

1 **ONLINE SUPPLEMENTARY INFORMATION**

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3 **Host heterozygosity and genotype rarity affect viral dynamics in an avian**
4 **subspecies complex**

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17 **Supplementary Table S1: F_{st} values between each subspecies dyad calculated using Alequin.**

Subspecies	<i>P. e. elegans</i>	Western slopes hybrid	<i>P. e. flaveolus</i>	<i>P. e. adelaidae</i>
<i>P. e. elegans</i>	0.00	-	-	-
Western slopes hybrid	0.03	0.00	-	-
<i>P. e. flaveolus</i>	0.07	0.04	0.00	-
<i>P. e. adelaidae</i>	0.02	0.05	0.06	0.00

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19 **Supplementary Table S2:** Summary statistics of each loci used in this study assuming all subspecies
 20 are one continuous population. Each loci was tested for linkage disequilibrium within each
 21 subspecies. **Loci C12 had a high proportion of null alleles which ranged between 0.10 and 0.17 across**
 22 **subspecies. Excluding C12 from the analysis did not influence the results of this study.**

Loci	Number of individuals	Number of alleles per locus	Allele size range	Estimated proportion of null alleles	Evidence of linkage disequilibrium?
AgGT07	359	27	251-286	0.1	No
Cp03E01	361	23	184-234	0.1	No
AgGT21	361	4	315-328	0.02	No
Cfor2627	362	10	132-159	0.04	No
C12	362	6	61-78	0.17	No
C13	363	8	189-209	0.09	No
CP52A09	359	20	361-401	0.04	No
Ero03	358	12	192-218	0.06	No
Ero08	362	17	119-155	0.01	No

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24 **Supplementary Table S3: Arlequin results for observed and expected heterozygosities used for testing**
 25 **Hardy-Weinberg equilibrium for each subspecies (n = 363 individuals) at each of the nine microsatellite**
 26 **loci. * denotes significance after Bonferroni correction ($P < 0.001$).**

