RESEARCHSPACE@AUCKLAND

http://researchspace.auckland.ac.nz

ResearchSpace@Auckland

Copyright Statement

The digital copy of this thesis is protected by the Copyright Act 1994 (New Zealand).

This thesis may be consulted by you, provided you comply with the provisions of the Act and the following conditions of use:

- Any use you make of these documents or images must be for research or
 private study purposes only, and you may not make them available to any
 other person.
- Authors control the copyright of their thesis. You will recognise the author's
 right to be identified as the author of this thesis, and due acknowledgement
 will be made to the author where appropriate.
- You will obtain the author's permission before publishing any material from their thesis.

To request permissions please use the Feedback form on our webpage. http://researchspace.auckland.ac.nz/feedback

General copyright and disclaimer

In addition to the above conditions, authors give their consent for the digital copy of their work to be used subject to the conditions specified on the Library Thesis Consent Form.

Development of a microarray for *Potyvirus* detection and Identification

Ting Wei

PhD Thesis 2008

Development of a microarray for *Potyvirus* detection and Identification

A thesis presented in partial fulfilment
of the requirements for the degree of

Doctor of Philosophy in Biological Sciences
The University of Auckland, New Zealand

Ting Wei

2008

Abstract

Potyvirus is the largest and one of the most economically important of the virus genera infecting plants. The complexities of potyvirus identification resulting from many different species, mixed infections, emerging new viruses, new hosts, and new vectors, etc., often requires the use of multiple detection methods which is time consumable and costly. Therefore an assay that can test for a range of potyviruses simultaneously, with good specificity and sensitivity, is desirable. This study looked at the feasibility of producing an oligonucleotide microarray for detection and identification of potyviruses at both species and strain level.

Thirty plant samples with suspected potyvirus infections were collected from field and research laboratories in New Zealand and partial NIb gene, complete CP gene and 3'UTR were sequenced. Twelve definitive potyviruses, one tentative potyvirus, one non-potyvirus, and one novel potyvirus-like sequence were identified, six of which were first records for New Zealand.

Sequence analysis showed that NIb and CP genes and the 3'UTR contained both conserved and variable sequences which were used to design both species and strain level specific probes. Four *Potyvirus* species were chosen for a "proof of concept" study and probes were designed using two different software programs (ROSO and CAG software). A total of eighty five probes including 33 perfect-match and 52 mismatch probes were selected to represent the four targeted potyviruses. Each probe was synthesized with spacers of either 6 or 12 poly-cytosine or poly-thymine at the 5' terminus. Arrays showed high specificity to the targets when tested using nineteen different geographically diverse potyvirus isolates representing the four target species, four distinct but closely related New Zealand potyviruses, and four healthy plant species. Factors affecting the hybridization efficiency, e.g. the size of the target fragments, secondary structure of probes and targets, label type, strandedness, Tm and GC content of probes, were also investigated.

The approaches and protocols developed in this study should form a useful basis for developing other potyviruses arrays and the results also provide useful insights into issues of generic interest for the development of arrays for detecting other pathogens.

Acknowledgements

I would particularly like to express my sincere thanks and appreciations to the following people and institutions who gave the advice, support, help and encouragement to complete this PhD thesis.

My chief supervisor, associate professor Dr. Mike N. Pearson, for offering me this opportunity and guiding and support throughout the whole PhD study.

My co-supervisor, Dr. Dave Saul for advice on the problems of sequence analysis.

Dr. Karen Armstrong, for advice and support, especially the introduction of microarray expert professor Dietmar Blohm for help in the microarray development.

Professor Dietmar Blohm, the chairman of Centrum für Angewandte Genesensorik (CAG, Centre of Applied Microarray), Bremen University, Germany, for his kind help and support on the development of microarray.

Dr. Manfred Nölte, from Bioinformatic Department, Bremen University, Germany, for the design of probes using their proprietary software (CAG software).

Dr. Sascha Todt, from The Centre of Applied Microarray, Bremen University, Germany, and Dr. Lei Zhan, from The Dental Research Institute, University of California, Los Angeles, for advice and discussion on the problems of microarray hybridisation and data analysis.

Mr. Frank Meyerjürgens and Mr. Sven Roll, from Department of Biotechnology and Molecular Genetic, Bremen University, Germany) for assistance in printing the arrays.

