CZECH UNIVERSITY OF LIFE SCIENCES PRAGUE
FACULTY OF ENVIRONMENTAL SCIENCE
DEPARTMENT OF ECOLOGY

Development of microsatellite markers set for population genetic structure estimation of *Peucedanum cervaria* (Apiaceae)

Diploma Thesis 2019

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9 Appendix 1

Appendix 1-1: Population Localities

Population ID	Locality	Latitude	Longitude
10	Romania, Cluj-Napoca, Bărăi	46.85796	23.90922
11	Romania, Suceava, Moara Carp	47.57491	26.25542
2	Hungary, Dorog, Kis-Strázsa-hegy, Nagy-Strázsa-hegy	47.750617	18.741983
64	Austria, Hundsheim (distr. Bruck an der Leitha): Hundsheimer Berg 1.0-1.2 km NW-N of the village	48.1281389	16.9333611
15	Poland, Skorocice	50.41889	20.66948
54	Czech Republic, Pavlovské vrchy	48.834861	16.639778
36	Czech Republic, Srbsko	49.946837	14.133322
169	Slovakia, Ružomberok Distr., Ružomberok: Dry grassland developed on limestone slopes of the Čebrat Hill, NW edge of the town	49.09425	19.29616667
31	Germany, Nissmitz	51.195998	11.763920
9	Hungary, Bükk, Eger	48.012401	20.578951

Appendix 1-2: All Primer Sequence Data

Primer	Motif	Left Sequence (Tag)	Right Sequence
PC-di-01	$(AG)_{19}$	GGAAACAGCTATGACCATCTCTCACGTAAACTCGCCG	CAGAGCCTCAAATCGAAGTCTC
PC-di-02	$(AG)_{19}$	GGAAACAGCTATGACCATGAACCACCACCGCTTCAC	GGACAGCGGTAGAGAGGC
PC-di-03	$(AG)_{19}$	GGAAACAGCTATGACCATCCACATACACTTGTCTCGTCC	CAACAGATGAGGACGTACTGAC
PC-di-04	$(AG)_{19}$	GGAAACAGCTATGACCATCACCGGAAACCAACCCATC	GTGATGGCCGTGAAGTGAAG
PC-di-05	$(AG)_{19}$	GGAAACAGCTATGACCATTTCCGGCGAGTCAGTGG	CCCGAAACTCCTCTTTGATCC
PC-di-06	$(AG)_{19}$	GGAAACAGCTATGACCATAAACCCTAAGTGAGACTGCG	ATTTCAATTTCCCGGGCCAG
PC-di-07	$(AG)_{19}$	GGAAACAGCTATGACCATGCTAAGACAAGTACAGCGCC	CCATTCCTAGCCTGAGTCGG
PC-di-08	$(AC)_{19}$	GGAAACAGCTATGACCATCTCTCTCGGCCCTTTACC	GTTCGGGTGTGGGTGTATCC
PC-di-09	$(AG)_{19}$	GGAAACAGCTATGACCATCTCTCTCCAACTCACCCAGC	TTTACGTGCTGGGTGGGTTG
PC-di-10	$(AG)_{19}$	GGAAACAGCTATGACCATAAATCGGGAAGGAGGAGGG	ATCCGCAAACAACCCATCAC
PC-di-11	$(AG)_{19}$	GGAAACAGCTATGACCATACCTTTCCGATGACCACCG	AGGAGAGATTGTTGGCGGAG
PC-di-12	$(AT)_{19}$	GGAAACAGCTATGACCATGCACAATCGGCGAAGATGG	TTGGGTGTAAACGCGAGATC
PC-di-13	$(AG)_{19}$	GGAAACAGCTATGACCATCCGCCACTGATTTCAACCC	GCTTCCCGCCTATATTCACC
PC-di-14	$(AT)_{19}$	GGAAACAGCTATGACCATCCTCCCATGTCCTGCAC	TGCTCCTGGTCATACGATCC
PC-di-15	$(AG)_{19}$	GGAAACAGCTATGACCATACACACGCAGAGAAGATAAAGG	CACCTGCAGTTCCAACACAC

