

Livestock grazing systems and sustainable development in the Mediterranean and Tropical areas

Recent knowledge on their strenghts and weaknesses

Alexandre Ickowicz and Charles-Henri Moulin, editors



perception of the nutritional status of ewes and prefer ewes in good body condition to lean ewes. Moreover, they can discriminate ewes within a flock based on their body weight (Alhamada *et al.*, 2017b).

We demonstrate for the first time, the behavioural origin of the subfertility observed in undernourished ewes: the rams do not primarily seek lean ewes that are responsive for a shorter time than ewes in good condition. Underfed ewes with insufficient body reserves are therefore less likely to be mated. This means that they can replenish their body reserves and focus on survival rather than on completing a difficult pregnancy. This sub-fertility can be quickly overcome by re-feeding the animals. Our study demonstrates that ewes adapt individually to nutritional hazards in order to preserve their integrity and that at the flock level, male × female interactions favour the most productive females. From a practical point of view, these results indicate that a different breeding management is required (male/female ratio, batch management, *flushing*, etc.) depending on the nutritional status of the animals.

Genetic diversity and adaptation of local breeds to their breeding environment

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The use of animal genetic diversity is one of the main levers to be considered so as to improve the adaptation of livestock systems to the major current changes. Among domestic ruminants, there is a high intraspecific diversity, as illustrated by the high number of cattle breeds registered (more than 800) and classified as zebu (*Bos taurus indicus*), taurine (*Bos taurus taurus*) and zebu × taurine crossbreeds, or the more than 1,500 sheep breeds documented globally⁴. The main factors that have contributed to the generation of this diversity are domestication, the sometimes distant migration of ruminants from their domestication centers, and the different pressures of recent natural (such as exposure to new climatic conditions and pathogens, and the abundance or scarcity of food and water resources) and artificial selection (selection of animals by farmers based on morphological criteria, coat colouring, docility, or their performance, for example). Local hardy and heritage breeds, mainly considered in grazing systems, are the result of an evolutionary process that has determined their ability to live in a specific environment.

In order to conserve and make the best use of this genetic diversity within sustainable breeding systems, it is essential to characterise it well (for example at the population level or within the herd in relation to traits of interest such as feed efficiency or the dynamics of mobilisation-reconstitution of body reserves), to understand the demographic history of these breeds and to identify the genetic mechanisms underlying their

4. www.fao.org/dad-is/fr/

adaptive capacities. It is also necessary to characterise the perceptions that breeders have of the adaptation of their breeds, their herds and their animals and to better understand how they take this adaptation into account and manage it through their practices.

I Genetic characterization of local breeds adapted to tropical and Mediterranean conditions

Over the last twenty years, the genomic revolution accompanied by the development of new high-throughput⁵ genotyping and sequencing tools has greatly facilitated the fine genetic characterization of ruminant breeds. These tools have, for example, provided reference genotyping data for many cattle and sheep breeds stored in the Widde database⁶ (Sempéré *et al.*, 2015).

Exploring the structure of genetic diversity in local breeds (through multivariate approaches or supervised and unsupervised hierarchical clustering) applied to individual genotyping data is an essential step in describing these breeds and a prerequisite for further study of their demographic and adaptive histories. In cattle, for example, this exploratory approach has made it possible to better characterise the genetic diversity structure of some local breeds by comparing them to a panel of breeds representative of the genetic diversity of the species and to suggest historical hypotheses based on their origin, as exemplified by the Zebu of Mayotte and the Mediterranean cattle breeds (Ouvrard *et al.*, 2019; Flori *et al.*, 2019).