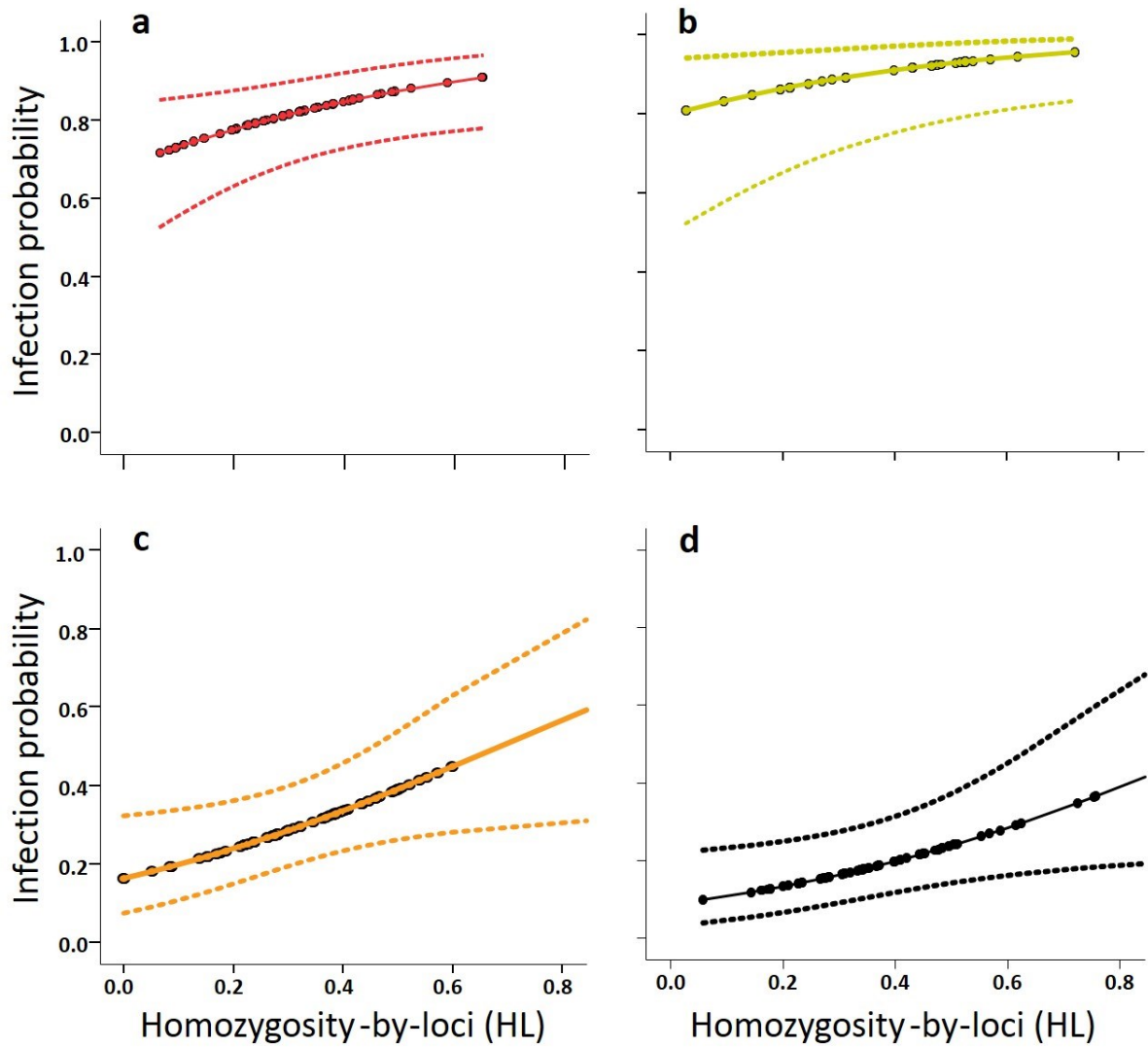
Loci	Heterozygosity	<i>P. e. elegans</i>	Western Slopes	<i>P. e. flaveolus</i>	<i>P. e. adelaidae</i>	Pooled data
AgGT07	H_o	0.83	0.73	0.77	0.71*	0.75*
	H_e	0.93	0.85	0.88	0.86	0.92
CPO3E01	H_o	0.86	0.49*	0.59	0.86	0.72*
	H_e	0.90	0.88	0.81	0.88	0.89
AgGT21	H_o	0.43	0.33	0.17	0.32	0.33
	H_e	0.41	0.35	0.20	0.31	0.34
Cfor2627	H_o	0.63	0.63	0.54	0.5	0.58
	H_e	0.69	0.67	0.59	0.52	0.63
CI2	H_o	0.40	0.29	0.27	0.40	0.35*
	H_e	0.52	0.40	0.34	0.50	0.50
CI3	H_o	0.55	0.58	0.58	0.51*	0.55*
	H_e	0.61	0.63	0.67	0.59	0.65
CP52A09	H_o	0.78	0.73	0.77	0.79	0.77*
	H_e	0.81	0.87	0.84	0.82	0.84
Ero03	H_o	0.70	0.60	0.55	0.66	0.64*
	H_e	0.73	0.64	0.66	0.75	0.72
Ero08	H_o	0.87	0.81	0.65	0.73	0.78*
	H_e	0.84	0.82	0.60	0.76	0.80

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28 **Supplementary Table S4:** The set of candidate models considered in this study, ranked by the AIC_c
 29 values for each of the two response variables (lower AIC_c values indicates greater support for
 30 model). Addition sign represents delta AIC_c compared to top model.

Response variable	Candidate models	AIC _c
BFDV infection status	Subspecies + Age + HL	222.54
	Subspecies + Age + Sex + HL	+0.59
	Subspecies + Age + Sex	+2.22
	Subspecies + Age	+2.51
	Subspecies + Age + Sex + APR	+4.21
	Subspecies + Age + APR	+4.35
	Subspecies + HL	+11.94
	Subspecies + Sex + HL	+14.05
	Subspecies	+14.72
	Subspecies + APR	+15.99
	Subspecies + Sex	+16.7
	Subspecies + Sex + APR	+17.98
	Age + Sex	+37.14
	Age + Sex + APR	+38.39
	Age + Sex + HL	+38.95
	Age	+40.36
	Age + APR	+41.67
	Age + HL	+41.74
	Null (intercept only)	+89.37
	HL	+90.46
Sex	+90.66	
APR	+91.16	
Sex + HL	+91.99	
Sex + APR	+92.47	
BFDV viral load	Subspecies + Age + Sex + APR	414.97
	Subspecies + Age + Sex	+1.56
	Subspecies + Age + Sex + HL	+3.8
	Subspecies + Age + APR	+4.32
	Subspecies + Age	+5.79
	Subspecies + Sex + APR	+6.15
	Subspecies + Age + HL	+7.29
	Subspecies + APR	+8.75
	Subspecies + Sex	+11.01
	Subspecies + Sex + HL	+12.8
	Subspecies	+13.3
	Subspecies + HL	+14.31
	Age + Sex	+23.23
	Age + Sex + HL	+25.01
	Age + Sex + APR	+25.32
	Age	+28.88
	Age + APR	+30.99
	Age + HL	+31.07
	Sex	+43.99
	Sex + APR	+44.96
Sex + HL	+45.96	
Null (intercept only)	+46.41	
APR	+47.51	
HL	+48.53	

