Title: Similar world-wide patterns in the sex pheromone signal and response in the oriental fruit moth, Grapholita molesta (Lepidoptera: Tortricidae)

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Supplementary file "suppl.R.codes". Contains the R codes for the statistical analyses for the paper

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```
library(lme4)
library(multcomp)
library(pgirmess)
library(nparcomp)
library(lattice)
library(reshape)
```

```
*****************************************************************************************
////////////////////////////////////////////////////////////////////////////////////////////////////////////////
*****************************************************************************************
1. FIELD TRAPPING EXPERIMENT
*****************************************************************************************
////////////////////////////////////////////////////////////////////////////////////////////////////////////////
*****************************************************************************************
```

```
##############################
# 1-Factor pop, trt, date and plot #
##############################

fields$pop <- factor(fields$pop)
fields$trt <- factor(fields$trt)
fields$date <- factor(fields$date)
fields$plot <- factor(fields$plot)

########################
# 2-Descriptive statistics  #
########################

#This produces a table with the mean and SEM of the captures per treatment and population, as shown in Table S1

fmean=by(fields[,5],list(fields$pop, fields$trt),mean)##mean for each population and concentration of E isomer
fn=by(fields[,5],list(fields$pop,fields$trt),length)##sample size(N) for number of plots and days
fsdv=by(fields[,5],list(fields$pop,fields$trt),sd)##standard deviation
fse=fsdv/sqrt(fn-1)##standard error
round(data.frame(MEAN=cbind(fmean), SEM=cbind(fse)),digits=2)##grouping means and SEM for each population and treatment

########################################
##3-Add a value when there are no captures  ##
########################################

##In some treatments there were zero captures, this results in zero variability and erroneous analysis. We opted for adding a single #insect capture to those #treatments where there were zero captures. The trap, plot and date that received the “1” value was chosen at random

fields[fields$pop=="girona"& fields$trt=="hexane",]$male[3] <- 1
fields[fields$pop=="Lleida"& fields$trt=="hexane",]$male[15] <- 1
fields[fields$pop=="Korea"& fields$trt=="hexane",]$male[30] <- 1

#Check that the transformation has taken place
```

```
fmean=by(fields[,5],list(fields$pop, fields$trt),mean)##mean for each population and concentration of E isomer
fn=by(fields[,5],list(fields$pop,fields$trt),length)##sample size(N) for number of plots and days
fsdv=by(fields[,5],list(fields$pop,fields$trt),sd)##standard deviation
fse=fsdv/sqrt(fn-1)##standard error
data.frame(MEAN=cbind(fmean), SEM=cbind(fse))##grouping means and SEM for each population and treatment
#Now there should be no zero values

#################
# 4-Model fitting ##
#################

#Models from simplest to most complex were produced and compared statistically

model.0 <- lmer(male~(1|date/plot),data=fields,family=poisson)#Model with just random effects
model.trt <- lmer(male~0+trt+(1|date/plot),data=fields,family=poisson)  #model with random effects and trt as fixed effect
model.pop <- lmer(male~0+pop+(1|date/plot),data=fields,family=poisson)  #Model with random effects and pop a fixed
model.trt.pop <- lmer(male~0+trt+pop+(1|date/plot),data=fields,family=poisson)#Model with all componenents but no interaction
model.trt.int.pop <- lmer(male~0+trt*pop+(1|date/plot),data=fields,family=poisson)  #Complete model with interaction

#model comparison
anova(model.0,model.trt)
anova(model.0,model.pop)
anova(model.trt,model.trt.pop)
anova(model.trt.pop,model.trt.int.pop)

##This comparison shows that the most complex model explains better the variability of the data. Variability among dates is very large and this is why it needs to be included in the model as a random effect. Plot is also included as a random effect. Population and treatment are included as fixed effects.

##################################
##5 - Overdiperssion and Pearson  ####
##################################

#These parameter estimate the goodness of the models

model1 <- lmer(male~trt*pop+(1|date/plot),data=fields,family=poisson)
summary(model1)
(Pearson.model1 <- sum((model1@y-model1@mu)^2/model1@mu)) #pearson's residuals)
df.residual <- 1526-48-2
(p.value.Pearson.model1 <- 1-pchisq(Pearson.model1,df.residual))
(deviance.model1 <- deviance(model1))
(overdispersion.model1 <- deviance(model1)/(df.residual))


#########################################
# 6 - New variable trt.pop for easy stimation ##
#########################################

##Create a composite variable of pop and trt to facilitate the tast of creating matrices for multiple contrats
```

```
fields$trt.pop <- factor(paste(fields$pop,fields$trt,sep="-"))

#model using this new parameter
model1 <- lmer(male~0+trt.pop+(1|date/plot),data=fields,family=poisson)
summary(model1)
#The fit of this model is the same as lmer(male~trt*pop+(1|date/plot),data=fields,family=poisson)

################################
# 7 - Matix for multiple comparison##
################################

#We want to compare tratments within each population. For this we make a matrix for each population in which
the treatments to be compared pairwise are # specified with "1" and "-1".