My colleague, PhD student Kelvin Lau, for help in the use of probe design ROSO software, microarray scanning machine and microarray hybridisation procedure. Dr. Franz Pichler for discussing the problems from microarray hybridisation.

Associate professor Cristin Print, from Department of Molecular Medicine & Pathology, The University of Auckland, for discussing microarray data analysis.

Dr. Francisco M. Ochoa-Corona from Investigation and Diagnostic Centre, Biosecurity, Ministry of Agriculture and Forestry, New Zealand, Dr. Dan Cohen from HortResearch, Auckland, New Zealand and Dr. John D. Fletcher from Crop & Food Research, Christchurch, New Zealand, for providing suspected virus infecting plant samples.

My colleagues, Catia Delmiglio and Scott Harper for their kind assistances in many experimental and computing analysis issues; Kristine Boxen for sequencing service; Terry Gruijters for computer assistance.

National centre for advanced bio-protection technologies, for providing me this PhD funding.

Department of School of Biological Sciences, Auckland University, for providing research facilities.

The last but not the least, I would like to thank my dear parents, my husband Guangjin Lu, my two daughters, my relatives and good friends, for their love and support throughout the whole process of this study.

Table of Contents

Abstracti
Acknowledgementsii
Table of Contentsiv
List of Figuresx
List of Tablesxiv
Abbreviationsxvi
Chapter 1. General Introduction1
1.1. Literature review1
1.1.1 Introduction of plant virus disease
1.1.1.1 History and development of plant virus disease
1.1.1.2 Impact of plant virus diseases
1.1.1.3 Infection and transmission
1.1.1.4 Control
1.1.2 <i>Potyvirus</i> 5
1.1.2.1 Introduction
1.1.2.2 Potyvirus genome
1.1.2.3 <i>Potyvirus</i> taxonomy8
1.1.2.4 Potyviruses in New Zealand9
1.1.3 Plant virus diseases diagnosis
1.1.3.1 Development of techniques for plant virus disease diagnosis11
1.1.3.2 Problems with current plant virus detection and identification with particular
reference to potyviruses
1.1.4 DNA Microarray
1.1.4.1 Introduction of DNA microarray
1.1.4.2 Application of DNA microarray
2. Project overview

Chapter 2. Collection and identification of potyviruses	22
2A. General information on potyvirus collection and identification	22
2A.1. Introduction	22
2A.2. Materials and methods	23
2A.2.1 Source of virus isolates	23
2A.2.1.1 Virus infected plant samples	23
2A.2.1.2 RNA samples	25
2A.2.1.3 Control samples	25
2A.2.2 Antisera.	26
2A.2.3 Mechanical inoculation of herbaceous hosts	26
2A.2.4 Enzyme-linked immunosorbent assay (ELISA)	26
2A.2.5 RNA extraction and cDNA synthesis	27
2A.2.6 Polymerase chain reaction (PCR)	28
2A.2.6.1 <i>Potyvirus</i> universal primers	28
2A.2.6.2 Virus specific primers	29
2A.2.6.3 PCR	29
2A.2.7 Cloning, sequencing and data analysis	29
2A.2.8 Submission of sequences to GenBank	30
2A.3. Results	31
2A.3.1 Plant inoculations.	31
2A.3.2 ELISA results.	31
2A.3.2.1. Results of samples from Pukekohe, Auckland, New Zealand	32
2A.3.2.2. Results of samples from HortResearch and Crop & Food Research.	32
2A.3.4 Results from molecular biological tests	33
2A.3.4.1 Results of RT-PCR	33
2A.3.4.2 Sequence results.	35
2A.3.4.3 Sequence analysis	39
2A.3.4.4 New primer design and the consequent PCR and sequencing results	42
2A A Discussion	13

