

Diversity of performance patterns in dairy goats: multi-scale analysis of milk yield, body condition score and body weight trajectories

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Abstract

In the French dairy goat sector, low longevity is a key issue leading to higher replacement rate in the herd and poor dilution of does rearing costs. There is a need to better understand determinants of lifetime performance. The general objective of this work was to analyze the variability of lifetime phenotypic trajectories (milk yield (MY), body weight (BW) and body condition score (BCS)) through a 3-step approach: (1) characterize individual phenotypic trajectories, (2) explore the associations between MY, BW and BCS trajectories at the lactation scale and (3) assess the diversity of phenotypic trajectories on successive lactations. Routine data from two experimental farms Le Pradel (Dataset 1, Ardeche department, France) and MoSAR experimental farm (Dataset 2, Yvelines department, France) were used. Dataset 1 included 793 Alpine goats from 1996 to 2020. Dataset 2 included 339 Alpine and 310 Saanen goats from 2006 to 2022. Weekly MY records (Dataset 1) and daily MY records (Dataset 2) were fitted using a lactation model with explicit representation of perturbations. Monthly BW records (Dataset 1) and BCS record (Dataset 1&2) were fitted using the Grossman multiphasic model. Daily BW records (Dataset 2) were fitted using a weight model. Each individual trajectory modelled for MY, BW and BCS was then summarized with synthetic indicators of level and dynamics. Principal component analysis was performed on MY, BW and BCS indicators separately to generate clusters of dynamic profiles. At the lactation scale, associations between milk yield, body weight and body condition clusters were evaluated by contingency tables with a chi-square test. Lifetime-scale bar plots were used to display cluster changes throughout parities. For MY trajectories, four and three profiles were found for primiparous and multiparous goats respectively. For BW, lumbar and sternal BCS trajectories, three profiles were found for all parities. At the lactation scale, no major association was found between phenotypic trajectories suggesting a diversity of energy partitioning strategies between life functions. At the lifetime scale, change between profiles was more pronounced for primiparous goats while a pattern of cluster membership appeared for multiparous goats. Further analysis are needed to include reproductive performance in analyzing lifetime performance profiles and better identify profiles or combinations of profiles at risk in terms of culling.

Key words : Dairy goats, milk yield trajectories, body weight trajectories, body condition score trajectories, lactation scale, lifetime scale

44 **Implications**

45 In the context of **agroecological transition**, **finding management strategies improving**
46 animal robustness and efficiency is more and more important. To characterize **robust**
47 goats, it's essential to better understand the associations between phenotypic
48 trajectories (e.g., milk yield, body weight, body condition score). The present study
49 showed that no major associations existed between phenotypic trajectories at the
50 lactation scale. At the lifetime scale, change between profiles was more pronounced
51 for primiparous goats while a pattern of cluster membership appeared for multiparous
52 goats. Our results challenge mainstream management strategies that are based on an
53 average animal performance. Rather, considering diversity of performance profiles can
54 be a way to better adapt to individuals or groups of individuals to improve their
55 robustness.

56 **Introduction:**

57 The French dairy goat sector faces many challenges such as animals with low
58 longevity (Palhière et al., 2018) and high replacement costs. In the future design of
59 livestock farming, breeding and managing robust animals is in the agenda of many
60 research programs. One of the key elements of robustness is to consider goats as a
61 biological system within which productive trajectories (e.g., lactation, growth,
62 reproduction, etc...) interact through complex mechanisms involving nutrient
63 partitioning (Bauman and Currie, 1980; Friggens et al., 2017). Nutrient partitioning
64 implies that energy cannot be maximized across all productive trajectories and
65 therefore some functions are given priority over others, in particular to support some
66 physiological stages (e.g. lactation). Hence, individual variability of performance could
67 be explained by differences in nutrient partitioning strategies between functions. A first
68 important aspect to explain changes in nutrient partitioning is the succession of
69 reproductive cycles throughout life, which modifies priorities among functions to
70 support a given physiological stage (e.g. gestation, lactation). In addition to these
71 homeorhetic drivers, priorities can be modified by various aspects of the farming
72 system environment. For instance, it is well documented that genetic selection for milk
73 production has altered priorities among functions in dairy cattle leading to health and
74 reproductive disorders (Pryce et al., 2001; Roche et al., 2009; Friggens et al., 2010).
75 Indeed, high genetic merit for milk has led to energy partitioning in favor of lactation
76 over other biological functions. It is also known that priorities can be modified if
77 nutritional environment is impaired (Friggens, 2003). As a central function supporting
78 lactation and as a buffer for variation in nutritional environment, body reserves play a
79 central role in energy partitioning among productive trajectories.

