: Restriction fragment sizes from Southern blot analyses of sequences flanking integrated genetic elements in *D. nodosus*

Strain of <i>D. nodosus</i>	<i>aska</i> - pDT17(1)		<i>pnpA</i> - pGW19(2)	
	<i>EcoRI</i>	<i>HindIII</i>	<i>EcoRI</i>	<i>HindIII</i>
A198	7.6 ¹	5.8 ¹	9.1 ¹	4.9 ¹
C3051*			14.8 ¹ , 6.6 ¹	6.6 ¹ , 5.8 ¹
C3052	9.3 ¹	6.7 ¹	13.1 ¹	7.1 ² , 4.1 ¹
I311	13.1 ¹ , 3.3 ⁵	6.9 ¹ , 3.5 ⁵	9.1 ¹	4.9 ¹
I311A	3.3 ¹	3.5 ¹	9.1 ¹	4.8 ¹
AC3577	15.5 ¹ , 3.3 ³	7.9 ¹ , 3.6 ³	12.3 ¹	12.2 ³ , 6.5 ² , 4.8 ¹
B1006	15.5 ¹	9.3 ¹	12.3 ¹	7.1 ² , 4.9 ¹
G1220	7.6 ¹	9.3 ¹	12.3 ¹	4.9 ¹
H1204	3.3 ¹	3.5 ¹	12.3 ¹	4.9 ¹
H1215	3.3 ¹	3.5 ¹	6.9 ¹	4.8 ² , 4.1 ¹
819	16.9 ¹ , 8.5 ¹	11.2 ⁴ , 6.6 ¹	17.0 ⁵ , 6.3 ¹	7.6 ² , 5.9 ¹
1169	3.3 ¹	3.5 ¹	17.0 ¹	7.1 ² , 4.1 ¹
2483	7.7 ¹	6.6 ¹	17.0 ¹	7.1 ² , 4.1 ¹
1493	16.9 ¹	6.6 ¹	17.0 ¹	7.1 ² , 4.1 ¹
3138		9.3 ¹ , 6.7 ¹	6.3 ¹	7.1 ¹
1469		6.6 ¹	17.0 ¹	4.1 ¹
AC390 (JIR1212)	5.2 ¹	3.6 ¹	12.1 ¹	3.3 ¹
D1172 (JIR1214)	15.2 ¹	7.4 ¹	9.4 ¹	5.1 ¹
lab book	5.215	5.279	6.66	6.72
reference	5.202	5.265	6.71	6.74
	7.229	7.229	6.76	6.77
			7.231	7.231
			7.237	7.237
			7.272*	7.272*
			7.292*	7.292*

Notes regarding tabulated data as per appendix 4

Appendix 9

Table A9: Restriction fragment sizes from Southern blot analyses *vtI* sequences in different strains of *D. nodosus*

Strain of <i>D. nodosus</i>	RH <i>vtI</i> - pJIR590		LH <i>vtI</i> - pJIR743	
	EcoRI	HindIII	EcoRI	HindIII
A198	3.7 ¹	14.3 ¹	13.7 ¹ , 3.7 ²	13.7 ¹
C305	-	-	-	-
1311	3.7 ¹	14.3 ¹	13.7 ¹ , 3.7 ²	19.0 ¹ , 13.7 ²
1311A	3.7 ¹	14.3 ¹	13.7 ¹ , 3.7 ²	19.0 ¹ , 13.7 ²
AC3577	-	-	-	-
B1006	-	14.3 ¹	-	-
G1220	-	-	-	-
H1204	-	-	-	-
H1215	-	14.3 ¹	-	-
819	-	-	-	-
1169	-	-	-	-
2483	-	-	-	-
1493	-	-	-	-
3138	-	-	-	-
1469	-	-	-	-
AC390 (JIR1212)	-	-	-	-
D1172 (JIR1214)	-	-	-	-
lab book	7.271	7.271	7.283	7.283
reference	7.276	7.276	7.290	7.290
		8.262		