PC-di-16	$(AG)_{19}$	GGAAACAGCTATGACCATGAAACAAGACCGGATCGC	TCTTTCTCTCTCGAACTAGCCG
PC-di-17	$(AG)_{18}$	GGAAACAGCTATGACCATGTAGAGGCGGAAAGGGAG	TGTCTCGACCTCCCTCCC
PC-di-18	$(AG)_{18}$	GGAAACAGCTATGACCATGTTGATCTGAGCTTCCCTGG	GAACCATGCCACACAAGTCC
PC-di-19	$(AG)_{18}$	GGAAACAGCTATGACCATCTACATTCACCTCATCCTCCC	GGCCCAGTAACTCCATGAAC
PC-di-20	$(AG)_{18}$	GGAAACAGCTATGACCATCCTTCTGCACTCTCATGTAAGC	GTCGAAACCTAGTGCCAATGG
PC-di-21	$(AG)_{18}$	GGAAACAGCTATGACCATGCTCGGAAAGTCAAGCCATC	GGAAGGTTGTGTTGTGGAGG
PC-di-22	$(AG)_{18}$	GGAAACAGCTATGACCATCGGAAGCAAGTAAAGGTGTG	AACTTCTCCTCACCTGGCTG
PC-di-23	$(AT)_{18}$	GGAAACAGCTATGACCATGCACAGCCTCACTCTCTTAG	TCTGTGAAGGTGTATGTAGCTG
PC-di-24	$(AG)_{18}$	GGAAACAGCTATGACCATCGATTTCAATTCGACCCACC	GAGGTAGGAAGGCAGGTGG
PC-di-25	$(AT)_{18}$	GGAAACAGCTATGACCATGCGCGCCCAGGTATTATAC	GGAACTCTCAAGGTACGTTCTC
PC-di-26	$(AG)_{13}$	GGAAACAGCTATGACCATACCCAACACCAATGAACTCC	TGGCTCCAAACCAGATTAGAG
PC-di-27	$(AG)_{13}$	GGAAACAGCTATGACCATCTTTGCCAGCTTGTACTTCC	CGTGTGGGAACTGAAACGAC
PC-di-28	$(AT)_{13}$	GGAAACAGCTATGACCATACATCAGGAAGACACCAACC	TGCAGCACCACTTAATCTCG
PC-di-29	$(AG)_{13}$	GGAAACAGCTATGACCATACAATCGGGCCACAACG	ATGGGTTGGAGGTGGAATGG
PC-di-30	$(AG)_{13}$	GGAAACAGCTATGACCATACGATTCGATCCGGAAATCAC	GGAGGTAAGTTAAATCGGGCTC
PC-di-31	$(AT)_{13}$	GGAAACAGCTATGACCATACTTGCCAGAACCACCATTG	TGGCTCCCATTGATTGACTC
PC-di-32	$(AG)_{13}$	GGAAACAGCTATGACCATCACAACACATGAATCCACATCC	CCTCATCGCTGAAAGATCTGG