80 Assessing the diversity of phenotypic trajectories reflecting productive functions (e.g.,
81 milk yield (MY)) and body reserves (body weight (BW), body condition score (BCS)) is
82 a way to understand interactions among biological functions and potential trade-offs.
83 With time series data based on more frequent measures (e.g., MY, BW, BCS...), using
84 **interpretation models** can provide information about individual phenotypic trajectories
85 and their variability. Models can be used to transform raw data into biological
86 meaningful information. Over the past decades, authors proposed mathematical

87 models to capture the shape of the lactation curve (Wood, 1967; Cobby & Le Du, 1978;
88 Dhanoa, 1981; Wilmink, 1987) and some wanted to have models based on a biological
89 framework (Dijkstra et al., 1997; Pollott, 2000). With more frequent data, a recent
90 model was developed to characterize the lactation curve with an explicit representation
91 of perturbations (Ben Abdelkrim et al., 2020). This model allowed a better estimation
92 of a lactation potential for a given animal. Having the shape of lactation curve can help
93 to look for goats that need specific feeding management (Arnal et al., 2018). Works on
94 modelling the shape of body weight or body condition (Macé et al., 2023) are less
95 frequent, some mathematical functions with exponential approach were used (Sauvant
96 et al., 2012) or random regression approach (Berry et al., 2003). In dairy cows, Ollion
97 et al., (2016) developed a method to characterize trade-offs among biological
98 functions. This method was based on Principal Component Analysis (PCA) followed
99 by Agglomerative Hierarchical Classification (AHC) using milk dynamics, body
100 condition changes and reproduction performance.

101 Studying the diversity of **phenotypic trajectories' sequences** on a lifetime scale open
102 the perspective to look at potential changes in priorities among functions and see how
103 early lifetime performance can impact the whole productive lifetime. Most of culling
104 rules rely on different criterions (e.g., milk production, reproductive disorders, sanitary
105 problems etc...) (Astruc et al., 2021). Understanding the career diversity in a herd will
106 enable to develop adaptive management strategies linked to a specific trajectory and
107 increase animal resilience. To our knowledge, no recent studies in dairy goats have
108 used models to cross milk, body weight and body condition dynamics at a lactation
109 scale or at a lifetime scale. In this study, we hypothesized that a multi-scale approach
110 (lactation and lifetime scale) on phenotypic trajectories will bring insights on energy
111 partitioning strategies between biological functions and better understand the
112 variability of lifetime phenotypic trajectories. The general objective of this work was to
113 analyze variability of lifetime phenotypic trajectories through a 3-step approach: (1)
114 characterize individual phenotypic trajectories, (2) explore the associations between
115 MY, BW and BCS trajectories at the lactation scale and (3) assess the diversity of
116 phenotypic trajectories on successive lactations.

117 **Material and methods**

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119 **Datasets**

120

121 *Dataset 1 (1996-2020).*

122 Data came from the experimental farm Le Pradel (agricultural high school Olivier de
123 Serres) located in the French department Ardeche (44° 34' 58.4364" N; 4° 29' 53.2068"
124 E). The data set contained 2,460 lactations from 793 Alpine goats including 93,965
125 weekly milk records, 28,099 monthly body weight records and 26,271 monthly body
126 condition score (BCS) records. Over this period, goats were milked twice daily, and the
127 recorded value was a sum of the two milkings. **Body weight was measured one time**
128 **on a weighing balance.** Body condition score was evaluated at lumbar and sternal
129 regions on a 0 to 5 scale (Morand-Fehr and Hervieu, 1999). Le Pradel farm had a

