

**Table S1.** Results of pairwise comparisons between apiaries with respect to propolis composition. Analyses were performed subsequent to a significant permutational ANOVA in 'RRPP' using the 'pairwise' function.

Comparison	Distance between Means	Z-Score	Pr > d
A:B	12.00	-0.03	0.502
<b>A:C</b>	<b>25.74</b>	<b>1.71</b>	<b>0.044</b>
<b>AD</b>	<b>26.43</b>	<b>1.86</b>	<b>0.031</b>
A:E	22.09	1.27	0.107
<b>B:C</b>	<b>27.91</b>	<b>2.10</b>	<b>0.016</b>
B:D	18.14	1.12	0.146
B:E	11.29	-0.18	0.557
<b>C:D</b>	<b>40.75</b>	<b>3.16</b>	<b>0.001</b>
<b>C:E</b>	<b>32.98</b>	<b>2.34</b>	<b>0.006</b>
D:E	14.70	0.54	0.301

The bolded text represents only those that were statistically significant.

### Script S1

#### Supplementary R script of analyses from this study

```
library(RRPP)
```

```
library(ape)
```

```
library(vegan)
```

```
##Sum abundance vs cropland
```

```
PropSum<-read.csv('PropSumAbundance.csv')
```

```
summary(lm(PropSum$Mean_peak_sum_abundance~PropSum$Cropland_coverage))
```

```
##GCMS comparisons among apiaries
```

```
PropGCMS<-read.csv('PropGCMS.csv')
```

```
apiary<-PropGCMS[,2]
```

```
compounds<-PropGCMS[,-(1:2)]
```

```
####Euclidean
```

```
pca.Euc<-prcomp(compounds)$x
```

```
summary(prcomp(compounds))
```

```
summary(lm.rrpp(pca.Euc~ apiary))
```

```
pair<-pairwise(lm.rrpp(pca.Euc~ apiary),groups=apiary)
```

```
summary(pair,test.type='dist')
```

```

####Jaccard

distJac<-vegdist(compounds,method='jaccard')

pcoa.Jac<-pcoa(distJac)$vectors

summary(lm.rrpp(pcoa.Jac~ apiary))


##MIC50

PropMIC50_bigmodel<-read.csv('PropMIC50_bigmodel.csv')

summary(aov(PropMIC50_bigmodel$MIC50~PropMIC50_bigmodel$pathoge
n*PropMIC50_bigmodel $apiary))

PropMIC50_bigmodel$pathogen<-
factor(PropMIC50_bigmodel$pathogen,levels=c('Serratia_marcescens','Klebsi
ella_pneumoniae','Lysinibacillus_sphaericus','Paenibacillus_larvae'))

TukeyHSD(aov(PropMIC50_bigmodel$MIC50~
PropMIC50_bigmodel$pathogen))


PropMIC50<-read.csv('PropMIC50.csv')cfa

PropMIC50_noF<-subset(PropMIC50, PropMIC50$apiary!='F')


summary(lm(PropMIC50_noF$Klebsiella_pneumoniae~ PropMIC50_noF
$apiary))

TukeyHSD(aov(PropMIC50_noF$Klebsiella_pneumoniae~ PropMIC50_noF
$apiary))

summary(lm(PropMIC50_noF$Serratia_marcescens~ PropMIC50_noF
$apiary))

TukeyHSD(aov(PropMIC50_noF$Serratia_marcescens~ PropMIC50_noF
$apiary))

```