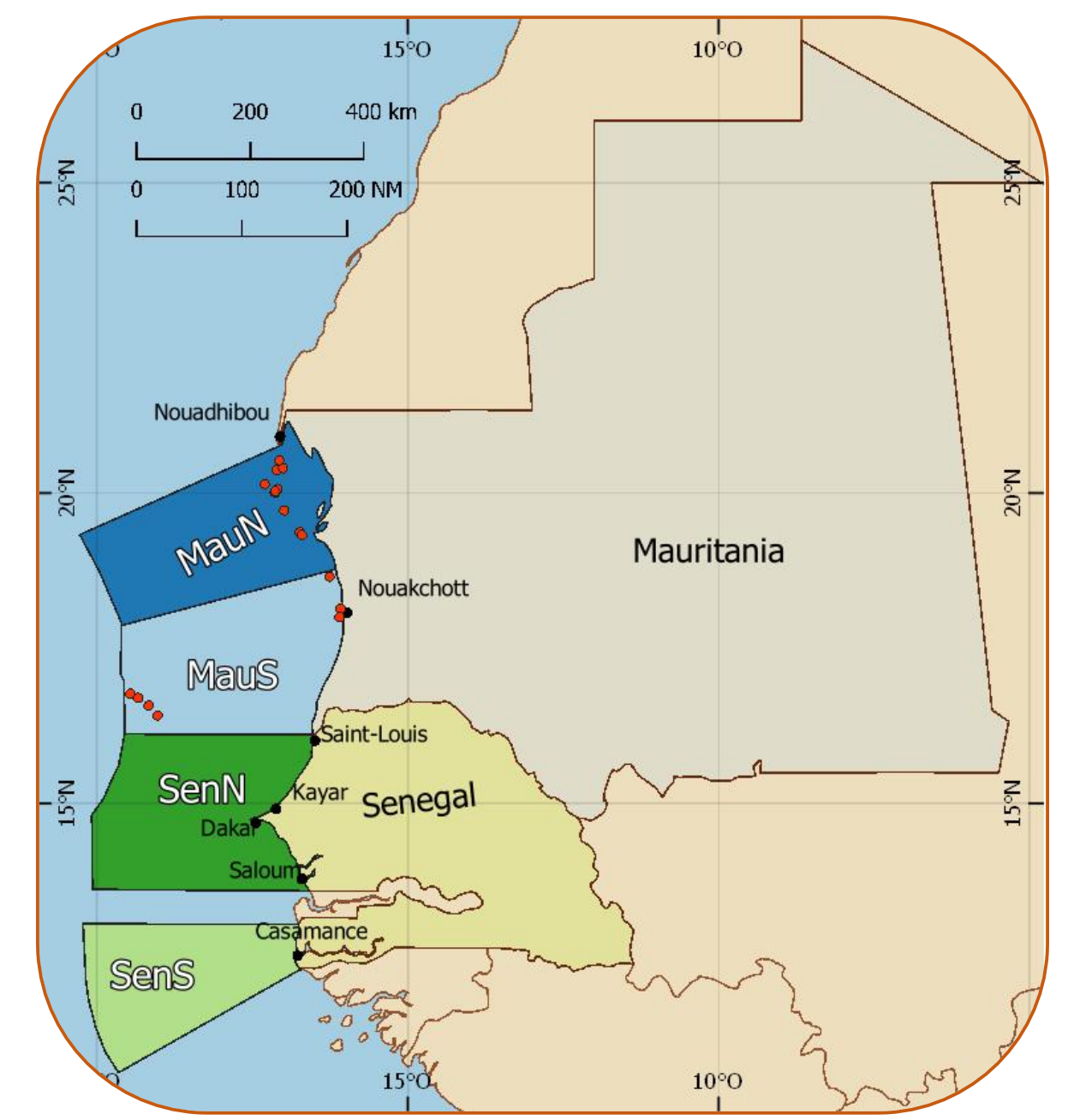


### 1 Introduction

The thiof *Epinephelus aeneus* (GPW) is assumed by CECAF as a single management unit for Mauritania, Senegal and the Gambia.

The application of stock identification methods can reveal inconsistencies between the spatial structure of biological populations and the definition of stock units used in assessment and management.

The aim of the genetic analyses is to identify the geographical boundaries of the stocks using microsatellite markers.