130 seasonal system with a kidding period between January and February. During
131 breeding period in August, only goats inseminated received a hormonal treatment.
132 Male were introduced 18 days after AI. Male stayed until October to mate the goats
133 that will return to heat after AI and those who were not inseminated. Goats produced
134 milk from January to November-December. All lactations retained for milk records had
135 a first record less than 30 days after kidding, a last record after 240 days in milk and
136 had less than 30 days' interval between two records. All lactations retained for body
137 weight and body condition score records had a first record less than 17 days after
138 kidding, a last record after 240 days, more than 8 records per lactation and less than
139 100 days' interval between two records. Lactations lasted on average 289.6 ± 28.5
140 days. The final dataset 1 concerned 2,271 lactations for milk records, 1,935 lactations
141 for body weight records and 1,851 lactations for body condition score records (Table
142 1).

143 *Dataset 2 (2006-2022).*

144 Data came from the MoSAR experimental farm (INRAE- AgroParisTech) located in the
145 French department of Yvelines ($48^{\circ} 50' 31.4801''$ N; $1^{\circ} 56' 56.5843''$ E). The data set
146 contained 1,608 lactations from 339 Alpine and 310 Saanen goats including 396,814
147 daily milk records, 252,725 daily body weight records and 11,525 monthly body
148 condition score records. The farm has a rotary parlour with automatic weighing
149 platform, goats were milked and weighed twice a day. The recorded value for milk was
150 a sum of the two milkings. The recorded value for body weight was an average of the
151 two measures. Body condition score was assessed as the same way as in dataset 1.
152 MoSAR experimental farm had a seasonal system with a kidding period between
153 January and February. During breeding period in August, all goats received a hormonal
154 treatment. Goats inseminated will be on a fixed date on August. Goats that will be
155 naturally mated, small groups of 10-12 goats per day over 6-7 days. Goats produced
156 milk from January to November-December. All lactations retained for milk records had
157 a first record less than 5 days after kidding, a last record after 240 days in milk and had
158 less than 30 days' interval between two records. All lactations retained for body weight
159 and body condition score records had a first record less than 20 days after kidding, a
160 last record after 240 days, more than 8 records per lactation and less than 80 days'
161 interval between two records. Lactations lasted on average 280.1 ± 35.1 days. The final
162 dataset 2 concerned 1,256 lactations for milk records, 1,299 lactations for body weight
163 records and 381 lactations for body condition score records (Table 1).

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172 **Table 1.** Lactation selection criteria for milk yield, body weight and body condition score records with
 173 parity and breed distribution for dataset 1 and 2.

		Milk yield		Body weight		Body condition score	
		Dataset 1	Dataset 2	Dataset 1	Dataset 2	Dataset 1	Dataset 2
Lactation stage (d)	First record	<30	<5	<17	<20	<17	<20
	Last record	>240	>240	>240	>240	>240	>240
Interval between records (d)		<30	<30	<100	<80	<100	<80
Record per lactation		/	/	>=8	>=8	>=8	>=8
Parity	Primiparous	671	520	606	499	549	143
	Multiparous	1,600	736	1,329	800	1,302	238
Breed	Alpine	2,271	716	1,935	742	1,851	191
	Saanen	0	540	0	557	0	190
Total		2,271	1,256	1,935	1,299	1,851	381

