



HAL
open science

Genes flow by the channels of culture: the genetic imprint of matrilocality in Ngazidja, Comoros Islands

Stéphane Mazières, Pauline Oviedo, Célia Kamel, Pascal Bailly, Caroline Costedoat, Jacques Chiaroni

► To cite this version:

Stéphane Mazières, Pauline Oviedo, Célia Kamel, Pascal Bailly, Caroline Costedoat, et al.. Genes flow by the channels of culture: the genetic imprint of matrilocality in Ngazidja, Comoros Islands. European Journal of Human Genetics, 2018, 26, pp.1222-1226. 10.1038/s41431-018-0154-y . hal-01783534

HAL Id: hal-01783534

<https://hal.science/hal-01783534>

Submitted on 2 Dec 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

1 **Genes flow by the channels of culture: the genetic imprint of matrilocality in**
2 **Ngazidja, Comoros Islands**

3

4 Stéphane Mazières¹, Pauline Oviedo¹, Célia Kamel¹, Pascal Bailly^{1,2}, Caroline
5 Costedoat¹, Jacques Chiaroni^{1,2}

6

7 ¹Aix Marseille Univ, CNRS, EFS, ADES, "Biologie des Groupes Sanguins", Marseille,
8 France,

9 ²Etablissement Français du Sang Alpes-Méditerranée

10

11 Addresses:

12 ¹ Faculté de Médecine secteur Nord, 51 bd Pierre Dramard Bât A, 13344 Marseille
13 cedex 15, France

14 ² EFS Alpes Méditerranée, Biologie des Groupes Sanguins, Aix Marseille Université,
15 Faculté de médecine secteur Timone, 27 boulevard Jean Moulin, 13385 Marseille
16 Cedex 5

17

18 **Running title:** Social and genetic structure in Ngazidja

19

20 **Correspondence:** stephane.mazieres@univ-amu.fr

21

22 **Conflict of interest:** the authors declare no conflict of interest

23 **Abstract**

24 Post-marital residence of spouses is one of the architects of population genetic structure.
25 In the present study, we tested how the uxori-matrilocality in Ngazidja, Comoros Islands,
26 has unequally channelled the dispersal of male and female gene diversity amongst the
27 villages. Using sequences of the hypervariable segment I of the mitochondrial DNA
28 (mtDNA HVS-I) and seven Y-chromosome microsatellites (Y-STRs), we measured the
29 genetic variation and male-to-female ratios based on F_{ST} values and revealed a genetic
30 structure driven by male gene flow across villages but one. This genetic feature illustrates
31 the social place of residence of males and females which is inherited from the matrilocal
32 Bantu expansion. Exception is Bandamadji whose past military status made patrilocality
33 necessary.

34

35 **Keywords:** Comoros, matrilocality, mtDNA, Y-STRs, gene diversity

36 **Introduction**

37 The Comoros Islands are an archipelago of four island, Ngazidja (Great
38 Comoros), Nzduani (Anjouan), Mwali (Mohéli), and Mahore (Mayotte), located at the
39 northern end of the Mozambique Channel in the Indian Ocean. Historical, social,
40 religious, linguistic and genetic studies showed that the Comorian population arose from
41 the encounter of East African Bantu metallurgists with Islamic Middle Eastern traders
42 and to a lesser degree, with Austronesian people ¹⁻⁵.

43 The social structure in Comoros Islands results from the interactions between
44 Islam’s laws and ancestral rites from East Africa, with a mix distribution of matrilineal
45 and patrilineal traits in various domains of social organization: kinship, inheritance of
46 property, succession to titles, mode of residence, and detention of authority ^{2,6}. In the four
47 islands, the post-marital residence is largely uxori-matri-local: the husband resides with
48 his wife and the children (girls) marry in the place of their mother. Under African’s
49 costumes and Islam’s laws, men are allowed to practice polygyny. However, in order to
50 rise its social position, a man has to realize his “great marriage” with a woman from his
51 own village. This specific union happens while he is able to assume the great expenses
52 needed for this unique event and in for his adult’s life. Before, he may or has to conclude
53 others unions that are not necessarily with women from his own maternal village, called
54 “little marriage”. Men are thus considered as “itinerant” husbands moving from one to
55 other village and will have between two to five unions in their life. Meanwhile, for her
56 wedding the bride is given a house from her mother’s family. The oldest maternal uncle
57 looks after their education and the one of the children, but these rules are not applied if
58 the woman leaves the village. Furthermore, each Comorian individual and its social rights

59 are as a priority identified by his matriline, called *hinya*. All these conditions create a real
60 economic pressure to stay in a village ^{2,6}.

