Genetic diversity and structure in Cameroon native goat populations using microsatellites

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Indigenous/local goat breeds are critical for subsistence of smallholders in the world (Pollot and Wilson, 2009).

In most developing countries, goats breeds have been merely considered and documented (Wilson, 1990) .

=> Consequences: low performances, unpredictable crossings and genetic erosion (Groenevald *et al.,* 2010).

Genetic status of majority of livestock in developing world is still very scanty (Guimarães *et al*., 2007).

With about 5millions heads, Cameroon hosts a variety of goats types (MINEPIA, 2010)

Common names from literature: *Cameroon Dwarf*, *West African Dwarf Goat*-*Chèvre Naine de Guinée*, *Djallonke Goat, Nigerian Goat*, *Pygmy Goat*, *Dwarf Goat*-*Chèvre Naine, Fouta Djallon Goat et chèvre Kirdi* (Epstein, 1962; Devendra and Burns, 1982; Lauvergne *et al.*, 1993).

These various names = possible genetic variability in goats from the coastal Atlantic ocean =➜ northen arid Sahelian region?

Background

Genomic application in farm animal is at its initial stage in Cameroon.

Short tandem repeat **(STR) or short sequence repeats (SSR)** markers or microsatellites developed did not take into account sub saharan goat populations variability (Hanotte et al., 2004).

Their application are popularized in tropics as a tool to assess in very efficient way the diversity in livestock

Research Objective

Characterize the genetic relationships between 08 Cameroonian goats ecotypes by the application of a panel of 17 SSR markers

Sampling approach
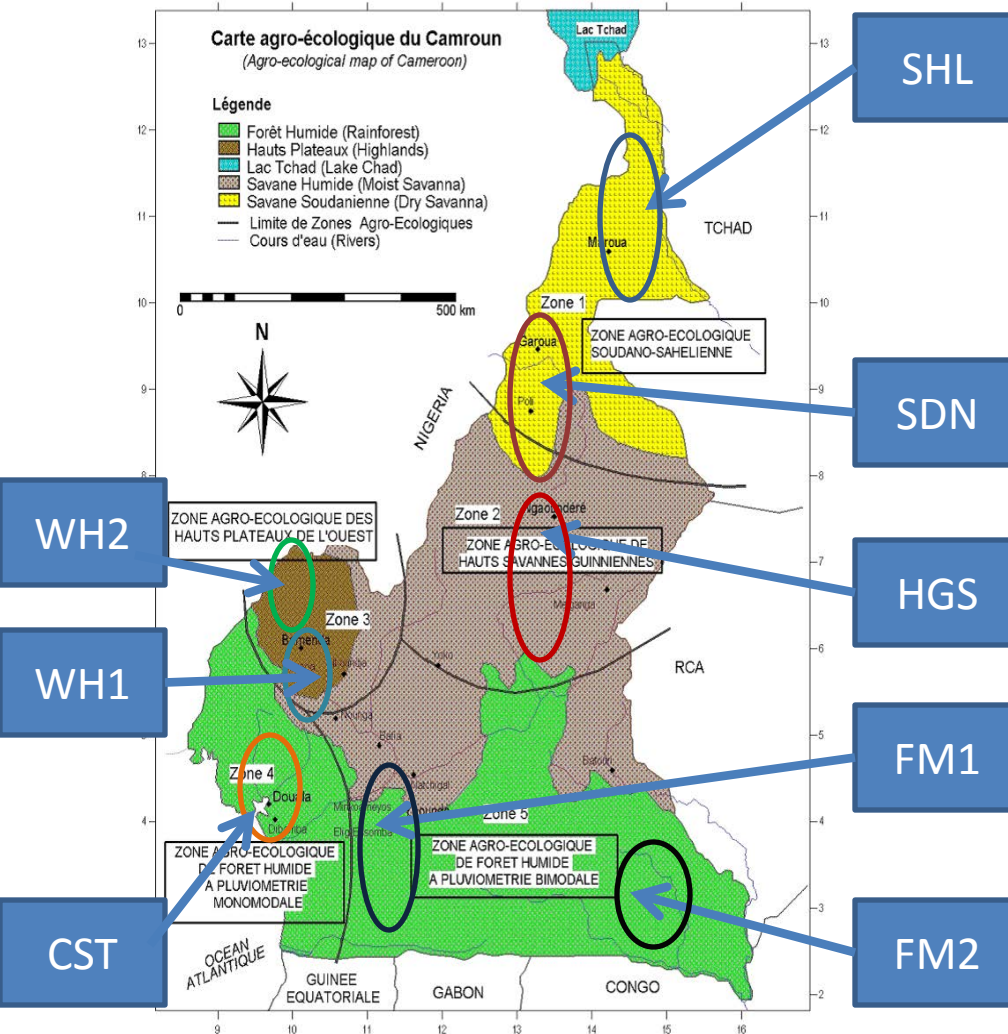
- 190 goats (M/F) not related and randomly

