

A brief, speculative history of avipoxvirus in New Zealand

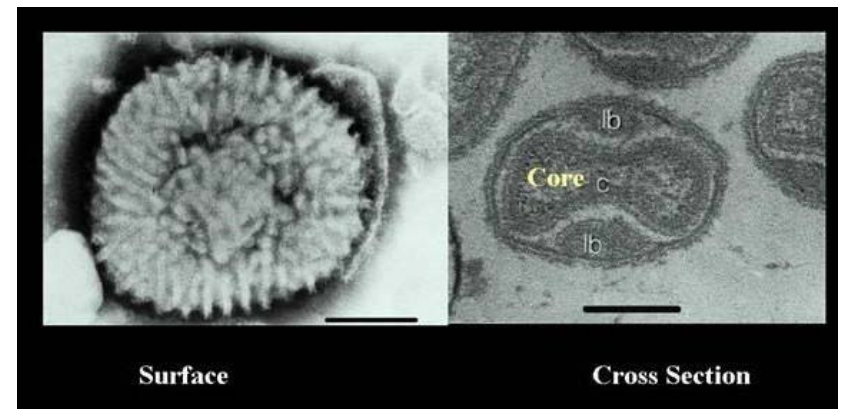
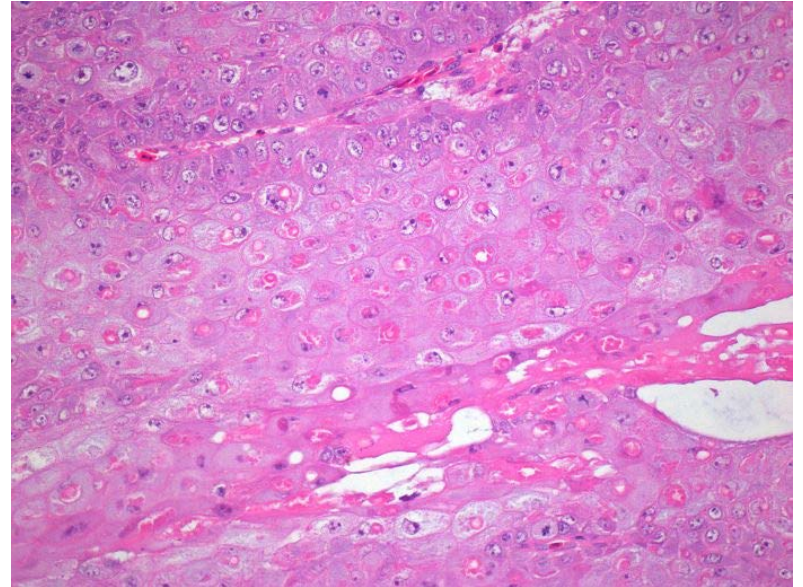


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Intro to avipoxvirus (APV)

- Global distribution
- Reports in >280 bird species, 70 families, 20 orders globally
- Economic losses in domestic poultry
- Biodiversity losses in island ecosystems (Hawaii, Galapagos, Canary Islands) in conjunction with avian malaria



(vaccinia virus, copyright E. Niles).

APV infection characteristics

- Excellent environmental stability
- Need a break in the epithelium for infection to establish
- Insect and mechanical vectors are main route of infection
- Host specificity varies between strains