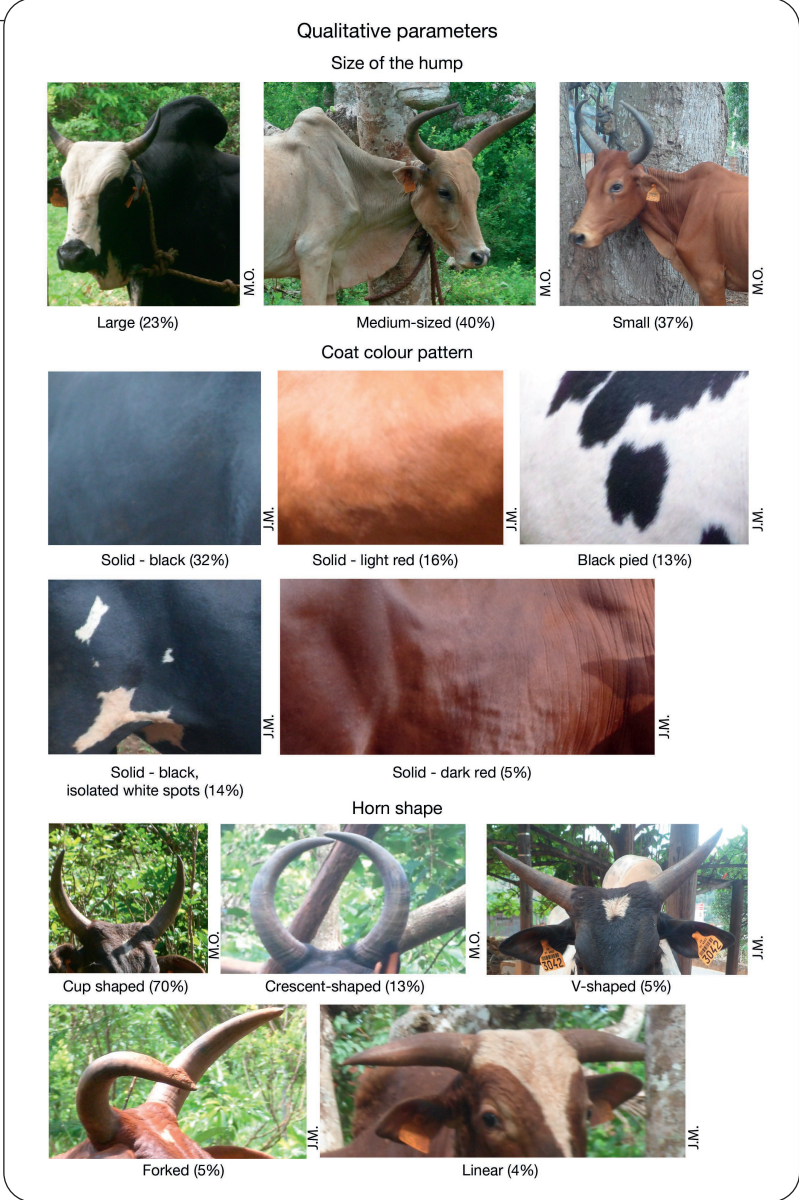
The genetic study of the Zebu of Mayotte⁷ has effectively confirmed its originality and initiated the implementation of conservation measures. This local population (approximately 70% of the 20,000 head counted in Mayotte), whose presence on the island could date back several centuries according to archeozoological data (Boivin, 2013), is used in traditional local production systems (in family farms of a few head) and has a significant ceremonial and cultural value. However, some breeders have started to crossbreed with improved European taurine breeds (i.e. Montbeliarde, Jersiaise, Gasconne and Brune breeds) over the last twenty years, which is threatening the Zebu of Mayotte. Consequently, a process of recognition of this local breed was undertaken by the constitution of a file integrating a joint phenotypic and genetic characterization and led to its official recognition in 2018 (Ouvrard *et al.*, 2019). The phenotypic study of this breed, which is a prerequisite for the selection of animals to be genetically characterised, showed a significant heterogeneity of coat color patterns and of some morphological parameters in the 400 animals studied and established a detailed description useful for defining the breed standard (Figure 2.10).

5. These enable the simultaneous study of several thousand to several hundred thousand biallelic markers spread over the whole genome.

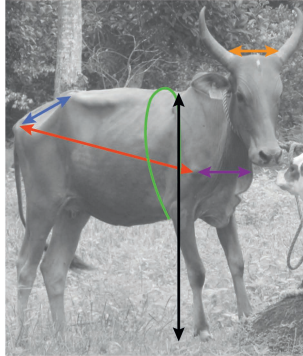
6. <http://widde.toulouse.inra.fr/widde/>.

7. Conducted thanks to a collaboration between the Coopadem farmers' cooperative and CIRAD, assisted by INRAE geneticists within the framework of the Rita project (agricultural innovation and transfer network) Defi-Animal, coordinated by Emmanuel Tillard (Selmet, La Réunion).

Figure 2.10. Example of parameters measured in 400 Zebus of Mayotte from 178 different farms selected on the entire territory of Mayotte.

