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# **Speciation genes in native New Zealand Leafroller moths**

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A THESIS SUBMITTED IN FULFILLMENT OF THE REQUIREMENTS OF  
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# Abstract

This thesis tests predicted characteristics of speciation genes made by the 'genic view' of speciation. The genic view states that the genome of a species is mosaic, and is divided into regions that contribute to a speciation event (speciation genes) and regions that do not (neutral genes). These speciation loci are characterized by the absence of ancestral polymorphism and diminished or no gene flow. This work investigates whether Pheromone Binding Protein 1 (*PBP1*) fulfils the criteria of a speciation gene in a complex of native New Zealand Leafroller moths. *Ctenopseustis* and *Planotortrix* comprise five and seven species, respectively. Intraspecific sampling resolved many allelic variants in four neutral genes (*COI*[barcoding region], *COI-COII*, *EF-1 $\alpha$*  and *TPI*). These loci show evidence of purifying selection and typically are not reciprocally monophyletic for *P. octo* + *P. excessana* and *C. obliquana* + *C. herana*. *PBP1* is no better at recovering monophyly of species groups than any of the neutral genes. The phylogenetic patterns are different among loci confirming a mosaic genome for recently speciated groups. *PBP1* is under purifying selection or functional constraint, however there are indications of excess non-synonymous substitutions within *PBP1* in *P. octo*, *P. excessana* and *P. avicenniae*. Some of these amino acid changes are in positions predicted to be involved in pheromone binding and receptor interactions. In addition the lineage leading to the species *C. fraterna* and *C. filicis* show evidence of positive selection in the *PBP1* gene tree. In conclusion, *PBP1* may be a speciation gene for some of the speciation events that gave rise to this species complex.

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# Contents

<b>Abstract</b>	<b>i</b>
<b>Acknowledgments</b>	<b>ii</b>
<b>Table of Contents</b>	<b>iv</b>
<b>List of Figures</b>	<b>viii</b>
<b>List of Tables</b>	<b>x</b>
<b>1 General Introduction</b>	<b>1</b>
1.1 Species Concepts . . . . .	2
1.1.1 Modes of Speciation . . . . .	4
1.2 The genic view of speciation . . . . .	6
1.3 Speciation genes . . . . .	9
1.4 Lepidopteran sex pheromones . . . . .	13
1.4.1 Sex pheromone biosynthesis in female moth . . . . .	13
1.4.2 Sex pheromone reception in male moth . . . . .	15
1.4.3 Sex pheromone evolution . . . . .	16
1.5 A model system for speciation . . . . .	17
1.5.1 Morphology of <i>Planotortrix</i> and <i>Ctenopseustis</i> moths . . . . .	17
1.5.2 Phylogenetics . . . . .	19
1.5.3 Distribution and host plants . . . . .	20
1.5.4 Sex pheromones in native Leafroller . . . . .	20
1.5.5 Sex pheromone biosynthesis <i>Planotortrix</i> and <i>Ctenopseustis</i> . . . . .	24

---

1.5.6	Pheromone binding proteins in Leafroller moths . . . . .	24
1.5.7	Genetic study on behaviour in male <i>Ctenopseustis</i> moths . . . . .	25
1.6	Thesis objectives . . . . .	26
<b>2</b>	<b>Evolutionary patterns in the DNA barcoding region of the <i>Cytochrome c oxidase subunit 1</i> gene</b>	<b>29</b>
2.1	Introduction . . . . .	29
2.1.1	Aims . . . . .	30
2.2	Materials and Methods . . . . .	30
2.2.1	Specimens . . . . .	30
2.2.2	PCR amplification and sequencing . . . . .	33
2.2.3	Data analysis . . . . .	33
2.3	Results . . . . .	34
2.4	Discussion . . . . .	37
<b>3</b>	<b>Evolutionary patterns in non-speciation genes</b>	<b>40</b>
3.1	Introduction . . . . .	40
3.2	Aims . . . . .	42
3.3	Data limitations . . . . .	43
3.4	Materials and Methods . . . . .	43
3.4.1	Insect collection . . . . .	43
3.4.2	Genomic DNA extraction from adult moths . . . . .	44
3.4.3	PCR amplification and sequencing . . . . .	44
3.4.4	Sequence alignment . . . . .	47
3.4.5	Phylogenetic analysis . . . . .	47
3.4.6	PAML analysis for testing selection . . . . .	48
3.4.7	Constraint analysis and monophyly tests . . . . .	49
3.5	Results . . . . .	49
3.5.1	Gene tree phylogenies . . . . .	49
3.5.2	Tree topology tests . . . . .	54
3.5.3	Testing sites and lineages under selection . . . . .	58
3.6	Discussion . . . . .	60