##Matrix for each population

#chile
mxch <- matrix(c(
1,-1,0,0,0,0,rep(0,48-6),
1,0,-1,0,0,0,rep(0,48-6),
1,0,0,-1,0,0,rep(0,48-6),
1,0,0,0,-1,0,rep(0,48-6),
1,0,0,0,0,-1,rep(0,48-6),
0,1,-1,0,0,0,rep(0,48-6),
0,1,0,-1,0,0,rep(0,48-6),
0,1,0,0,-1,0,rep(0,48-6),
0,1,0,0,0,-1,rep(0,48-6),
0,0,1,-1,0,0,rep(0,48-6),
0,0,1,0,-1,0,rep(0,48-6),
0,0,1,0,0,-1,rep(0,48-6),
0,0,0,1,-1,0,rep(0,48-6),
0,0,0,1,0,-1,rep(0,48-6),
0,0,0,0,1,-1,rep(0,48-6)),
nrow=15,ncol=48,byrow=TRUE)

#girona
mxgir <- matrix(c(
rep(0,6),1,-1,0,0,0,0,rep(0,48-12),
rep(0,6),1,0,-1,0,0,0,rep(0,48-12),
rep(0,6),1,0,0,-1,0,0,rep(0,48-12),
rep(0,6),1,0,0,0,-1,0,rep(0,48-12),
rep(0,6),1,0,0,0,0,-1,rep(0,48-12),
rep(0,6),0,1,-1,0,0,0,rep(0,48-12),
rep(0,6),0,1,0,-1,0,0,rep(0,48-12),
rep(0,6),0,1,0,0,-1,0,rep(0,48-12),
rep(0,6),0,1,0,0,0,-1,rep(0,48-12),
rep(0,6),0,0,1,-1,0,0,rep(0,48-12),
rep(0,6),0,0,1,0,-1,0,rep(0,48-12),
rep(0,6),0,0,1,0,0,-1,rep(0,48-12),
rep(0,6),0,0,0,1,-1,0,rep(0,48-12),
rep(0,6),0,0,0,1,0,-1,rep(0,48-12),
rep(0,6),0,0,0,0,1,-1,rep(0,48-12)),
```

```
nrow=15,ncol=48,byrow=TRUE)

#italy
mxit <- matrix(c(
rep(0,12),1,-1,0,0,0,0,rep(0,48-18),
rep(0,12),1,0,-1,0,0,0,rep(0,48-18),
rep(0,12),1,0,0,-1,0,0,rep(0,48-18),
rep(0,12),1,0,0,0,-1,0,rep(0,48-18),
rep(0,12),1,0,0,0,0,-1,rep(0,48-18),
rep(0,12),0,1,-1,0,0,0,rep(0,48-18),
rep(0,12),0,1,0,-1,0,0,rep(0,48-18),
rep(0,12),0,1,0,0,-1,0,rep(0,48-18),
rep(0,12),0,1,0,0,0,-1,rep(0,48-18),
rep(0,12),0,0,1,-1,0,0,rep(0,48-18),
rep(0,12),0,0,1,0,-1,0,rep(0,48-18),
rep(0,12),0,0,1,0,0,-1,rep(0,48-18),
rep(0,12),0,0,0,1,-1,0,rep(0,48-18),
rep(0,12),0,0,0,1,0,-1,rep(0,48-18),
rep(0,12),0,0,0,0,1,-1,rep(0,48-18)),
nrow=15,ncol=48,byrow=TRUE)

#korea
mxkor <- matrix(c(
rep(0,18),1,-1,0,0,0,0,rep(0,48-24),
rep(0,18),1,0,-1,0,0,0,rep(0,48-24),
rep(0,18),1,0,0,-1,0,0,rep(0,48-24),
rep(0,18),1,0,0,0,-1,0,rep(0,48-24),
rep(0,18),1,0,0,0,0,-1,rep(0,48-24),
rep(0,18),0,1,-1,0,0,0,rep(0,48-24),
rep(0,18),0,1,0,-1,0,0,rep(0,48-24),
rep(0,18),0,1,0,0,-1,0,rep(0,48-24),
rep(0,18),0,1,0,0,0,-1,rep(0,48-24),
rep(0,18),0,0,1,-1,0,0,rep(0,48-24),
rep(0,18),0,0,1,0,-1,0,rep(0,48-24),
rep(0,18),0,0,1,0,0,-1,rep(0,48-24),
rep(0,18),0,0,0,1,-1,0,rep(0,48-24),
rep(0,18),0,0,0,1,0,-1,rep(0,48-24),
rep(0,18),0,0,0,0,1,-1,rep(0,48-24)),
nrow=15,ncol=48,byrow=TRUE)