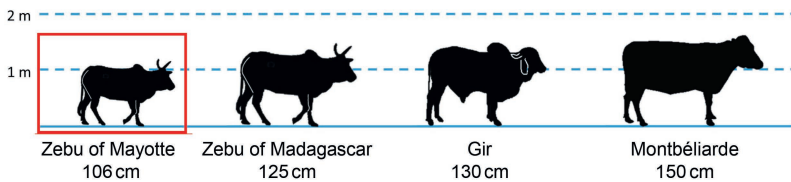


Quantitative parameters



Measured parameters	Mean in cm (standard deviation)
Height at withers	106 (7)
Oblique body length	118 (9)
Chest circumference	139 (10)
Chest width	34 (5)
Pelvic length	39 (3)
Length between horns	15 (2)

Size comparison with other breeds



Sources: M.O., Mélissa Ouvrard ; J.M., Jessica Magnier.

In contrast, the genetic characterization of 150 of these unrelated animals, based on the genotyping of 50,000 biallelic markers distributed over their genome, revealed a high genetic homogeneity and proximity to Zebus of Madagascar (Ouvrard *et al.*, 2019), both breeds having a higher indicine cattle ancestry⁸ than the African cattle breeds and a low African taurine ancestry. In 16% of the individuals, a low European taurine ancestry (<5%), probably resulting from recent crosses with European taurine breeds, is also observed. The aim now is to extend the population inventory and to organise its management by setting up a conservation and management plan. These first genetic studies will also be continued by estimating certain demographic parameters and studying the production and adaptation capacities of this breed, which are still poorly known. Indeed, the Zebu of Mayotte population has developed adaptive capacities specific to the constrained environment of the island (hot and humid climate, pathogen pressure, low availability of water and food resources).

This exploratory approach was also applied on a larger scale to study the structure of the genetic diversity of 21 local Mediterranean cattle breeds (640 individuals genotyped for more than 50,000 biallelic markers) from Algeria (i.e. Cheurfa, Chelifienne, Guelmoise), Cyprus, Egypt (i.e. Baladi), Greece (i.e. Brachykeratiki), Italy (i.e. Maremmana, Romagnola, Sarda, Sardo-modicana, Cinesara, Modicana), Morocco (i.e. Oulmes Zaër, Tidili, Atlas brown), Spain (i.e. Mallorquina, Menorquina, Marismena, Negra andaluza), and France (i.e. Raço di Biou and Corse) (Flori *et al.*, 2019⁹). As the Mediterranean basin has been crossed by several migration routes used by herders, the demographic history of these breeds appears relatively complex. The genetic study indicates that the majority of breeds studied have European and African taurine ancestry, the proportions of which depend on the latitude. However, a certain proportion of indicine ancestry is also detected in the Egyptian, Greek and Cypriot breeds and to a lesser extent in the Italian breeds Maremmana, Modicana and Sarda-modicana and in the Corsican breed, testifying to crossbreeding with populations of indicine ancestry in Southern Europe, the level of which decreases from East to West. This ancestry pattern is consistent with the known migration history of Neolithic farmers from the centre of taurine domestication in the Fertile Crescent westward via the Mediterranean and its main islands along the so-called “Mediterranean route”, 6,000 to 6,500 years ago. It is also consistent with the migration of taurines from North Africa to Spain after their introduction into Africa via Egypt, 6,500 years ago. The intersection in Egypt, at roughly the same time, of several migration routes taken by human communities through Europe and Africa may have simultaneously favoured the interbreeding of different bovine populations. Populations of indicine ancestry or admixed with zebus were probably imported into southern Europe (between 200 BC and 1720) by the Silk Road that connected Asia to the Mediterranean Sea, ending in Italy, in accordance with the decreasing gradient of indicine ancestry observed from Sicily to mainland Italy and Corsica. The weak indicine ancestry also detected in some Algerian breeds (i.e. Cheurfa

8. From *Bos indicus*.

9. Galimed project (Inra, Métaprogramme Accaf), coordinated by Denis Laloë (Gabi, Jouy-en-Josas).

and Guelmoise) probably results from a residual crossbreeding between African taurine and zebu, while the European taurine ancestry detected in the other North African breeds indicates more recent crossbreeding, during the last century, with European taurine. All of these more or less complex scenarios suggested by these exploratory approaches of the genetic structure will, however, have to be confirmed by more detailed modelling of demographic processes.