Notes regarding tabulated data as per appendix 4

Appendix 10

Table A10: PCR analyses of integration sites in fifteen strains of *D. nodosus*

Strain of <i>D. nodosus</i>	<i>aska/intC</i>		<i>aska/intB</i>		<i>aska/intA</i>		<i>pnpA/intC</i>		<i>pnpA/vapG</i>		<i>pnpA/intB</i>	
	BCH12-GBSEQ3	BCH12-GB1	BCH12-GB1	BCH12-BCH3	BCH10-GBSEQ3	BCH10-BCH7	BCH10-GBSEQ3	BCH10-BCH7	BCH10-GB1	BCH10-GB1		
A198	-	-	-	2.5	-	-	-	2.6	-	-	-	-
C305	2.5	-	-	-	-	-	-	-	-	-	-	0.65
I311	2.5	1.1*	-	-	-	-	-	2.6	-	-	-	-
I311A	-	1.1	-	-	-	-	-	2.6	-	-	-	-
AC3577	2.5	1.1*	-	-	-	-	-	2.6	-	-	-	0.65*
B1006	2.5	-	-	-	-	-	-	2.6	-	-	-	-
G1220	2.5	-	-	-	-	-	-	2.6	-	-	-	-
H1204	-	1.1	-	-	-	-	-	2.6	-	-	-	-
H1215	-	1.1	-	-	-	-	-	2.6	-	-	-	-
819	2.5	-	-	-	-	-	-	-	-	-	-	0.65*
1169	-	1.1	-	-	-	-	-	-	-	-	-	0.65
2483	2.5	-	-	-	-	-	-	-	-	-	-	0.65
1493	2.5	-	-	-	-	-	-	-	-	-	-	0.65
3138	2.5	-	-	-	-	-	-	-	-	-	-	0.65*
1469	2.5	-	-	-	-	-	-	-	-	-	-	0.65

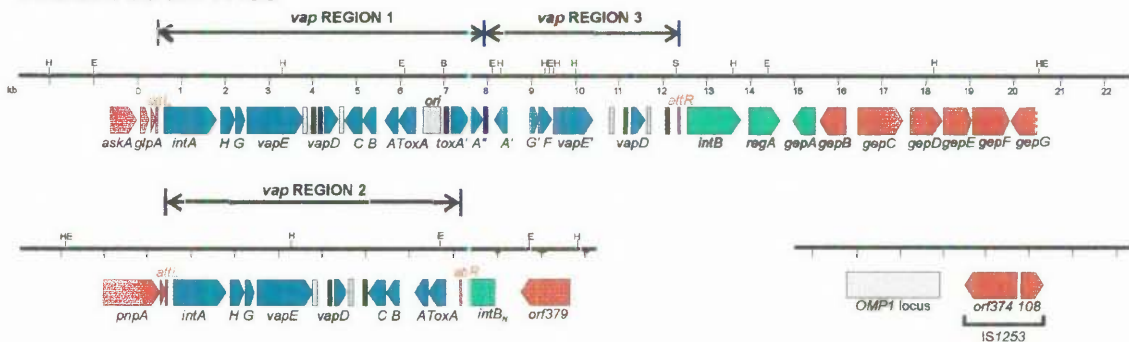
Note: PCR results are not shown for *D. nodosus* strains AC390 or D1172 because at the time these PCR experiments were performed these strains were not available in our laboratory. Where PCR products were amplified the size of the product is indicated in kb. If a product was not detected a dash is shown. Asterisks indicate products which are amplified from a small population of cells of the indicated strain, due to loss of an integrated element from the indicated position (discussed in Chapter 7).

Appendix 11

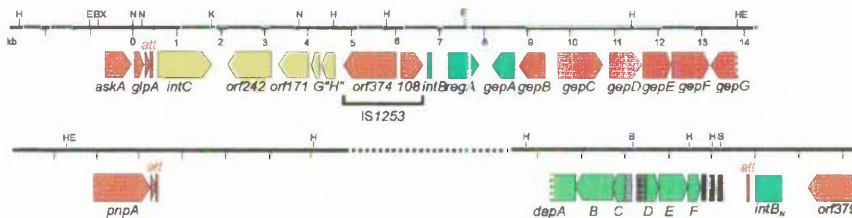
Maps of the *vap*, *intB*, *intC* and *intD* elements in different strains of *D. nodosus*, as determined from Southern blot analyses.