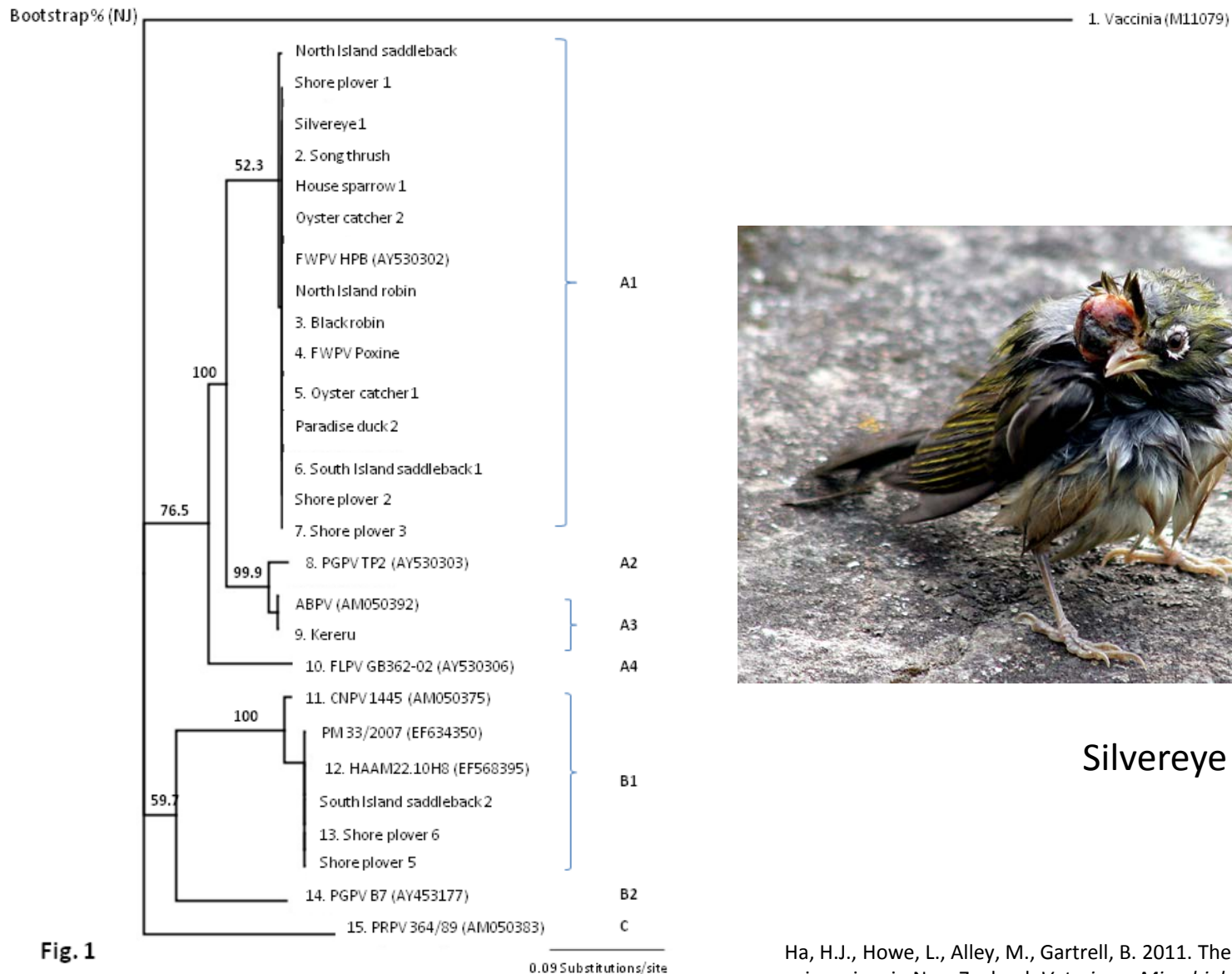
APV molecular characteristics

- *Fowlpox virus* is the type species of the *Avipoxvirus* genus
- complete genomic sequences of *Fowlpox virus* and *Canarypox virus*
- The two genomes are highly diverged, sharing only ca. 70% sequence identity
- The 365-kbp genome of *Canarypox virus* is larger than that of *Fowlpox virus* (288 kbp) and shows significant differences in gene content

APV phylogeny

- Initially assigned strain/species status on host affected but confused by multi-host pathogenic strains
- DNA sequences of the 4b core protein coding genomic region currently used.
- Wide variation in genome has limited other pan-genus PCR primers
- the vast majority of avian poxvirus isolates clustered into three major clades, represented by the *Fowlpox virus* (clade A), the *Canarypox virus* (clade B), and the *Psittacinepox virus* (clade C)

APV phylogeny from NZ birds (HJ Ha PhD)

