

# *T. mopan* description - R codes

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February 7, 2018

## Libraries used

```
library(ape)
```

## CytB and ITS-2 alignments

```
cytb<-read.FASTA("Cyt_b__mopan.fst")
```

```
its2<-read.FASTA("its2_mopan_align.fst")
```

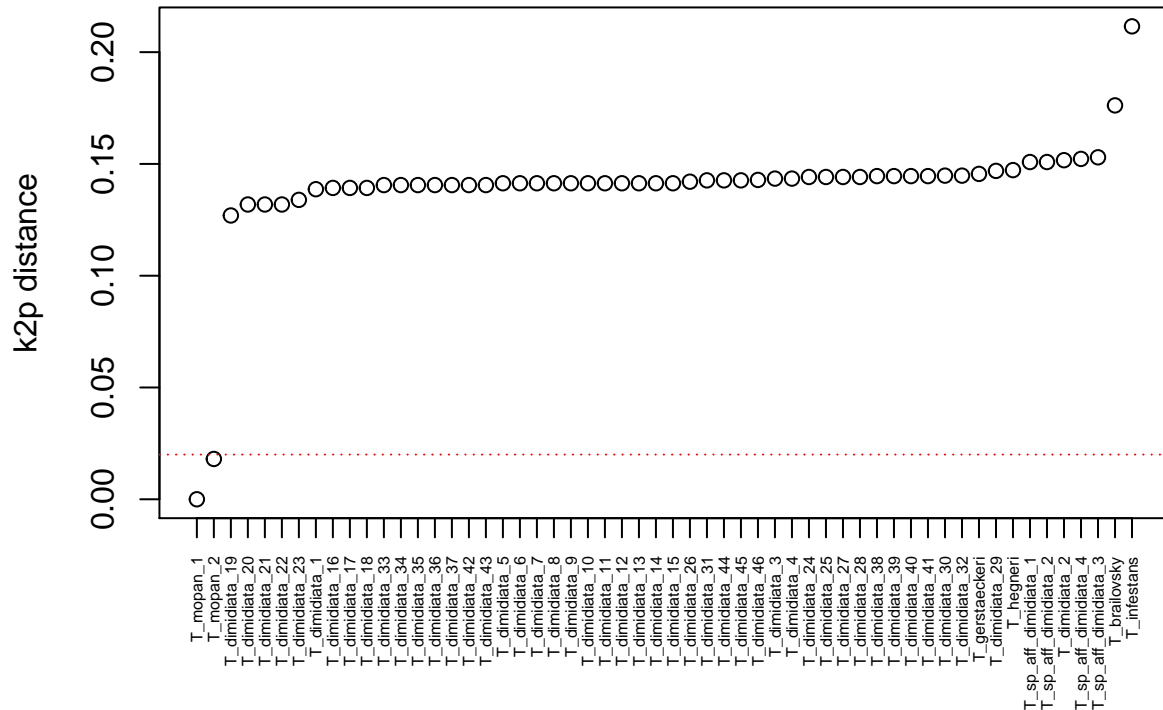
Calculating pairwise k2p distances. This model was used to make the distances comparable to previously published data.

```
dist_cytb <- dist.dna(cytb, model = "k80", as.matrix = TRUE, pairwise.deletion = T)
```

Ordering the distances from smallest to largest to plot and visualize it. Red dotted line corresponds to a distance of 2%.

```
T_mopan <- subset(dist_cytb, select = "T_mopan_1")
T_mopan_sorted <- as.matrix(T_mopan[order(T_mopan[, 1]), ])
plot(T_mopan_sorted, pch = 1, main = "K2p pairwise distances", xaxt = "n", xlab = "",
     ylab = "k2p distance")
axis(1, at = 1:nrow(T_mopan_sorted), labels = row.names(T_mopan_sorted), las = 2,
     cex.axis = 0.5)
abline(h = 0.02, col = "red", lty = 3)
```