#lleida
mxlle <- matrix(c(
rep(0,24),1,-1,0,0,0,0,rep(0,48-30),
rep(0,24),1,0,-1,0,0,0,rep(0,48-30),
rep(0,24),1,0,0,-1,0,0,rep(0,48-30),
rep(0,24),1,0,0,0,-1,0,rep(0,48-30),
rep(0,24),1,0,0,0,0,-1,rep(0,48-30),
rep(0,24),0,1,-1,0,0,0,rep(0,48-30),
rep(0,24),0,1,0,-1,0,0,rep(0,48-30),
rep(0,24),0,1,0,0,-1,0,rep(0,48-30),
rep(0,24),0,1,0,0,0,-1,rep(0,48-30),
rep(0,24),0,0,1,-1,0,0,rep(0,48-30),
rep(0,24),0,0,1,0,-1,0,rep(0,48-30),
```

```
rep(0,24),0,0,1,0,0,-1,rep(0,48-30),
rep(0,24),0,0,0,1,-1,0,rep(0,48-30),
rep(0,24),0,0,0,1,0,-1,rep(0,48-30),
rep(0,24),0,0,0,0,1,-1,rep(0,48-30)),
nrow=15,ncol=48,byrow=TRUE)

##new zealand
mxnz <- matrix(c(
rep(0,30),1,-1,0,0,0,0,rep(0,48-36),
rep(0,30),1,0,-1,0,0,0,rep(0,48-36),
rep(0,30),1,0,0,-1,0,0,rep(0,48-36),
rep(0,30),1,0,0,0,-1,0,rep(0,48-36),
rep(0,30),1,0,0,0,0,-1,rep(0,48-36),
rep(0,30),0,1,-1,0,0,0,rep(0,48-36),
rep(0,30),0,1,0,-1,0,0,rep(0,48-36),
rep(0,30),0,1,0,0,-1,0,rep(0,48-36),
rep(0,30),0,1,0,0,0,-1,rep(0,48-36),
rep(0,30),0,0,1,-1,0,0,rep(0,48-36),
rep(0,30),0,0,1,0,-1,0,rep(0,48-36),
rep(0,30),0,0,1,0,0,-1,rep(0,48-36),
rep(0,30),0,0,0,1,-1,0,rep(0,48-36),
rep(0,30),0,0,0,1,0,-1,rep(0,48-36),
rep(0,30),0,0,0,0,1,-1,rep(0,48-36)),
nrow=15,ncol=48,byrow=TRUE)

##usa
mxusa <- matrix(c(
rep(0,36),1,-1,0,0,0,0,rep(0,48-42),
rep(0,36),1,0,-1,0,0,0,rep(0,48-42),
rep(0,36),1,0,0,-1,0,0,rep(0,48-42),
rep(0,36),1,0,0,0,-1,0,rep(0,48-42),
rep(0,36),1,0,0,0,0,-1,rep(0,48-42),
rep(0,36),0,1,-1,0,0,0,rep(0,48-42),
rep(0,36),0,1,0,-1,0,0,rep(0,48-42),
rep(0,36),0,1,0,0,-1,0,rep(0,48-42),
rep(0,36),0,1,0,0,0,-1,rep(0,48-42),
rep(0,36),0,0,1,-1,0,0,rep(0,48-42),
rep(0,36),0,0,1,0,-1,0,rep(0,48-42),
rep(0,36),0,0,1,0,0,-1,rep(0,48-42),
rep(0,36),0,0,0,1,-1,0,rep(0,48-42),
rep(0,36),0,0,0,1,0,-1,rep(0,48-42),
rep(0,36),0,0,0,0,1,-1,rep(0,48-42)),
nrow=15,ncol=48,byrow=TRUE)

##turkey
mxtur <- matrix(c(
rep(0,42),1,-1,0,0,0,0,rep(0,48-48),
rep(0,42),1,0,-1,0,0,0,rep(0,48-48),
rep(0,42),1,0,0,-1,0,0,rep(0,48-48),
rep(0,42),1,0,0,0,-1,0,rep(0,48-48),
rep(0,42),1,0,0,0,0,-1,rep(0,48-48),
rep(0,42),0,1,-1,0,0,0,rep(0,48-48),
rep(0,42),0,1,0,-1,0,0,rep(0,48-48),
```