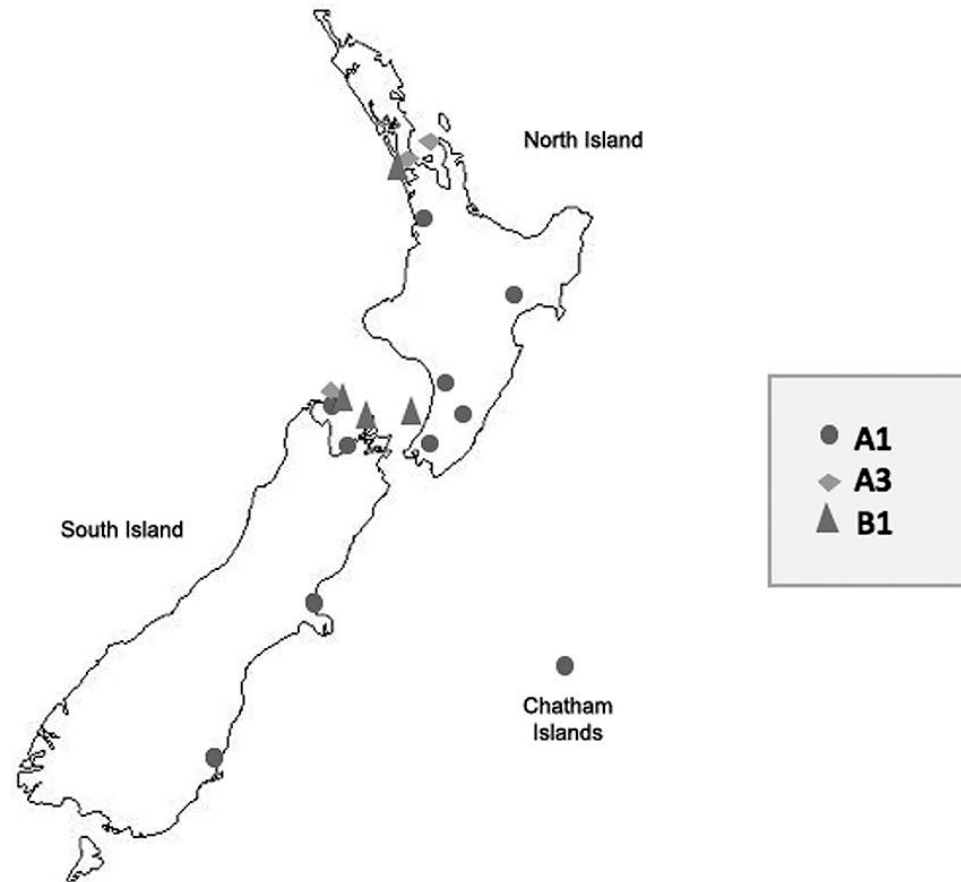


Silvereye © P Sorrell

Fig. 1

Ha, H.J., Howe, L., Alley, M., Gartrell, B. 2011. The phylogenetic analysis of avipoxvirus in New Zealand. *Veterinary Microbiology* 150: 80–87