31 APR = average pairwise relatedness, HL = homozygosity-by-loci, AIC_c = Akaike Information Criterion (corrected
32 for small sample size)

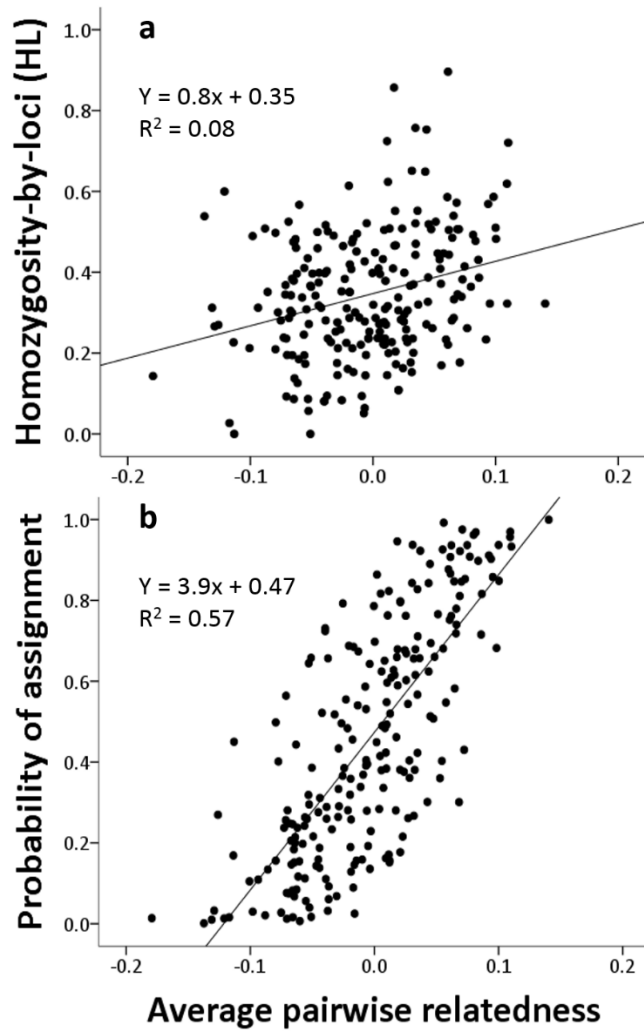


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35 **Supplementary Figure S1:** The model predicted effects of individual host homozygosity (measured as36 homozygosity-by-loci) on the probability of infection with beak and feather disease virus in **(a)**37 *Platycercus elegans elegans*, **(b)** *P. e. flaveolus*, **(c)** *P. e. adelaidae*, and **(d)** the Westerns Slopes

38 population. Dotted lines indicate the 95% confidence interval, and circles indicate the levels of HL