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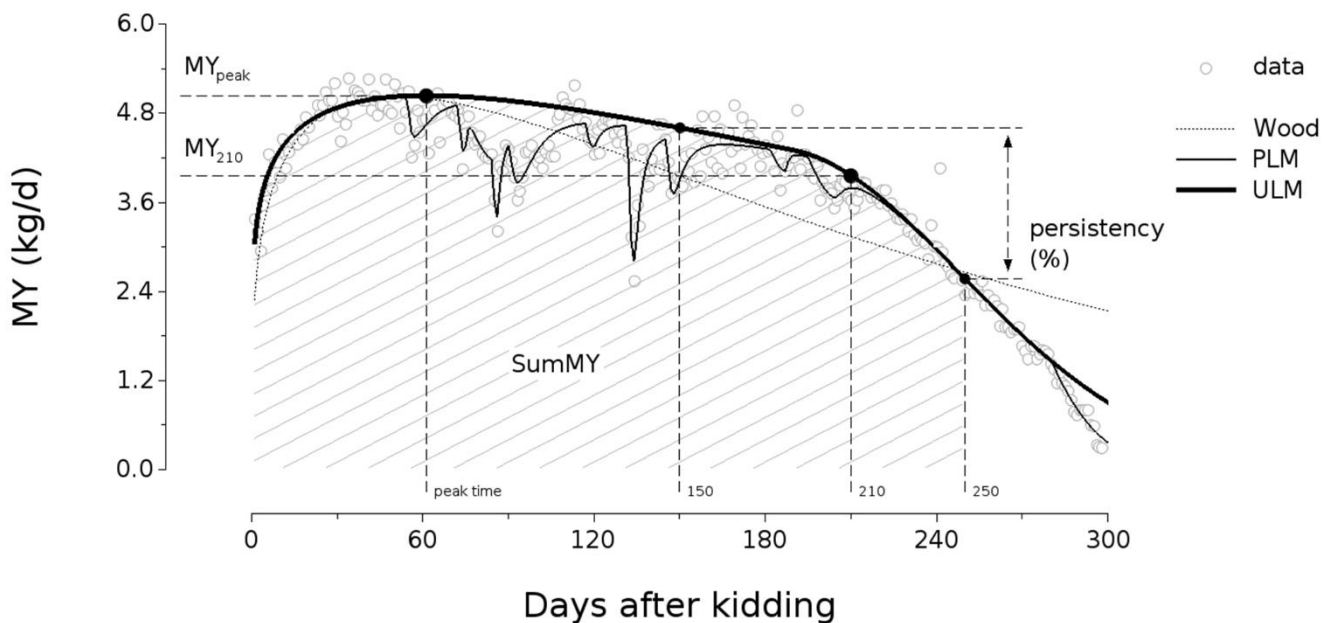
196 **Models of individual phenotypic trajectories**

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198 Models were selected according to data frequency.

199 *Lactation curve fitting of both daily and monthly data (dataset 1 and 2)*

200 The perturbed lactation model proposed by Ben Abdelkrim et al., (2020) was fitted
201 to milk yield time series data (Figure.1). This model was designed to decompose
202 lactation dynamics into two components: a theoretical unperturbed lactation curve and
203 perturbations. This approach was selected to characterize lactation trajectories
204 corrected for perturbations because it allows to capture a proxy of the lactation
205 potential. The model used for the unperturbed lactation was a modified version of the
206 Wood model (Wood, 1967) integrating a late lactation decrease. The model was fitted
207 in Scilab (Version 6.1.1, www.scilab.org) using an updated version (Martin,
208 unpublished/personnal communication) of the fitting protocol described in Ben
209 Abdelkrim et al., (2020). For further details about the model and the fitting procedure
210 (see Appendix A section 1).



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213 **Figure.1** Example of daily milk records fitted using the model proposed by Ben Abdelkrim et al., (2020)
214 with empty white points representing raw data, black bold straight lines representing the unpertubed
215 lactation model (ULM), black straight lines representing the perturbed lactation model (PLM) and dotted
216 lines representing the Wood model. The ULM trajectory was represented with synthetic indicators:
217 MY_{peak} = highest milk yield value; MY_{210} = milk yield value at 210 days; SumMY = sum of daily milk yield
218 values on 250 days; Peak time = time of the highest milk yield value; Persistency = $(MY_{250} - MY_{150}) / MY_{150}$
219 $\times 100$.