### 2 Methods

#### Samples (Country-Sampling year)

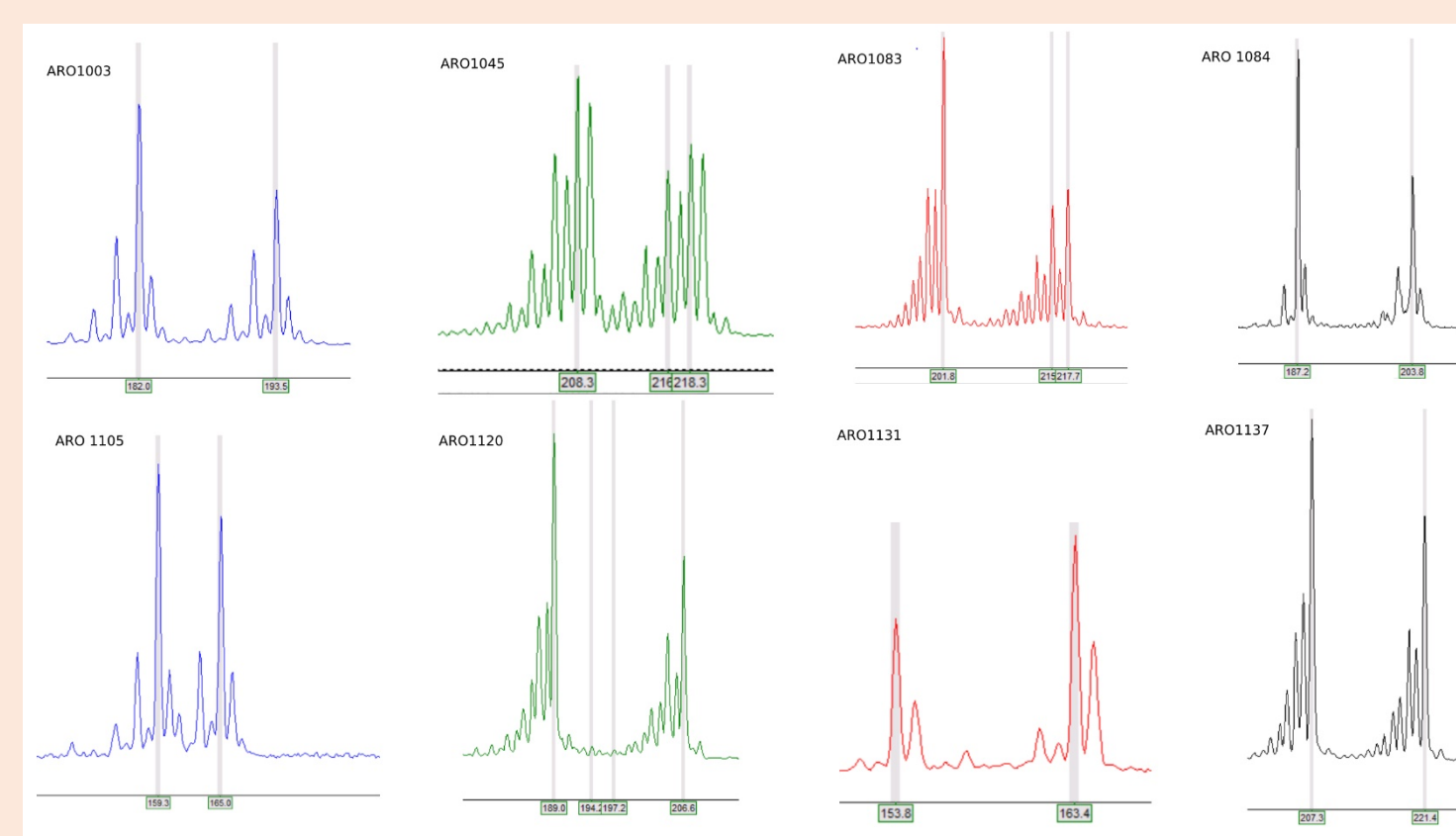


#### Microsatellite markers (Dor et al., 2014)

The final design allowed amplification of eight microsatellite loci in two multiplex PCR (M1 and M2) and a single PCR (M3).

Multiplex	Locus	Primer F	Primer R
M1	ARO1105	TGATAGCTTTACATGCACCTCA	CTGAACCTCACCTGAAA
M1	ARO1045	CACGAAGTATTGGCTGAT	GAGAAAGTGCAATATTGAC
M1	ARO1083	CCGGTCTTCTCTCTCCC	TTACTGTTGATTGAGTTGTTGT
M1	ARO1084	GGGTTATTTCAAAGGTCAG	CCCAATGAGGTGTTCAATAT
M2	ARO1003	GTGCAAGGCAAGCTGTGTTA	AGCAGGCATCTTGTATCTGG
M2	ARO1120	CTCTGATGCTGTTACACAAC	TCTCCATCGAAGGTAAAGG
M2	ARO1137	ATGGGTATAATTAGGACACACT	AGGAAAGGAGGGAGGAAA
M3	ARO1131	TGTGTGTCAGAGGTGGTT	TGAATTTCACTCATGTTTC

#### Allele calling



GeneMarker®

The established internal threshold for missing data per individual was 25% (two loci with missing data), resulting in genetic data for 354 GPW.