2B. Further investigation of particular sequences identified from section 2A47		
2B.1. Introduction	47	
2B.2. Materials and methods	48	
2B.2.1 Plant samples.	48	
2B.2.2 Antisera	48	
2B.2.3 Purification of virus from infected garlic leaves	48	
2B.2.4 Serological tests	49	
2B.2.4.1 ELISA	49	
2B.2.4.2 Immuno-sorbent electron microscopy (ISEM)	49	
2B.2.5 Single-strand conformational polymorphism analysis (SSCP)	50	
2B.2.6 Sequence analysis	50	
2B.3. Results	51	
2B.3.1 Identification of GYSV	51	
2B.3.1.1 Optimization of polyclonal antisera	51	
2B.3.1.2 Serological identification of the virus from garlic samples	51	
2B.3.1.3 Electronic microscopy and ISEM results	52	
2B.3.1.4 SSCP results.	53	
2B.3.1.5 Analysis of sequences from garlic samples	54	
2B.3.2 Characteristics of the four novel sequences	56	
2B.4. Discussion.	59	
Chapter 3. Microarray Development: in silico design		
3.1. Introduction		
3.2. Materials and methods		
3.2.1 Sequence selection and alignment		
3.2.2 Sequences analysis and design of microarray oligonucleotides		
3.2.3 Virus sequences		
3.2.4 The selection of oligonucleotide probes		
3.2.5 Modification of oligonucleotide probes		
3.3. Results		
3.3.1 Sequences selected for analysis		
3.3.2 Selection of suitable viruses and genome regions for probe design	66	

3.3.3 Generation of potential specific oligonucleotide probes with desirable length	68
3.3.4 Selection of the optimal oligonucleotide probes	69
3.3.4.1 Principle of oligonucleotide probe selection	69
3.3.4.2 Summary of probes selected for DsMV	74
3.3.4.3 Summary of probes selected for LYSV	75
3.3.4.4 Summary of probes selected for PVY	76
3.3.4.5 Summary of probes selected for ZYMV	77
3.3.4.6. Mismatch oligonucleotide probes	78
3.3.5 The selection of negative control probes	80
3.3.6 Addition of spacers to oligonucleotide probes	80
3.3.7 Diagrammatic recording of the test results	81
3.4. Discussion.	84
Chapter 4. Array validation	91
Part A. Array validated using different size PCR products under different condition	ons91
4A.1 Introduction	91
4A.2 Materials and methods	92
4A.2.1 Oligonucleotides synthesis and microarray fabrication	92
4A.2.2 Generation of PCR products.	92
4A.2.2.1 Direct fluorescent dye labeling of PCR products	92
4A.2.2.2 Indirect fluorescent dye labeling of PCR products	93
4A.2.3 Hybridization of microarray	93
4A.2.3.1 Hybridization protocol.	93
4A.2.3.2 Hybridization temperature and time	95
4A.2.3.3 Template concentration.	95
4A.2.4 Scanning and data analysis	96
4A.3 Results	97
4A.3.1 Microarray fabrication	97
4A.3.2 Generation of PCR products.	98
4A.3.3 Specificity of the array	99
4A.3.3.1 Reaction of individual viruses with array under two different	labeling
systems	99
4A.3.3.2 Hybridization of array with four mixed viruses	109

4A.3.4 Sensitivity of the array	111
4A.3.5 Effects of different spacers and probe location	114
4A.3.6 Impact of GC content and Tm of the probes to the hybridisation efficiency	122
4A.4 Discussion	124
Part B. Further investigation of possible factors affecting array hybridization	130
4B.1 Introduction	130
4B.2 Materials and methods	
4B.2.1 Hybridization period	
4B.2.2 Generation of hybridization templates	
4B.2.2.1 Single strand DNA fragments	
4B.2.2.2 Short PCR fragments	
4B.2.3 Microarray hybridization and data analysis	
4B.2.4 Analysis of the impact of secondary structures of probes and targets	
4B.3 Results	133
4B.3.1 Overnight hybridization	133
4B.3.2 Array hybridized with ssDNA fragments	134
4B.3.3 Generation of specific short PCR products using specific primers	135
4B.3.4 Hybridization of array using indirect-labeled specific short PCR product	138
4B.3.4.1 Short fragments from DsMV	139
4B.3.4.2 Short fragments from LYSV	139
4B.3.4.3 Short fragments from PVY	141
4B.3.4.4 Short fragments from ZYMV	141
4B.3.5 Relationships between hybridization efficiency and secondary structures	142
4B.3.5.1 Impact of secondary structures of probes	142
4B.3.5.2 Impact of secondary structures of targets	143
4B.4 Discussion	150
Chapter 5. Evaluation of the stain and species specificity of the micro	oarrav
	·
5.1 Introduction	
5.2 Materials and methods	153