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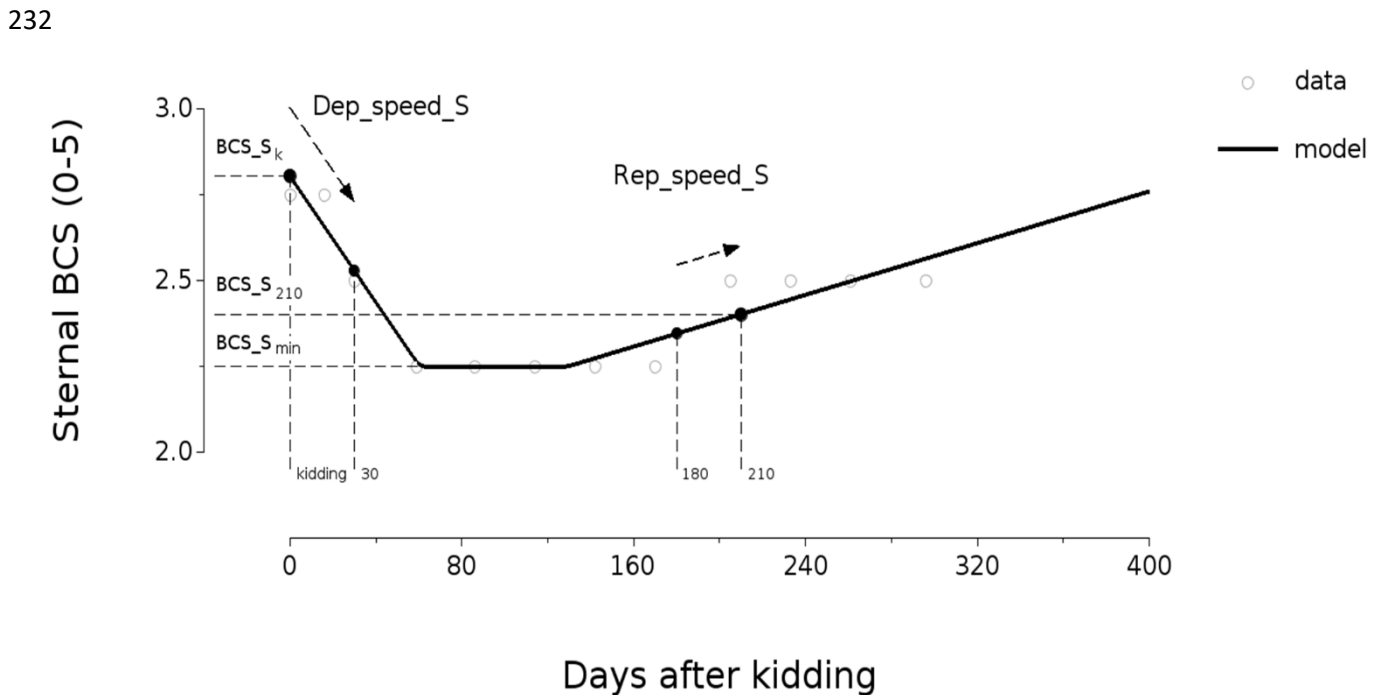
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224 *Body condition score curve fitting of monthly data (dataset 1 and 2)*

225 The triphasic model proposed by Grossman et al., (1999) was fitted to monthly body
 226 condition score time series data (Figure.2). This model was designed to decompose
 227 body condition dynamics into three parts: a depletion phase, a plateau phase and a
 228 repletion phase. This model allows to characterize trajectories with less frequent data
 229 (at least five records were needed). The model was fitted using RStudio (version
 230 2023.06.01). For further details about the model and the fitting procedure (see
 231 Appendix A section 3).



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234 **Figure. 2** Example of monthly sternal body condition records fitted using the model proposed by
 235 Grossman et al.,1999 with empty white points representing raw data, black straight lines representing
 236 the fitted trajectory. This fitted trajectory was represented with synthetic indicators: BCS_{S_k} = sternal
 237 BCS at kidding; $BCS_{S_{min}}$ = minimum sternal BCS; $BCS_{S_{210}}$ = sternal BCS at 210 days;
 238 $Dep_speed_S_{k \rightarrow 30} = (BCS_{S_{30}} - BCS_{S_k}) / 30$; $Rep_speed_S_{180 \rightarrow 210} = (BCS_{S_{210}} - BCS_{S_{180}}) / 30$.