## K2p pairwise distances

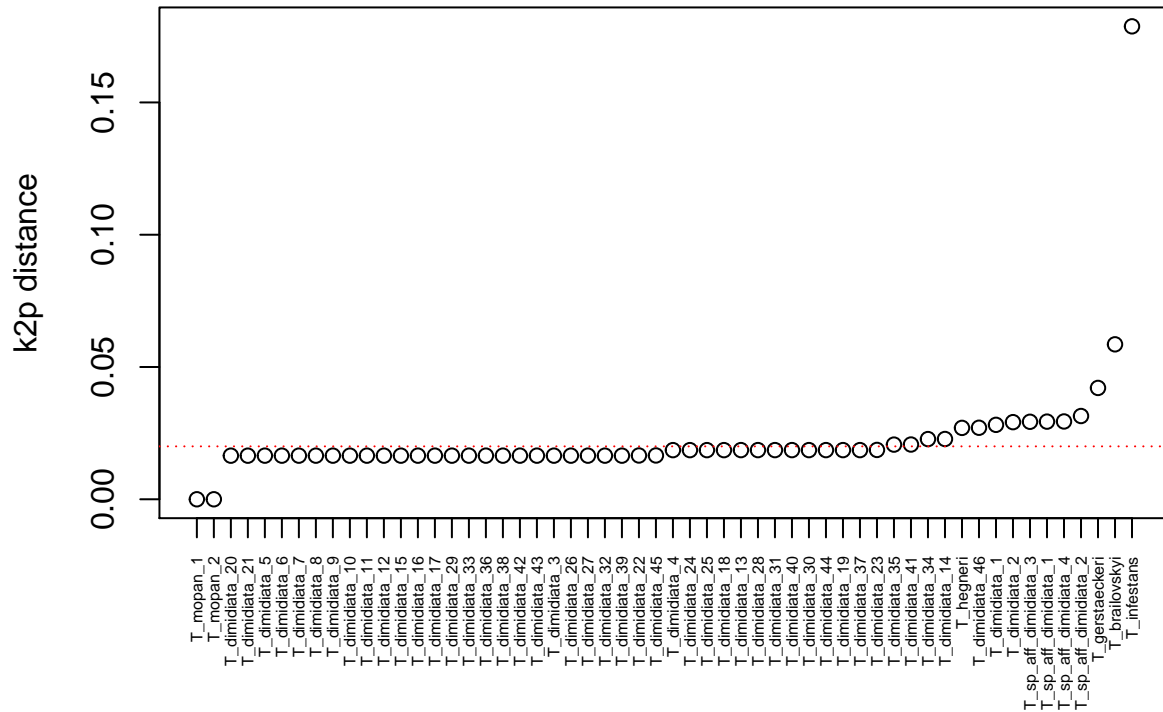


```
dist_its2 <- dist.dna(its2, model = "k80", as.matrix = TRUE, pairwise.deletion = T)
```

Ordering the distances from smallest to largest to plot and visualize it. Red dotted line corresponds to a distance of 2%.