5. 2.1 Overseas potyvirus isolates	153
5.2.2 Closely related, non-target potyviruses	154
5.2.3 Healthy plants	154
5.2.4 Generation of hybridization target fragments	155
5.2.5 Microarray hybridisation and data analysis	155
5.3. Results	156
5.3.1 Selection of phylogenetically closely related potyviruses	156
5.3.2 Generation of PCR products.	158
5.3.3 Array hybridization with PCR products from overseas potyviruses	158
5.3.3.1 DsMV	158
5.3.2.2 LYSV	161
5.3.2.3 PVY	164
5.3.2.4 ZYMV	168
5.3.4 Array hybridization with PCR products from closely related potyviruses	171
5.3.5 Hybridization with healthy plant cDNA	174
5.4. Discussion	176
Chapter 6. General discussion	178
6.1. Identification of potyviruses in plants	178
6.2. Microarray technology for detecting plant potyviruses	179
6.3. Limits and potential improvements of potyvirus arrays in the future	
References	186
Appendices	222
Appendix I. Diagrammatic recording of the hybridisation results of positi	ve fragments
from New Zealand potyviruses	223
Appendix II. Relationship of the hybridisation results and the target fragmen	nts secondary
structures of New Zealand potyviruses	239
Appendix III. Publications based on this PhD study	285

List of Figures

Fig. 1.1. Genomic organization of <i>Potyvirus</i> genome
Fig. 2A.1. The location of <i>Potyvirus</i> universal primers: U335 & D335 (Langeveld et al., 1991)
PV2I/T7 & PV1/SP6 (Mackenzie et al., 1998), and the expected sizes of the
fragments from potyvirus infected samples
Fig. 2A.2. Symptoms on <i>N. benthamiana</i> infected with suspected ZYMV31
Fig. 2A.3. Example of different size of PCR products from potyvirus infected samples35
Fig. 2A.4. Graphic overview of nt sequences of nzNovel-DC3, nzNovel-DC4a, nzNovel-DC4b
and nzNovel-DC6 when blast in GenBank during the period 200638
Fig. 2A.5. Alignment of CP gene aa sequences of DsMV1, DsMV2 with other DsMV and
VanMV isolates from GenBank
Fig. 2A.6. Alignment of aa sequence of the NIb gene of the New Zealand garlic and potato
isolates of PVY with other PVY isolates from GenBank
Fig. 2A.7. Alignment of coat protein amino acid sequences of nzZaMMV with the other two
ZaMMV isolates in GenBank
Fig. 2B.1. Immunosorbent electron microscopy of partially purified viruses from garlic
samples using various potyvirus antisera53
Fig. 2B.2. SSCP analysis for virus infected garlic and WMV infected zucchini samples54
Fig. 2B.3. Alignment of CP aa sequences of nzLYSVg1, nzLYSVg2 with selected LYSV
isolates from GenBank55
Fig. 2B.4. Neighbour-joining tree for nzLYSVg1, nzLYSVg2 sequences from NZ garlic and
LYSV, OYSV sequences from GenBank56
Fig. 2B.5. Neighbour-joining tree for the newly identified novel sequence nzNovel-DC6 and
selected sequences covering partial NIb gene, complete CP gene and 3'UTR region
and representing six genera of <i>Potyviridae</i> from GenBank
Fig. 3.1. BLAST result of a 25-mer oligonucleotide probe (AACCCGTAGTATCCTT
ACCT) from New Zealand LYSVg isolate71
Fig. 3.2. BLAST result of a 25-mer oligonucleotide probe (GTGGTGACTCTATCTGTTAAT
TCCG) from New Zealand PVY isolate72
Fig. 3.3. BLAST result of a 25-mer oligonucleotide probe (CTCGAACTCTATGATAGTGA TGTGC) from New Zealand LYSVg isolate
Fig. 3.4. Linker and spacer modifications to oligonucleotide probes
Fig. 3.5. An example of diagrammatic figure for hybridization result recording using different
size of fragments from DsMV83