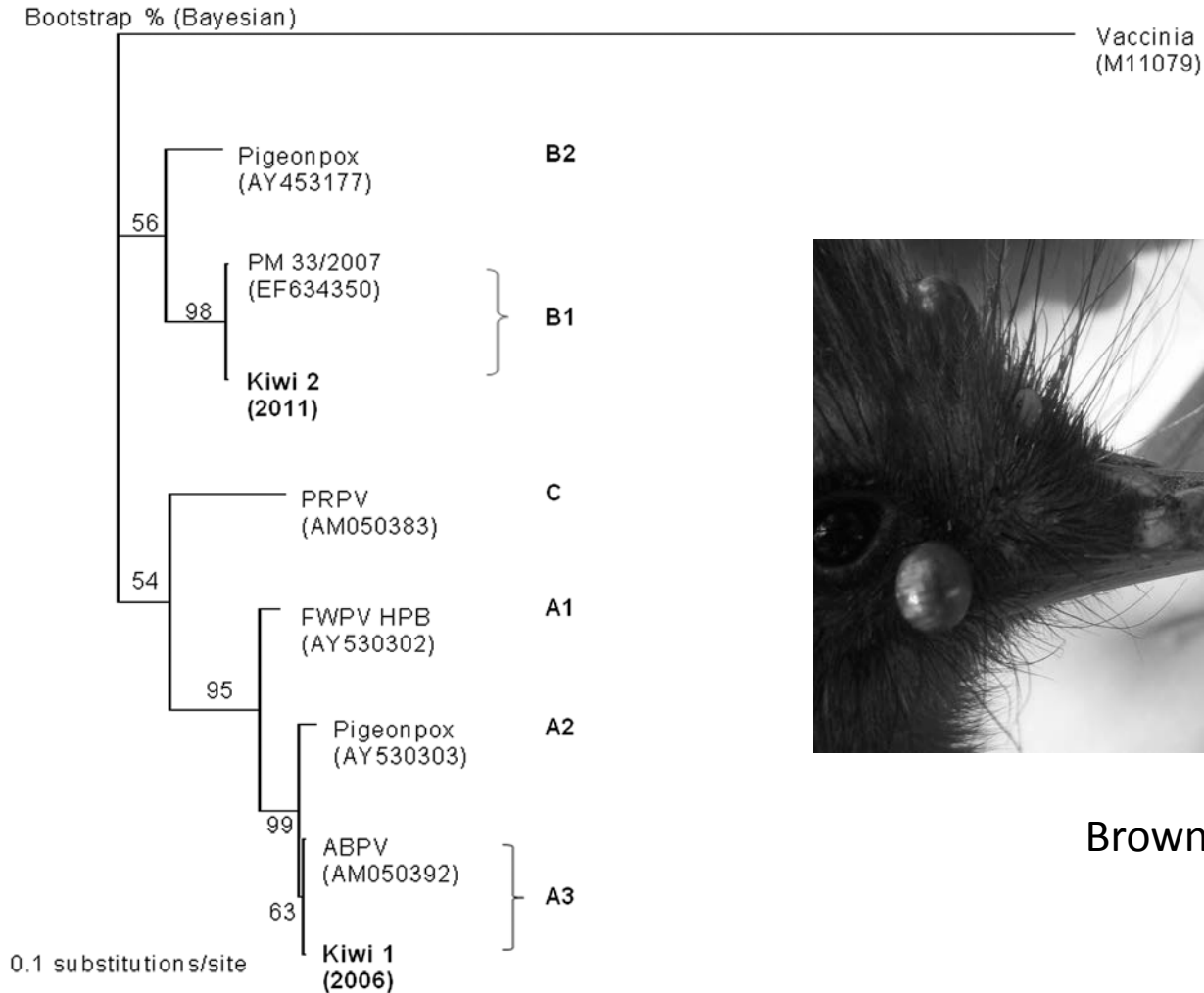
APV distribution in NZ



Sequence divergence of NZ APV isolates

| | Lineage | | | | | | | | | | | | | | |
|----|------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|
| | 1 ^A | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
| 1 | 0.0 ^B | - | - | - | - | - | - | - | - | - | - | - | - | - | - |
| 2 | 55.0 | 0.0 | - | - | - | - | - | - | - | - | - | - | - | - | - |
| 3 | 54.8 | 0.2 | 0.0 | - | - | - | - | - | - | - | - | - | - | - | - |
| 4 | 54.8 | 0.2 | 0.0 | 0.0 | - | - | - | - | - | - | - | - | - | - | - |
| 5 | 54.8 | 0.2 | 0.0 | 0.0 | 0.0 | - | - | - | - | - | - | - | - | - | - |
| 6 | 54.8 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | - | - | - | - | - | - | - | - | - |
| 7 | 54.8 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | - | - | - | - | - | - | - | - |
| 8 | 54.4 | 9.1 | 9.3 | 9.3 | 9.3 | 9.3 | 9.3 | 0.0 | - | - | - | - | - | - | - |
| 9 | 55.1 | 8.1 | 8.3 | 8.3 | 8.3 | 8.3 | 8.3 | 2.4 | 0.0 | - | - | - | - | - | - |
| 10 | 54.9 | 11.7 | 11.9 | 11.9 | 11.9 | 11.9 | 11.9 | 11.2 | 11.7 | 0.0 | - | - | - | - | - |
| 11 | 53.4 | 22.1 | 22.4 | 22.4 | 22.4 | 22.4 | 22.4 | 23.8 | 24.0 | 22.3 | 0.0 | - | - | - | - |
| 12 | 53.9 | 23.3 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 24.0 | 24.8 | 23.6 | 2.1 | 0.0 | - | - | - |
| 13 | 54.0 | 23.3 | 23.6 | 23.6 | 23.6 | 23.6 | 23.6 | 24.1 | 24.8 | 23.6 | 2.1 | 0.0 | 0.0 | - | - |
| 14 | 55.2 | 21.7 | 21.9 | 21.9 | 21.9 | 21.9 | 21.9 | 20.8 | 21.0 | 20.5 | 17.6 | 15.9 | 16.0 | 0.0 | - |
| 15 | 58.4 | 24.0 | 23.8 | 23.8 | 23.8 | 23.8 | 23.8 | 24.5 | 25.0 | 26.2 | 24.0 | 23.3 | 23.3 | 22.9 | 0.0 |