#### Genetic diversity estimation



Number of alleles (Na), No. of Effective Alleles (Ne), Observed Heterozygosity (Ho), Expected Heterozygosity (He), Unbiased Expected Heterozygosity (uHe)



Departures from Hardy-Weinberg equilibrium (HWE), Inbreeding coefficient  $F_{IS}$

#### Genetic differentiation and migration



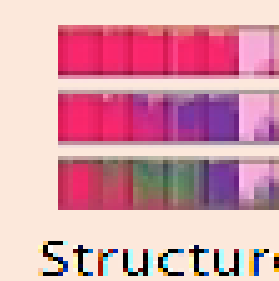
pairwise  $F_{ST}$ , Number of migrants (Nm)



pairwise  $F_{ST}$ , Number of migrants (Nm)

adegenet R package

Discriminant Analysis of Principal Components (DAPC), distance-method approach



STRUCTURE with STRUCTURE HARVESTER and CLUMPAK: model-based clustering, Bayesian approach

### Genetic analysis by country-zone

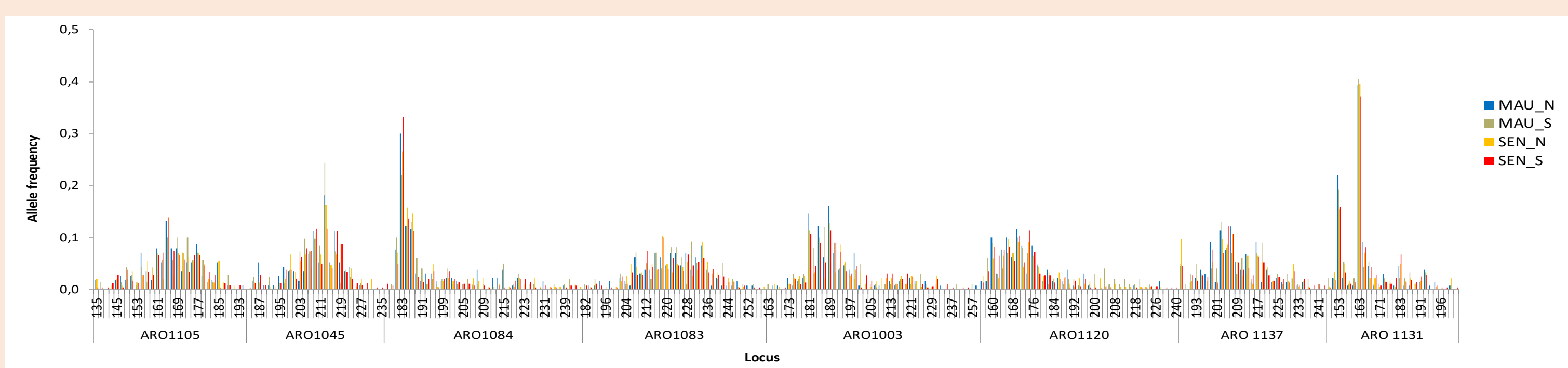
### 3 Results

#### Characterization of genetic diversity at GPW microsatellite loci

Pop <sup>a</sup>	ARO1105	ARO1045	ARO1084	ARO1083	ARO1003	ARO1120	ARO 1137	ARO 1131
MAU_N	57/23	58/21	65/22	65/30	65/27	65/26	66/24	66/19
MAU_S	35/23	41/18	50/27	49/26	50/30	50/28	50/24	47/19
SEN_N	72/26	71/22	92/31	93/30	93/33	93/35	93/26	91/22
SEN_S	120/28	120/24	143/35	140/33	145/33	145/24	144/28	141/24

<sup>a</sup>Pop refers to each port where GPW were collected. Number of GPW individuals (N) and number of alleles (Na) characterized for each microsatellite loci. Each cell indicates data for N/Na.