```r
rep(0,42),0,1,0,0,-1,0,rep(0,48-48),
rep(0,42),0,1,0,0,0,-1,rep(0,48-48),
rep(0,42),0,0,1,-1,0,0,rep(0,48-48),
rep(0,42),0,0,1,0,-1,0,rep(0,48-48),
rep(0,42),0,0,1,0,0,-1,rep(0,48-48),
rep(0,42),0,0,0,1,-1,0,rep(0,48-48),
rep(0,42),0,0,0,1,0,-1,rep(0,48-48),
rep(0,42),0,0,0,0,1,-1,rep(0,48-48)),
nrow=15,ncol=48,byrow=TRUE)

##This next is to name the contrasts of the matrices

h0=c("0 vs 10","0 vs 100","0 vs 30","0 vs 5","0 vs hexane","10 vs 100","10 vs 30","10 vs 5","10 vs hexane","100 vs 30","100 vs 5","100 vs hexane","30 vs 5","30 vs hexane", "5 vs hexane")

rownames(mxch)=paste(h0)
rownames(mxgir)= paste(h0)
rownames(mxit)= paste(h0)
rownames(mxkor)=paste(h0)
rownames(mxkor)= paste(h0)
rownames(mxlle)= paste(h0)
rownames(mxnz)= paste(h0)
rownames(mxusa)=paste(h0)
rownames(mxtur)=paste(h0)

########################
# 8 Multiple comparison  ##
########################

chile.mcp <- glht(model1,linfct=mxch)
girona.mcp <- glht(model1,linfct=mxgir)
italy.mcp <- glht(model1,linfct=mxit)
korea.mcp <- glht(model1,linfct=mxkor)
lleida.mcp <- glht(model1,linfct=mxlle)
nz.mcp <- glht(model1,linfct=mxnz)
usa.mcp <- glht(model1,linfct=mxusa)
turkey.mcp <- glht(model1,linfct=mxtur)

summary(chile.mcp)
summary(girona.mcp)
summary(italy.mcp)
summary(korea.mcp)
summary(lleida.mcp)
summary(nz.mcp)
summary(usa.mcp)
summary(turkey.mcp)
```

```
******************************************************************************************
/////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
******************************************************************************************
2. WIND TUNNEL EXPERIMENT WITH LIVE FEMALES
******************************************************************************************
/////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
******************************************************************************************
################################
##1. Descriptive statistics #########
################################

#This will produce the data shown in Table S4

n=xtabs(~male+female,tunnel)##sample size
tab1=table(tunnel$male,tunnel$female,tunnel$land)#number of individuals landing or not landing
tab2=as.data.frame(tab1)
tab3=rename(tab2,c(Var1="male",Var2="female",Var3="land"))
###load library “reshape”
posit=subset(tab3, land=="Y")
negat=subset(tab3,land=="N")
posit$percY=posit$Freq/(posit$Freq+negat$Freq)
posit

####################
# 2. Factor variables##
####################

tunnel$ndat=as.factor(tunnel$nday)
tunnel$male=as.factor(tunnel$male)
tunnel$female=as.factor(tunnel$female)


#####################
# 3. Model selection ###
#####################

#According to Zuur et al. 2009. Mixed Effects Models and Extensions in Ecology with R. Springer
#1. Overparameterised model
#2. Optimal structure for random effects using REML and either LRT or AIC
#3. Optimal structure for fixed effects using ML
#4. Refit final model with REML

land.glmm=lmer(land~male*female+(1|nday),tunnel,family=binomial,REML=TRUE)

#overparameterised model
land.glm=glm(land~male*female,tunnel,family=binomial) #This is a glm to test for variance due to day (recoded)
#We are testing at the boundary of the parameter (H0: variance=0),
#therefore the appropriate distribution under H0 is 1/2 spike on 0 + 1/2 chi2 with 1 df
#pval=p(LRT>0.5Chi^2 with 1df)=p(LRT>Chi^2 with 1df)/2
pchisq(deviance(land.glm)-deviance(land.glmm),1,lower.tail=FALSE)/2 #Random effect nday required
```

```
land1.glmm=lmer(land~male+female+(1|nday),tunnel,family=binomial,REML=TRUE) #Dropping trt x pop
interaction
anova(land.glmm,land1.glmm) #Interaction term is NOT important, stop model selection

land.best=lmer(land~male+female+(1|nday),tunnel,family=binomial,REML=TRUE) #Best model fitted with REML
summary(land.best) #Pring output