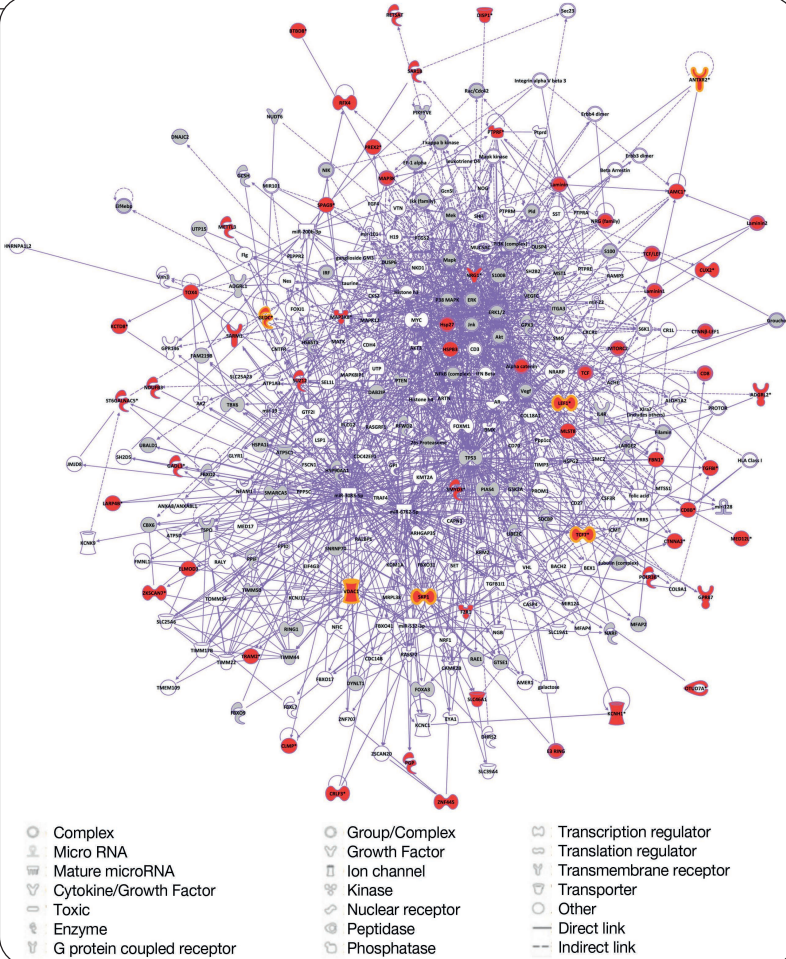
I Genetic study of the adaptive history of local Mediterranean breeds

The identification of the genes involved in the adaptation of local breeds to their specific environment, coupled with the dissection of the underlying molecular mechanisms, allows a better understanding of the adaptive mechanisms. It can also be considered as an additional means to characterise local breeds and reveal their originality from a genetic point of view. It involves locating footprints (or signatures) of natural and artificial selection in the genome by analysing the dense genetic information of several dozen individuals. Functional annotation of candidate genes identified in regions under selection using systems biology tools (Flori *et al.*, 2012; 2014; 2019) allows to make hypotheses about the key functions, biological pathways, and gene networks in which genes under selection are involved and about the selection pressures that may have occurred. The complementary use of association methods with population-specific phenotypes or environmental variables (Gautier, 2015) can make a connection between genomic selection signatures and these variables and hence confirm some of these hypotheses.

The 21 previously studied Mediterranean breeds have been subjected for centuries to the different variants of the Mediterranean climate. The joint screening of selection signatures in their genomes and of associated chromosomal regions with population-specific variables discriminating the different subtypes of the Mediterranean climate made it possible to establish a direct link between some selection signatures and climatic variables and to propose a genetic map of the association with climate (Flori *et al.*, 2019). Nine regions under selection and 17 candidate genes located on five separate chromosomes were identified, including several candidate genes (LEF1, ANTXR2, VDAC1, TCF7 and SKP1) that are also associated with climate variables. The 55 genes associated with at least one climate variable (Figure 2.11) are involved in several biological functions that play a role in adaptation to the Mediterranean climate, such as thermotolerance, ultraviolet (UV) protection, pathogen resistance or metabolism. The main selection pressures affecting cattle in the Mediterranean area are likely to be variations in heat and UV exposure, availability of food and water resources and exposure to pathogens. Among the strong candidate genes associated with climate (e.g. NDUF3, FBN1, METTL3, LEF1, ANTXR2 and TCF7), the ANTXR2 gene, already found under selection in West African cattle breeds and associated with climatic variables in humans and sheep, encodes the receptor for the *Bacillus anthracis* anthrax toxin. These results suggest that anthrax, the oldest known zoonosis with a global distribution, must have exerted significant selection pressure on cattle breeds in the Mediterranean basin

and West Africa and illustrates a clear link between this disease and climate. The *Bacillus anthracis* spores can persist in the soil for years and climatic factors such as temperature and precipitation are decisive in the occurrence of anthrax epizootics.