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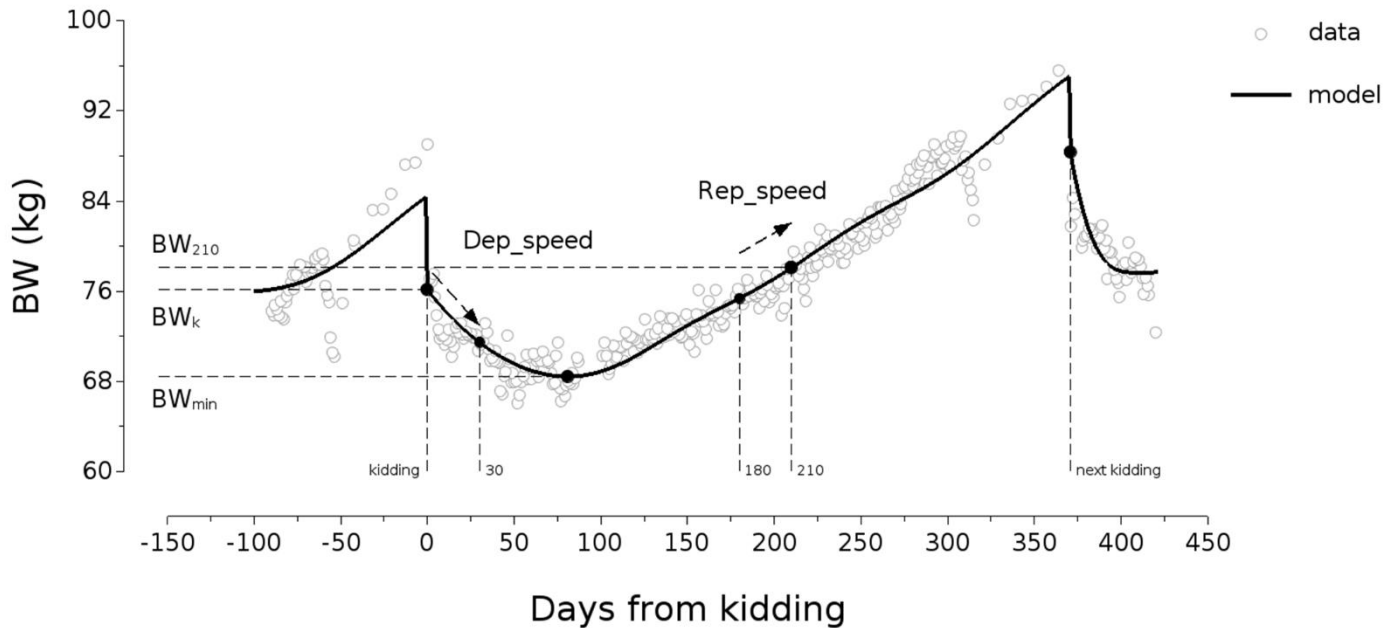
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248 *Body weight curve fitting of daily data*

249 The unperturbed weight model proposed by (Martin and Ben Abdelkrim, 2019) was
250 fitted to daily body weight time series data (Figure.3). This model was designed to
251 decompose body weight dynamics during a lactation into a sequence of
252 depletion/repletion of body weight. This model was built to be flexible and to capture
253 various shapes of body weight trajectories. The model was fitted using RStudio
254 (version 2023.06.01). For further details about the model and the fitting procedure (see
255 Appendix A section 2).
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258 **Figure. 3** Example of daily body weight records fitted using the model proposed by Martin and Ben
259 abdelkrim (2019) with empty white points representing raw data, black straight lines representing the
260 fitted trajectory. This fitted trajectory was represented with synthetic indicators: BW_k = body weight at
261 kidding; BW_{min} = minimum body weight; BW_{210} = body weight at 210 days; $Dep_speed_{k \rightarrow 30} = (BW_{30} -$
262 $BW_k) / 30$; $Rep_speed_{180 \rightarrow 210} = (BW_{210} - BW_{180}) / 30$.