PC-di-33	$(AT)_{13}$	GGAAACAGCTATGACCATGCATTGTGAATAGTCCCGC	AACGTGCAAGTGTTGGGTAC
PC-di-34	$(AT)_{13}$	GGAAACAGCTATGACCATGACCAGTATTTCAAACACAGGC	TAGAACACTCCCAGACGACG
PC-di-35	$(AG)_{13}$	GGAAACAGCTATGACCATGGTTCGAAAGTCAAGCCACC	GAGTTCGATTTGGGCCAAGG
PC-di-36	$(AG)_{13}$	GGAAACAGCTATGACCATGAGCAGCAACCAAGAAGATG	GCAGGCATAATCACCCAGAG
PC-di-37	$(AG)_{13}$	GGAAACAGCTATGACCATCGACCCGGAGATAAGCTTC	GGTGTTGCCTTAGAAACCCG
PC-di-38	$(AT)_{13}$	GGAAACAGCTATGACCATGAACACAAGACTCTGGCAC	GGCGGAATCCAAGGTGTACC
PC-di-39	$(AT)_{13}$	GGAAACAGCTATGACCATTCTCCACGGTTCTCCACG	CTATTTGCCCACGTCAGCAC
PC-di-40	$(AG)_{13}$	GGAAACAGCTATGACCATACCCACCGGAAGAATCTCTC	GGTGGAGGTTGTGAAGAGGG
PC-di-41	$(AG)_{13}$	GGAAACAGCTATGACCATTTGCCAGGTCCACTCTCC	AGCAATTGAGATTTGGAGCGG
PC-di-42	$(AG)_{13}$	GGAAACAGCTATGACCATGGACGAAGGGACAACTTATC	ACACTTGACACGACATTCTCAC
PC-di-43	$(AT)_{13}$	GGAAACAGCTATGACCATGACAAGGAGTGGGAGCAAAC	CAGCTGCTGGTTACACGG
PC-di-44	$(AG)_{13}$	GGAAACAGCTATGACCATACCAAGTTCGCCACAAACG	TTTGTACTTGGCGAATATTGGC
PC-di-45	$(AT)_{13}$	GGAAACAGCTATGACCATCCAACCAACCAAATATCCCATG	ACTGTTGGTGTCTCGGTTTG
PC-di-46	$(AC)_{13}$	GGAAACAGCTATGACCATAACCAAGCAAGCAACAACTC	TGAGAAATGGTGCTTTGATGTG
PC-di-47	$(AC)_{13}$	GGAAACAGCTATGACCATGCAACTGGAAGTGAGTGTC	TGCCCATGTAAGACGTAGGG
PC-di-48	$(AT)_{13}$	GGAAACAGCTATGACCATGACCAATAGCGTCCGTTG	ATCCAAACCCGATCCGAACC
PC-di-49	$(AT)_{13}$	GGAAACAGCTATGACCATAACATTCCACCGAGATCTGC	TCATCAGTGACGTGGCAGTG

PC-di-50	$(AG)_{13}$	GGAAACAGCTATGACCATCACACGAACGTCCGATCATC	GCTGCTATACATCTTGAGAGGC
PC-di-51	$(AC)_{13}$	GGAAACAGCTATGACCATAAGCGCGCAAACATCAC	TCGTTAGCTGTACATCTTGAGG
PC-di-52	$(AT)_{13}$	GGAAACAGCTATGACCATCACCTTCTACCCGGACG	CACGGTTTAGGTTGCTCTCG
PC-di-53	$(AG)_{13}$	GGAAACAGCTATGACCATGAACCCGAACAGCCTGTAG	CAGGCGGGCTCAATCTTTG
PC-di-54	$(AT)_{13}$	GGAAACAGCTATGACCATGCCATCTACACAAAGGACC	GGATACCCGACCCTTGGATC
PC-di-55	$(AT)_{13}$	GGAAACAGCTATGACCATGGTGCCTGTGGAAATAAAGC	CGCCCATCCGATTCACTATG
PC-di-56	$(AT)_{12}$	GGAAACAGCTATGACCATTCCGCCAAATTCACCTCTC	GTGTTCTCCATCACCTGCAC
PC-di-57	$(AC)_{12}$	GGAAACAGCTATGACCATACTCAGCACCCATTCATCCG	ATCGTCAAGGTCTCCAATGC
PC-di-58	$(AT)_{12}$	GGAAACAGCTATGACCATGAGACGTACACTGAGATTGGG	ATGGTCTCGTGTACTGTGGG
PC-di-59	$(AC)_{12}$	GGAAACAGCTATGACCATCACACAGAGGAGAGCACTG	GGTAGTCTAGAGGGCCAAGG
PC-di-60	$(AT)_{12}$	GGAAACAGCTATGACCATAAAGCCAAGGAAGCATCTCG	CTCAGCAATAGAGGTTCTCCC
PC-di-61	$(AT)_{12}$	GGAAACAGCTATGACCATGTAACAACCCAACTGCCG	TGTGGGCCTCAAATTTGGTC
PC-di-62	$(AG)_{12}$	GGAAACAGCTATGACCATGCACCCACTACACGTTACC	GGTTAGGGTGTGCATAAATCAC
PC-di-63	$(AG)_{12}$	GGAAACAGCTATGACCATAAATTGCTTGGCCACGTGTC	GTGCGGTTAGAGAGGTGAGG
PC-di-64	$(AC)_{12}$	GGAAACAGCTATGACCATGTATTTGTTGCAGCGTGTGG	AAATTCGAACCCACCTGCAC
PC-di-65	$(AC)_{12}$	GGAAACAGCTATGACCATACACTCCAAATATGCCTGCAC	GAGTGTGGAGGTTTCTGGTG
PC-di-66	$(AG)_{12}$	GGAAACAGCTATGACCATCCTCTCTTCCACAACGC	TGGCTGGTCGTGATGAGAG

