

Supplementary Information

Table S1 Amino acid accession and database sequence information for cytochrome b sequences used in trait evolution analyses including the resistance matrix for CWD (R = resistant, S = susceptible, U = unknown) for each species. For this analysis humans are used as the reference sequence and are assumed to be resistant to CWD infection.

| Family | Species | CWD | Accession | Database source | RefSeq accession | Citation |
|-----------------|-------------------------------------|-----|----------------|-----------------|------------------|----------------------------------|
| Antilocapridae | <i>Antilocapra americana</i> | U | YP_007625795.1 | RefSeq | NC_020679.1 | Hassanin et al. 2012 |
| Bovidae | <i>Bison bison</i> | U | YP_002791041.1 | RefSeq | NC_012346.1 | Achilli et al. 2008 |
| Bovidae | <i>Bos taurus</i> | R | YP_209217.1 | RefSeq | NC_006853.1 | Chung and Ha 2005 |
| Bovidae | <i>Oreamnos americanus</i> | U | YP_007625158.1 | RefSeq | NC_020630.1 | Hassanin et al. 2009 |
| Bovidae | <i>Ovis canadensis</i> | U | YP_004769596.1 | RefSeq | NC_015889.1 | Miller et al. 2011 |
| Canidae | <i>Canis latrans</i> | R | YP_626727.1 | RefSeq | NC_008093.1 | Björnerfeldt et al. 2006 |
| Cebidae | <i>Saimiri sciureus</i> | S | YP_002929489.1 | RefSeq | NC_012775.1 | Matsui et al. 2009 |
| Cercopithecidae | <i>Macaca fascicularis</i> | R | YP_002884238.1 | RefSeq | NC_012670.1 | Yi et al. 2009 |
| Cervidae | <i>Alces alces</i> | S | YP_007625769.1 | RefSeq | NC_020677.1 | Hassanin et al. 2012 |
| Cervidae | <i>Alces alces alces</i> | S | O47922.1 | UniProt | NA | Randi et al. 1998 |
| Cervidae | <i>Cervus canadensis canadensis</i> | S | AAL17840.1 | Protein | NA | Ludt et al. 2004 |
| Cervidae | <i>Muntiacus reevesi</i> | S | NP_663804.1 | RefSeq | NC_004069.1 | Zhang et al. 2010 |
| Cervidae | <i>Odocoileus hemionus</i> | S | YP_007626445.1 | RefSeq | NC_020729.1 | Hassanin et al. 2012 |
| Cervidae | <i>Odocoileus virginianus</i> | S | YP_004300520.1 | RefSeq | NC_015247.1 | Seabury et al. 2011 |
| Cervidae | <i>Rangifer tarandus</i> | S | YP_448945.1 | RefSeq | NC_007703.1 | Wada et al. 2007 |
| Cervidae | <i>Rangifer tarandus granti</i> | S | AAV84418.1 | Protein | NA | Cronin et al. 2005 |
| Cricetidae | <i>Phodopus sungorus</i> | R | ACG76170.1 | Protein | NA | Meshchersky and Feoktistova 2009 |
| Felidae | <i>Felis catus</i> | R | NP_008263.1 | RefSeq | NC_001700.1 | Lopez et al. 1996 |
| Hominidae | <i>Homo sapiens</i> | R | YP_003024038.1 | RefSeq | RefSeq | Anderson et al. 1981 |
| Mustelidae | <i>Mustela putorius</i> | R | YP_007625262.1 | RefSeq | NC_020638.1 | Yu et al. 2011 |

| | | | | | | |
|-------------|------------------------------|---|----------------|---------|-------------|--------------------|
| Mustelidae | <i>Mustela putorius furo</i> | R | BAB08027.1 | Protein | NA | Kurose et al. 2000 |
| Mustelidae | <i>Neovison vison</i> | R | YP_007625301.1 | RefSeq | NC_020641.1 | Kurose et al. 2000 |
| Procyonidae | <i>Procyon lotor</i> | R | YP_001096027.1 | RefSeq | NC_009126.1 | Takada et al. 2008 |