61 Previous surveys in matri- and patrilocally structured populations have shown a
62 contrasted pattern of within and between-population genetic variation when examined for
63 male and female genetic markers ^{7,8}. To what extent the matrilineal and matrilineal social
64 organization has left footprints in the genetic structure of the Great Comoros Island is of
65 the topic of the present study. To this aim, we explored the uniparental genetic variation
66 between five villages of Ngazidja in order to test to what extent matrilineality would have
67 shaped the gene diversity in the island.

68

69 **Material and Methods**

70

71 After informed consent approval, we collected 86 male samples from five villages
72 of Ngazidja: Bandamadji, Hahaya, Iconi, Male and Mitsoudje. We included only
73 unrelated men for at least two generations back in time and recorded ethnological
74 information including the name of the lineage village.

75 Samples were screened for seven Y-STRs (DYS389I, DYS389II, DYS19,
76 DYS390, DYS391, DYS392 and DYS393) (S1 Table) and sequenced for HVS-I (S2
77 File). Blood collection and lab methods are detailed in ⁹.

78 We first estimated the within-village gene diversity then tested the inter-village
79 genetic structure with a measure of F_{ST} and R_{ST} genetic distances and amount of variance
80 (AMOVA) ¹⁰. We also performed two median joining networks where we considered the
81 HVS-I poly-C region according to ¹¹ and weighted the Y-STRs loci as a function of their
82 variance ¹² after exclusion of DYS389I-II as recommended. Lastly, we measured the ratio

83 between effective numbers of male and female migrants per generation as described in ¹³
84 and ¹⁴. In this approach, populations are in the island model, considered as stable,
85 mutation as negligible and allele frequencies are assumed to result mainly from
86 differences in migration rate and/or effective population size. Hence, the expected value
87 of genetic differences between populations, F_{ST} , is seen as a function of N and m , the
88 effective number of males or female and their migration rate, per generation: $F_{ST}^{(Y-STRs)}$
89 $= 1/(1+N_{male}m_{male})$ and $F_{ST}^{(mtDNA)} = 1/(1+N_{female}m_{female})$ for haploid systems. Hence, the
90 male-to-female ratio per generation $N_{male}m_{male} / N_{female}m_{female}$ were inferred from F_{ST}
91 values ¹³.

92

93 **Results**

94 Figure 1 depicts the genetic relationships amongst the five Comoros villages based
95 on female and male genetic markers. For HVS-I, genetic similarities link the Iconi with
96 Bandamadji while Hayaya and Male stand at peripheral positions. As far as the Y-STRs
97 genetic variation is concerned, the Bandamadji village departs strongly from the four
98 remaining villages, separated with non-significant R_{ST} values. When compared on a
99 haplotype basis, networks mirror the gene diversity pattern showed in Table 1. Iconi,
100 Mitsoudje and Bandamadji encapsulate the highest HVS-I haplotype diversity with
101 numerous branches while most of the Hayaya and Male mtDNAs are included into one
102 main profile. As far as Y-STRs are concerned, every village are spread over the nodes,
103 but Bandamadji which is represented by almost exclusively one profile. Networks also
104 depict a higher pairwise differences (Pw) for HVS-I than for Y-STRs (mean $Pw_{HVS-I} =$
105 9.3 ; mean $Pw_{YSTRs} = 3.3$). Finally, one can notice twice more village-specific haplotypes
106 for HVS-I ($n= 24$) than for YSTRs ($n= 12$).

107 Table 1 shows the female and male gene diversity indices in the five Comoros
108 villages. The main pattern is a higher male than female gene diversity as observed in
109 Hayaya, Male and Mistoudje. Exceptions are Iconi which shows similar values for both
110 uniparental markers, and overall Bandamadji which distinguishes with a higher mtDNA
111 than Y-STRs gene diversity. AMOVA points out that HVS-I presents 3.2-times more
112 genetic variation amongst villages than Y-STRs (respectively 15.32% and 4.74%), but
113 less within-village variation (~0.9-fold, respectively 84.68% and 95.26%). Due to the
114 peculiar behaviour of Bandamadji above-mentioned, we ran an additional AMOVA
115 excluding this village. We noticed an strong increase of the contrasting patterns of within-
116 and between-population genetic variation as seen from HVS-I and Y-STRs (Table 1),
117 since the female genetic variation among populations reached almost 10-fold the male
118 one (17.08% and 1.74%).

