Title: Competition between strains of *Borrelia afzelii* inside the rodent host and the tick vector

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R Code

Transmission

Create table

cat1=data.frame(all.cor[,c(1:9, 13,19,25)])

y.call\_foc=with(cat1, ifelse(experiment==1, as.character(Call\_A3), as.character(Call\_A10)))

cat2=data.frame(cat1, "call\_foc"=y.call\_foc)

cat2$treat=as.character(cat2$treat)

cat2$treat=ifelse(cat2$treat=="single", 1, 2)

cat2$treat=factor(cat2$treat, labels=c("single", "double"))

cat2$experiment=as.factor(cat2$experiment)

cat3 <- cat2[!cat2$mouse.id %in% c("S17", "S20", "S25", "S29"), ]

result

library(lme4)

cat3$treat=ifelse(cat3$treat=="single", 1, 2)

cat3$treat=factor(cat3$treat, labels=c("single", "double"))

y.model20=glmer(call\_foc~experiment+treat+experiment\*treat+(1|mouse.id),data=cat3, family=binomial)

y.model21=glmer(call\_foc~experiment+treat+(1|mouse.id), data=cat3, family=binomial)

y.model22=glmer(call\_foc~experiment+(1|mouse.id), data=cat3, family=binomial)

y.model23=glmer(call\_foc~treat+(1|mouse.id), data=cat3, family=binomial)

summary(y.model20)

anova(y.model21,y.model20)

anova(y.model21,y.model22)

anova(y.model21,y.model23)

y.model30=glmer(call\_foc~treat+(1|mouse.id), data=cat3, subset=c(experiment=="1"), family=binomial)

y.model31=glmer(call\_foc~1+(1|mouse.id), data=cat3, subset=c(experiment=="1"), family=binomial)

anova(y.model31,y.model30)

summary(y.model30)

y.model32=glmer(call\_foc~treat+(1|mouse.id), data=cat3, subset=c(experiment=="2"), family=binomial)

y.model33=glmer(call\_foc~1+(1|mouse.id), data=cat3, subset=c(experiment=="2"), family=binomial)

anova(y.model33,y.model32)

summary(y.model33)

summary(y.model32)

Spirochete load

Create table

#### spiro.load : create predicted spiro.load from the ospC~FLAG ####

single.inf=read.table("single.inf.csv", header=T, sep=";")

model01=lm(log10.spiro\_A3~log10.spiro\_FLAG, data=single.inf)

model01b=lm(log10.spiro\_FLAG~log10.spiro\_A3, data=single.inf)

model02=lm(single.inf$log10.spiro\_A10~single.inf$log10.spiro\_FLAG)

model02b=lm(log10.spiro\_FLAG~log10.spiro\_A10, data=single.inf)

A3.cor$pred.lm\_A3=10^predict.lm(object=model01b, newdata=A3.cor)

A3.cor$pred.lm\_A10=10^predict.lm(object=model02b, newdata=A3.cor)

A3.cor$pred.lm\_A3=ifelse(is.na(A3.cor$pred.lm\_A3)==TRUE, 0, A3.cor$pred.lm\_A3)

A3.cor$pred.lm\_A10=ifelse(is.na(A3.cor$pred.lm\_A10)==TRUE, 0, A3.cor$pred.lm\_A10)

A3.cor$spiro.load\_A3.1=ifelse(is.na(A3.cor$spiro.load\_A3)==TRUE, 0, A3.cor$spiro.load\_A3)

A3.cor$spiro.load\_A10.1=ifelse(is.na(A3.cor$spiro.load\_A10)==TRUE, 0, A3.cor$spiro.load\_A10)

bat1=(A3.cor$pred.lm\_A3)/(A3.cor$pred.lm\_A3 + A3.cor$pred.lm\_A10)

bat3=(A3.cor$pred.lm\_A10)/(A3.cor$pred.lm\_A10 + A3.cor$pred.lm\_A3)

A3.cor$cor2\_A3=bat1\*A3.cor$spiro.load\_FLAG

A3.cor$cor2\_A10=bat3\*A3.cor$spiro.load\_FLAG

A3.cor$cor2\_A3[A3.cor$cor2\_A3==0] <- NA

A3.cor$cor2\_A10[A3.cor$cor2\_A10==0] <- NA

A3.cor$log10.cor2\_A3=log10(A3.cor$cor2\_A3)

A3.cor$log10.cor2\_A10=log10(A3.cor$cor2\_A10)

A10.cor$pred.lm\_A3=10^predict.lm(object=model01b, newdata=A10.cor)

A10.cor$pred.lm\_A10=10^predict.lm(object=model02b, newdata=A10.cor)

