**Source Code**

The following OPENBUGS code was used to fit the best fit functional relationships shown in Figure 2.

model{

##the relationship between bioassay mortality with and without PBO for different mosquito species (Figure 2B)

for(mrs in 1:n\_assays){ my\_assay\_rand[mrs]~dnorm(0,tauA)} ##Random effects

for(v in 1:n\_points) {c\_dead[v]~dbin(hp[v],c\_n[v])

pbo\_dead[v]~dbin(gp[v],pbo\_n[v])

my\_funG[v]<-k[1]+(k[2]\*(hp[v]-0.5))/(1+(hp[v]-0.5)\*k[3])

my\_funF[v]<-k[4]+(k[5]\*(hp[v]-0.5))

my\_fun[v]<-step(-abs(species[v]-2))\*my\_funF[v]+step(-abs(species[v]-1))\*my\_funG[v]

logit(mf[v])<-my\_fun[v]+my\_assay\_rand[assays[v]]

gp[v]<-max(0,min(mf[v],1))

hp[v]~dunif(0,1)}

##the relationship between assay mortality and hut trial mortality (Figure 2A)

for(mr in 1:n\_study){my\_rand[mr]~dnorm(0,tau)} ##Random effects

for (a in 1:n\_convert) {assay\_dead[a]~dbin(ap[a],assay\_N[a])

hut\_dead[a]~dbin(bp[a],hut\_N[a])

af[a]<-k[6]+k[7]\*(ap[a]-0.5)+my\_rand[assay\_study[a]]

logit(bp[a])<-af[a]

ap[a]~dunif(0,1)}

tauA<-k[8] tau<-k[9]

##Priors

k[1] ~dnorm(0,0) k[2] ~dnorm(0,0) k[3]~dnorm(0,0) k[4]~dnorm(0,0) k[5]~dnorm(0,0) k[6]~dnorm(0,0) k[7]~dnorm(0,0) k[8]~dnorm(0,0) k[9]~dnorm(0,0)}

The following OPENBUGS code was used to fit the best fit functional relationships shown in Figure 3.

model{

for (s in 1:n\_sites) {mean\_caught\_untreated[s]~dnorm(my\_caught,tau\_site)

site\_ind\_s[s]~dnorm(0,tau\_site\_s) } ##Random effects

## Relationship between hut trial mortality and deterrence (Figure 3A)

for (v in 1:n\_points) {mean\_caught[v]<-is\_treat[v]\*mean\_caught\_untreated[my\_site\_u[v]]\*(1-my\_det[v])+(1-is\_treat[v])\*mean\_caught\_untreated[my\_site\_u[v]]

my\_det[v]<-k[4]+k[5]\*(hp[v]-0.5)+k[6]\*pow((hp[v]-0.5),2)

caught\_u[v]~dnorm(mean\_caught[v],tau\_caught)

prop\_hp[v]<-dead\_u[v]/caught\_u[v]

dead\_u[v]~dbin(hp[v],caught\_u[v])

hp[v]~dunif(0,1)}

## Relationship between hut trial mortality and feeding success (Figure 3C)

for (x in 1:26) {my\_function[x]<-k[7]\*(exp(k[8]\*(1-hp[x]))-1)+site\_ind\_s[my\_site\_u[x]]

my\_all[x]<-min(1,max(0,my\_function[x]))

suc\_u[x]~dbin(my\_all[x],caught\_u[x])

prop\_u[x]<-suc\_u[x]/caught\_u[x]}

## Relationship between number of washes and LLIN halflife

for (w in 1:n\_points2) {dead\_w[w]~dbin(decay\_mort\_all[w],caught\_w[w])

decay\_mort\_tog[w]<-hp[n\_omit[w]]

decay\_mort\_all[w]<-min(1,max(0,decay\_mort\_tog[w]\*decay\_mort[w]))

logit(decayM[w])<-k[9]+(hp[n\_omit[w]])\*k[10]

decay\_mort[w]<-exp(-washes[w]\*decayM[w])}

tau\_site<-pow(k[1],-1) tau\_caught<-pow(k[2],-1) my\_caught<-k[3] tau\_site\_s<-pow(k[11],-1)

##Priors

k[1] ~dgamma(0.0000001,0.0000001) k[2] ~dgamma(0.0000001,0.0000001) k[3]~dgamma(0.0000001,0.0000001) k[4]~dnorm(0,0) k[5]~dnorm(0,0) k[6]~dnorm(0,0) k[7]~dgamma(0.0000001,0.0000001) k[8]~dgamma(0.0000001,0.0000001) k[9]~dnorm(0,0) k[10]~dnorm(0,0) k[11]~dgamma(0.0000001,0.0000001)}