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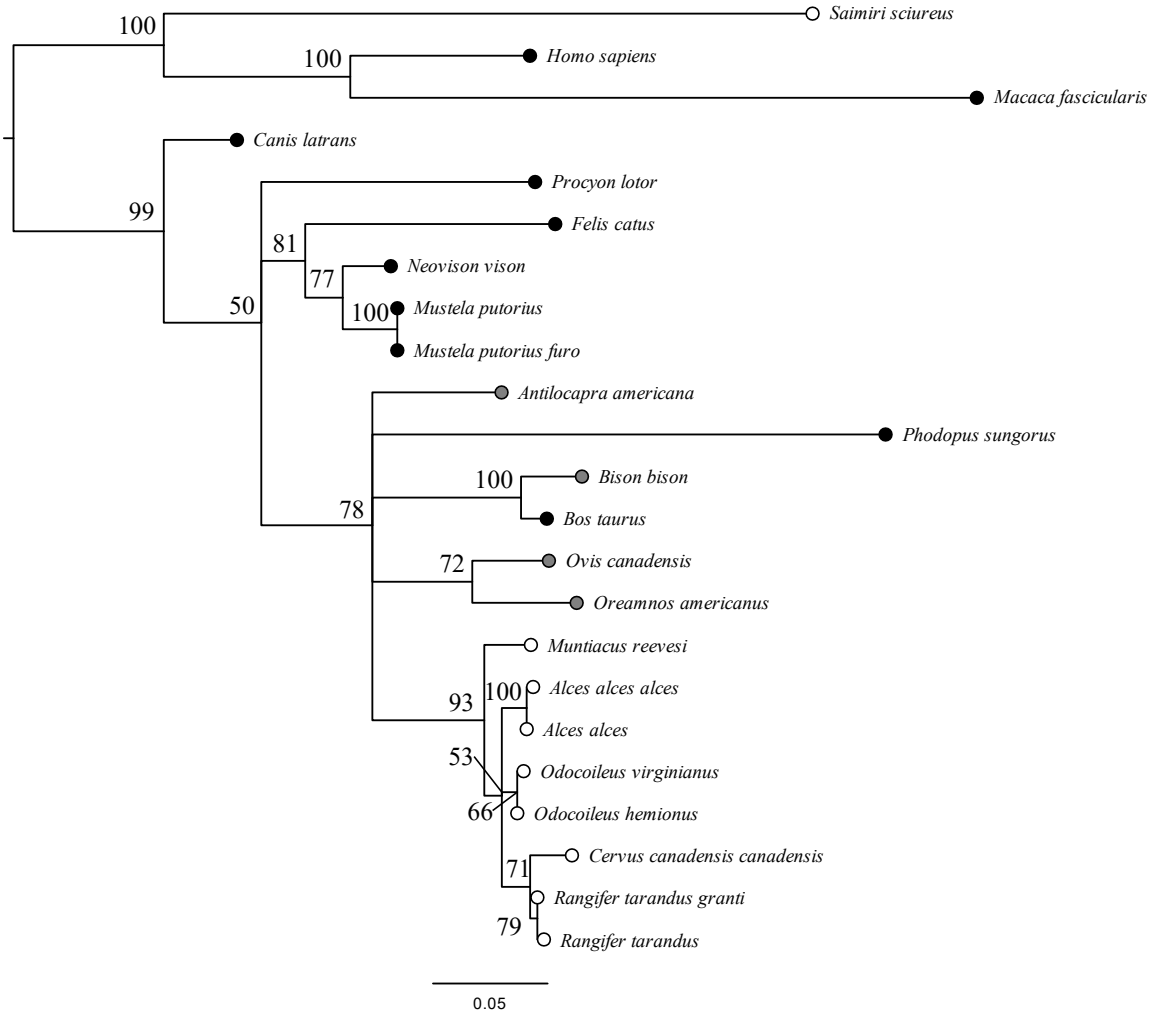


Figure S1. Maximum likelihood phylogram of cytochrome b used in ancestral and unknown state predictions. Branches with less than 50% bootstrap support were collapsed. Susceptible species indicated with white circles at branch tips, resistant species with black circles, and unknown with grey.