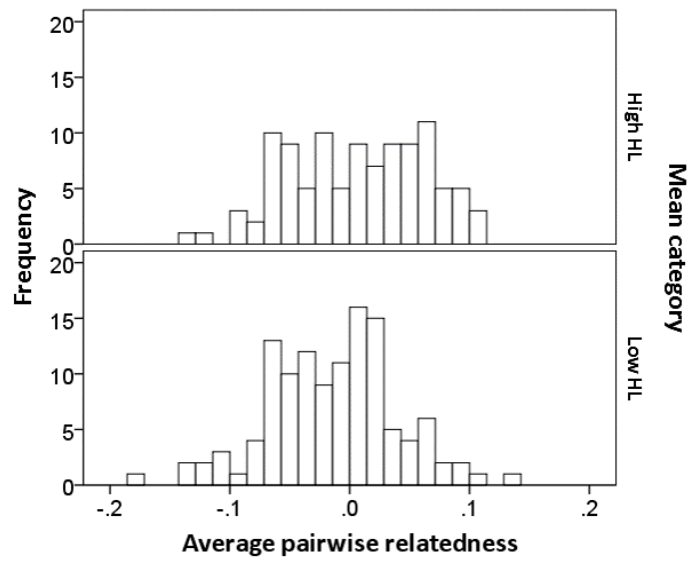
39 sampled in this study. Effects are averaged over age classes and sexes.



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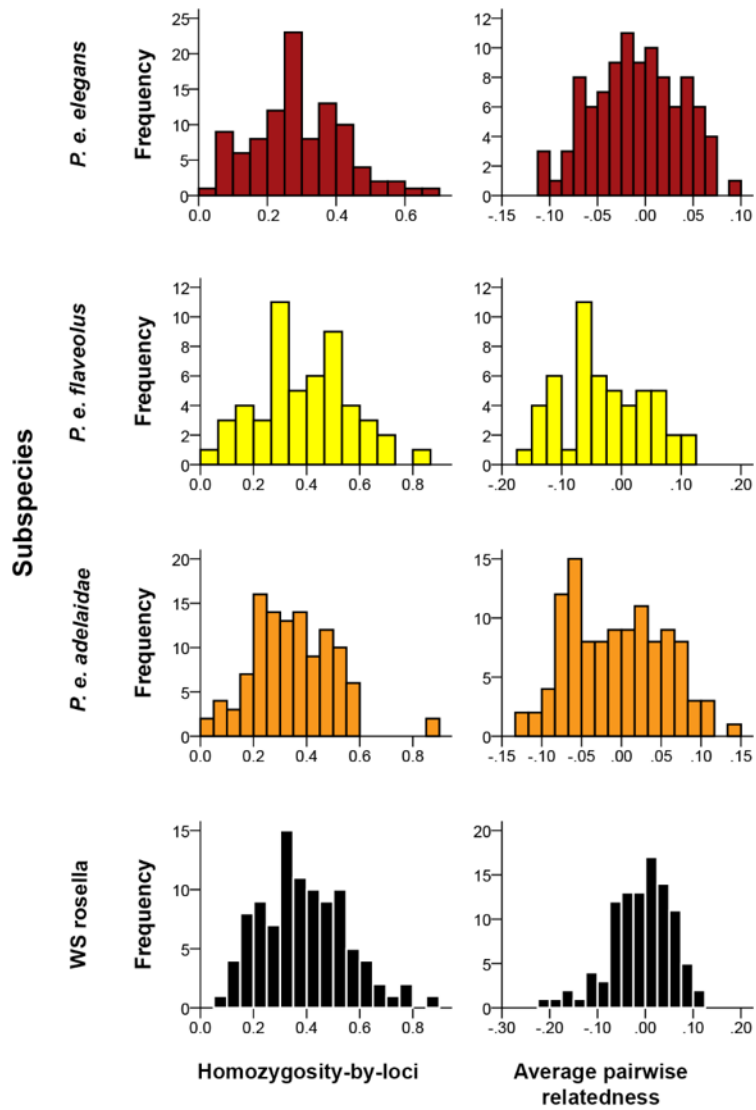
41 **Supplementary Figure S2:** To estimate an individual's genotype rarity within a population we
 42 calculated average pairwise relatedness (APR; see methods). (a) APR was weakly correlated with
 43 homozygosity-by-loci (HL) but explained only a small proportion of the variance. (b) The correlation
 44 between APR and the probability of assignment index (see methods) was much higher. Linear
 45 regression lines were calculated using ordinary least squares (N = 224).

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48 **Supplementary Figure S3:** The frequency distribution of average pairwise relatedness in two different
 49 groups. High HL contains individuals with higher than average (Mean HL = 0.34) homozygosity-by-loci
 50 (HL) values and Low HL contains individuals with lower than the average HL.



Genetic diversity measure

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52 **Supplementary Figure S4:** Frequency distribution of each individual genetic diversity measure was

53 similar across populations (n = 363 individuals).

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