- Dry spot blood on FTA Whatmann

- Georeferencing with GPS

- gDNA extraction using Invitrogen kit

- 35 cycles for 25µl total volume Rx

- Genotyping under ABI 3130 and GeneMapper v.4

Figure 1: Agro ecological regions and sampled ecotypes

SHL = Sahelian Longipes HW ≥ 65cm; LBW=20-45kg Variable coat color Meat, skin and milk	**SDN = Kirdi** Longipes-Mediopes HW ≈ 60cm; LBW=20-35kg Variable coat color Meat, skin and milk
WH1 = Djallonke Mediopes-Naine HW≤65cm; LBW=15-30kg Variable coat color Meat and goatlings	**HGS=Djallonke** Longipes-Mediopes HW≤65cm; LBW=15-40kg Variable coat color Meat and milk
WH2 = Djallonke Mediopes-Dwarf HW≤65cm; LBW=15-30kg Variable coat color Meat	**FM2=Djallonke** Dwarf HW ≤55cm; LBW=15-25kg Variable coat color Meat
FM1 = Djallonke Dwarf HW ≤50cm;LBW=15-25kg Variable coat color Meat	**CST= Djallonke** Dwarf HW ≤50cm;LBW=15-25kg Variable coat color Meat

Figure 2: Main features of local goat ecotypes

Table 1: Microsatellites Markers

N°	Microsatellite	Allele size (bp)	Annl. T°c	Dye
1	ILSTS029	148-170	**56.6**	NED
2	SRCRSP3	98-122	**56.6**	NED
3	ETH10	200-210	**57.0**	PET
4	CSRD247	220-247	**62.2**	PET
5	TCRVB6	217-255	**59.2**	PET
6	SRCRSP7	117-131	**50.7**	PET
7	SRCRSP9	99-125	**58.8**	PET
8	McM527	167-247	**59.0**	VIC
9	ILSTS005	172-208	**60.3**	VIC
10	MAF209	100-104	**56.6**	VIC
11	OarFCB20	80-130	**54.0**	VIC
12	MAF065	116-158	**62.5**	VIC
13	DRBP1	195-229	**63.0**	VIC
14	INRA063	164-186	**63.3**	VIC
15	MAF70	134-178	**60.6**	6-FAM
16	BM6444	118-200	**65.5**	6-FAM
17	SPS113	134-158	**62.5**	6-FAM

Some statistical parameters:

✓ Allele frequency and Heterozygosity

✓ Diversity and Polymorphism information content

✓ AMOVA under GenAlEX 6.5 (Peakall and Smouse 2012)

✓ FST values amongst populations (Arlequin)

✓ K probability, K = sub populations given by Evanno et al., (2005) under STRUCTURE

✓ Admixture estimation of caprine population following Pritchard et al., (2000) ; et Falush et al., (2003 et 2007).

Table 2: Statistical values obtained from microsatellites analyses

| Markers	Maj. Allele Freq.	Genotype Nbr	Obs. Nbr	Allele Nbr	Gene Diversity	He	PIC
BM6444	0.241	28	93	15	0.864	0.258	0.851
CSRD247	0.317	29	93	13	0.811	0.602	0.788
DRBP1	0.301	20	138	10	0.820	0.239	0.799
ETH10	0.357	10	157	5	0.677	0.561	0.608
ILSTS005	0.869	12	176	7	0.239	0.102	0.232
ILSTS029	0.237	43	150	12	0.853	0.793	0.836
INRA063	0.632	11	125	7	0.543	0.376	0.496
MAF065	0.383	26	64	10	0.782	0.453	0.758
MAF70	0.341	42	167	14	0.794	0.677	0.769
MAF209	0.424	11	170	5	0.677	0.529	0.615
MCM527	0.368	24	167	10	0.749	0.515	0.712
OarFCB20	0.237	33	173	10	0.821	0.555	0.798
SPS113	0.421	22	87	8	0.809	0.713	0.783
SRCPSP3	0.513	15	140	6	0.682	0.557	0.628
SRCRSP7	0.286	8	79	5	0.545	0.443	0.444
SRCRSP9	0.340	38	119	12	0.846	0.597	0.831
TCRVB6	0.386	25	119	9	0.776	0.697	0.743
Mean	0.386	23.35	130.412	9.294	0.723	0.510	0.688

Molecular Variance percentage
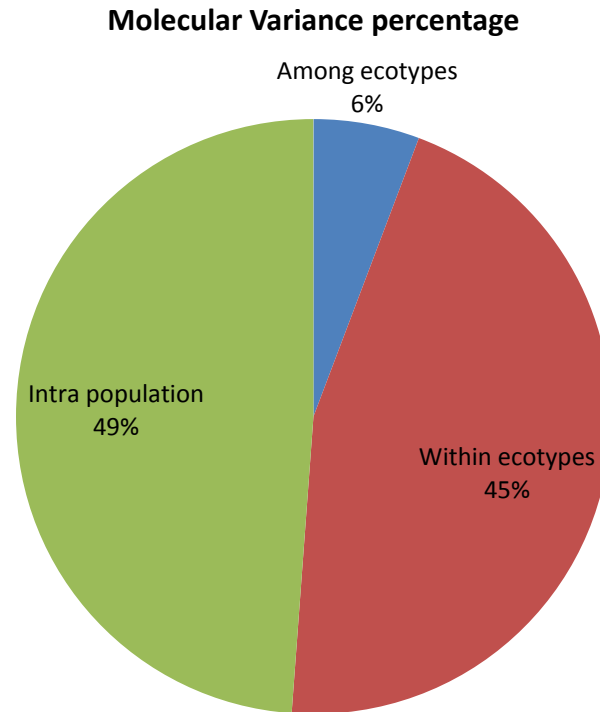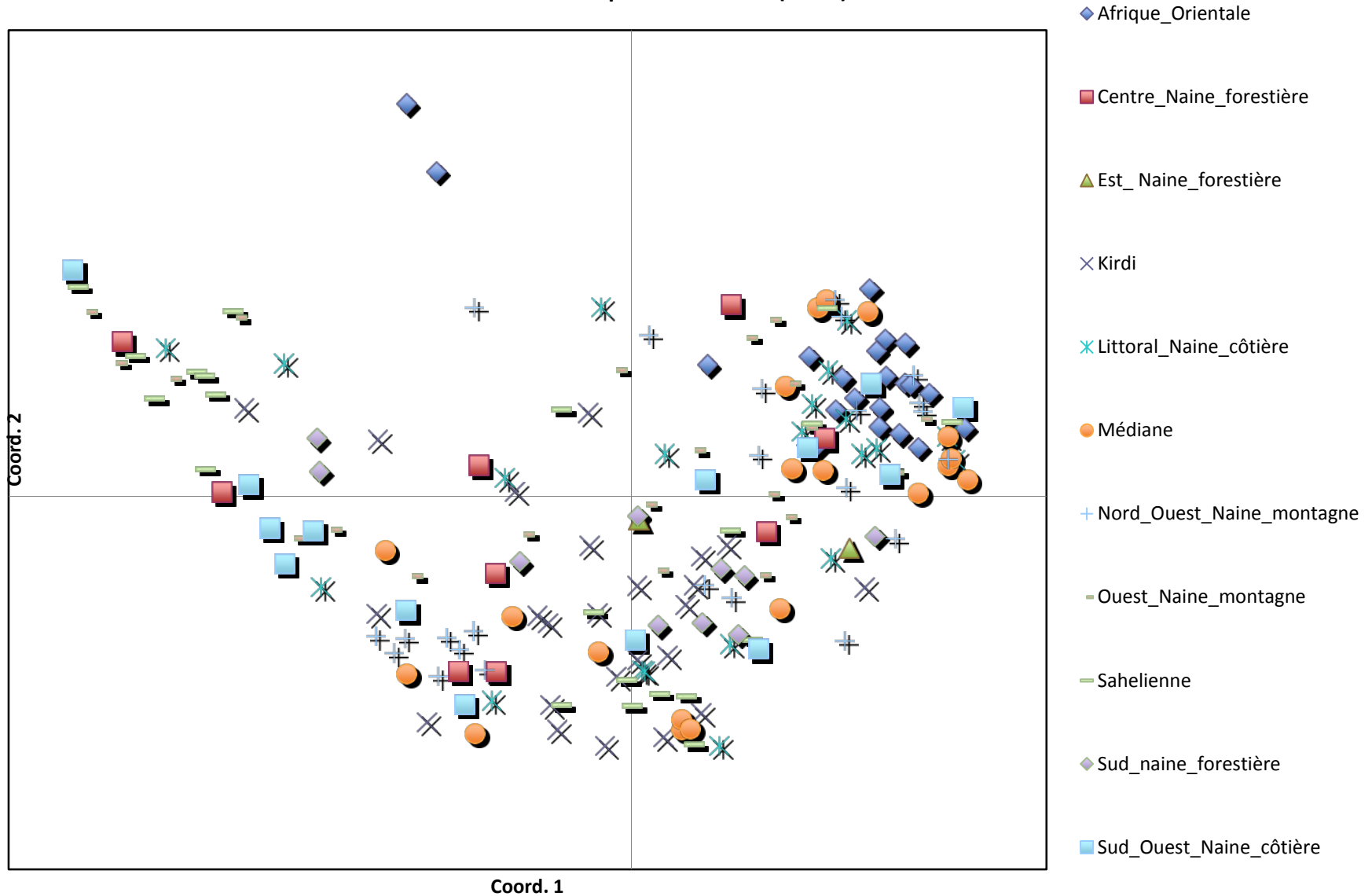
Figure 3: Molecular variance in Cameroon goat population

Figure 4: Principal Component Analysis in Cameroon goat population

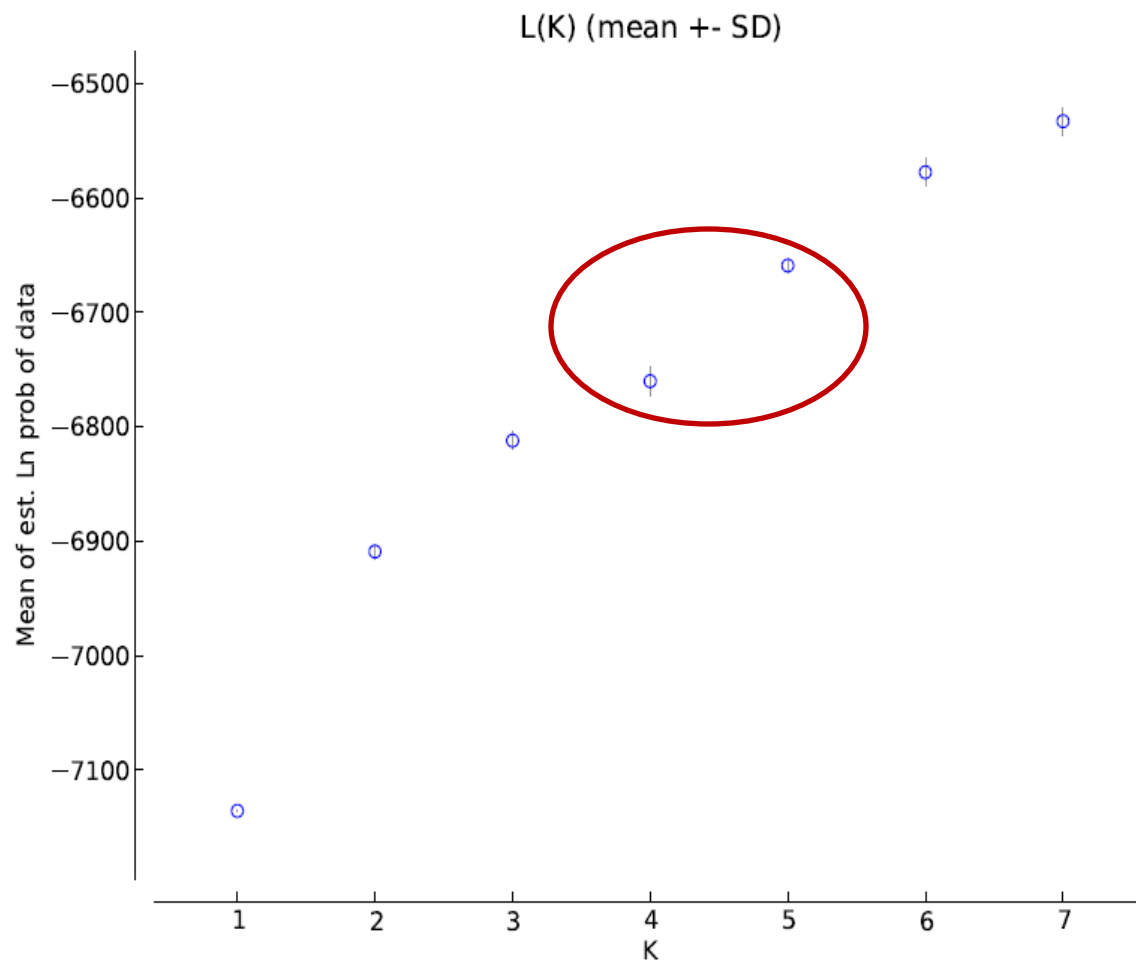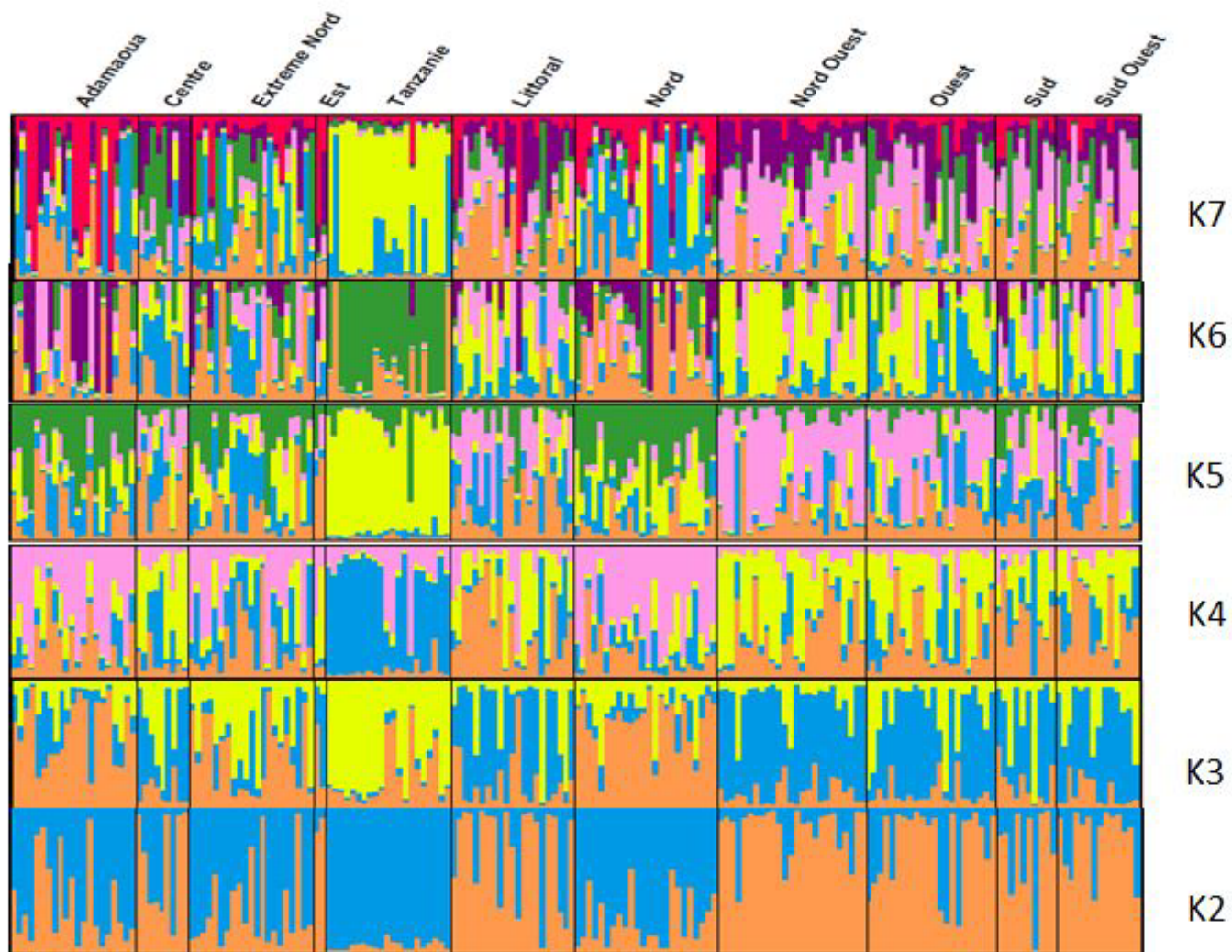Figure 5 : Estimation of Cameroon population structure by Evanno's procedure

Figure 6 : Admixture trend in Cameroon goat population

Conclusion

- All 17 SSR are polymorphic in different Cameroon goat ecotypes.
- Results suggest variability among Cameroon goat population
- At least 4 putative populations exist
- Admixture tendency => high

Further analysis and more specific SSR applications are needed.

Some measures are needed to avoid massive dilution of native goat population

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Thank You!!!