PC-di-67	$(AT)_{12}$	GGAAACAGCTATGACCATCAAGACAACATTCAACCCAAC	TCTGAGAACCTGAGTCCTTGTG
PC-di-68	$(AC)_{12}$	GGAAACAGCTATGACCATACCACTGACCCTAAACCTCG	TGCGGGCTGGTAGAACTTTC
PC-di-69	$(AG)_{12}$	GGAAACAGCTATGACCATCACACGAACGTCCGATTGTC	GCTGTTCCAACTGTTGAGAGG
PC-di-70	$(AG)_{12}$	GGAAACAGCTATGACCATAATAAACTCCGGGCCTGAAG	TTGTGTTCCGCCATTGAGAG
PC-di-71	$(AT)_{12}$	GGAAACAGCTATGACCATCCGATCCCTGCAGTTAATCC	GCTGAGCAATTCTTTCGCTC
PC-di-72	$(AG)_{12}$	GGAAACAGCTATGACCATCAGACACATCACACAAGTAGG	TGGATATGGAACCAGGCATTG
PC-di-73	$(AC)_{12}$	GGAAACAGCTATGACCATGATCCACCAAGAAGCAGATG	TGCACCTCCAGTCTTCCATC
PC-di-74	$(AT)_{12}$	GGAAACAGCTATGACCATCCCAGTAGTATGACCCTTGG	CAGTGAAGTGTGGTCAATAGGG
PC-di-75	$(AG)_{12}$	GGAAACAGCTATGACCATACCCTCCGAATCAAATCTCG	TGGTGGTGATGTTTGGGTCC

Appendix 1-3: R code for Genetic Analysis

```
install.packages("adegenet")
install.packages("hierfstat")
install.packages("PopGenReport")
install.packages("diveRsity")
install.packages("HWxtest")
install.packages ("tidyverse")
install.packages ("tibble")

library(adegenet)
library(diveRsity)
library(hierfstat)
library(PopGenReport)
library(tidyverse)

setwd("E:/2019/PrimerAnalysis/PopAnalysis")
MIKRODATA <-read.csv("PC_AllPopData.csv", head=TRUE,colClasses='character')
colnames(MIKRODATA)[1]<-"POPULACE"
MIKRODATA

## data conversion from table to genind
MIKRODATA_tibble <- as_tibble(MIKRODATA)
tt <-  unique(MIKRODATA_tibble[,1])
pop_data <- list()
for (i in tt$POPULACE)  {pop_data [[i]] <- filter(MIKRODATA_tibble, POPULACE == i)
}
## creates geneind objects from each df in a pop_data list
data_gen_pop <- list()
for (i in tt$POPULACE)  { data_gen_pop [[i]] <- assign(paste0("DATA_GEN_pop", i), df2genind(pop_data[[i]][-1],
pop=pop_data[[i]]$POPULACE, ploidy=2, type="codom",ncode=10))
}
## replace missing data (NA) by zero
nn<-colnames(DATA_GEN@tab)
DATA_GEN@tab[is.na(DATA_GEN@tab)] <- 0
DATA_GEN@tab<-matrix(as.integer(DATA_GEN@tab), nrow=nrow(DATA_GEN@tab),
ncol=ncol(DATA_GEN@tab))
colnames(DATA_GEN@tab)<-nn

library(HWxtest)
source("GenePopUnflatten.R") # konverze dat z dataframe do genepopu
source("transformdata.R") # uprava genepop formatu
source("transformdata2.R") # genpopformat adjustment, similar to transformdata, for missing data uses"000000"
source("HW_table.R") # uprava tabulky vysledku

Hw_test2 <- divBasic(infile = tabledata2, outfile = "results_divbasic2", HWEexact = TRUE, bootstraps = 1000, mcRep =
9999) # calculation in package diveRsity
str(Hw_test2)

nullalleles_pop_summaries <- list()
for (i in tt$POPULACE){nullalleles_pop_summaries [[i]] <- assign(paste0("null_alleles_pop_sum", i),
nullalleles_pops[[i]]$null.allele.freq$`summary1`)}
str(nullalleles_pop_summaries)
```