---

3.6.1	Discordant tree topologies . . . . .	60
3.6.2	<i>COI</i> , <i>COII</i> and <i>EF-1<math>\alpha</math></i> are under purifying selection . . . . .	63
<b>4</b>	<b>A Candidate Speciation Gene</b>	<b>64</b>
4.1	Introduction . . . . .	64
4.2	Aims . . . . .	65
4.3	Materials and Methods . . . . .	66
4.3.1	Specimen dataset . . . . .	66
4.3.2	PCR amplification and sequencing . . . . .	66
4.3.3	Sequence analysis . . . . .	67
4.4	Results . . . . .	69
4.4.1	PBP phylogeny . . . . .	69
4.4.2	Tests for selection in PBP . . . . .	70
4.4.3	PBP amino acid variation between <i>Planotortrix</i> and <i>Ctenopseustis</i> . . . . .	73
4.4.4	A 3D protein structure model of PBP for <i>Planotortrix octo</i> PBP1 . . . . .	75
4.4.5	Mapping amino acid changes in <i>C. fraterna</i> and <i>C. filicis</i> onto <i>P. octo</i> model structure . . . . .	78
4.5	Discussion . . . . .	80
<b>5</b>	<b>General discussion</b>	<b>84</b>
5.1	Sorting of alleles . . . . .	85
5.1.1	Taxon sampling and power . . . . .	85
5.1.2	Effective population sizes . . . . .	86
5.1.3	Hybridization and Introgression . . . . .	87
5.1.4	Taxonomy . . . . .	87
5.2	Mosaic genome . . . . .	88
5.2.1	Species tree . . . . .	89
5.3	Selection . . . . .	89
5.4	Functional work and future directions . . . . .	90
<b>A</b>	<b>Appendix A</b>	<b>93</b>
<b>B</b>	<b>Appendix B</b>	<b>94</b>





# List of Figures

1.1	Dobzhansky-Muller model of hybrid incompatibility . . . . .	6
1.2	The two horizontal bars represent the genomes of two diverging populations . . .	7
1.3	Contrasting gene genealogies at two types of loci . . . . .	9
1.4	Adults and larva of <i>Planotortrix</i> and <i>Ctenopseustis</i> moths . . . . .	18
1.5	Distribution maps of <i>Planotortrix</i> and <i>Ctenopseustis</i> moths . . . . .	21
2.1	Species collection sites for the North Island. Each individual dot represents a specimen sampled. . . . .	31
2.2	Species collection sites for the South Island. Each individual dot represents a specimen sampled. . . . .	32
2.3	Maximum likelihood tree constructed from the barcoding region of the Cytochrome c oxidase subunit 1 ( <i>COI</i> ) gene . . . . .	35
2.4	Comparison of maximal within species divergence with minimal between species divergence at the <i>COI</i> . . . . .	36
2.5	Comparison of maximal within species divergence with minimal between species divergence at the <i>COI</i> . . . . .	37
3.1	Bayesian inference gene tree phylogeny for <i>Planotortrix</i> and <i>Ctenopseustis</i> species based on combined <i>COI</i> and <i>COII</i> sequences . . . . .	51
3.2	Bayesian inference gene tree phylogeny for <i>Planotortrix</i> and <i>Ctenopseustis</i> species based on <i>EF-1<math>\alpha</math></i> sequences . . . . .	53
3.3	Maximum likelihood gene tree phylogeny for <i>Planotortrix</i> and <i>Ctenopseustis</i> species based on <i>TPI</i> exon sequences . . . . .	55

---

3.4	Bayesian inference gene tree phylogeny for <i>Planotortrix</i> and <i>Ctenopseustis</i> species based on <i>TPI</i> exon and intron sequences . . . . .	56
4.1	Bayesian inference gene phylogeny for <i>Planotortrix</i> and <i>Ctenopseustis</i> species based on <i>PBP</i> sequences . . . . .	71
4.2	Alignment of PBP1 across <i>Ctenopseustis</i> and <i>Planotortrix</i> showing only variable amino acid sites . . . . .	74
4.3	Structure-based sequence alignment of <i>P.octo-2</i> PBP1 . . . . .	75
4.4	Ribbon diagram of the predicted structure of <i>P.octo-2</i> PBP1 (blue) and the structure of <i>A. polyphemus</i> PBP1 (orange). . . . .	77
4.5	Ribbon diagram of the predicted structure of <i>P.octo-2</i> PBP1 (blue) and the structure of ApolPBP1 (orange) showing fixed amino acid changes between <i>C. fraterna</i> and <i>C. filicis</i> . . . . .	79

# List of Tables

1.1	Reproductive isolation mechanism . . . . .	2
1.2	Distribution and Host plants of <i>Planotortrix</i> and <i>Ctenopseustis</i> . . . . .	22
1.3	Sex pheromone components and their ratios for <i>Planotortrix</i> and <i>Ctenopseustis</i> species . . . . .	23
2.1	Shimodaira-Hasegawa test analysis for topological constraints . . . . .	36
3.1	Non-speciation gene dataset . . . . .	44
3.2	Additional dataset from (Newcomb & Gleeson, 1998) . . . . .	45
3.3	Primer list . . . . .	46
3.4	Species monophyly status . . . . .	57
3.5	Constraint tree analysis using Shimodaira-Hasegawa test . . . . .	58
3.6	Likelihood values and parameter estimates for mt genes <i>COI-COII</i> . . . . .	59
3.7	Likelihood values and parameter estimates for <i>EF-1<math>\alpha</math></i> . . . . .	60
3.8	Nested model results of PAML analysis . . . . .	60
3.9	Branch-model results of PAML analysis . . . . .	61
4.1	PBP1 gene dataset . . . . .	67
4.2	Primer list for PBP1 . . . . .	68
4.3	Likelihood values and parameter estimates for PBP . . . . .	72
4.4	Nested model results of PAML analysis . . . . .	72
4.5	Species monophyly status . . . . .	83