Figure 2.11. Gene network comprising genes under selection and those associated with climate variables in 21 Mediterranean breeds (Flori *et al.*, 2019).



The network was obtained using the Ingenuity Pathway Analysis software. Genes under selection are highlighted in red, those associated with at least one climate variable are in yellow. Shaded genes are not associated with any climate variable. The shape of the molecules is representative of their different families.

Taken together, these results indicate that local breeds are valuable genetic resources that should be preserved and integrated into appropriate management and genetic improvement schemes. This preservation appears crucial in the current context of the increasing incidence of crossbreeding with supposedly more productive breeds (under different environmental conditions) that can threaten these local breeds. It is also crucial in the context of climate change which imposes new environmental constraints. Genomic prediction of the vulnerability of breeds to these constraints is a new field of research, the results of which could make it possible to promote certain breeds that are less vulnerable in a given environment and to advise against others.

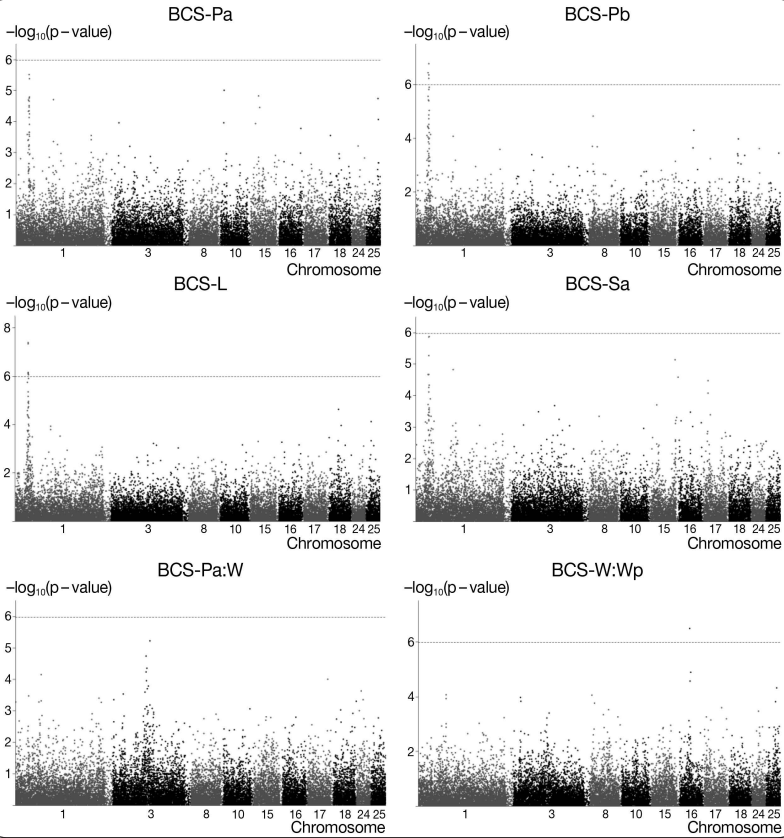
I Study of intra-herd genetic variability in adaptation to constrained feeding conditions

In addition to previously reported work on cattle, in the conditions of the Massif Central in France, bordering the Mediterranean, we demonstrated a significant genetic component accounting for intraflock variability in BR mobilisation-reconstitution processes in the Romane ovine meat breed (Macé *et al.*, 2018a; 2018b; 2019). We have identified and described the spectrum of PV and NEC profiles present in the females of the flock and demonstrated intra-flock variability of these parameters and their dynamics during the mobilisation and reconstitution phases of the production cycle, and during the entire ewe cycle. Values of heritability h^2 greater than 0.2 were obtained, confirming the influence of genetic factors in the variation of these parameters in the Romane breed. Strong phenotypic and genetic correlations between mobilisation and reconstitution phases were also estimated (Macé *et al.*, 2018; 2019). In addition, we identified quantitative trait loci (QTL) responsible for the variability detected in the BR dynamics (Figure 2.12). Several candidate genes were identified, including three of interest: the LEPR gene, which encodes the leptin receptor, a plasma hormone of major importance in the regulation of adiposity levels and intake in mammals, the metabotropic glutamate receptor 1 (GRM1) gene, and finally the TRPS1 (*Tricho-rhino-phalangeal syndrome 1*) gene associated with weight gain during the post-weaning period, and regulator of the hypothalamic-pituitary-adrenal (HPA) axis acting on energy storage and expenditure. These results provide interesting avenues for the use of this (BR) adaptive trait in the design of genetic improvement schemes adapted to new challenges (climate change and agroecological transition of livestock systems), where the contribution of the animal component in the overall resilience of the systems should be important.