Appendix 1-4: Elimination of Primers Table

Primers	Gel	Sample Seq	Full Pop Seq	Amplification	Variability	Multiplex
PC1		X				
PC2			X			
PC3					P	
PC4	I					
PC5			X			
PC6			X			
PC7	0					
PC8			X			
PC9	I					
PC10	M					
PC11		X				
PC12	0					
PC13	I					
PC14	I					
PC15					P	
PC16	0					
PC17	0					
PC18						ACCEPTED
PC19						ACCEPTED
PC20	0					
PC21	I					
PC22				X		

PC23		X				
PC24	0					
PC25		X				
PC26	M					
PC27	I					
PC28				X		
PC29		X				
PC30						ACCEPTED
PC31				X		
PC32			X			
PC33			X			
PC34	M					
PC35	I					
PC36			X			
PC37	M					
PC38				X		
PC39	0					
PC40	I					
PC41	I					
PC42	0					
PC43		X				
PC44		X				
PC45					NV	
PC46		X				
PC47	I					
PC48	M					
PC49		X				
PC50		X				

PC51		X				
PC52					P	
PC53			X			
PC54	0					
PC55			X			
PC56	I					
PC57		X				
PC58						ACCEPTED
PC59					NV	
PC60	0					
PC61	0					
PC62		X				
PC63	M					
PC64			X			
PC65				X		
PC66			X			
PC67	M					
PC68						ACCEPTED
PC69		X				
PC70					P	
PC71				X		
PC72			X			
PC73						ACCEPTED
PC74		X				
PC75					NV	

X – Eliminated; 0 – Eliminated due to amplification failure; I – Eliminated due to Inconsistent amplification; M – Eliminated due to multiple alleles

Appendix 1-5: Population Summary Statistics

11	X68	X58	X73	X19	X30	X18	Overall
N	20	20	20	20	20	20	20
A	7	2	6	9	5	12	41
%	58.33	40	46.15	52.94	38.46	26.67	43.76
Ar	6.17	2	5.41	7.3	4.45	9.54	5.81
Ho	0.75	0.35	0.65	0.9	0.45	0.95	0.68
He	0.78	0.47	0.77	0.76	0.69	0.88	0.73
HWE	0.381	0.325	0.543	0.738	0.088	0.095	0.211
Fis	0.0385	0.2533	0.1586	-0.1765	0.3466	-0.0826	0.0695
Fis_Low	-0.1819	-0.193	-0.0864	-0.3396	0.0282	-0.172	-0.0009
Fis_High	0.2753	0.6772	0.4179	-0.018	0.6556	0.0301	0.1292
B	-0.07816	-0.2232	-0.0610	-0.0752	-0.0869	-0.0335	

169	X68	X58	X73	X19	X30	X18	Overall
N	19	15	19	19	17	19	18
A	3	2	8	5	4	10	32
%	25	40	61.54	29.41	30.77	22.22	34.82
Ar	2.5	2	6.37	3.99	3.33	6.7	4.15
Ho	0.21	0.33	0.89	0.58	0.12	0.63	0.46
He	0.27	0.49	0.76	0.54	0.6	0.63	0.55
HWE	0.218	0.282	0	0.148	0	0.014	0
Fis	0.2284	0.3213	-0.1745	-0.0636	0.8052	0	0.163
Fis_Low	-0.1259	-0.1499	-0.3431	-0.2893	0.478	-0.1894	0.0308
Fis_High	0.7589	0.8491	0.0131	0.1708	1.0153	0.1876	0.2908
B	-0.4019	-0.2064	-0.0760	-0.1626	-0.1917	-0.0989	

2	X68	X58	X73	X19	X30	X18	Overall
N	20	19	20	20	18	20	19.5
A	7	4	6	9	8	17	51
%	58.33	80	46.15	52.94	61.54	37.78	56.12
Ar	5.62	3.8	5.28	8.02	5.52	12.35	6.76