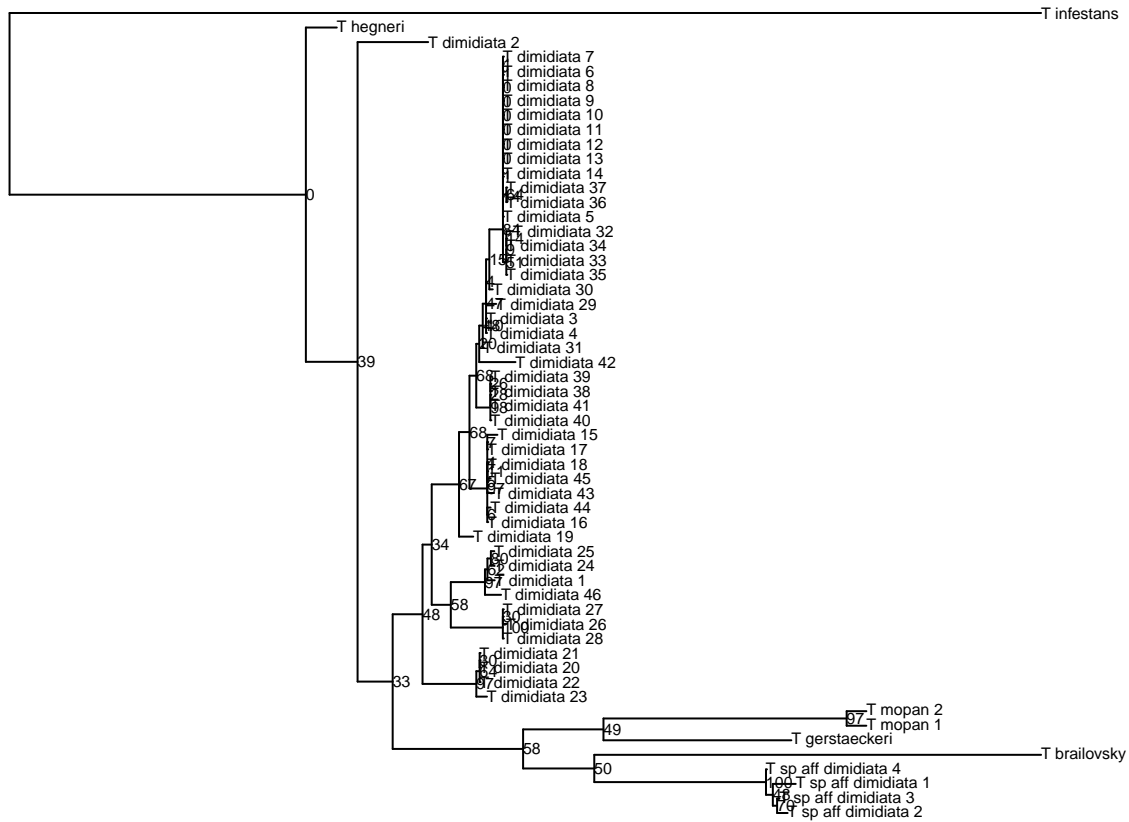
```
T_mopan_its2 <- subset(dist_its2, select = "T_mopan_1")
T_mopan_its2sorted <- as.matrix(T_mopan_its2[order(T_mopan_its2[, 1]), ])
plot(T_mopan_its2sorted, pch = 1, main = "K2p pairwise distances", xaxt = "n",
     xlab = "", ylab = "k2p distance")
axis(1, at = 1:nrow(T_mopan_its2sorted), labels = row.names(T_mopan_its2sorted),
     las = 2, cex.axis = 0.5)
abline(h = 0.02, col = "red", lty = 3)
```

## K2p pairwise distances



## Reading as displaying the phylogenies reconstructed using PhyML

```
cytb_tree<-read.tree("cytb_mopan.tre")
plot(cytb_tree, type = "phylogram", use.edge.length = TRUE,
     node.pos = 1, show.tip.label = TRUE,
     show.node.label = TRUE,
     edge.color = "black",
     edge.width = 1,
     edge.lty = 1,
     font = 1,
     cex = 0.5,
     no.margin = TRUE,
     root.edge = TRUE,
     label.offset = 0,
     underscore = FALSE,
     x.lim = NULL, y.lim = NULL,
     direction = "rightwards",
     lab4ut = NULL, tip.color = "black", plot = TRUE,
     rotate.tree = 0, open.angle = 0, node.depth = 1,
     align.tip.label = FALSE)
```



```

its2_tree<-read.tree("its2_mopan.tre")
plot(its2_tree, type = "phylogram", use.edge.length = TRUE,
     node.pos = 1, show.tip.label = TRUE,
     show.node.label = TRUE,
     edge.color = "black",
     edge.width = 1,
     edge.lty = 1,
     font = 1,
     cex = 0.5,
     no.margin = TRUE,
     root.edge = TRUE,
     label.offset = 0,
     underscore = FALSE,
     x.lim = NULL, y.lim = NULL,
     direction = "rightwards",
     lab4ut = NULL, tip.color = "black", plot = TRUE,
     rotate.tree = 0, open.angle = 0, node.depth = 1,
     align.tip.label = FALSE)

```