Fig. 4A.1. Arrangement of oligonucleotide probes within the microarray	98
Fig. 4A.2. PCR products generated for microarray hybridization) 9
Fig. 4A.3. Results from hybridization of DsMV ~1.3 kb fragment with the microarray10)1
Fig. 4A.4. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using direct- and indirect-labeled DsMV ~1.3 kb fragments10)2
Fig. 4A.5. Results from hybridization of LYSV ~1.0 kb fragment with the microarray10)2
Fig. 4A.6. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using direct- and indirect-labeled LYSVg2 ~1.0 kb fragments10)3
Fig. 4A.7. Results from hybridization of PVY ~0.8 kb fragment with the microarray10)4
Fig. 4A.8. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using direct- and indirect-labeled PVY ~0.8 kb fragments10)5
Fig. 4A.9. Results from hybridization of ZYMV ~0.7 kb fragment with the microarray10)5
Fig. 4A.10. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using direct- and indirect-labeled ZYMV ~0.7 kb fragments10	16
Fig. 4A.11. Effect of different labelling systems on negative probes from positive fragments	
)8
Fig. 4A.12. Results from hybridization of a mixture containing fragments from four	
potyviruses11	.0
Fig. 4A.13. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using four-virus mixtures11	0
Fig. 4A.14. Results from the hybridization of the ZYMV ~0.7 kb fragment at six different	
concentrations with the microarray	12
Fig. 4A.15. Fluorescent intensities of probes without spacer and with 12T spacer from the	
hybridization using the direct-labelled ZYMV ~0.7 kb fragment at six different	
concentrations11	4
Fig. 4A.16. Effect of different spacers to the positive probes from direct- and indirect-labeled	
DsMV ~1.3 kb fragment.	5
Fig. 4A.17. Effect of different spacers to the positive probes from direct- and indirect-labeled	
LYSVg2 ~1.0 kb fragment	6
Fig. 4A.18. Effect of different spacers to the positive probes from direct- and indirect-labeled	
PVY ~0.8 kb fragment	1
Fig. 4A.19. Effect of different spacers to the positive probes from direct- and indirect-labeled	
ZYMV ~0.7 kb fragment11	.8
Fig. 4A.20. Effect of different spacers to the positive probes from a mixture containing direct-	-
and indirect-labeled fragments representing four different potyviruses11	9

Fig. 4A.21.	Fluorescent intensities of all positive probes without spacer and with different
	spacers from the triplicate hybridizations using direct-labeled positive fragments
Fig. 4B.1. R	Results of overnight hybridization using PVY ~1.3 kb fragment133
Fig. 4B.2. I	mages of ssDNA and dsDNA fragments from PVY and ZYMV hybridized with
n	nicroarray
Fig. 4B.3. L	Location of specific primers and relevant specific short fragments
Fig. 4B.4. P	PCR products generated using newly designed specific primers
Fig. 4B.5. H	Hybridization results for the DsMV specific short fragment Ds1139
	Hybridization results of three specific short fragments Ls1, Ls2 and Ls3 from LYSV
_	Hybridization results of specific short fragments Ps2 and Ps3 from PVY141
Ū	Hybridization results of specific short fragments Zs1 and Zs2 from ZYMV142
	Relationship between hybridization results and the probes computing self annealing
	and looping143
_	Relationship between the hybridisation results and the target fragment secondary
	structure for DsMV ~1.3 kb fragment at 55°C
Fig. 4B.11.	Relationship between the hybridisation results and the target fragment secondary
	structure for specific short fragment Ds1 from DsMV at 55°C146
Fig. 4B.12.	Relationship between the hybridisation results and the target fragment secondary
	structure for specific short fragment Ls1 from LYSV at 55°C147
Fig. 4B.13.	Relationship between hybridisation results and the target fragment secondary
	structure for specific short fragment Ls2 from LYSV at 55°C148
Fig. 4B.14.	Relationship between the hybridisation results and the target fragment secondary
	structure for specific short fragment Ps3 from PVY at 55°C149
Fig. 5.1. Ph	ylogenetic analysis (neighbour joining tree) of the nucleic acid sequences of 21
Ne	w Zealand potyviruses
Fig. 5.2. Im	ages and fluorescent intensity results from the hybridization using ~1.3 kb
fra	gments from Agdia and Florida DsMV (agD13 and flD13 fragments)159
Fig. 5.3. Co	emparison of fluorescent intensities of positive probes from different DsMV isolates
Fig. 5.4. Im	ages and fluorescent intensity results from the hybridization using ~1.0 kb
fra	gments from The Netherlands and Taiwan LYSV isolates (nL10 and tL10