Maps of integrated genetic elements are shown for the following strains of *D. nodosus*: A198, C3051, C3052, 1311, 1311A, AC3577, B1006, G1220, H1204, H1215, 819, 1169, 2483, 1493, 3138, 1469, AC390 and D1172. Genetic elements are indicated as follows: the *vap* element (blue), *intB* element (green), *intC* element (yellow) and the *intD* element (purple). Those sequences which are not part of the aforementioned genetic elements are shown in red. Where the integration site of an element has been determined to be next to *askA*, *pnpA*, the OMP1 locus or in the right-hand end of another genetic element it has been shown. Repeated sequences are as follows: attachment sites, *attL* or *attR* (narrow red boxes), 102 bp repeats or partial copies thereof (filled boxes), 103 bp repeats (grey boxes). Restriction enzyme sites shown include *Bam*HI (B), *Eco*RI (E), *Hind*III (H), and *Sac*I (S). For many strains there are multiple copies of IS1253 (Section 7.2.1), *vapHG* (Section 7.2.1) and *intB* (Section 5.2.8.3), however only those copies that have a known position in the genome of a given strain are shown on the maps. The *intC* element of *D. nodosus* strain 1311 is known to contain a copy of the IS1253 (Figure 7.2.4), however its position relative to genes *intC*, *orf242* and *orf171* are unknown and hence have not been shown in the map for this strain. Those sequences indicated by slashed lines are of an as yet undetermined size. The dashes below the lines representing DNA sequences are one kb apart as indicated by the numbers.