119 Lastly, from the F_{ST} values we inferred the magnitude of male-to-female
120 migration ratio per generation for each village and across villages (Table 1 and Figure 2).
121 The main pattern is a male-to-female ratio above 1 in Ngazidja where the male gene flow
122 ranges from 2.6 and 7.1 (mean ratio = 3.5) in four villages (Hayaya, Iconi, Male, and
123 Mitsoudje). Exception is Bandamadji with a male-to-female ratio under 1 (ratio = 0.9),
124 which could signify an equal or slightly more female than male gene flow.

125

126 **Discussion**

127

128 A great variety of human social organizations defined by rules of marriage,
129 residence, descent and mode of subsistence has been described worldwide¹⁵, which in
130 return can substantially impact the genetic diversity^{7,8,16}. At the global scale, populations

131 would be genetically more structured for male than for female genetic markers, mirroring
132 sex-biased gene flows involving mostly women and thus, patrilocality ⁷. Nevertheless,
133 matrilocality rules other societies (e.g.¹⁷) and in the Indian Ocean, the earliest inhabitants
134 of the Comoros originated from the Shambara in East Africa, as the extension of the
135 matrilineal belt that encompassed Africa Bantu which opens to the east since the 11th
136 century ^{3,18}.

137 When examined for uniparental genetic systems, inter- and intra-village genetic
138 diversity in Ngazidja indicate male-oriented gene flows amongst villages. Exception is
139 Bandamadji which behaves as a patrilocal population. Oral and historical knowledge
140 evokes that Bandamadji was the military basis of one of the great Comorian clan
141 M'Dombozi, where men have sworn fidelity to their sultan Hachim ben Ahmed (died
142 1889) to stay to protect the city (¹⁹ and Kassim Papa, pers. com.).

143 Finally, the Comorian villages are organized according to the social space in
144 which males and females participate distinctly, and the present data agree with the ethno-
145 historical records ². Human gene diversity results mainly from demography, natural and
146 cultural selection. The present study evidences that amongst and within human
147 populations, genes also flow through the channels dug by culture. It especially illustrates
148 the positive collaboration between geneticists and anthropologists to search together how
149 distribution maps of biological phenomena and cultural phenomena illuminate each other
150 ²⁰.

151 **Acknowledgements**

152 We are grateful to all the people who volunteered to participate in the study. We also
153 thank Yannick Bernardie, and Adem Miraoui from the UMR7268 ADES for their help in
154 handling the data, as well as Julie DiCristofaro from the UMR7268 ADES and
155 Etablissement Français du Sang for her constructive comments. Lastly, we thank Kassim
156 Papa, responsible for preparation of blood-derived products at the EFS Reunion, for
157 helpful insights on village history.

158

159

160 **References**

161

162 1. Fontes P, Coudray J, Eberschweiler C, Fontes J-C: Datation et conditions
163 d'occupation du site de Koungou (Ile de Mayotte). *Revue d'Archéométrie* 1987;
164 11: 77-82.

165

166 2. Blanchy S: Famille et parenté dans l'archipel des Comores. *Journal des*
167 *africanistes* 1992; 62: 7-53.

168

169 3. Allibert C, Vérin P: The early pre-Islamic history of the Comores Islands: links
170 with Madagascar and Africa; in: Reade J (ed): *The Indian Ocean in Antiquity*.
171 London: Kegan Paul International, 1996, pp 461-470.

172

173 4. Pauly M: La diffusion de l'islam à Mayotte à l'époque médiévale. *Revue des*
174 *archives départementales de Mayotte* 2014; Taarifa 4: 63-89.

175

176 5. Brucato N, Kusuma P, Beaujard P, Sudoyo H, Cox MP, Ricaut FX: Genomic
177 admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean
178 trading network. *Scientific reports* 2017; 7: 2919.

179

180 6. Blanchy S: *Maisons des femmes, cités des hommes. Filiation, âge et pouvoir à*
181 *Ngazidja (Comores)*. Nanterre: Société d'ethnologie, 2009.

182

183 7. Oota H, Settheetham-Ishida W, Tiwawech D, Ishida T, Stoneking M: Human
184 mtDNA and Y-chromosome variation is correlated with matrilineal versus
185 patrilineal residence. *Nat Genet* 2001; 29: 20-21.