263 The same fitting procedure for body condition score was used to fit monthly body
264 weight data.

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273 **Fitting convergence**

274 Non-convergence of the fitting procedure occurred in situations where the model was
 275 irrelevant to describe data. Non-convergence of the fitting procedure accounted for 0
 276 % of lactations of the datasets for MY, 3 % of lactations of the datasets for BW and 30
 277 % of lactations of the datasets for lumbar BCS and 22 % of lactations of the two
 278 datasets for sternal BCS. Modelled curves with extreme features were removed using
 279 the Tukey’s rule (Tukey, 1977) applied to estimates of model parameters and root
 280 mean square error (RMSE) (exclusion of values above the third quartile plus three
 281 times the interquartile range). The loss associated to extreme features accounted for
 282 3 % of lactations of the datasets for MY, 7 % of lactations of the datasets for BW and
 283 6 % of lactations of the datasets for lumbar and sternal BCS.

284 **Synthetic indicators to describe fitted individual phenotypic trajectory**

285 Finally, we used synthetic indicators derived from modelled curves to describe
 286 lactation, body weight and body condition score dynamics during lactation. Two types
 287 of indicators were used: level indicators were considered to characterize performance
 288 at specific times and dynamic indicators were considered to characterize temporal
 289 changes in performance (Table 2).

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291 **Table 2.** Description of the set of synthetic indicators to describe fitted individual phenotypic trajectory
 292 for milk yield, body weight and body condition score.

Trajectory	Type	Indicator	Calculation	Unit
Milk production	L ²	SumMY	Sum of daily milk yield values on 250 days from Wood model	kg
	L	MY _{peak}	Highest daily milk yield	kg/d
	L	MY ₂₁₀	Daily milk yield at 210 days	kg/d
	D	Peak time	Time of highest milk yield value	d
	D	Persistency	$(MY_{250}-MY_{150}/MY_{150}) \times 100$	%
Body weight	L	BW _k	Daily body weight at kidding	kg
	L	BW _{min}	Minimum daily body weight	kg
	L	BW ₂₁₀	Daily body weight value at 210 days	kg
	D	Dep_speed _{k->30}	Body weight depletion speed: $(BW_{30} - BW_k) / 30$	kg/d
	D	Rep_speed _{180->210}	Body weight repletion speed: $(BW_{210} - BW_{180}) / 30$	kg/d
Lumbar or sternal body condition score ¹	L	BCS_X _k	Lumbar/sternal BCS at kidding	[0-5] scale
	L	BCS_X _{min}	Minimum lumbar/sternal BCS	[0-5] scale
	L	BCS_X ₂₁₀	Lumbar/sternal BCS at 210 days	[0-5] scale
	D	Dep_speed_X _{k->30}	Lumbar/sternal BCS depletion speed : $(BCS_X_{30} - BCS_X_k) / 30$	[0-5] scale/d
	D	Rep_speed_X _{180->210}	Lumbar/sternal BCS repletion speed : $(BCS_X_{210} - BCS_X_{180}) / 30$	[0-5] scale/d

¹ X stands for lumbar (L) or sternal (S).

² L = level; D = dynamic.

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294 **Statistical analysis**

295 *Clusters of phenotypic trajectories at lactation scale*

296 All statistical analysis were performed using RStudio (version 2023.06.01). Data and
 297 scripts can be found in the repository linked to this manuscript (Gafsi et al., 2023). To