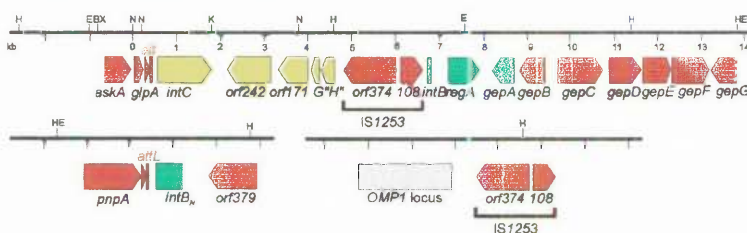
Virulent Strain A198



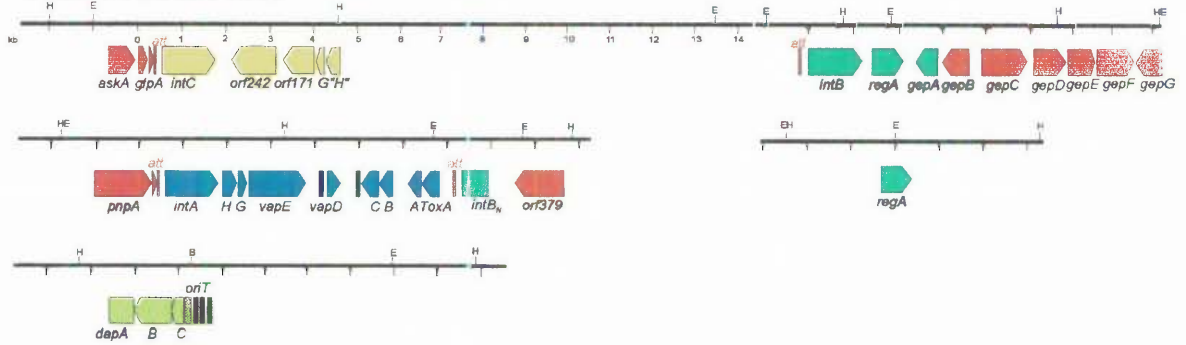
Benign Strain C3051



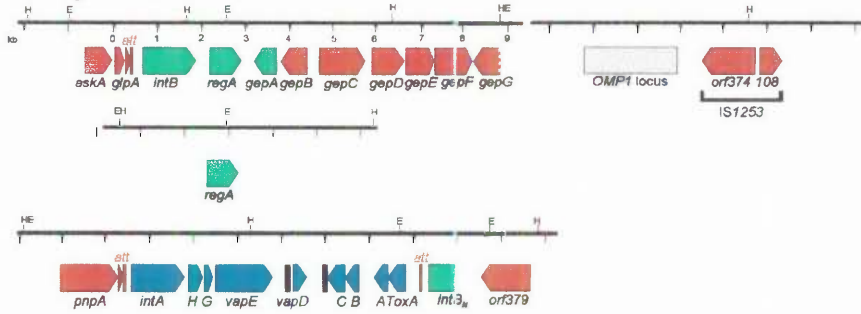
Benign Strain C3052



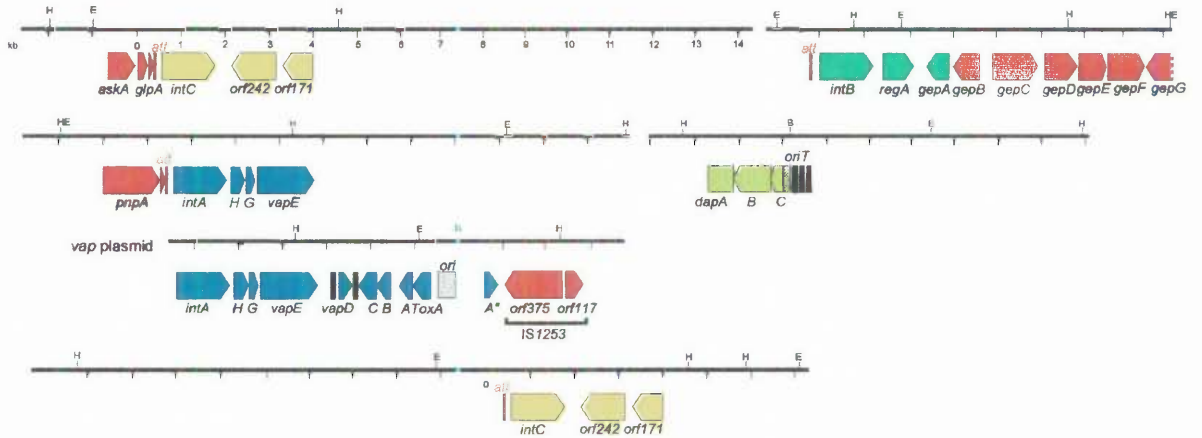
Virulent Strain 1311



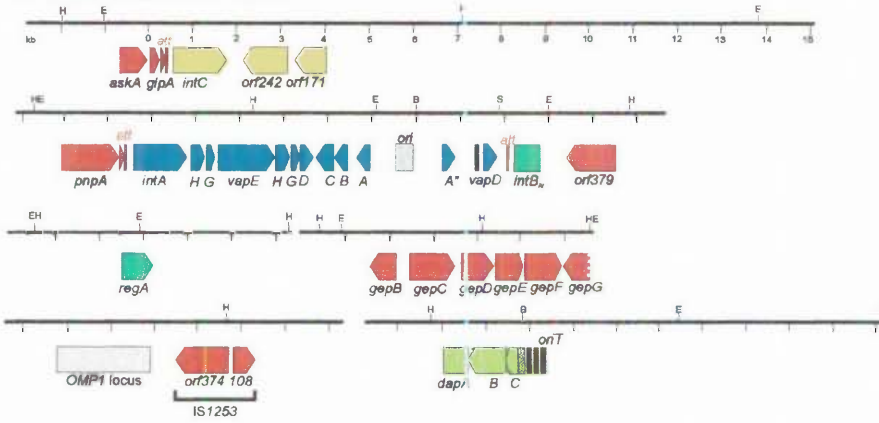
Benign Strain 1311A



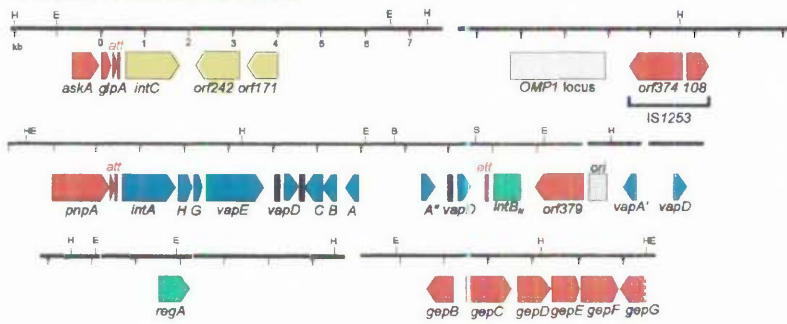
