

Title	Sibship assignment to the founders of a Bangladeshi Catla catla breeding population
Authors	Hamilton, Matthew G.;Mekkawy, Wagdy;Benzie, John A. H.
Publication date	2019-04-29
Original Citation	Hamilton, M.G., Mekkawy, W. and Benzie, J.A., 2019. Sibship assignment to the founders of a Bangladeshi Catla catla breeding population. Genetics Selection Evolution, 51(1), (17). DOI:10.1186/s12711-019-0454-x
Type of publication	Article (peer-reviewed)
Link to publisher's version	https://gsejournal.biomedcentral.com/articles/10.1186/s12711-019-0454-x - 10.1186/s12711-019-0454-x
Rights	© The Author(s) 2019 - https://creativecommons.org/licenses/by/4.0/ . The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated
Download date	2024-04-19 00:00:39
Item downloaded from	https://hdl.handle.net/10468/9093

Additional file 2: Peripheral Figures

Contents

Figure S1 Minor allele frequency across all river populations and within populations using a) all SNP and founders prior to quality control and b) SNP and founders used in population genetic analyses. The minor allele for each locus was identified in the dataset containing all rivers for a and b separately. White filled bars less than zero represent SNP loci in which the minor allele was absent (i.e. MAF is exactly zero).

Figure S2. The mean number of a) distinct alleles per locus and b) private alleles per locus, as functions of standardized sample size for three rivers (excluding known relatives).

Figure S3. Bayesian Information Criterion (BIC) against the number of clusters (K) from unsupervised K-means clustering.