#### Allele frequency



#### Population structure $F_{ST}$ – Number of migrants

Pop <sup>a</sup>	N	Na	Ne	$H_o$	$H_e$	$uH_e$
MAU_N	63	24	13	0.871	0.903	0.910
MAU_S	47	24	13	0.893	0.909	0.919
SEN_N	88	28	14	0.861	0.913	0.919
SEN_S	137	90	14	0.866	0.912	0.915

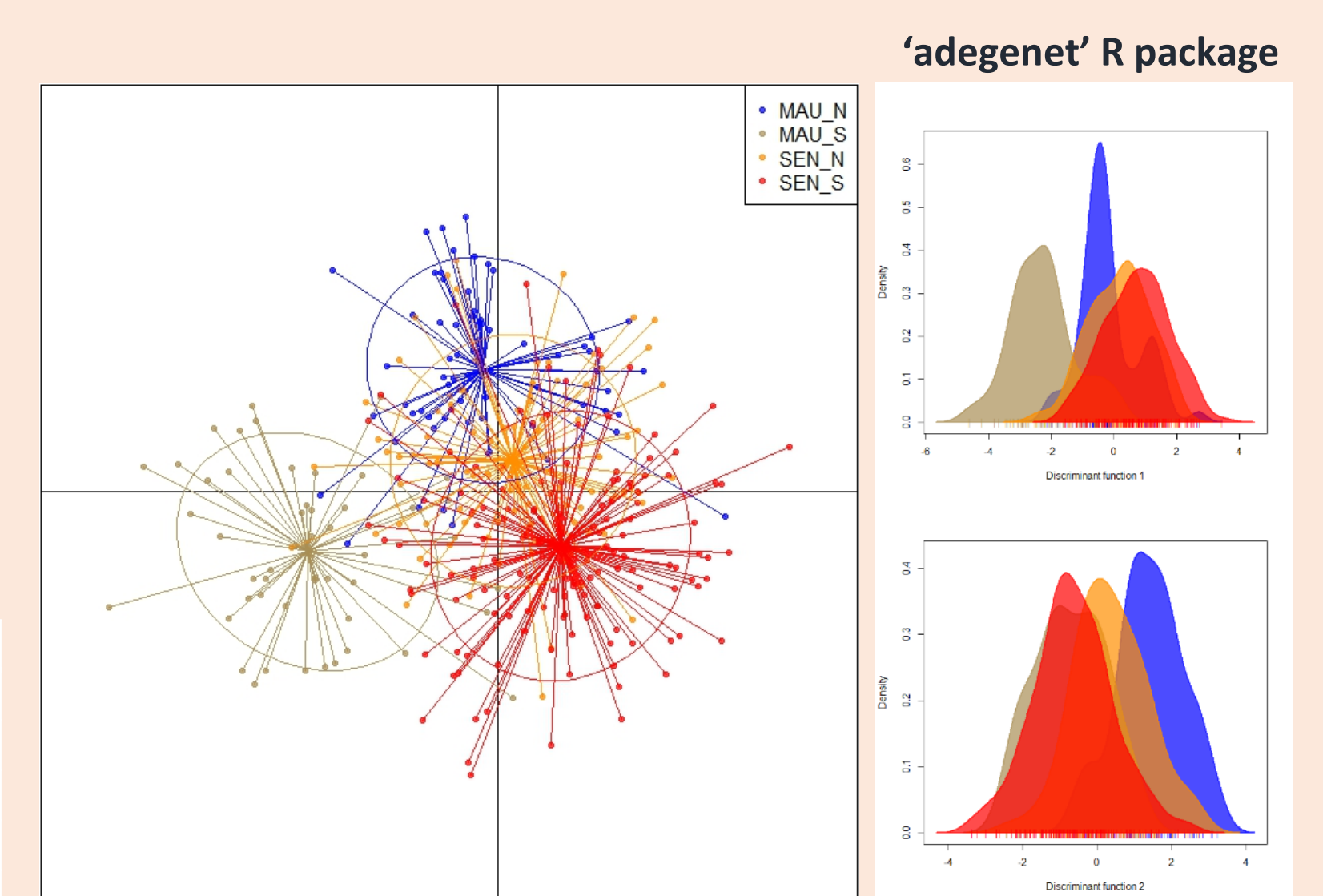
N, number of individuals analyzed; Na, number of different alleles; Ne, number of effective or equally frequent alleles;  $H_o$ , observed heterozygosity;  $H_e$ , expected heterozygosity according to allele frequencies;  $uH_e$ , unbiased expected heterozygosity according to sample size

#### Number of migrants

Locus	All Pops
ARO1105	52
ARO1045	37
ARO1084	47
ARO1083	48
ARO1003	35
ARO1120	55
ARO1137	54
ARO1131	84
Mean ± SE	51 ± 5