A10.cor$pred.lm\_A3=ifelse(is.na(A10.cor$pred.lm\_A3)==TRUE, 0, A10.cor$pred.lm\_A3)

A10.cor$pred.lm\_A10=ifelse(is.na(A10.cor$pred.lm\_A10)==TRUE, 0, A10.cor$pred.lm\_A10)

A10.cor$spiro.load\_A3.1=ifelse(is.na(A10.cor$spiro.load\_A3)==TRUE, 0, A10.cor$spiro.load\_A3)

A10.cor$spiro.load\_A10.1=ifelse(is.na(A10.cor$spiro.load\_A10)==TRUE, 0, A10.cor$spiro.load\_A10)

bat.1=(A10.cor$pred.lm\_A3)/(A10.cor$pred.lm\_A3 + A10.cor$pred.lm\_A10)

bat.3=(A10.cor$pred.lm\_A10)/(A10.cor$pred.lm\_A10 + A10.cor$pred.lm\_A3)

A10.cor$cor2\_A3=bat.1\*A10.cor$spiro.load\_FLAG

A10.cor$cor2\_A10=bat.3\*A10.cor$spiro.load\_FLAG

A10.cor$cor2\_A3[A10.cor$cor2\_A3==0] <- NA

A10.cor$cor2\_A10[A10.cor$cor2\_A10==0] <- NA

A10.cor$log10.cor2\_A3=log10(A10.cor$cor2\_A3)

A10.cor$log10.cor2\_A10=log10(A10.cor$cor2\_A10)

all.cor=rbind(A3.cor,A10.cor)

#### spiro.load : create table with focal strains ####

dog1=all.cor

z.log10.spiro\_foc=with(dog1, ifelse(experiment==1, log10.spiro\_A3, log10.spiro\_A10))

z.cor.log10\_foc=with(dog1, ifelse(experiment==1, cor.log10\_A3, cor.log10\_A10))

z.log10.cor2\_foc=with(dog1, ifelse(experiment==1, log10.cor2\_A3, log10.cor2\_A10))

dog2=data.frame(dog1[,c(1:9, 12)], "log10.spiro\_foc"=z.log10.spiro\_foc, "cor.log10\_foc"=z.cor.log10\_foc, "log10.cor2\_foc"=z.log10.cor2\_foc)

dog2$experiment=as.factor(dog2$experiment)

dog2$treat=as.character(dog2$treat)

dog2$treat=ifelse(dog2$treat=="single", 1, 2)

dog2$treat=factor(dog2$treat, labels=c("single", "double"))

#remove S17, S20, S25, S29, only infected with strain A3 #

dog3 <- dog2[!dog2$mouse.id %in% c("S17", "S20", "S25", "S29"), ]

Result

library(lme4)

# method 1 #

z.model31=lmer(log10.spiro\_foc~experiment\*treat+(1|mouse.id), data=dog3, REML=F)

z.model32=lmer(log10.spiro\_foc~experiment+treat+(1|mouse.id), data=dog3, REML=F)

z.model33=lmer(log10.spiro\_foc~experiment+(1|mouse.id), data=dog3, REML=F)

z.model34=lmer(log10.spiro\_foc~treat+(1|mouse.id), data=dog3, REML=F)

anova(z.model32, z.model31)

anova(z.model33, z.model32)

anova(z.model34, z.model32)

summary(z.model32)

summary(z.model31)

# method 2 #

z.model41=lmer(cor.log10\_foc~experiment\*treat+(1|mouse.id), data=dog3, REML=F)

z.model42=lmer(cor.log10\_foc~experiment+treat+(1|mouse.id), data=dog3, REML=F)

z.model43=lmer(cor.log10\_foc~experiment+(1|mouse.id), data=dog3, REML=F)

z.model44=lmer(cor.log10\_foc~treat+(1|mouse.id), data=dog3, REML=F)

anova(z.model42, z.model41)

anova(z.model43, z.model42)

anova(z.model44, z.model42)

summary(z.model41)

summary(z.model42)

# method 3 #

z.model51=lmer(log10.cor2\_foc~experiment\*treat+(1|mouse.id), data=dog3,REML=F)

z.model52=lmer(log10.cor2\_foc~experiment+treat+(1|mouse.id), data=dog3,REML=F)

z.model53=lmer(log10.cor2\_foc~experiment+(1|mouse.id), data=dog3,REML=F)

z.model54=lmer(log10.cor2\_foc~treat+(1|mouse.id), data=dog3,REML=F)

anova(z.model52, z.model51)

anova(z.model53, z.model52)

anova(z.model54, z.model52)

summary(z.model51)

summary(z.model52)