I Managing the adaptation of local breeds at the farm level through farmer practices

The characteristics of adaptation of local breeds to their environment mean that they are theoretically interesting resources to be mobilised by farmers in the areas concerned. However, as we shall see, it is not so simple and the notion of adaptation can refer to a diversity of definitions and perceptions, but also to multiple practices implemented to manage or promote it.

Figure 2.12. Identification of QTLs that determine body condition score (BCS) in Romane ewes during several physiological stages (Macé *et al.*, 2022).



The $-\log_{10}(p - \text{value})$ for all SNP (single nucleotide polymorphism) was plotted for chromosomes 1, 3, 8, 10, 15, 16, 17, 18, 24 and 25. The dotted line indicates the genome-wide significance threshold (BONFgen = 5,94). Chromosome-wide significance thresholds were OAR1: 5,02, OAR3: 4,96, OAR8: 4,57, OAR10: 4,52, OAR15: 4,49, OAR16: 4,45, OAR17: 4,42, OAR18: 4,43, OAR24: 4,14, OAR25: 4,26. Candidate genes related to fat traits and lipid metabolic pathways.
 BCS-Pa: body condition score during early gestation.
 BCS-Pb: body condition score during late gestation.
 BCS-L: body condition score during lactation .
 BCS-Sa: body condition score for the period during early lactation, after lambing.

BCS-Pa:W: body condition score for the period from early gestation to just after weaning.
 BCS-W:Wp : body condition score for the period beginning just after weaning and ending 1 month after weaning.
 Five major regions identified on chromosomes OAR1, 3, 8, 9, 11.
 Candidate genes related to fat traits and lipid metabolic pathways.
 Pa: beginning of gestation.
 Pb: end of gestation.
 L: during lactation.
 Sa: early lactation phase, after lambing.
 W: just after weaning.
 Wp: up to 1 month after weaning.

The livestock breeders perception of the adaptation of local breeds refers to a diversity of animal characteristics

In the framework of the genetic study of the local Mediterranean cattle breeds mentioned above, twenty surveys were carried out among breeders of the Corsican cattle breed so as to improve their perception of the breed's adaptation¹⁰. These semi-structured interviews, with mountain and plain breeders, breeders or not, crossing or not with other breeds, and belonging or not to the breed's management association, involved the following themes: history of the farm, characteristics of the breeding system, points of view and practices related to the adaptation and the link to collective action related to the breed. Not only do these surveys capture the diversity of adaptation characteristics cited by breeders (Table 2.4), but the thematic analysis of the interviews made it possible to clarify the diversity of ways of seeing each adaptation characteristic. In analysing the parts of the interviews associated with "animal autonomy for feeding" for example, we note that according to the breeders, this theme is associated with various animal characteristics: low animal needs, feeding behaviour, body condition that is seen by the breeders as a positive or negative characteristic of the breed, and various food resources valued by the breed. This analysis also provides elements on the perceived consequences of this autonomy, including the associated low cost, ease of management, the fact that the activity is not very time-consuming, and the fact that this autonomy could be out of line with social expectations. Finally, this analysis provides an explanation of the farmers view on the causes of this autonomy: some breeders consider that the morphology of the breed allows this adaptation, some consider it to be innate while others consider that it can be acquired, and finally some breeders consider that the practices can influence this adaptation favourably or unfavourably (Lauvie *et al.*, 2013).

Table 2.4. The frequency of quotation of adaptation characteristics mentioned by the Corsican cattle breeders surveyed.

