README

Data for: Heritability of plumage colour morph variation in a wild population of promiscuous, long-lived Australian magpies

**File 1: HDY-18-AO311 Microsatellite genotype data.**

Excel spreadsheet file containing genotype scores for eight microsatellite loci used for parentage analysis. Column 1 “ind\_code” = code number of individual bird; Column 2 “territory\_code” = code of social territory group to which individual bird was a member; Columns 3-18 = allele scores for eight microsatellite loci where the two alleles of each locus appear in separate columns. Locus names in header: 43, 115b, 115a, 112, 67, 201, 206, 208.

**File 2: HDY-18-AO311 Back colour morph scores.**

Excel spreadsheet file containing back colour morph scores recorded for individual birds at the time they were first trapped and also for all subsequent field observations made on that individual. Each row represents data for an individual bird. Column 1 “territory\_code” = code of social territory group to which individual bird was a member; Column 2 “ind\_code” = code number of individual bird; Column 3 “Notes\_when\_trapped” = data on age, sex and back colour morph score recorded when bird was first trapped and banded (\*\*see key below); “Average\_back\_score” = mean back colour morph score across all observations of an individual bird; “back\_score\_when\_trapped” = back colour morph score recorded when bird was trapped and in the hand; “back\_scores\_when\_sighted” = remaining values in row represent back colour morph scores recorded for subsequent field observations of that individual. Number of observation vary across individuals.

\*\*key to “Notes when trapped”: This code contains information on age, sex and back colour morph score. The letter represents age and sex (if adult) i.e. C = chick; J = juvenile (sometimes recorded as “S” subadult); M = adult male; F = adult female. The number represents the back colour morph score recorded when bird was trapped and in the hand (see Supplementary File 1 for information on back colour morph score coding). For example, “C1” means a chick with back colour morph score of 1.

**File 3: HDY-18-AO311 Back colour morph scores for genetically assigned family groups.**

Excel spreadsheet file containing back colour morph scores for family groups where chicks have a genetically assigned mother and father. Column 1 “territory\_code” = code of social territory of family group; Column 2 “parent\_midP” = mean back colour morph score of mother and father; Column 3 ”mom\_BC” = back colour morph score of mother; Column 4 “dad\_BC” = back colour morph score of father; Column 5 “#full\_sibs” = number of full sib offspring assigned to mother and father combination; Column 6 “chick\_BC” = back colour morph score of individual chick; Column 7 “mean\_sibs\_bc” = mean back colour morph score across full sibs assigned to mother and father combination; Column 8 “sibs\_BC\_SD” = standard deviation of back colour morph score across full sibs assigned to mother and father combination; Column 9 “unique\_identifier” = unique identifier for family group.

**File 4: HDY-18-AO311 animal model R script**

Script containing R commands used for running animal models using R package MCMCglmm. Requires libraries: MCMCglmm, pedigree, MasterBayes. Associated input data required is in files “pedigreetxt.txt” (see File 5) and “phenotypestxt.txt” (see File 6).

**File 5: pedigreetxt.txt**

Text file containing data on pedigree relationships among individual birds used for calculating heritability using animal models (see File 4 animal model R script). This file is required input data for running animal models.

**File 6: phenotypestxt.txt**

Text file containing data for individual birds on back colour morph score “BC”, year of birth i.e. cohort “YEAROFBIRTH”, and territory membership i.e. social group “TERRITORY”. This file is required input data for running animal models (see File 4 animal model R script).