186

187 8. Seielstad MT, Minch E, Cavalli-Sforza LL: Genetic evidence for a higher female
188 migration rate in humans. *Nat Genet* 1998; 20: 278-280.

189

190 9. Msaidie S, Ducourneau A, Boetsch G et al: Genetic diversity on the Comoros
191 Islands shows early seafaring as major determinant of human biocultural
192 evolution in the Western Indian Ocean. *Eur J Hum Genet* 2010; 19: 89-94.

193

194 10. Excoffier L, Laval G, Schneider S: Arlequin (version 3.0): An integrated software
195 package for population genetics data analysis. *Evolutionary bioinformatics online*
196 2005; 1: 47-50.

197

198 11. Bandelt HJ, Parson W: Consistent treatment of length variants in the human
199 mtDNA control region: a reappraisal. *Int J Legal Med* 2008; 122: 11-21.

200

201 12. Qamar R, Ayub Q, Mohyuddin A et al: Y-chromosomal DNA variation in
202 Pakistan. *Am J Hum Genet* 2002; 70: 1107-1124.

203

- 204 13. Segurel L, Martinez-Cruz B, Quintana-Murci L et al: Sex-specific genetic
205 structure and social organization in Central Asia: insights from a multi-locus
206 study. PLoS Genet 2008; 4: e1000200.
- 207
- 208 14. Destro-Bisol G, Donati F, Coia V et al: Variation of female and male lineages in
209 sub-Saharan populations: the importance of sociocultural factors. Mol Biol Evol
210 2004; 21: 1673-1682.
- 211
- 212 15. Marlowe F: Paternal investment and the human mating system. Behav Processes
213 2000; 51: 45-61.
- 214
- 215 16. Hunley KL, Spence JE, Merriwether DA: The impact of group fissions on genetic
216 structure in Native South America and implications for human evolution. Am J
217 Phys Anthropol 2008; 135: 195-205.
- 218
- 219 17. Besaggio D, Fuselli S, Srikumool M et al: Genetic variation in Northern
220 Thailand Hill Tribes: origins and relationships with social structure and linguistic
221 differences. BMC Evol Biol 2007; 7 Suppl 2: S12.
- 222
- 223 18. Jones D: The matrilineal tribe: an organization of demic expansion. Hum Nat
224 2011; 22: 177-200.
- 225

226 19. Martin J: Les débuts du protectorat et la révolte servile de 1891 dans l'île
227 d'Anjouan. Revue française d'histoire d'outre- mer 1973; 60: 45-85.

228

229 20. Levi-Strauss C: Le regard éloigné, Plon edn. Paris: EDI8, 1983.

230

Titles and legends to tables and figures

231

232

233 Table 1. Summary statistics of mtDNA and Y-STRs genetic variation within and between
234 five villages of Ngazidja. Pw: mean number of pairwise differences. Values in the
235 Ngazidja column were obtained from the AMOVA. Male-to-female ratio was inferred
236 from Ségurel et al. 2008.

237

238 Fig 1. Multidimensional Scaling of F_{ST} and R_{ST} genetic distances and haplotype networks
239 (NETWORK 5.0) for mtDNA HVS-I (left panel) and Y-STRs (right panel)

240

241 Fig.2 Intensity of female and male gene flow amongst the five villages understudy. Width
242 of the tip of the arrows is proportional to $\log_{10}(F_{ST}^r \text{ ratio})$. Grey: female/male ratio >1 ,
243 white: male/female ratio >1 . Background map was taken from www.d-maps.com©.

244

245 S1Table (.xlsx). Y-STRs haplotypes in five Comorian villages

246

247 S2 File (.doc). HVS1 profiles in five Comorian villages

248

249

250 Table 1. Summary statistics of mtDNA and Y-STRs genetic variation within and between five villages of N'gazidja. Pw: mean number of pairwise
 251 differences. Values in the Ngazidja column were obtained from the AMOVA. Male-to-female ratio was inferred from Ségurel et al. 2008.