APV in kiwi



Brown kiwi © I Castro

APV seroprevalence and avian malaria in introduced passerines (Palmerston North)

| Species | Common Name | APV ELISA Positive (%) | <i>Plasmodium</i> PCR Positive (%) | No. of <i>Plasmodium</i> positive birds seropositive to APV (%) | <i>Plasmodium</i> lineages identified (GenBank no.) |
|----------------------------|-------------|------------------------|------------------------------------|---|--|
| <i>Turdus merula</i> | Blackbird | 31/32 (97%) | 11/28 (39.2%) | 11/11 (100%) | Mixed (unresolved) <i>P. (Novyella) spp. SYATO5</i> (DQ847271) <i>Plasmodium</i> spp AFTRU5 (DQ847263) |
| <i>Fringila coelebs</i> | Chap finch | 6/11 (54.6%) | 0/10 (0%) | 0/0 (0%) | - |
| <i>Careulis chloris</i> | Gold finch | 0/2 (0%) | 0/2 (0%) | 0/0 (0%) | - |
| <i>Cardeulis cardeulis</i> | Green finch | 1/4 (25%) | 0/4 (0%) | 0/0 (0%) | - |
| <i>Turdus philomelos</i> | Song thrush | 4/4 (100%) | 1/1 (100%) | 1/1 (100%) | <i>Plasmodium</i> spp AFTRU5 (DQ847263) |
| <i>Stunus vulgaris</i> | Starling | 3/12 (25%) | 3/10 (30%) | 2/3 (67%) | <i>P. (Huffia) elongatum</i> GRW6 (DQ368381) |
| | Total | 45/65 (69.2%) | 15/55 (27.3%) | 14/15 (93.3%) | |