	-
	fragments)
Fig. 5.5	Comparison of fluorescent intensities of positive probes from different LYSV isolates
Fig. 5.6	Images and fluorescent intensity results from the hybridization using \sim 0.7 kb and \sim 1.3
	kb fragments from different PVY isolates
Fig. 5.7	Comparison of fluorescent intensities of positive probes from different fragments of
	different PVY isolates
Fig. 5.8.	Images and fluorescent intensity results from the hybridization using ~0.7 kb
	fragments from different ZYMV isolates
Fig. 5.9.	Comparison of fluorescent intensities of positive probes from different fragments of
	different ZYMV isolates171
Fig. 5.10	D. Images and fluorescent intensity results from the hybridization using ~1.3 kb and
	~0.7 kb fragments from four phylogenetic closely related poryviruses173
Fig. 5.1	1. Images and fluorescent intensity results from the hybridization using cDNA from
	four healthy plants175
Fig. 6.1.	Photograph of the new DNA chip from recent publication (Nagino et al., 2006)183

List of Tables

Table 1.1. Potyviruses in New Zealand (up to December 2003)	9
Table 2A.1. Details of suspected potyviruses infected plant samples	24
Table 2A.2. Information of RNA samples	25
Table 2A.3. Sequences of <i>Potyvirus</i> universal primers	28
Table 2A.4. Reaction of Pukekohe plant samples with universal <i>Potyvirus</i> McAb	32
Table 2A.5. Reaction of ornamental plant samples with universal <i>Potyvirus</i> McAb	33
Table 2A.6. Potyvirus infected samples available for RT-PCR	34
Table 2A.7. Details of potyvirus clones sent for sequencing	36
Table 2A.8. BLAST results for the nt and aa sequences of the investigated potyvirus isolate	es.
	37
Table 2A.9. Information about New Zealand potyvirus sequences identified in this study	39
Table 2A.10. Specific primers for particular potyviruses	43
Table 2B.1. Effect of healthy sap pre-absorption on <i>Alium</i> virus polyclonal antisera	51
Table 2B.2. Reaction of virus from garlic, LYSV, and OYDV to various antisera	52
Table 2B.3. Re-BLAST results for the four novel sequences	59
Table 3.1. Summary of sequences available for the eleven selected potyviruses found in Ne	W
Zealand	66
Table 3.2. Summary of the longest conserved sequences from eleven New Zealand potyviru	ıses
	67
Table 3.3. The number of potential oligonucleotide probes for different lengths, as generate	d
by ROSO	69
Table 3.4. Summary of selected oligonucleotide probes	73
Table 3.5. The oligonucleotide probes for DsMV	74
Table 3.6. The oligonucleotide probes for LYSV	
Table 3.7. The oligonucleotide probes for PVY	76
Table 3.8. The oligonucleotide probes for ZYMV	77
Table 3.9. Information of MM oligonucleotdes	78
Table 3.10. Negative control oligonucleotide probes	80
Table 4A.1. Reagents and buffers used for microarray hybridization	95
Table 4A.2. Preparation of microarray hybridization mixture	95
Table 4A.3. The information of the visual determination of the array image results	97
Table 4A.4. Size and designation of the PCR products used for microarray hybridization	99
Table 4A.5. Summary of positive probes with positive reactions to the different potyviruses	š

	109
Table 4A.6.	P values and ratio of average fluorescent intensity values for the comparison of the
	fluorescent intensity of positive probes, with and without spacers, from the direct-
	labeled DsMV ~1.3 kb, LYSVg2 ~1.0 kb, PVY ~0.8 kb and ZYMV ~0.7 kb PCR
	fragments
Table 4A.7.	The distance of each positive probe to the fluorescent labeling end in the direct
	labeling system
Table 4B.1.	Primer sequences used to generate specific short PCR products fro DsMV,
	LYSVg2, PVY and ZYMV136
Table 4B.2.	Information of specific short fragments and the probe identification numbers on
	each fragment
Table 5.1. C	Overseas potyvirus isolates used to validate the microarray

Abbreviations

A Adenine aa amino acid

agD Agdia DsMV isolate Am6C 6 carbon linker arm

ANOVA one-way-analysis of variance
ATCC American Type Culture Collection

BCMV Bean common mosaic virus

BLAST Basic Local Alignment Search Tool

bp base pairs

BtMV Beet mosaic virus

BYMV Bean yellow mosaic virus

C cytosine

CAG Centre of Applied Gensensorik (microarray)