252

Genetic marker	Estimator	Bandamadji	Hahaya	Iconi	Male	Mitsoudje	Ngazidja
mtDNA	Sample size	11	20	17	18	11	77
	Gene diversity	0.946	0.742	0.985	0.699	0.927	0,864
	Pw	10.1	4.3	10.8	10.4	10.8	
	Mean F_{ST} with the other villages	0.108	0.220	0.071	0.150	0.098	0.136
Y-STRs	Sample size	9	16	22	22	17	86
	Gene diversity	0.722	0.942	0.952	0.987	0.971	0.953
	Pw	2.3	3.3	3.7	3.6	3.5	
	Mean F_{ST} with the other villages	0.114	0.043	0.018	0.062	0.032	0.048
	Mean male-to-female ratio	0.9	7.1	7.0	2.6	3.3	3.6

253

Figure 1

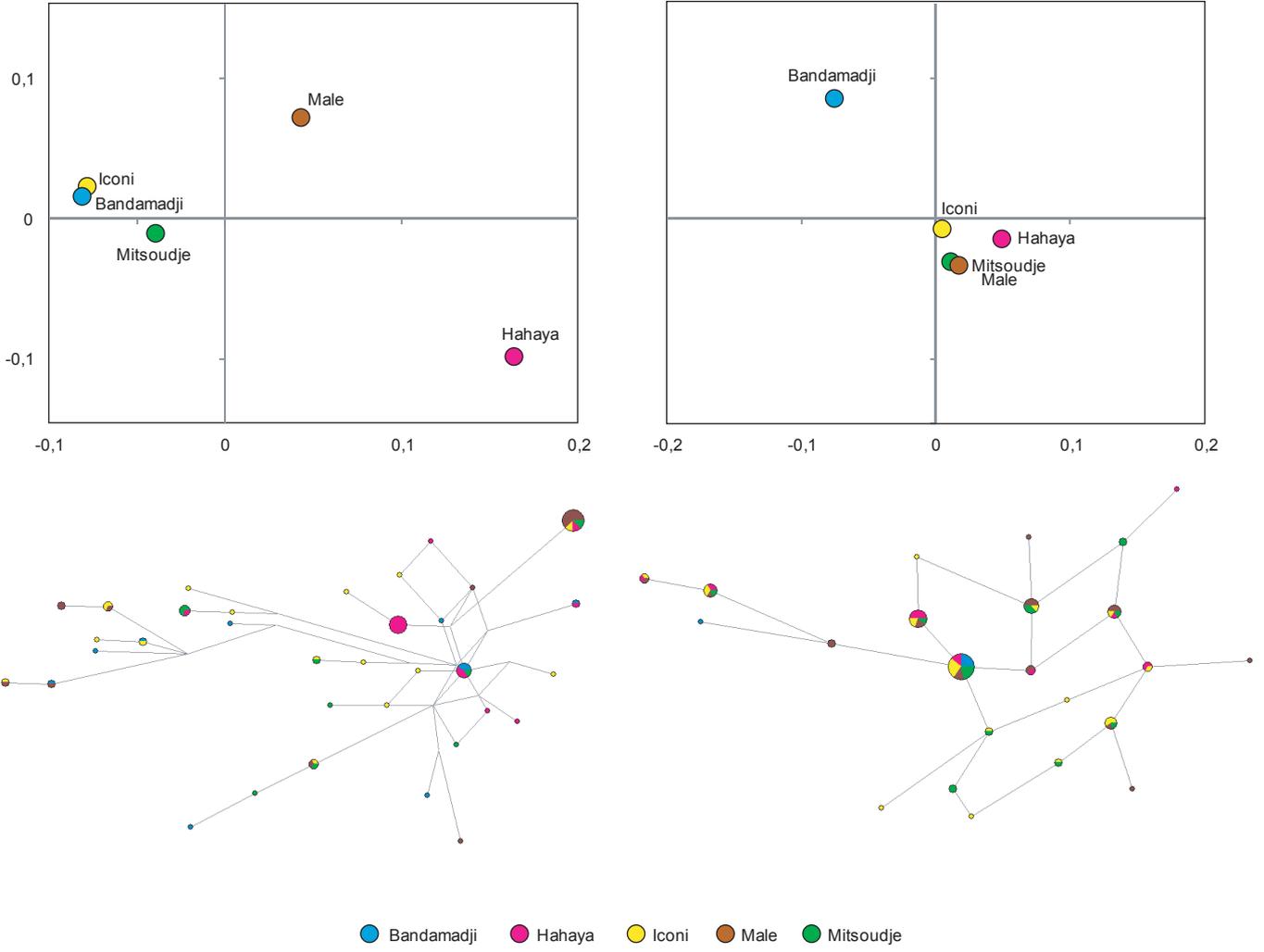


Figure 2