#Model appropriateness statistics
summary(land.best)@AICtab

#Function to calculate overdispersion obtained from http://glmm.wikidot.com/faq
overdisp_fun <- function(model) {
  ## number of variance parameters in
  ##   an n-by-n variance-covariance matrix
  vpars <- function(m) {
    nrow(m)*(nrow(m)+1)/2
  }
  model.df <- sum(sapply(VarCorr(model),vpars))+length(fixef(model))
  rdf <- nrow(model.frame(model))-model.df
  rp <- residuals(model,type="pearson")
  Pearson.chisq <- sum(rp^2)
  prat <- Pearson.chisq/rdf
  pval <- pchisq(Pearson.chisq, df=rdf, lower.tail=FALSE)
  c(chisq=Pearson.chisq,ratio=prat,rdf=rdf,p=pval)
}
overdisp_fun(land.best)

#####################
# 4. Multiple contrats  ##
#####################

# Create a composed variable (male.female) that will help extract the fixed effects necessary for the contrasts

tunnel$male.female <- factor(paste(tunnel$male,tunnel$female,sep="-"))
model1 <- lmer(land~0+male.female+(1|nday),data=tunnel,family=binomial,REML=TRUE)
summary(model1)

##Make matices to compare among 4 male pops within each female pop and among 4 female pops within each
male pop, and for each of these compare all pops #with the same-pop pair (i.e.: for  French females compare
Italian males with French males, lleida males with French males and USA males with French males, etc.).

#France males matrix
malefr = matrix(c(
1,-1,0,0,rep(0,12),
1,0,-1,0,rep(0,12),
1,0,0,-1,rep(0,12)),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs it","fr vs llei","fr vs usa")
rownames(malefr)=paste(h0)
mcp.malefr=glht(model1,linfct=malefr)
summary(mcp.malefr)

#Italy2 males matrix
```

```
maleit = matrix(c(
0,0,0,0,-1,1,0,0,0,rep(0,7),
0,0,0,0,0,1,0,-1,0,rep(0,7),
0,0,0,0,0,1,0,0,-1,rep(0,7)),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs it","it vs llei","it vs usa")
rownames(maleit)=paste(h0)
mcp.maleit=glht(model1,linfct=maleit)
summary(mcp.maleit)

##Spain2 males matrix
malellei = matrix(c(
rep(0,8),-1,0,1,0,rep(0,4),
rep(0,8),0,-1,1,0,rep(0,4),
rep(0,8),0,0,1,-1,rep(0,4)),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs llei","it vs llei","llei vs usa")
rownames(malellei)=paste(h0)
mcp.malellei=glht(model1,linfct=malellei)
summary(mcp.malellei)

#USA2 males
maleusa = matrix(c(
rep(0,12),-1,0,0,-1,
rep(0,12),0,-1,0,1,
rep(0,12),0,0,-1,1),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs usa","it vs usa","llei vs usa")
rownames(maleusa)=paste(h0)
mcp.maleusa=glht(model1,linfct=maleusa)
summary(mcp.maleusa)

#France females
femafr = matrix(c(
1,rep(0,3),-1,rep(0,11),
1,rep(0,7),-1,rep(0,7),
1,rep(0,11),-1,0,0,0),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs it","fr vs llei","fr vs usa")
rownames(femafr)=paste(h0)
mcp.femafr=glht(model1,linfct=femafr)
summary(mcp.femafr)

#Italy2 females
femait = matrix(c(
0,-1,0,0,0,1,rep(0,10),
0,0,0,0,0,1,0,0,0,-1,rep(0,6),
0,0,0,0,0,1,rep(0,7),-1,0,0),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs it","it vs llei","it vs usa")
rownames(femait)=paste(h0)
mcp.femait=glht(model1,linfct=femait)
summary(mcp.femait)
```

```
#Spain2 females
femallei = matrix(c(
0,0,-1,rep(0,7),1,rep(0,5),
rep(0,6),-1,0,0,0,1,rep(0,5),
rep(0,10),1,0,0,0,1,0),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs llei","it vs llei","llei vs usa")
rownames(femallei)=paste(h0)
mcp.femallei=glht(model1,linfct=femallei)
summary(mcp.femallei)

#USA3 females
femausa = matrix(c(
0,0,0,-1,rep(0,11),1,
rep(0,7),-1,rep(0,7),1,
rep(0,11),-1,0,0,0,1),
nrow=3,ncol=16,byrow=TRUE)
h0=c("fr vs usa","it vs usa","usa vs usa")
rownames(femausa)=paste(h0)
mcp.femausa=glht(model1,linfct=femausa)
summary(mcp.femausa)