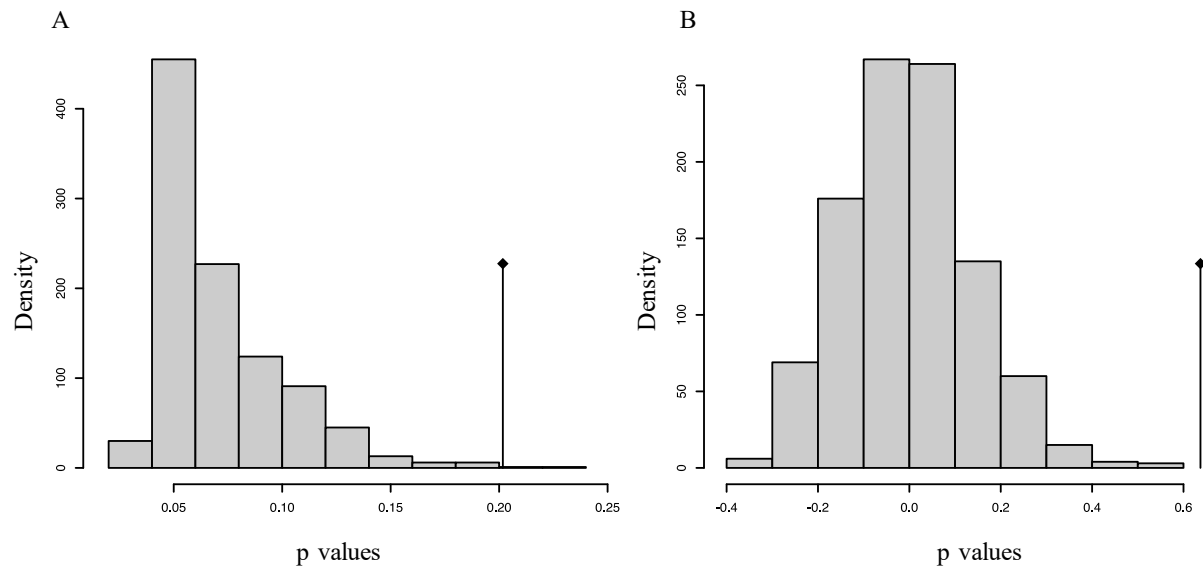


Figure S2. Susceptibility to CWD and phylogenetic signal are correlated with (A; $p = 0.003$) and without branch lengths (B; $p = 0.001$) as a factor. Significance of correlation tested using Moran's I with relationships among taxa inferred from the 19 species cytochrome b phylogeny (Fig. 2A) that does not have any missing infection data.

Additional File 1 - scripts

Model testing:

```
phymml -i infile.phy -d aa -m MTMAM -f m -v e -a e -c 4 -o tlr  
raxmlHPC-SSE3 -s infile.phy -m PROTGAMMAIMTMAM -n EXEC_NAME -p PARSIMONY_SEED  
raxml-ng --msa infile.phy --model MTMAM+I+G4  
paup -s infile.phy  
iqtree -s infile.phy -m MTMAM+I+G4
```

Running raxml:

```
raxmlHPC-HYBRID -T 4 -s infile -N autoMRE -n result -k -f a -p 12345 -x 12345 -m PROTCATMTMAMF
```

Adding BS values to raxml best tree:

```
raxmlHPC-AVX -f b -t RAxML_bestTree.result -z RAxML_bootstrap.result -m PROTCATMTMAMF -n BStree
```

Phylogenetic correlation

```
setwd("~/Documents/sidePieces/CWD/prnpsequencedata")  
library(adephylo)  
library(ape)  
library(phylobase)  
prnpTre <- read.tree("RAxML_bipartitions.BStree")  
plot(prnpTre)  
suscpetMatr <- read.table("SusceptMatr.txt", header = T, sep = "\t", as.is = 1)  
suscpetMatr <- data.frame(suscpetMatr, row.names = 1)  
prnpTre$node.label <- c()  
prnpData <- phylo4d(prnpTre, suscpetMatr)  
table.phylo4d(prnpData)  
prnp.abTest <- abouheif.moran(prnpData)  
prnp.abTest  
plot(prnp.abTest)  
prnp.prox <- vcv.phylo(prnpTre)  
prnp.abTest2 <- abouheif.moran(prnpData, W=prnp.prox)  
prnp.abTest2
```