Ho	0.75	0.37	0.5	0.85	0.44	0.9	0.64
He	0.75	0.69	0.66	0.76	0.62	0.91	0.73
HWE	0.03	0.01	0.752	0.997	0.002	0	0
Fis	0.005	0.4669	0.2481	-0.1221	0.2836	0.0123	0.1332
Fis_Low	-0.2965	0.1395	0.0097	-0.2645	-0.0944	-0.1158	0.0311
Fis_High	0.3032	0.7798	0.53	0.0226	0.661	0.1663	0.2387
B	-0.0899	-0.0989	-0.1080	-0.0471	-0.125	-0.0282	
54	X68	X58	X73	X19	X30	X18	Overall
N	19	12	19	19	19	19	17.83
A	5	4	10	9	6	19	53
%	41.67	80	76.92	52.94	46.15	42.22	56.65
Ar	4.47	3.6	8.15	6.93	5.12	14.01	7.05
Ho	0.68	0.33	0.84	0.74	0.26	0.89	0.63
He	0.58	0.71	0.83	0.78	0.67	0.93	0.75
HWE	1	0.002	0.022	0.294	0	0	0
Fis	-0.1706	0.5294	-0.0116	0.0584	0.6074	0.0415	0.1678
Fis_Low	-0.3494	0.0452	-0.1783	-0.1284	0.3497	-0.0886	0.0629
Fis_High	0.0248	0.9159	0.177	0.2704	0.863	0.2	0.2499
B	-0.1159	-0.1338	-0.0478	-0.0540	-0.1589	-0.0299	
64	X68	X58	X73	X19	X30	X18	Overall
N	18	17	18	18	17	18	17.67
A	6	4	6	9	7	18	50
%	50	80	46.15	52.94	53.85	40	53.82
Ar	4.3	3.41	5.25	7.11	5	12.9	6.33
Ho	0.44	0.35	0.72	0.83	0.35	0.72	0.57
He	0.6	0.64	0.74	0.79	0.45	0.92	0.69
HWE	0.135	0.001	0.82	0	0.078	0	0
Fis	0.2615	0.4457	0.0209	-0.0485	0.2093	0.2108	0.1704
Fis_Low	-0.1064	-0.0271	-0.244	-0.2486	-0.1384	0.0117	0.0601
Fis_High	0.5995	0.8363	0.3071	0.1616	0.65	0.4246	0.2658
B	-0.125	-0.1491	-0.0657	-0.0657	-0.2324	-0.0384	

10	X68	X58	X73	X19	X30	X18	Overall
N	19	17	18	19	13	17	17.17
A	3	3	5	8	5	10	34
%	25	60	38.46	47.06	38.46	22.22	38.53
Ar	2.83	2.77	4.55	5.96	4.26	7.53	4.65
Ho	0.47	0.24	0.67	0.58	0.15	0.76	0.48
He	0.48	0.38	0.75	0.63	0.74	0.78	0.63
HWE	1	0.252	0.793	0	0	0.002	0
Fis	0.0144	0.3818	0.1148	0.0752	0.792	0.0243	0.2366
Fis_Low	-0.3384	-0.1278	-0.1837	-0.2409	0.4979	-0.178	0.0792
Fis_High	0.408	0.8718	0.4147	0.3957	1.014	0.2492	0.3825
B	-0.2013	-0.2988	-0.0657	-0.1056	-0.1229	-0.0528	