################################
#5. Expected landing probabilities#
################################

#This is a backtransformation of the estimated parameters.
#These data are used in Table 3 in the main text

land.log=fixef(model1)
land.conv=exp(land.log)
land.prob=land.conv/(1+land.conv)
land.prob

#Surrogate standard errors=sqrt(pq/n)
n=xtabs(~male+female,tunnel)
sqrt(land.prob*(1-land.prob)/n)
```

```
****************************************************************************************************
/////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
****************************************************************************************************
3. WIND TUNNEL EXPERIMENT WITH SYNTHETIC PHEROMONE
****************************************************************************************************
/////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
****************************************************************************************************

########################
# 1. Descriptive statistics ##
########################

##This will produce a table with the data shown in supplementary table S7

tab1=table(tunnel$pop,tunnel$trt,tunnel$land)#number of individuals landing or not landing
tab2=as.data.frame(tab1)
tab3=rename(tab2,c(Var1="pop",Var2="trt",Var3="land"))
posit=subset(tab3, land=="yes")
negat=subset(tab3,land=="no")
posit$percY=posit$Freq/(posit$Freq+negat$Freq)
posit

###################
# 2. Factor variables #
###################

tunnel$nday=as.factor(tunnel$nday)
tunnel$pop=as.factor(tunnel$pop)
tunnel$trt=as.factor(tunnel$trt)

###########################################################
# 3. Add one value (“y”) when no insects responded (when all = “n” ) #
###########################################################

tunnel[tunnel$pop=="USA"& tunnel$trt=="100",]$land[1] = "yes"

################################################
#4. Model selection  (as described for live females) ####
################################################

#Mixed Effects Models and Extensions in Ecology with R. Springer
#1. Overparameterised model
#2. Optimal structure for random effects using REML and either LRT or AIC
#3. Optimal structure for fixed effects using ML
#4. Refit final model with REML

land.glmm=lmer(land~trt*pop+(1|nday),tunnel,family=binomial,REML=TRUE) #overparameterised model
land.glm=glm(land~trt*pop,tunnel,family=binomial) #This is a glm to test for variance due to day (recoded)
#We are testing at the boundary of the parameter (H0: variance=0),
#therefore the appropriate distribution under H0 is 1/2 spike on 0 + 1/2 chi2 with 1 df
#pval=p(LRT>0.5Chi^2 with 1df)=p(LRT>Chi^2 with 1df)/2
pchisq(deviance(land.glm)-deviance(land.glmm),1,lower.tail=FALSE)/2 #Random effect nday required
```

```
land1.glmm=lmer(land~trt+pop+(1|nday),tunnel,family=binomial,REML=TRUE) #Dropping trt x pop interaction
anova(land.glmm,land1.glmm) #Interaction term is important, stop model selection

land.best=lmer(land~trt*pop+(1|nday),tunnel,family=binomial,REML=TRUE) #Best model fitted with REML
summary(land.best) #Pring output

#Model appropriateness statistics
summary(land.best)@AICtab

#Function to calculate overdispersion obtained from http://glmm.wikidot.com/faq
overdisp_fun <- function(model) {
  ## number of variance parameters in
  ##   an n-by-n variance-covariance matrix
  vpars <- function(m) {
    nrow(m)*(nrow(m)+1)/2
  }
  model.df <- sum(sapply(VarCorr(model),vpars))+length(fixef(model))
  rdf <- nrow(model.frame(model))-model.df
  rp <- residuals(model,type="pearson")
  Pearson.chisq <- sum(rp^2)
  prat <- Pearson.chisq/rdf
  pval <- pchisq(Pearson.chisq, df=rdf, lower.tail=FALSE)
  c(chisq=Pearson.chisq,ratio=prat,rdf=rdf,p=pval)
}
overdisp_fun(land.best)

#####################
# 4. Multiple contrats  ##
#####################

# Create a composed variable (trt.pop) that will help extract the fixed effects necessary for the contrasts

tunnel$trt.pop <- factor(paste(tunnel$pop,tunnel$trt,sep="-"))
model1 <- lmer(land~0+trt.pop+(1|nday),data=tunnel,family=binomial,REML=TRUE)
summary(model1)

# Matrices for multiple comparison

Cfrance = matrix(c(
1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
1,0,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,1,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
```

```
0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
nrow=21,ncol=28,byrow=TRUE)

Citaly=matrix(c(
0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,1,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,1,0,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,1,0,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,0,0),
nrow=21,ncol=28,byrow=TRUE)

Clleida=matrix(c(
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,-1,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,-1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,-1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0,0,
```

