**Code S1.** Calculating principal components analysis (PCA)-based genetic distance using the method developed by Shirk *et al.* (2010). Code courtesy of Dr. Shirk (AShirk@uw.edu).

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## **INPUT DATA FILE PARAMETERS:** The first column should contain individual ID's. ## ## The second column can contain population identifiers (optional). Each subsequent column ## ## represents a locus (a single locus occupies two consecutive columns for diploid ##

## organisms). Allelic data for a given sample is entered in a single row following the ##

## individual ID. The ADEGENET package accepts GENEPOP, STRUCTURE, GENETIX, ##

## or FSTAT file formats. We used the Export Data function in GenAlEx 6.5 (Peakall and ## ## Smouse 2012) to convert our input .csv file to STRUCTURE format; the output file must ## ## then be appended with ".str". ##

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## Set working directory.

setwd("C:/Path/to/my/data")

library(ecodist)

library(adegenet)

## Convert microsatellite (MSAT) data to a matrix of allele frequencies.

alleles <- import2genind("MSAT\_data.str",quiet=T)@tab

write.csv(alleles,"alleles.csv")

## Generate PCA-based pairwise genetic distance matrix.

pca <- princomp(alleles,cor=F)

pca\_1 <- predict(pca)[,1] # Eigenvector of the first pc axis

pca\_1dist <- distance(pca\_1, method="euclidean")

GD <- as.dist(pca\_1dist)

GD.mat <- as.matrix(GD)

## Label and export PCA-based genetic distance matrix.

data <- read.csv("MSAT\_data.csv")

rownames(GD.mat) <- colnames(GD.mat) <- as.character(data[,1])

write.csv(GD.mat,"PCA\_GD.csv")