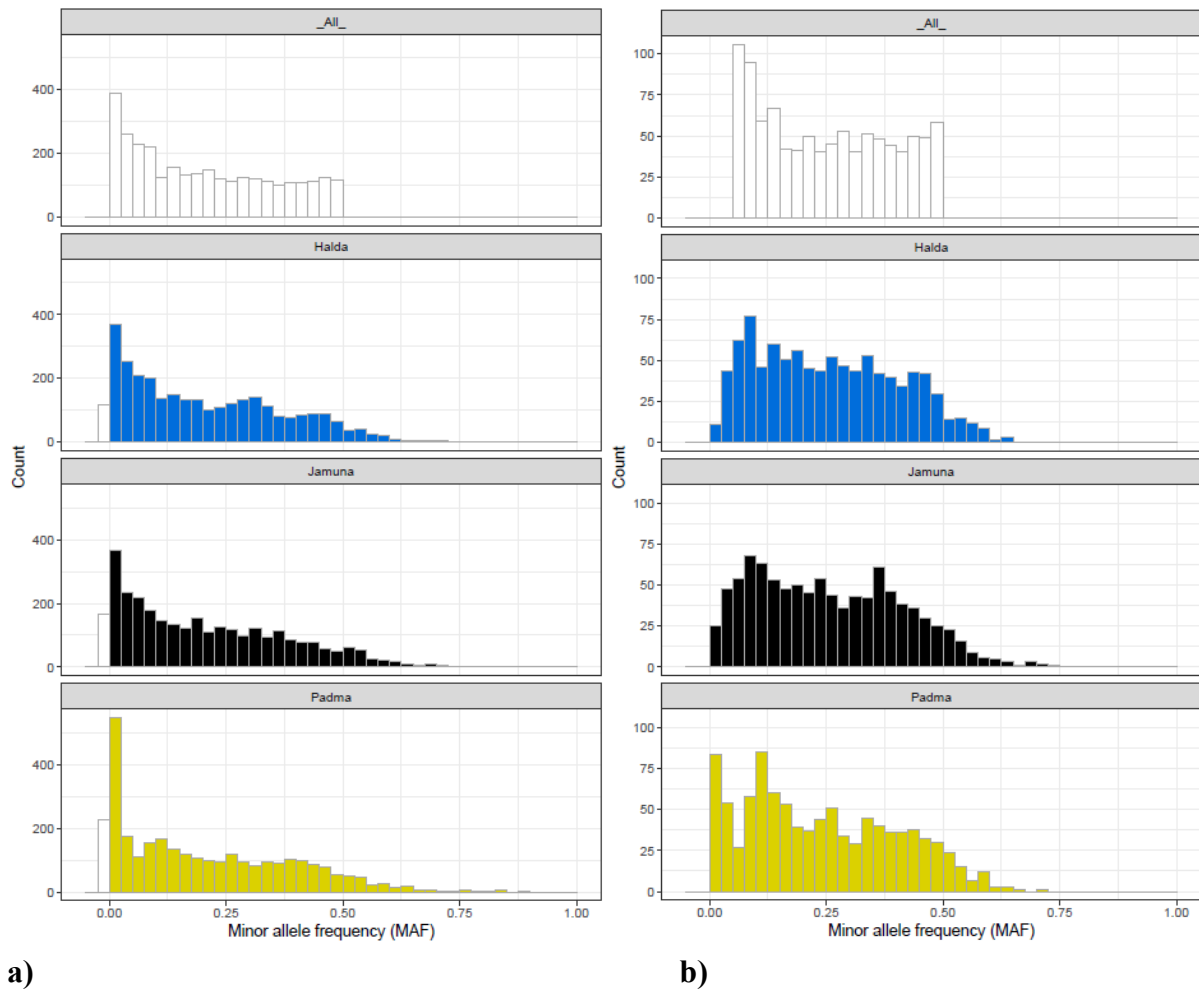


Figure S1 Minor allele frequency across all river populations and within populations using a) all SNP and founders prior to quality control and b) SNP and founders used in population genetic analyses. The minor allele for each locus was identified in the dataset containing all rivers for a and b separately. White filled bars less than zero represent SNP loci in which the minor allele was absent (i.e. MAF is exactly zero).

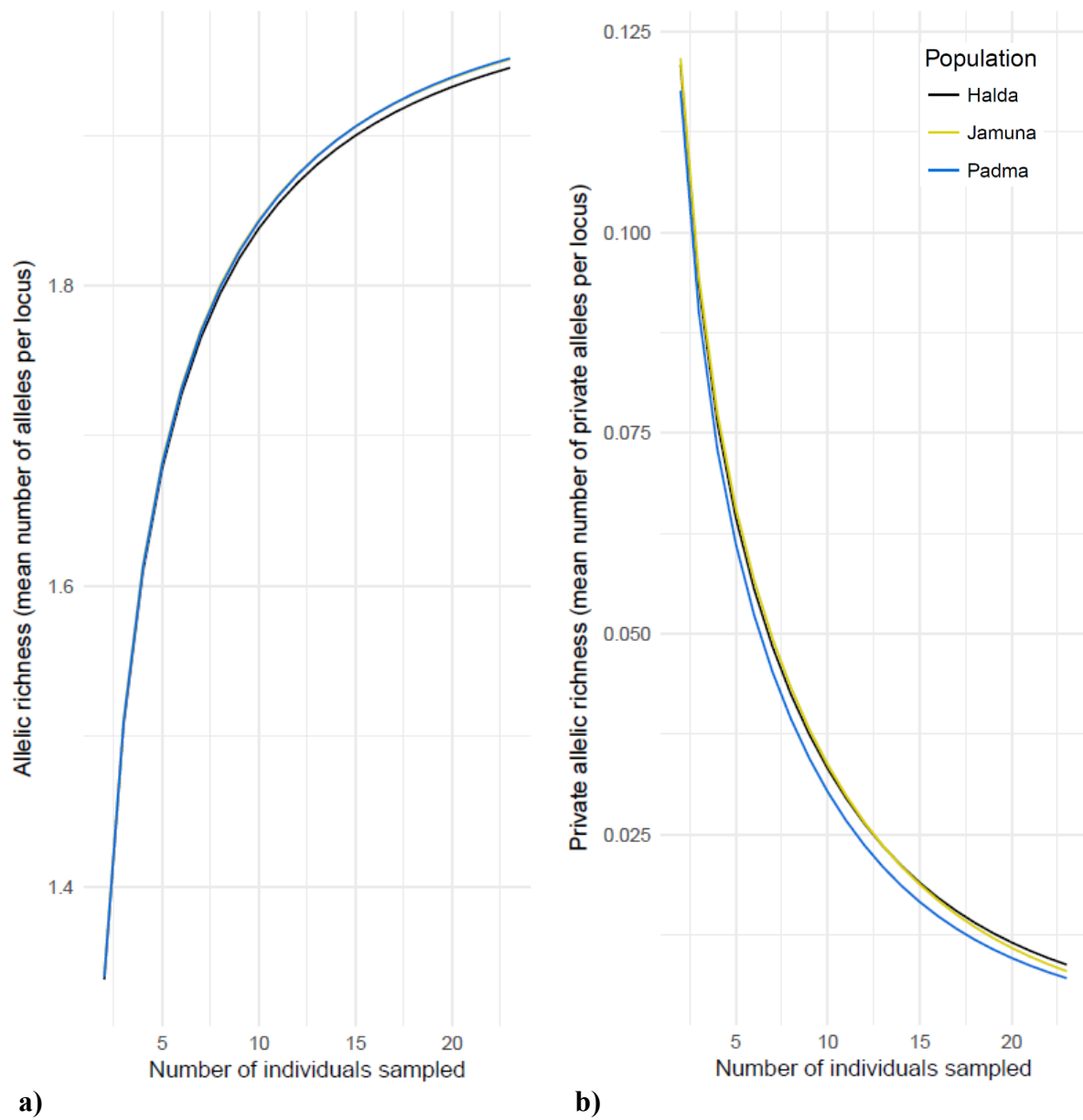


Figure S2. The mean number of a) distinct alleles per locus and b) private alleles per locus, as functions of standardized sample size for three rivers (excluding known relatives).