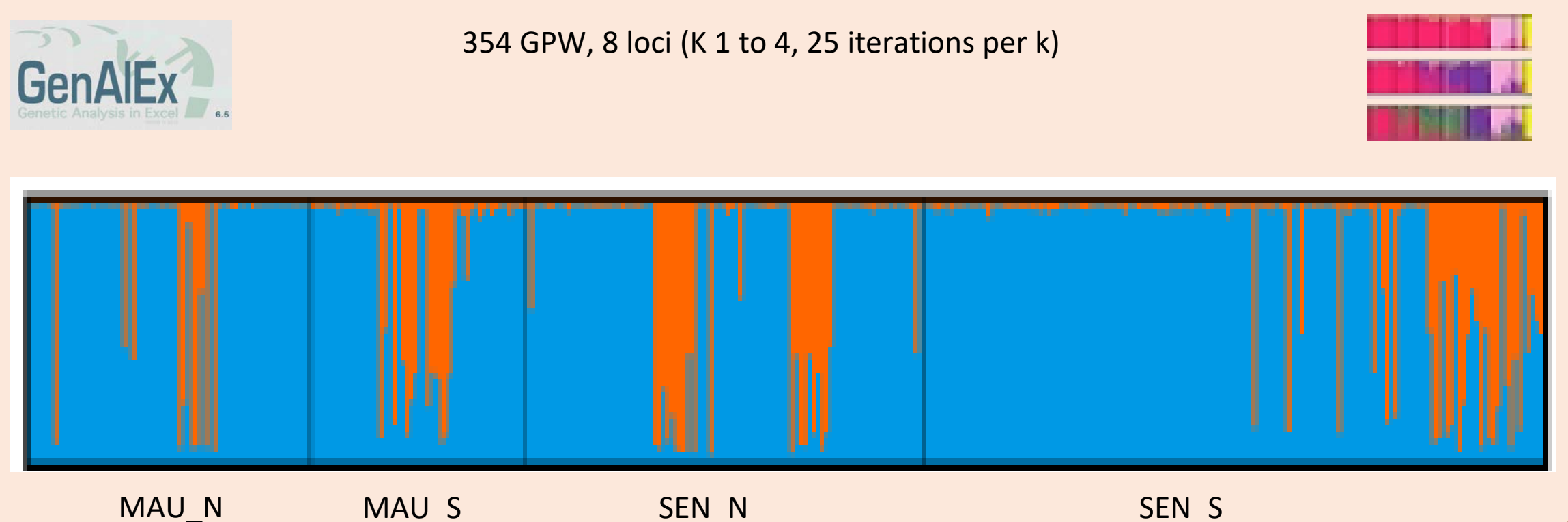
#### Discriminant Analysis of Principal Components (DAPC)

4 pops, 354 GPW, 8 loci



#### STRUCTURE - Bayesian analysis

354 GPW, 8 loci (K 1 to 4, 25 iterations per k)



Pop <sup>a</sup>	ARO1105	ARO1045	ARO1084	ARO1083	ARO1003	ARO1120	ARO 1137	ARO 1131
MAU_N	0.0508	-0.0259	0.0482	0.0185	0.2504***	0.0508	-0.0329	-0.0221
MAU_S	0.0084	0.0537**	-0.0128	-0.0047	0.1752***	0.0131	-0.0129	0.0105
SEN_N	0.0302	0.0263	0.1438*	0.0771***	0.1345*	0.0161	0.0643	0.0078
SEN_S	0.0092	0.0682	0.0730	0.0495	0.1659***	0.0304*	0.0218	0.0144

Each cell indicates the value of the inbreeding coefficient  $F_{IS}$  calculated according to (Weir and Cockerham, 1984), followed by the significance level (\*  $p < 0.05$ , \*\*  $p < 0.01$ , or \*\*\*  $p < 0.001$ ) of the probability p value obtained with the exact probability test for Hardy-Weinberg equilibrium calculated by the Markov chain method (10,000 dememorization, 1,000 batches, 1,000 iterations per batch).

$F_{ST}$  pairwise comparison of GPW genetic diversity at 8 loci in 4 populations.

### 4 Conclusions (preliminary)

The selected microsatellite markers have a high variability. The designed genetic tool (3 PCR reactions, 8 loci) is suitable for the assessment of connectivity in the species. All genetic analyses show high gene flow and homogeneity in the study area. Introgression detected with the Bayesian analysis performed with *Structure* suggests the presence of migrants from other regions in the area.

The extension of this study to longer periods and to northern and southern areas is highly recommended to determine appropriate geographic boundaries, needed to define the structure and distribution of this West African stock.



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