CeMV Celery mosaic virus
ClYVV Clover yellow vein virus

CP coat protein

CI cylindrical inclusion

CVMV Carnation vein mottle virus
Cy3 cyanine 3 fluorescent dye
Cy5 cyanine 5 fluorescent dye

D13 ~1.3kg PCR product from DsMV

DAG Asp-Ala-Gly DC Dr. Dan Cohen

DNA deoxyribonucleic acid

Ds specifc short PCR product from DsMV

dsDNA double strand DNA

DsMV Dasheen mosaic potyvirus

DSMZ German Resource Centre for Biological Material

DVY Daphne virus Y

ELISA enzyme-linked immunosorbent assay

EM electron microscopy
eZ Egypt ZYMV isolate
flD Florida DsMV isolate
flZ Florida ZYMV isolate
FreMV Freesia mosaic virus
frP France PVY isolate

G Guanine

gP Germany PVY isolate
GYSV Garlic yellow streak virus
HC-Pro helper component protein
hP Hungary PVY isolate
HyB hybridization buffer

ICTV The International Committee on Taxonomy of Viruses

IMMV Iris mild mosaic virus iP Italy PVY isolate

ISEM immunosorbent electron microscopy

iZ Italy ZYMV isolate

JGMV Johnsongrass mosaic virus

JF Dr. John D. Fletcher

L1-10 ~1.0kb PCR product from New Zealand LYSV isolate 1 L2-10 ~1.0kb PCR product from New Zealand LYSV isolate 2

LAMP loop-mediated isothermal amplification

LBR Liquid Blocking Reagent LMV Lettuce mosaic virus

Ls specifc short PCR product from LYSV

LYSV Leek yellow stripe virus
MacMV Maclura mosaic virus

MAF Ministry of Agriculture and Forestry McAb monoclonal potyvirus antibodies

MM mismatch

NC negative control

NeYSV Nerine yellow stripe potyvirus NIa-Pro nuclear inclusion a protein

NIa-VPg nuclear inclusion a linked VPg protein

NIb nuclear inclusion b protein nL The Netherland LYSV isolate

NLV Narcissus latent virus

nP The Netherland PVY isolate

nt nucleotide NVY Nerine virus Y

NYSV Narcissus yellow stripe virus

OD optical density
OMV Oat mosaic virus

OrMV Ornithogalum mosaic virus
OrV2 Ornithogalum virus 2
OYDV Onion yellow dwarf virus

P7 ~0.7kb PCR product from overseas PVY isolates P8 ~0.8kb PCR product from New Zealand PVY

PC positive control

PCR polymerase chain reaction

PcAb polyclonal antisera

pGYSV purified Garlic yellow streak virus

PK Pukekohe (a sampling site in Auckland, New Zealand)

poly-A poly adenines PM perfect-match

PMMA poly methyl methacrylate PNP p-nitrophenylphosphate

Ps specifc short PCR product from PVY

PPV Plum pox virus

PsbMV *Pea seed-borne mosaic*PTA potassium phosphotungstate

PVA Potato virus A PVY Potato virus Y

PVYg Potato virus Y from garlic PWV Passionfruit woodiness virus

RNA ribonucleic acid

RdRp RNA-dependent-RNA-polymerase

RT reverse transcription
SCMV Sugarcane mosaic virus
SD standard deviation
SMV Soybean mosaic virus

SNP single-nucleotide polymorphism

SpDNA Salmon Sperm DNA

SPFMV Sweet potato feathery mottle virus
SpMM Species level mismatched probes

SpS species-specific

SSCP Single-strand conformational polymorphism analysis

ssDNA single strand DNA StS strain-specific thymine

TaMV Tamarillo mosaic virus **TBV** Tulip breaking virus Taiwan LYSV isolate tL melting temperature Tm TMVTobacco mosaic virus Turnip mosaic virus TuMV TV Tuberose virus **UTR** untranslated region

VPg viral genome linked protein WMV Watermelon mosaic virus

Z7 ~0.7kb PCR product from ZYMV ZaMMV Zantedeschia mild mosaic virus ZaMV Zantedeschia mosaic virus

Zs specifc short PCR product from ZYMV

ZYMV Zucchini yellow mosaic virus