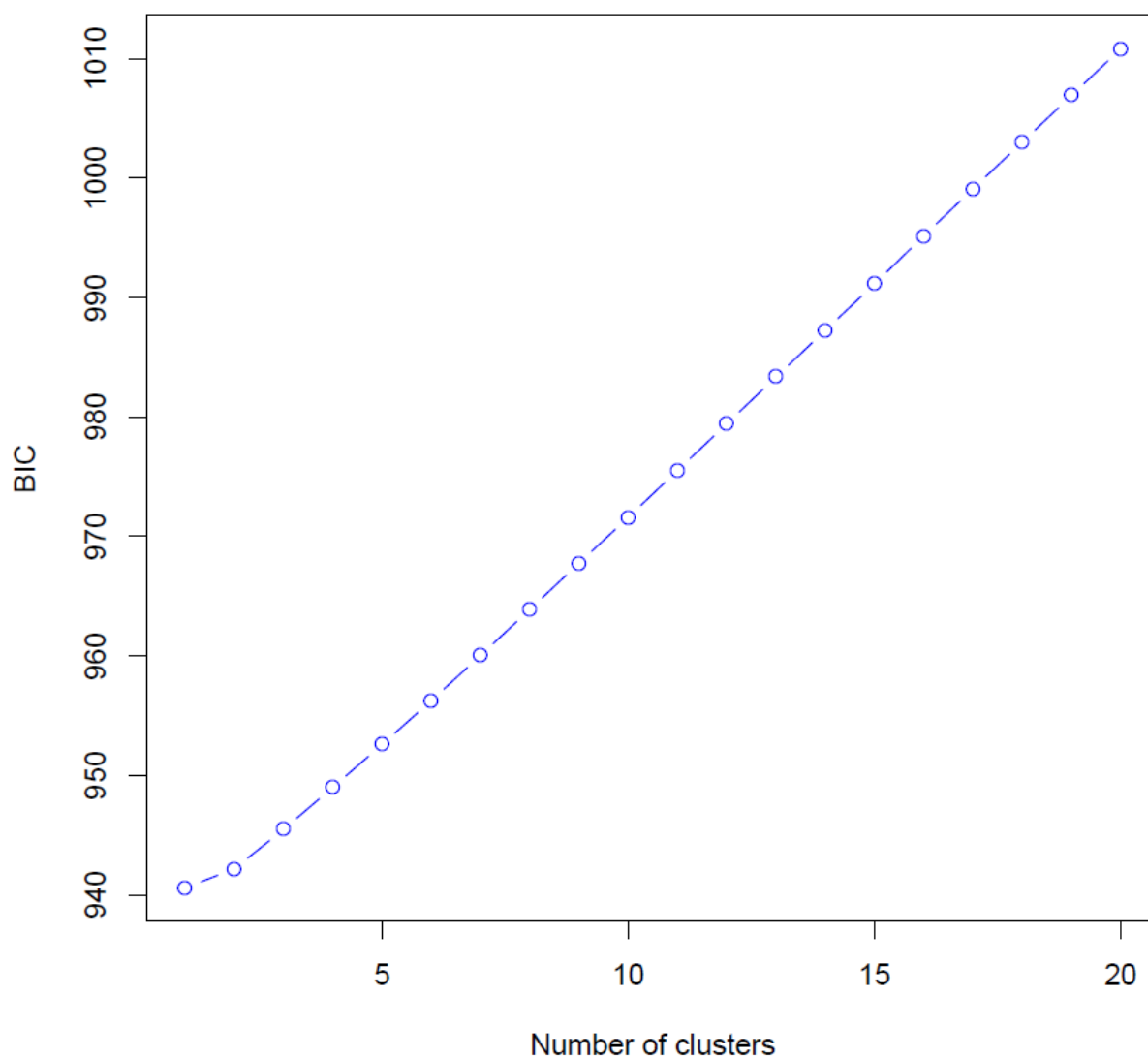


Figure S3. Bayesian Information Criterion (BIC) against the number of clusters (K) from unsupervised K-means clustering.