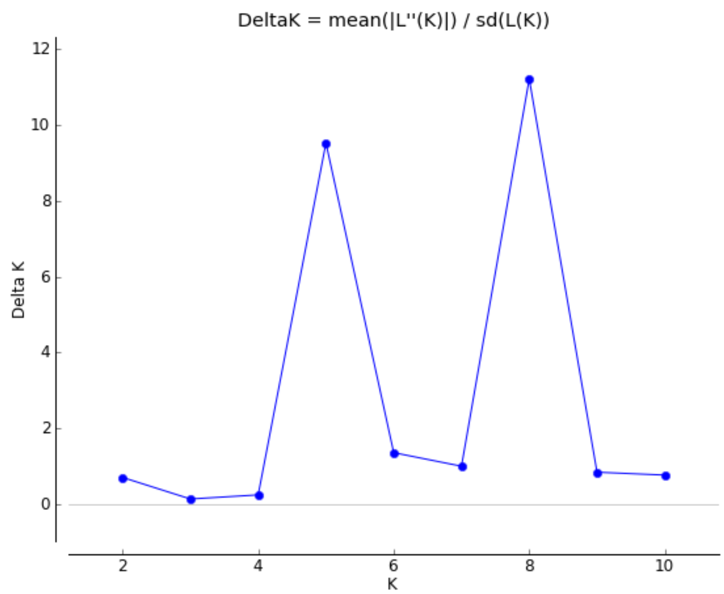
15	X68	X58	X73	X19	X30	X18	Overall
N	20	20	20	20	18	20	19.67
A	6	3	5	8	3	6	31
%	50	60	38.46	47.06	23.08	13.33	38.66
Ar	4.64	2.98	4.7	6.16	2.7	4.9	4.35
Ho	0.55	0.5	0.95	0.9	0.11	0.75	0.63
He	0.51	0.59	0.72	0.78	0.37	0.69	0.61
HWE	0.001	0.748	0.263	0	0.001	0.038	0
Fis	-0.0837	0.1471	-0.3287	-0.1502	0.6987	-0.0909	-0.0311
Fis_Low	-0.3294	-0.1511	-0.4996	-0.3042	-0.0204	-0.3663	-0.1326
Fis_High	0.1534	0.491	-0.1618	0.0321	1.0357	0.2207	0.0629
B	-0.1834	-0.1363	-0.1428	-0.0695	-0.3728	-0.1204	

31	X68	X58	X73	X19	X30	X18	Overall
N	20	20	20	20	15	20	19.17
A	7	3	3	9	5	13	40
%	58.33	60	23.08	52.94	38.46	28.89	43.62
Ar	5.62	2.53	2.56	7.33	4.06	9.96	5.34
Ho	0.8	0.45	0.25	0.85	0.27	0.8	0.57
He	0.73	0.52	0.52	0.83	0.64	0.8	0.67

HWE	0.09	0.355	0.004	0.964	0.001	0.244	0.001
Fis	-0.094	0.1283	0.5227	-0.0256	0.5862	0.0062	0.1563
Fis_Low	-0.3056	-0.2913	0.1037	-0.19	0.2216	-0.1297	0.0304
Fis_High	0.1172	0.54	0.8304	0.1821	0.8981	0.1431	0.2789
B	-0.0810	-0.1940	-0.1940	-0.0362	-0.1508	-0.0443	
36	X68	X58	X73	X19	X30	X18	Overall
N	19	18	19	19	13	19	17.83
A	6	2	6	5	6	17	42
%	50	40	46.15	29.41	46.15	37.78	41.58
Ar	5.69	1.99	5.45	3.78	4.62	11.89	5.57
Ho	0.63	0.22	0.74	0.37	0.31	0.84	0.52
He	0.79	0.28	0.77	0.32	0.74	0.9	0.64
HWE	1	1	0.856	1	0.015	0	0.007
Fis	0.2028	0.2	0.0466	-0.1368	0.5857	0.0675	0.1846
Fis_Low	-0.055	-0.1874	-0.1697	-0.2464	0.1928	-0.0971	0.0452
Fis_High	0.4813	0.7314	0.2869	-0.046	0.9204	0.2576	0.3018
B	-0.0448	-0.4025	-0.0571	-0.2824	-0.0868	-0.0358	
9	X68	X58	X73	X19	X30	X18	Overall
N	15	14	15	15	9	15	13.83
A	7	3	9	7	2	13	41
%	58.33	60	69.23	41.18	15.38	28.89	45.5
Ar	5.44	2.67	8.23	6.32	1.86	10.24	5.79
Ho	0.47	0.14	0.87	0.8	0.11	0.87	0.54
He	0.53	0.48	0.85	0.74	0.28	0.84	0.62
HWE	0.002	0.001	1	0.043	0.125	0.29	0
Fis	0.1176	0.7037	-0.0209	-0.0778	0.6	-0.029	0.1258
Fis_Low	-0.1287	0.2585	-0.2031	-0.3097	-0.086	-0.1656	-0.0004
Fis_High	0.3559	1.0187	0.1801	0.1384	1.1117	0.1279	0.2432
B	-0.1936	-0.2645	-0.0440	-0.1056	-0.4594	-0.0392	

Appendix 1-6: Delta K and Likelihood Graphs

A:



B: