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Original Research Paper

Multivariate analysis of local pig populations in the rural areas of High-Katanga province, DR Congo

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Abstract

Morpho-biometric characteristics of 342 local pigs from the rural areas of Kasenga and Kambove in Haut-Katanga province were studied with the objective to analyzing genetic variability, determining population structure, establishing phylogenetic relationships between the pig populations studied and identifying probable genetic types. The data collected were subjected to principal component analysis (PCA), hierarchical clustering (HCA) and discriminant factor analysis (DFA). The main results showed that the first two principal components (F1 and F2) explained more than 61.5% of the total phenotypic variability observed in the pig population studied. The highly correlated variables are height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, muzzle length, tail length, hind leg length, hock length, foreleg length. The F1 axis is clearly related to height at withers, body length, shoulder length and body length seem to be the most discriminating variables. The study population would consist of three genetic types, which can be grouped into two subgroups based on intra/inter population variation and genetic distances. The quantitative parameters studied, and sex are the variables that best characterize the pig populations (p<0.05). The local pig is therefore an animal genetic resource with high breeding potential due to its biodiversity.

Keywords: Morphometry; multivariate analysis; pig; High-Katanga **Introduction**

In the different regions of Africa, the breed most raised by the African population is the local pig because it requires few inputs and is characterized by its ability to adapt to difficult farming conditions. (Mopaté et al. 2010). In developing countries, livestock production provides income to poor subsistence farmers in the tropics (FAO, 2012) and is therefore well suited to fighting poverty (Mopate et al.; 2010). The improvement of the genetic potential of local animal resources in Africa in general and in D.R. Congo in particular remains unsatisfactory, less documented and information on the characteristics of local pigs is insufficient (Akilimali et al. 2017), There is a lack of political will to support the development and implementation of specific breeding programs for different local animal genetic resources.

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Therefore, the characterization of phenotypic biodiversity of animal populations in general and local pigs in particular in developing countries plays a role in maintaining genetic resources as a basis for the future improvement of animal productions. Domestic animal diversity is a boundary that has been used to define the genetic differences between and within species used for food and agriculture (Cardellino et Boyazoglu, 2009, Dongmo et al.2020). The greatest genetic diversity of animal populations in the world is found in these countries where local breeds are still poorly characterized; this leads to a significant loss of biodiversity and consequently of genetic variation in populations (Kastelic et al. 2005; Adamczyk et al. 2008). Phenotypic characterization of domestic animals is essential for the development of sustainable strategies for the management and conservation of alternative local animal genetic resources and for their genetic improvement (Lauvergne, 1982; FAO, 1998; 2013). In Africa, some studies have been conducted on the characterization of local pigs, notably in Ghana (Adjei et al. 2015) and in Benin (Djimenou et al. 2018) et Youssao et al. 2018). However, most of this work has been restricted to the use of one-factor analysis of variance, whereas the current trend in breed classification involves the use of multivariate statistical tools (Yakubu and Akinyemi, 2010). Multifactor discriminant analyses have proven to be more appropriate for assessing variation within a breed and for discriminating different population types when all variables are considered together (Dossa et al. 2007).

Thus, on the basis of morphometric traits, it was a question of using principal components and discriminant multifactor analysis to characterize and describe local pig populations in the rural areas of Haut-Katanga province in order to guide the implementation of sustainable management and conservation strategies for this genetic resource and consequently its genetic improvement and preservation. It is in this context that this study was initiated with the aim of analyzing genetic variability, structuring the local pig population, establishing phylogenetic relationships, and identifying genetic types. There would be a phenotypic diversity of pigs in the study areas and the pigs in these environments would be structured into several types or groups of populations.

Materials and Methods

Presentation of the study area

The study was conducted in 11 different villages located along the Kasenga road (sampwe1, sampwe2, maxeme, malambwe, kakana) and the Likasi road (luisha, kapolowe gare, kapolowe mission, lupepamshi, Katanga, chinakwa). These villages were chosen according to accessibility, the presence of pig farms and the financial means available.

In general, these rural areas of the province are characterized by a CW6 type climate according to Koppen's classification (Leteinturier, 2002). This is characterized by the alternative of a rainy season of 185 days (November to May) and a dry season of 118 days (May to September) with October and April as the transition months, July and August being dry. The average annual temperature is 20°C (Leteinturier, 2002).

October and November are the warmest months with a daily maximum average of 32° C and a monthly average temperature of 23° C. On the other hand, July is the coldest month with a daily minimum average of 8° C and a monthly average temperature of 17° C (Kidinda et *al*. 2015). Humidity varies greatly throughout the year, with a minimum of 50% at the end of the dry season to over 80% in the middle of the rainy season (Leteinturier, 2002).

The vegetation is dominated by clear savannahs, including trees and shrubs. More than 10 km south of the city, one can see the clear forest of Miombo resulting from the regeneration of the wastelands of the Muhulu primary mowed to practice agriculture and the manufacture of embers. The vegetation suffers from the impact of pollution due to the effects of the mining companies' discharges. (Leteinturier, 2002 and Kidinda et *al.* 2015)



Figure 1. Map of the territories of Kambove and Kasenga

Data collection

Based on the principles of characterization of local pig genetic resources described by FAO (2013) and adapted by AU-IBAR (2015), the data set was collected on a population of 342 adult and relatively unrelated local pigs. Quantitative traits considered were live weight, head length, snout length, ear length, face length, thoracic girth, Height at withers, shoulder length, forelimb length, hindlimb length, pelvis length, hip width, tail length, hock length, body length, neck girth, number of teat procedures, number of Djimenou et al, (2018) and Youssao et *al.* (2018).

A scale with a capacity of 100 kg was used for weighing the animals. And linear measurements (cm) were made using a tape measure. Qualitative traits were described by visual and direct daylight observations based on a color scale (AU-IBAR, 2015); qualitative parameters collected were coat color, coat pattern, muzzle shape, ear type, tail type, hair type, skin, ear orientation, head profile (Djimenou et al. 2017 and Youssao et *al.* 2018). Information on origins was confirmed through interviews with 110 breeders.

Statistical analysis

Based on 17 biometric traits, Principal Component Analysis (PCA) was performed to assess the genetic variability of the study population (FAO, 2013). Population structure analysis was performed using Discriminant Factor Analysis (DFA) based on the 17 body measurements (FAO, 2013) to identify the traits that best distinguish the sampled pigs. The construction of the phylogenetic tree or dendrogram following the Hierarchical Ascending Classification (HAC) protocol, using Pearson's full linkage correlation was performed in order to identify the genetic types and the relationships between them (Roux 2006). The typology of the pig population was highlighted using analysis of variance (ANOVA). When the effects of the factors were significant, the Turkey test was used to compare the means at the $\alpha = 5\%$ threshold. The statistical model used for data analysis was as follows:

Yij= $\mu + \alpha i + eij$ With Yij = Observation corresponding to the studied character

$\mu = Population means$

ai =Effect of genetic type i

eij = Residual error

The contingency test was used to test the association or independence between the factors (genetics type) and the qualitative characteristics. All of these analyses were performed using XLSTAT 2014 and Mnitab 16.

Results

Genetic variability of the local pig population in rural areas of Haut-Katanga province

Principal Component Analysis (PCA) was performed to show the contribution of 17 quantitative variables in explaining the total genetic variability observed in the population.

Table 1.Eigenvalue and cumulative variance of principal components in the analysis of the variability observed in the pig population

Main components (F)	Own value	Variability (%)	% Cumulative
F1	9,3393	54,9369	54,9369
F2	1,1079	6,5170	61,4540
F3	1,0573	6,2192	67,6732
F4	0,9170	5,3939	73,0671
F5	0,7911	4,6534	77,7205
F6	0,6262	3,6837	81,4043
F7	0,5645	3,3207	84,7250
F8	0,4792	2,8189	87,5439
F9	0,4388	2,5812	90,1251
F10	0,3362	1,9777	92,1027
F11	0,3006	1,7683	93,8710
F12	0,2517	1,4808	95,3519
F13	0,2324	1,3673	96,7192
F14	0,1862	1,0952	97,8144
F15	0,1598	0,9398	98,7542
F16	0,1178	0,6931	99,4473
F17	0,0940	0,5527	100,0000

% : percent

The own value and cumulative variance of the different principal components in the analysis of the variability observed in the pig population are presented in Table 1.

Table 1 shows that the first two principal components (F1 and F2) have eigenvalues of 9.3393 and 1.1079 respectively and cumulatively account for 61.4540% of the total phenotypic variability observed in rural pig populations in Haut-Katanga province. This means that if we represent the data on two axes, then we will always have a preservation of more than 61.4540% of the total variability. Each eigenvalue has a corresponding factor. The factors have the particularity of not being correlated

with each other. On the other hand, they can be in association with the variables. In general, the factor is equal to the dimension of the PCA which is equal to the axis of the PCA.

The factor being a linear combination of the 17 quantitative variables, it is thus necessary to highlight the contribution of each variable to the explanation of the total phenotypic variability observed and the correlations between the variables.

Table 2: Squared cosinus of the variables of the local pig population

	F1	F2
Weight	0,4728	0,0372
Lenght of the body	0,7910	0,0270
Lenght of the head	0,7656	0,0002
Lenght of the muzzle	0,6429	0,0189
Lenght of the ear	0,3155	0,0021
Lenght of the face	0,2825	0,1256
Circumference of the neck	0,6895	0,0197
Thoracic perimeter	0,3418	0,0041
Height at withers	0,8301	0,0192
Lenght of the sholder	0,8201	0,0069
Lenght of the front limb	0,3144	0,4843
Lenght of hind leg	0,5285	0,1791
Number of hips	0,0894	0,0000
Width of the hip	0,7030	0,0818
Lenght of the pelvis	0,6948	0,0740
Lenght of the hock	0,5092	0,0243
Lenght of the tail	0,5484	0,0036



Figure 2. Circle of correlations

Table 2 shows that the variables that contribute the most to the total variability observed in the pig population are height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, muzzle length, tail length, hind leg length, and hock length for the main

component F1, while the component F2 is mainly concerned with foreleg length and weight. The correlation circle (Figure 2) corresponds to a projection of the initial variables on a two-dimensional plane constituted by the first two factors. It shows that height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, muzzle length, tail length, hind leg length, hock length, foreleg length are strongly and positively correlated to each other while live weight is weakly and negatively associated to the other linear measures mentioned above. We can also see from this Figure 1 and confirm from Table 2 that the variables height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, muzzle length, tail length, hind limb length, hock length are associated with the F1 axis while the F2 axis is essentially related to the forelimb length because the squared cosines of these variables in absolute values are particularly higher.

Pig population structure in the rural areas of Haut-Katanga province, DR Congo

Discriminant Factor Analysis (DFA) was used to graphically identify that the subpopulations of pigs are distinct. It then identified the characteristics of the different groups on the basis of explanatory variables. SFM is both an explanatory and predictive method (Fisher, 1936). Table 3 shows the average biometric characteristics of three genetic types

From Table 3 it can be seen that genetic type 3 is characterized by the lowest live weight and measurements; genetic type 2 has the highest weight and measurements and type 1 has the average live weight and measurements.

Table 4 presents the eigenvalues and the corresponding percentage of variance, while the graph in Figure 3 constructed from Table 4 of the coordinates of the variables shows the correlations between the 17 variables and the factors (F1 and F2).

It can be seen in Table 4 that over 96.6115% of the variance is represented by the first factor (F1)

Classe Variable	PV	LC	LT	LMU	LO	LV	CCO U	РТН	HG	LE	LMEM ANT	LMEM POST	NT	lH	LB A	LJA R	LQ
1	53,8	68, 6	22, 0	11,0	10,9	9,4	47,6	63,2	44,6	23,7	14,4	18,9	6,6	15,7	18,8	5,6	16,7
2	61,1	92, 3	25, 8	12,7	11,9	10,0	62,3	72,2	55,7	30,4	14,9	20,8	10,4	20,8	24,3	6,6	20,1
3	37,2	56, 1	19, 3	9,5	10,0	7,8	41,5	52,4	36,9	19,2	12,6	16,8	7,4	13,2	15,6	5,3	15,0

Table 3: Biometric characteristics of the 3 genetic types

PV: Poids vif, LC: Body length, LT: Head length, LMU: Muzzle length, LO: Ear length, LV: Face length, CCOU:Neck circumference, PTH: Thoracic perimeter, HG: Height at withers, LE: Shoulder length, LMEMANT: Hind leg length, LMEMPOST: Hind leg length, NT: Teat number, lH: Hip width, LBA: Pelvis length, LJAR:Hock length

Figure 3 shows that F1 is most correlated with withers height, body length, shoulder length, and neck circumference, while F2 is most correlated with weight and forelimb length. Height at withers, shoulder length and body length appear to be the most discriminating variables.

Figure 4 shows the distribution of pig genetic types on the factorial axes (F1 and F2)

Figure 4 confirms that the individuals are well differentiated on the factorial axes obtained from the 17 initial explanatory variables. Thus, it can be seen that the F1 axis best discriminates the three genetic types whose traits are described in Table 3.

Table 4. Own values and percentage of variance.

	F1	F2	
Own values	8,2206	0,2883	
Discrimination (%)	96,6115	3,3885	
% Cumulative	96,6115	100,0000	





Figure 4. Distribution of pigs on the factorial axes (F1 and F2)

Phylogenetic analysis of local pig populations raised in rural areas of High-Katanga province

The dendrogram in Figure 5 illustrates the relationships between the 3 genetic types in the study population based on similarity

The phylogenetic tree (Figure 5) allowed us to identify three genetic types and to establish relationships between them. This dendrogram shows that the pig population is made up of two subgroups, the first consisting of T2 and the second consisting of T1 + T3.

Table 5: Variance	decomposition	for optimal	classification.
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	Absolute	Percentage	
Intra-classe	454,1079	40,13%	
Inter-classes	677,5313	59,87%	
Total	1131,6392	100%	

It appears from Table 5 that the variation within the population is lower than the variation between populations, which is higher.



Figure 5. Dendrogram of genetic types in the rural pig population

	Type 1	Type 2	Type 3	
Type 1	0			
Type 2	34,4183	0		
Type 3	26,4847	58,5442	0	

It can be observed in Table 6 that the distance between the barycenters of genetic types 1 and 2 is the highest while that between types 1 and 3 is the lowest; the distance between types 2 and 3 is greater than the latter.

Typology of the three genetic types

The description of the genetic types that make up the local pig population in the Haut-Katanga province area is summarized in Tables 6 and 7.

The analysis of variance (table 6) reveals that, with the exception of face length, forelimb length and number of teats which have comparable values between genetic types 1 and 2, the genetic type factor has statistically significant effects on the other quantitative variables. Thus, we can see for example that type 2 has pigs with the highest values of live weight, thoracic perimeter and height at withers, followed by type 1 and then type 3.

The contingency test (Table 7) revealed that all the qualitative parameters studied were significantly different between genetic types (p<0.05) except for ear orientation, skin appearance and head profile. Thus, genetic types 2 and 3 are predominantly characterized by female pigs having semi erect ears with curly tail and are of white coat with plain pattern and short cylindrical muzzle with long and dense hair. Only the significantly different qualitative traits would better characterize the pig population of the study area.

	Genetic Types			
Quantitative Variable	TYPE 1	TYPE 2	TYPE 3	
	M±ES	M±ES	M±ES	Р
Weight	53,776±4,703b	61,107±8,026a	37,241± 9,441c	0,000
Lenght of the body	68,5 ±9,95b	92,28 ± 10,07a	56,15 ± 11,22c	0,000
Lenght of the head	22,013±2,131b	25,793±2,987a	19,284±2,363c	0,000
Lenght of the muzzle	22,013±2,131b	12,653±1,852a	9,517±1,956c	0,000
Lenght of the ear	22,013±2,131b	11,947±1,878a	10,000±1,460c	0,000
Lenght of the face	9,447±3,454a	10,007 ± 1,631a	7,759±1,112b	0,000
Lenght of the museau	47,632 ±7,154b	62,273 ± 8,387a	$41,483 \pm 5,288c$	0,000
Thoracic perimeter	63,18±5,80b	72,16 ± 14,65a	$52,41 \pm 7,00c$	0,000
Height at withers	44,566±5,303b	55,700 ± 5,430a	36,897 ± 4,629c	0,000
Shoulder length	23,684±3,030b	30,367 ±3,977a	19,224 ± 2,999c	0,000
Lenght of front limb	14,368±3,057a	14,887± 1,827a	12,578 ± 2,175c	0,000
Lenght of hind leg	18,855±3,083b	20,753 ± 2,099a	$16,750 \pm 2,475c$	0,000
Number of teats	6,632±5,467a	$10,400 \pm 2,702a$	7,448 ± 5,098b	0,000
Width of the hip	15,697±2,238b	20,793 ± 3,382a	$13,153 \pm 1,786c$	0,000
Lenght of the pelvis	18,816±2,541b	24,300 ± 3,749a	15,629 ± 2,218c	0,000
Lenght of the hock	5,5526±0,822b	6,5733 ±0,7359a	5,2845 ±0,9741c	0,000
Lenght of the tail	16,737±3,218b	20,093± 3,244a	14,991 ± 2,216c	0,000

Tableau 6: Quantitative variables of the local pig according to genetic types in the province of High-Katanga.

 $M \pm SE$: mean plus/or minus standard error; a, b, c: values with the same letters on the same line are not significantly different

Table 7: Distribution of qualitative variables of the local pig according to genetic type in High-Katanga province.

Qualitative parameters	1	2	3	Total	p-value
Sex	n (%)	n (%)	n (%)	n (%)	
Femelle	46(17,16)	142(52,99)	80(29,85)	268(78,36)	$\mathbf{D} = 0.000$
Male	30(40,54)	8(10,81)	36(48,65)	74(21,64)	-P = 0,000
Ear type	1	2	3	Total	
Dresser	22(20,75)	54(50,94)	30(28,3)	106(30,99)	
Half-address	24(22,22)	56(51,85)	28(25,93)	108(31,58)	
Semi-dropping	14(20,59)	20(29,41)	34(50)	68(19,88)	- r _0,000
Falling	16(27,59)	18(31,03)	24(41,38)	58(16,96)	_
Ear Orientation	1	2	3	Total	
Towards the front	40(22,99)	74(42,53)	60(34,48)	174(50,88)	
Downward	14(25)	18(32,14)	24(42,86)	56(16,37)	P =0,176
To the top	22(19,64)	58(51,79)	32(28,57)	112(32,75)	_
Skin	1	2	3	Total	
Smoooth	64(22,07)	126(43,45)	100(34,48)	290(84,8)	D_0.871
Ride	12(23,08)	24(46,15)	16(30,77)	52(15,2)	- r_0,0/1
Tail type	1	2	3	Total	
Curly	38(18,45)	86(41,75)	82(39,81)	206(60,23)	D -0.010
Straite	38(27,94)	64(47,06)	34(25)	136(39,77)	- P=0,010
Head profil	1	2	3	Total	
Concave	14(17,95)	38(48,72)	26(33,33)	78(22,81)	P=0,091

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Convex	20(23,81)	44(52,38)	20(23,81)	84(24,56)	_	
Staight	42(23,33)	68(37,78)	70(38,89)	180(52,63)		
Coat color	1	2	3	Total		
White	38(23,5)	76(46,9)	48(29,6)	162(47,368)	_	
White and black	14(16,3)	34(39,5)	38(44,2)	86(25,146)		
White and brown	0(0)	0(0)	2(100)	2(0,585)	_	
White and red	0(0)	2(100)	0(0)	2(0,585)	_	
Rusty brown	0(0)	2(100)	0(0)	2(0,585)	_	
Brown	2(100)	0(0)	0(0)	2(0,585)	_	
Brown and black	2(50)	2(50)	0(0)	4(1,17)	- D_0.010	
Black	18(31)	26(44,8)	14(24,1)	58(16,959)	- F_0,010	
Black and red	0(0)	0(0)	1(100)	1(0,292)	_	
Roan	0(0)	0(0)	2(100)	2(0,585)	-	
Roan and white	e0(0)	0(0)	2(100)	2(0,585)		
Roan and black	0(0)	0(0)	2(100)	2(0,585)	—	
Red	0(0)	4(100)	0(0)	4(1,17)		
Red and white	0(0)	2(100)	0(0)	2(0,585)	_	
Dress color model	1	2	3	Total		
Uni	60(25,64)	106(45,3)	68(29,06)	234(68,42)	P=0.000	
Pie	16(15,09)	42(39,62)	48(45,28)	106(30,99)	- 1 -0,000	
Type of muzzle	1	2	3	Total		
Short and cylindrical	34(22,08)	48(31,17)	72(46,75)	154(45,03)		
Long and cylindrical	30(27,27)	64(58,18)	16(14,55)	110(32,16)	P=0,000	
Long and thin	12(15,38)	38(48,72)	28(35,9)	78(22,81)	_	
Weight Type	1	2	3	Total		
Sparseness	10(13,89)	40(55,56)	22(30,56)	72(21,05)		
Short and dense	2(50)	2(50)	0(0)	4(1,17)	_	
Short and straight	28(28)	34(34)	38(38)	100(29,24)	P=0,000	
Long and curly	4(13,33)	10(33,33)	16(53,33)	30(8,77)	_	
Long and dense	32(23,53)	64(47,06)	40(29,41)	136(39,77)		
n : effectif, (%) : percentage						

Discussion

Principal component analysis was performed to show the contribution of 17 quantitative variables in explaining the total genetic variability observed in the population. The quantitative parameters used in this study are identical to those used in several studies of phenotypic characterization of local pigs in Africa, notably in Benin and Ghana, in order to provide a good structuring of the population studied (FAO, 2013; Djimènou et *al.* 2017).

Discriminant Factor Analysis (DFA) was used to graphically identify that the subpopulations of pigs are distinct. Three morphological types were observed: Genetic type 3 was characterized by the lowest live weight (37.2 kg) and measurements (Height at withers (36.9 cm); Shoulder length (19.2 cm), Body length(56.1cm)); Genetic type 2 had the highest weight (61.1 Kg), (Height at withers (55.7cm); Shoulder length (30.3 cm), body length (92.2 cm)) and superior measurements and the type 1 has the live weight (53.8 kg) and average measurements (Height at withers (44.5 cm); Shoulder length (23.6 cm), body length (68.5 cm)) These quantitative parameters allow us to have the idea on the development and conformation of the body indicates good butchery skills that allow breeders to get a high income (Somenutse et *al.*2019). The results of this production study suggest the existence of small, large and medium sized animals in the rural pig population of High-Katanga Province. The differences observed may be due to endogenous factors on the one hand (breed, strain...) or exogenous

factors on the other hand (climate, husbandry...) and/or the interaction between the two factors (Djimènou et *al*.2017).

Traditional or peasant pig farming is characterized by a minimization of inputs and investments; feeding and management remain hazardous (Bastianelli et *al.* 2006). Other authors have shown that improved husbandry conditions that provide welfare would allow the animal to express its full potential (Dourmad et *al.* 2010; Paboeuf et *al.* 2010). However, several authors have confirmed that this type of breeding contributes to the improvement of pork production and provides a regular income to producers (Muir et *al.* 2008; Ollivier, 2009).

The F1 factor was more correlated with height at withers, body length, shoulder length, and neck circumference, while F2 is more correlated with weight and foreleg length. Height at withers, shoulder length and body length appear to be the most discriminating variables. These results are contradictory to those found by Youssao et *al.* (2017) after discriminant factor analysis only muzzle length was the discriminant trait. These same authors support that discriminant body measurements can be used to select animals to improve productivity.

The variation within the population was higher than that observed between populations. This suggests that the local pig population in rural Haut-Katanga province is related with a relatively high inbreeding rate.

It can be observed that the distance between the barycenters of genetic types 1 and 2 is the highest while that between types 1 and 3 is the lowest; the distance between types 2 and 3 is greater than the latter. Thus, genetic types 1 and 3 would share a larger gene pool.

The phylogenetic tree identified three genetic types and established relationships between them. The dendrogram reveals that the pig population would be made up of two subgroups, the first made up of Type 2 and the second made up of Type 1 plus Type 3. This relationship would probably be related either to variation within and/or between populations, or to genetic distances between the three types. According to the (Wiener and Rouvier, 2009; FAO, 2013; FAO, 2012). Phenotypic characterization is among the prerequisites to effectively assess the diversity of zoo genetic resources and determine their degree of introgression or genetic purity.

Knowledge of genetic variability is fundamental in animal and plant breeding. The identification of this genetic variability for certain morphological traits is the first essential step in the description of genetic resources (FAO, 2013). In this study three genetic types were found of which type 1 is characterized by average live weight and measurements, type 2 has higher weight and measurements, and type 3 has the lowest live weight and measurements. These results are comparable to those found by (Djimenou et *al.* 2018; Youssao et *al.*2018). However, the results of the hierarchical principal component classification (CHCP) and hierarchical ascending classification (HAC) revealed three morphotypes along a size gradient with the weight of the best morphotype estimated to average 56.29 kg (CHCP) and 65.13 kg (HAC), respectively. The use of the two classification analysis models allowed for a more accurate location of the phenotypic structure within the local pig resource. These results also revealed that among the local pigs there are individuals with a weight performance of more than 65.13 kg at 50 kg as also reported in Benin by d'Orgeval (1997). This is at odds with the apprehensions of several authors that the local African pig hardly reaches an adult weight of 60 kg (Klooster and Wingelaar, 2011; Muys et *al.* 2003; d'Orgeval, 1997).

This difference may be linked on the one hand to the poor management of breeding in Benin where the best boars are sold (Houndonougbo et *al.* 2012; Djimènou et *al.*2017) to obtain the best income while some should be retained for breeding. On the other hand, the observed performance gap can also be explained by the genetic diversity between the pig population of the Kambove and Kasenga territory and that of Bangladesh, but also and above all to the interaction between the animals and their production environments (Wiener and Rouvier, 2009) that are not very favorable to breeding. However, the local African pig is essentially raised according to traditional production practices. These practices are characterized by extensive breeding, with low input, with an often precarious

habitat without any hygiene measures and not respecting modern zootechnical standards (low nutritional quality feed) (Djimènou et *al.* 2017). This explains the fact that the expression of the zootechnical potential of local pigs is limited (Serres, 1989). This morphological variance is an indicator of the molecular genetic diversity between the local animal from these different countries. The factors such as coat color, agro-ecological zone, sex, and types of feed used did not discriminate local pigs in southern Benin (Djimènou et *al.* 2017).

Conclusion

The general objective of this study was to contribute to a better knowledge of the phenotypic biodiversity of local pigs through principal component and discriminant analyses in order to develop sustainable management and conservation strategies as well as genetic improvement and preservation. The results of this study show that there is a great phenotypic diversity within the local pigs of the rural areas of Kasenga and Kambove. Thus, the first two principal components (F1 and F2) explain the total phenotypic variability observed within the studied pig population. The highly correlated variables are height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, snout length, tail length, hind leg length, hock length, foreleg length. The F1 axis is clearly related to height at withers, body length, shoulder length, and neck circumference, while F2 is essentially related to weight and foreleg length. Height at withers, shoulder length and body length seem to be the most discriminating variables. The pig population would consist of three genetic types, which can be grouped into two subgroups on the basis of intra/inter population variations and genetic distances. The typology of genetic types revealed that height at withers, shoulder length, body length, head length, hip width, pelvis length, neck circumference, snout length, tail length; hind leg length, hock length, foreleg length, live weight and sex are the variables that best characterize pig populations. The local pig would thus constitute an alternative pig genetic resource with a high breeding potential due to its biodiversity and its strong capacity of adaptation.

Impact

Principal component and discriminant analyses of local pig populations allow the development of strategic plans for sustainable management and conservation as well as genetic improvement of this animal genetic resource.

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