	Percentage of farmers surveyed who mention the criterion at least once in the entire interview
Animal autonomy in feeding	100%
Morphology and external aspects	100%
Reproduction	95%
Adaptation to the territory	90%
Behaviour	85%
Resistance	80%
Meat quality	20%
Territory maintenance	50%

10. Interviews conducted during the internship of C. Rolland, INRAE, UR LRDE (2012-2013).

Taking adaptation into account in breeders practices and collective management

Perceptions of the adaptation of local breeds by livestock farmers are significant as they interact with their management practices and choices. Based on the cases of dairy sheep farming in Corsica and Thessaly, Lola Perucho's (2018) dissertation has made it possible to clarify the genetic management practices implemented by breeders in relation to their breeding system. This study highlights the different modes in which the adaptation characteristics of local breeds or individual animals are involved in these processes.

Adaptation characteristics may be involved in the choice of genetic types raised. Accordingly, the study of the trajectories of several breeders in Thessaly to analyse changes in breeds and in feeding systems (notably pastoral components of these systems) reveal that among livestock breeders who identify a mismatch between the genetic composition of the herd and the feeding system, three types of responses are possible: crossbreeding with a local breed, discontinuing the use of a highly productive breed, trying a different breed, or changing the feeding system. When the first response is chosen, it is clearly related to the adaptive characteristics attributed to the local breed (Perucho, 2018).

The notion of hardiness, frequently highlighted when referring to local breeds, can refer to a diversity of traits and also to various management methods according to the breeders. For some Corsican sheep breeders, for example, it can refer to different meanings: sensitivity to disease or climatic conditions, the development of rangelands in relation to production, walking skills, longevity of females (Perucho, 2018). Some breeders individually select their breeding stock on hardiness through indirect indicators, mainly morphological (coat, standard). Others consider that this hardiness is "acquired" via the breed or the breeding conditions. For example, transhumance enables a de facto selection by eliminating the ewes least able to follow the herd (animal loss) (Perucho, 2018).

For a same adaptation trait, the levers used by breeders to obtain a herd in line with their expectations are multiple: for example, out of 23 Corsican breeders mentioning susceptibility to disease as a trait of interest, only one breeder makes it a criterion for choosing internal renewal, while the majority only make it a criterion for culling (Perucho, 2018). In addition to internal renewal and culling practices, other levers may also come into play such as the criteria for choosing breeders who supply male breeding stock (Perucho, 2018).

The research conducted by Perucho (2018) also raises issues of interactions between individual breeder choices and collective breed management tools. Among the eight breeders of Corsican ewes surveyed in this study, all take into account the criteria of milk production and index (estimated genetic value) when choosing ewe lambs.

However, six of them also take into account other criteria (from two to four additional criteria depending on the breeder, including ancestry, fleece colour, breed standard, milking behaviour, dairy persistency and udder characteristics). As such, they combine the use of a collective tool and individual criteria to build a herd that is tailored to their expectations and systems (Perucho, 2018).

In addition, work on the practices of local breeders also reveals that in the processes that enable breeds to adapt to certain situations or constraints, other dimensions than biological ones can be considered, such as more social or organisational dimensions linked to the breeds. Consequently, Perucho et al. (upcoming) demonstrate how the group organisation of breeders around a breed can contribute to deal with a health hazard that the animals in that breed are facing.

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The issues of local breed adaptation therefore involve biological and genetic characteristics that are valued and managed by breeders in their individual and collective practices. The characterization of the biological and genetic mechanisms at work provide valuable information to improve the management of these breeds. Likewise, a better understanding of the practices of management stakeholders, and primarily of breeders, as well as the underlying views, contributes to the understanding of the evolution of genetic resources. The integration of approaches stemming from complementary disciplines is necessary for a better understanding of the interactions between human populations, animal populations and livestock environments, for which the adaptation of animal populations is one of the consequences.

The mechanisms of adaptation analysed at the level of families and local communities

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This section focuses on the analysis of adaptation processes of pastoral and agropastoral households in arid and Mediterranean zones, jointly addressing the social and biotechnical dimensions involved. Specifically, we analyse the contribution of three levers: (i) the diversity of situations considered at a household level from the point of view of a “capability portfolio” and at the local level from the point of view of a diversity of production systems, (ii) the importance of institutions and collective organisations considered through social networks and collective actions, (iii) the forms of learning while considering the references to standards and values that guide the action. The research conducted in Egypt, Chad, Morocco and France and described here illustrate the manner in which livestock owners mobilise and sometimes combine them, resulting in a shift from a situation that weakens households to one that strengthens solidarity and reinforces their sustainability.