```
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,0,0),
nrow=21,ncol=28,byrow=TRUE)

Cusa = matrix(c(
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,-1,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,-1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,-1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,-1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,-1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1,0,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,-1,
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,-1),
nrow=21,ncol=28,byrow=TRUE)

#Names for the contratsts
h0= c("0 vs 10","0 vs 100","0 vs 20","0 vs 30","0 vs 6","0 vs 60","10 vs 100","10 vs 20","10 vs 30","10 vs 6","10 vs 60","100 vs 20","100 vs 30","100 vs 6","100 vs 60","20 vs 30","20 vs 6","20 vs 60","30 vs 6","30 vs 60","6 vs 60")
rownames(Cfrance) <-  paste(h0)
rownames(Citaly) <-  paste(h0)
rownames(Clleida) <-  paste(h0)
rownames(Cusa) <-  paste(h0)

#Contrasts using glht function within multcomp package
land.multcomp.lleida=glht(model1,linfct=Clleida)
land.multcomp.france=glht(model1,linfct=Cfrance)
land.multcomp.italy=glht(model1,linfct=Citaly)
land.multcomp.usa=glht(model1,linfct=Cusa)

#Summary of contrasts within population
summary(land.multcomp.lleida)
summary(land.multcomp.france)
summary(land.multcomp.italy)
summary(land.multcomp.usa)

#######################
#5. Landing probabilities #
#######################

#This is a backtransformation of the estimated parameters.
```

```
#These data are used in Table 4 in the main text

treats=levels(tunnel$trt) #Treatments
pops=levels(tunnel$pop) #Populations

land.best=lmer(land~0+trt*pop+(1|nday),tunnel,family=binomial,REML=TRUE)
logOR=fixef(land.best) #Logarithm of Odds Ratios

logORpop.trt=matrix(0,nrow=length(pops),ncol=length(treats),dimnames=list(pops,treats)) #Results matrix
logORpop.trt

logORpop.trt[1,]=logOR[1:7] #Effecs fro France
logORpop.trt[2,1]=logOR["trt0"]+logOR["popitaly"] #Effects for italy trt=0
logORpop.trt[3,1]=logOR["trt0"]+logOR["poplleida"]
logORpop.trt[4,1]=logOR["trt0"]+logOR["popUSA"]

logORpop.trt[2,2]=logOR["trt5"]+logOR["popitaly"]+logOR["trt5:popitaly"] #effects for Italy trt=5
logORpop.trt[3,2]=logOR["trt5"]+logOR["poplleida"]+logOR["trt5:poplleida"]
logORpop.trt[4,2]=logOR["trt5"]+logOR["popUSA"]+logOR["trt5:popUSA"]

logORpop.trt[2,3]=logOR["trt10"]+logOR["popitaly"]+logOR["trt10:popitaly"]
logORpop.trt[3,3]=logOR["trt10"]+logOR["poplleida"]+logOR["trt10:poplleida"]
logORpop.trt[4,3]=logOR["trt10"]+logOR["popUSA"]+logOR["trt10:popUSA"]

logORpop.trt[2,4]=logOR["trt20"]+logOR["popitaly"]+logOR["trt20:popitaly"]
logORpop.trt[3,4]=logOR["trt20"]+logOR["poplleida"]+logOR["trt20:poplleida"]
logORpop.trt[4,4]=logOR["trt20"]+logOR["popUSA"]+logOR["trt20:popUSA"]

logORpop.trt[2,5]=logOR["trt30"]+logOR["popitaly"]+logOR["trt30:popitaly"]
logORpop.trt[3,5]=logOR["trt30"]+logOR["poplleida"]+logOR["trt30:poplleida"]
logORpop.trt[4,5]=logOR["trt30"]+logOR["popUSA"]+logOR["trt30:popUSA"]

logORpop.trt[2,6]=logOR["trt60"]+logOR["popitaly"]+logOR["trt60:popitaly"]
logORpop.trt[3,6]=logOR["trt60"]+logOR["poplleida"]+logOR["trt60:poplleida"]
logORpop.trt[4,6]=logOR["trt60"]+logOR["popUSA"]+logOR["trt60:popUSA"]

logORpop.trt[2,7]=logOR["trt100"]+logOR["popitaly"]+logOR["trt100:popitaly"]
logORpop.trt[3,7]=logOR["trt100"]+logOR["poplleida"]+logOR["trt100:poplleida"]
logORpop.trt[4,7]=logOR["trt100"]+logOR["popUSA"]+logOR["trt100:popUSA"]