Intermediate Strain AC3577



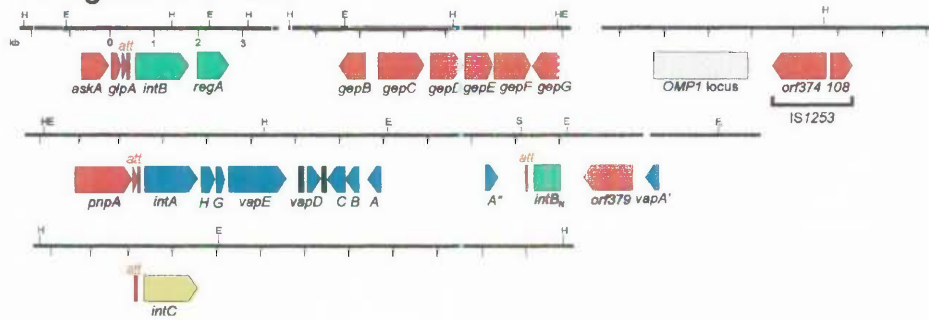
Virulent Strain B1006



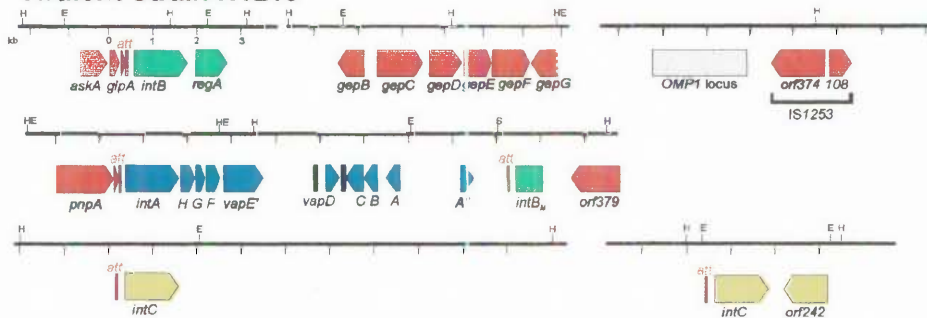
Virulent Strain G1220



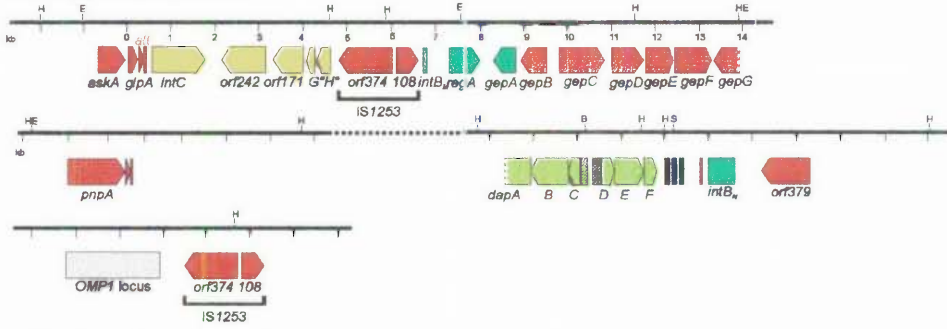
Benign Strain H1204



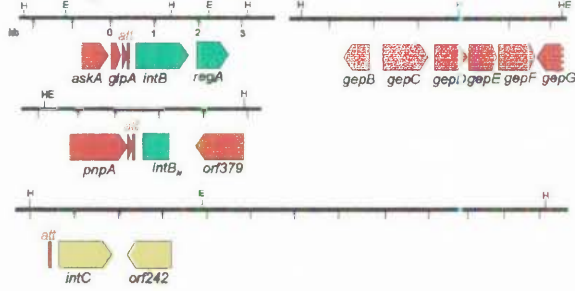
Virulent Strain H1215



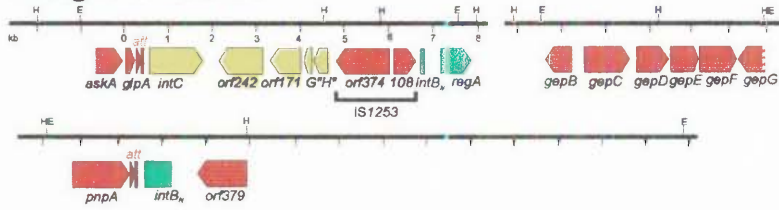