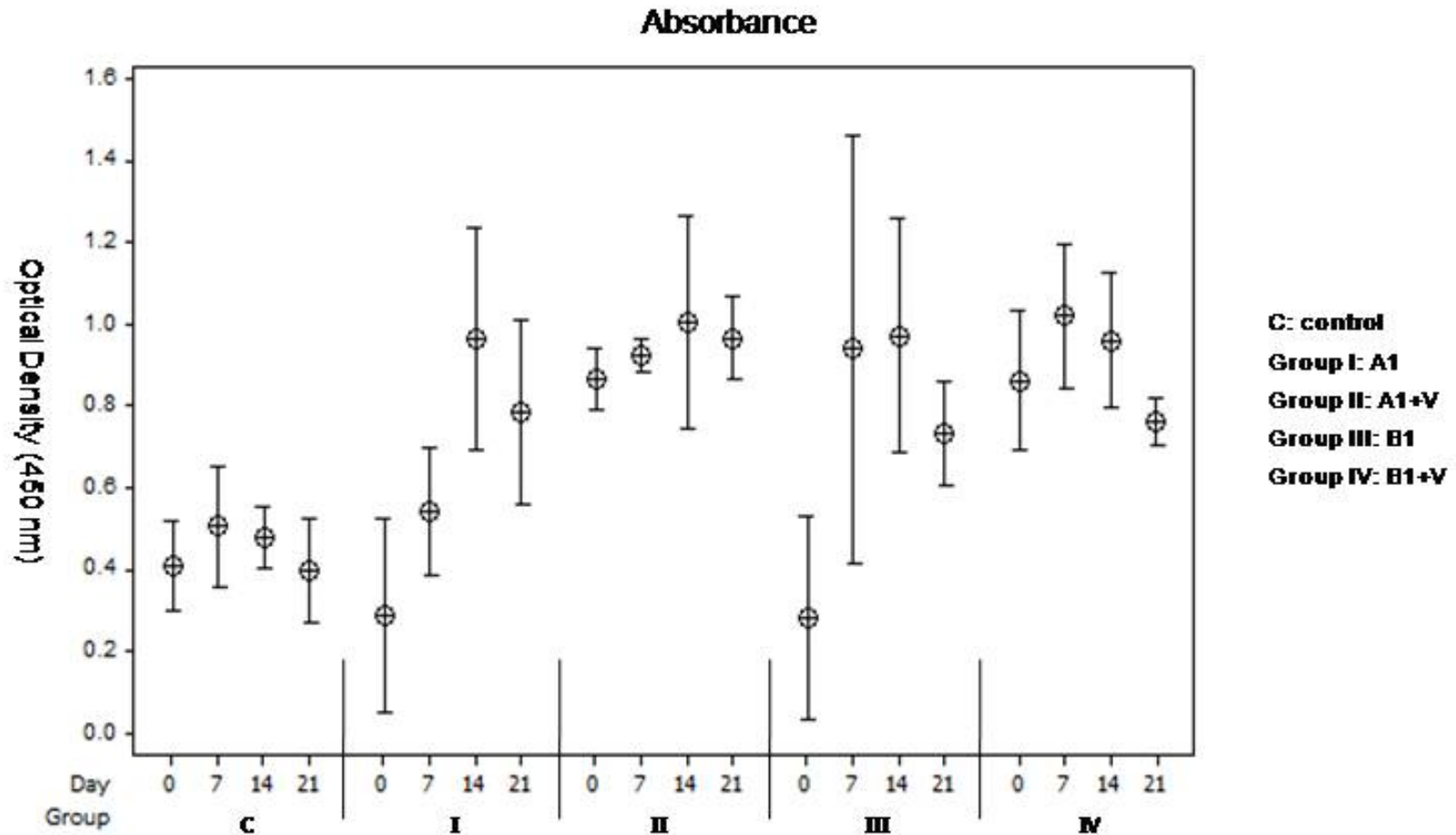
H. J. Ha , M. Banda , M. R. Alley , L. Howe , and B. D. Gartrell. 2013. The seroprevalence of avipoxvirus and its association with avian malaria (*Plasmodium* spp.) infection in introduced passerine birds in the southern regions of the North Island of New Zealand. *Avian Diseases*, 57(1):109-115. 2013

APV seroprevalence in NI Robins

- 15 North Island robins (*Petroica australis longipes*) from Kapiti Island sampled by Kate McInnes
- One bird with suspicious leg lesion
- Nine birds (60%, n = 15) were seropositive to APV
- The one robin with APV suspected leg lesion was serologically negative (early infection?)



Protection by vaccination against NZ field strains of APV in zebra finches



Current effects of APV on NZ birds

- In most species, APV causes seasonal self-limiting illness and occasional mortality especially in young individuals
- Cause of mortality and increased cost of captive rearing and translocations in endangered New Zealand shore plover
- Emerging as a possible cause of disease and death in kiwi populations
- Species with limited genetic diversity are potentially most at risk eg, black robins, little spotted kiwi



Wrybill © Phil Battley

Historical Hypotheses

- All strains of APV in New Zealand were introduced by exotic avian hosts
 - Alternative: robin immigration events as potential natural pathways
- No current evidence of “native” strains of APV
- Considerable reduction in APV strain diversity occurred (parasite dropout) which has biosecurity implications (especially clade C)



Chatham Island taiko © DOC



Yellow crowned amazon aka Bob

Historical Hypotheses 2

- Primary hosts and vectors spread across NZ has led to endemic reservoirs of APV and pollution of most environments
- Significant mortality of native bird species may have initially occurred
 - effect obscured by primary causes of biodiversity loss (predation and habitat loss)



Research questions

- Can museum specimens and molecular techniques be used to define when APV was introduced into NZ?
- Can commercial fowlpox vaccines be used safely in the conservation management of the endangered shore plover?
- Why are shore plovers so susceptible to APV disease?
- Can whole genome sequencing of APV give us insights into
 - molecular evolution of this pathogen
 - virulence genes present
 - risks to genetically limited populations of NZ birds?