ORpop.trt=exp(logORpop.trt) #Odds Ratios
Ppop.trt=round(ORpop.trt/(1+ORpop.trt),digits=3) #probabilities
print(Ppop.trt)###make a table

#Surrogate standard errors=sqrt(pq/n)
n=xtabs(~pop+trt,tunnel)
sqrt(Ppop.trt*(1-Ppop.trt)/n)
```

```
********************************************************************************************************
////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
********************************************************************************************************
4. PHEROMONE GLAND ANALYSIS
********************************************************************************************************
////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////////
********************************************************************************************************

#######################
## Quantity of E8-12:Ac ##
#######################

m.ng.e=tapply(glands$ng.e,glands$pop,mean, na.rm=TRUE)
n.ng.e=tapply(glands$ng.e,glands$pop,function(x) sum(!is.na(x)))
sdev.ng.e=tapply(glands$ng.e,glands$pop,sd, na.rm=TRUE)
se.ng.e=sdev.ng.e/sqrt(n.ng.e-1)
data.frame(MEAN=cbind(m.ng.e),SEM=cbind(se.ng.e))

kruskal.test(glands$ng.e~glands$pop)
##not significant

#######################
## Quantity of E8-12:OH ##
#######################

m.ng.oh=tapply(glands$ng.oh,glands$pop,mean, na.rm=TRUE)
n.ng.oh=tapply(glands$ng.oh,glands$pop,function(x) sum(!is.na(x)))
sdev.ng.oh=tapply(glands$ng.oh,glands$pop,sd, na.rm=TRUE)
se.ng.oh=sdev.ng.oh/sqrt(n.ng.oh-1)
data.frame(MEAN=cbind(m.ng.oh),SEM=cbind(se.ng.oh))

kruskal.test(glands$ng.oh~glands$pop)
##significant
kruskalmc(glands$ng.oh~glands$pop)
#italy and USA are different

#######################
## Quantity of Z8-12:Ac ##
#######################

m.ng.z=tapply(glands$ng.z,glands$pop,mean, na.rm=TRUE)
n.ng.z=tapply(glands$ng.z,glands$pop,function(x) sum(!is.na(x)))
sdev.ng.z=tapply(glands$ng.z,glands$pop,sd, na.rm=TRUE)
se.ng.z=sdev.ng.z/sqrt(n.ng.z-1)
data.frame(MEAN=cbind(m.ng.z),SEM=cbind(se.ng.z))

kruskal.test(glands$ng.z~glands$pop)
##not significant


#######################
## Ratio of E8-12:Ac ##
#######################
```

```
m.ratio.e=tapply(glands$ratio.e,glands$pop,mean, na.rm=TRUE)
n.ratio.e=tapply(glands$ratio.e,glands$pop,function(x) sum(!is.na(x)))
sdev.ratio.e=tapply(glands$ratio.e,glands$pop,sd, na.rm=TRUE)
se.ratio.e=sdev.ratio.e/sqrt(n.ratio.e-1)
data.frame(MEAN=cbind(m.ratio.e),SEM=cbind(se.ratio.e))

kruskal.test(glands$ratio.e~glands$pop)

##significant

kruskalmc(glands$ratio.e~glands$pop)
#no differences?
wilcox.test(ratio.e[pop=="France"],ratio.e[pop=="Italy2"])#p=0.42
wilcox.test(ratio.e[pop=="France"],ratio.e[pop=="Spain2"])#p=0.26
wilcox.test(ratio.e[pop=="France"],ratio.e[pop=="USA"])#p=0.36
wilcox.test(ratio.e[pop=="Italy2"],ratio.e[pop=="Spain2"])#p=0.62
wilcox.test(ratio.e[pop=="Italy2"],ratio.e[pop=="USA"])#p=0.02066
wilcox.test(ratio.e[pop=="Spain2"],ratio.e[pop=="USA"])#p=0.01256

#boferroni correction: 0.05/5=0.01
##The overall test is significant but there are no pairwise differences


######################
## Ratio of Z8-12:OH ##
######################

m.ratio.oh=tapply(glands$ratio.oh,glands$pop,mean, na.rm=TRUE)
n.ratio.oh=tapply(glands$ratio.oh,glands$pop,function(x) sum(!is.na(x)))
sdev.ratio.oh=tapply(glands$ratio.oh,glands$pop,sd, na.rm=TRUE)
se.ratio.oh=sdev.ratio.oh/sqrt(n.ratio.oh-1)
data.frame(MEAN=cbind(m.ratio.oh),SEM=cbind(se.ratio.oh))

kruskal.test(glands$ratio.oh~glands$pop)
##significant

kruskalmc(glands$ratio.oh~glands$pop)
#france and italy are different from USA
```