Benign Strain 819



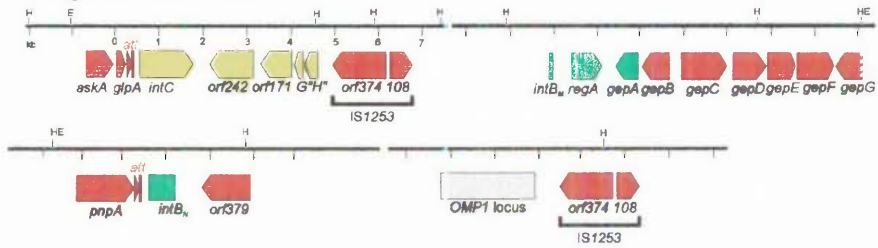
Benign Strain 1169



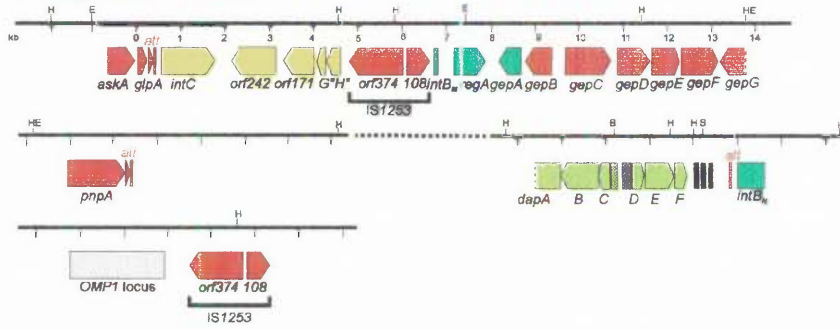
Benign Strain 2483



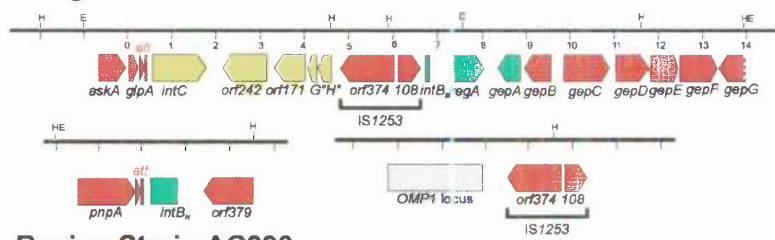
Benign Strain 1493



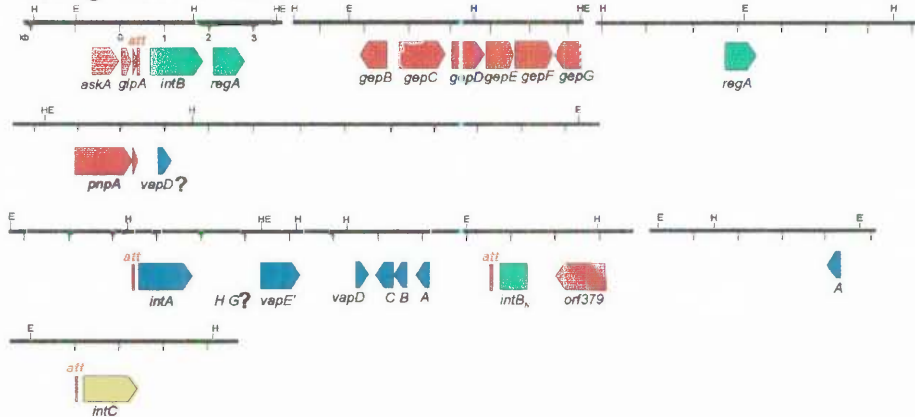
Benign Strain 3138



Benign Strain 1469



Benign Strain AC390



Virulent Strain D1172