298 characterize individual phenotypic trajectories, principal component analysis (PCA)
299 was performed on milk, body weight and body condition synthetic indicators
300 separately. The number of principal components (PC) was based on the cumulative
301 variance. To choose the number of PC at least 75 % of total variance was needed.
302 PCA was followed by an agglomerative hierarchical clustering (AHC) using Ward's
303 linkage procedure. Ward's method is a hierarchical procedure that iteratively merges
304 groups of individuals represented by points in an Euclidean space resulting in the
305 smallest increase in the sum of within-group sums of squares. This clustering method
306 produces groups that minimize intra-group dispersion and maximize inter-group
307 dispersion at each binary fusion. A specific clustering approach was used for each
308 phenotypic trajectory. Preliminary analysis was conducted considering the farming
309 systems, breed, and parities all together. Breed and farming systems did not play a
310 strong role on cluster characterization. Parity played a strong role on cluster
311 characterization only for milk yield and body weight. So, we performed a clustering by
312 parity (primiparous vs multiparous) for milk yield and body weight whereas we
313 performed a single clustering for all parities together for body condition score. The
314 optimal number of clusters was based on the higher relative loss of inertia criteria.
315 Differences between clusters were assessed for each synthetic indicator with a one-
316 way ANOVA followed by a Tukey test.

317 *At lactation scale, contingency tables between phenotypic clusters*

318 To assess the associations between MY, BW and BCS dynamics at the lactation scale,
319 we produced contingency tables. Contingency tables displayed the frequency of
320 individual lactations affected to two phenotypic clusters. Contingency tables are used
321 to assess if a cluster membership for a given phenotypic trajectory is associated to a
322 particular cluster membership for another phenotypic trajectory. This approach aimed
323 at seeking for combinations of dynamic profiles of MY, BW and BCS. MY, BW and
324 BCS records concerned different number of lactations, so each contingency tables
325 (e.g. MY with BW or MY with lumbar BCS) considered different sub-populations. Chi-
326 square tests were performed to assess for associations between phenotypic
327 trajectories. Cramer's V test was performed on significant associations to evaluate the
328 strength of the associations. Cramer's V values ranged from 0 to 1. Values close to 1
329 indicate a strong association whereas values close to 0 indicate a weak association.

330 *At lifetime scale, changes in cluster composition for each parity*

331 To assess the diversity of phenotypic trajectories at lifetime scale, we produced bar
332 plots of the composition of each cluster for parity n in terms of clusters in the next parity
333 $n+1$. With this visual display, it is possible to characterize if goat's assignment to a
334 cluster is stable across parities (reflecting goats with a stable type of dynamics across
335 parities) or if assignment to a cluster varies across parities (reflecting goats with various
336 dynamics during their lifetime). Chi-square tests were performed to assess for
337 associations between phenotypic trajectories. Cramer's V test was performed on
338 significant associations to evaluate the strength of the associations. For each
339 phenotypic trajectory, bar plots allow the visual display of cluster change from one
340 parity to another. Therefore, bar plots allow us to represent the sequence of cluster
341 memberships on over successive lactations.

342 **Results**

343 *Goodness-of-fit*

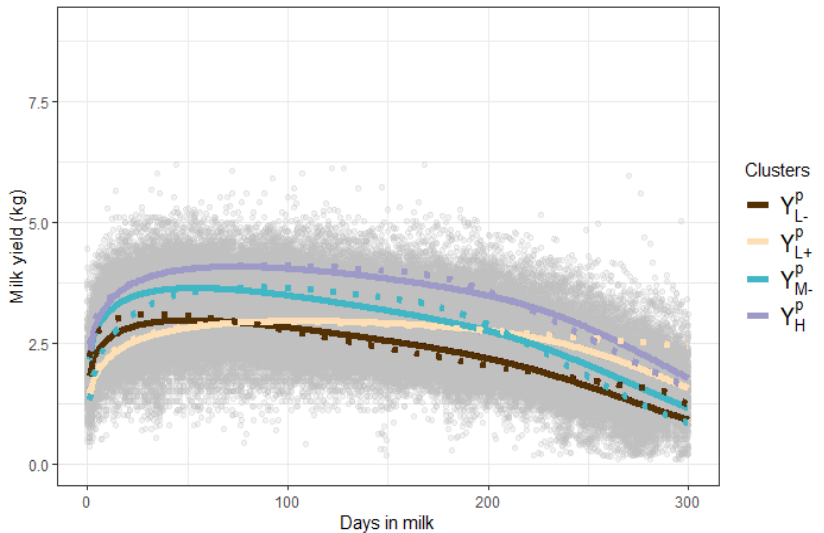
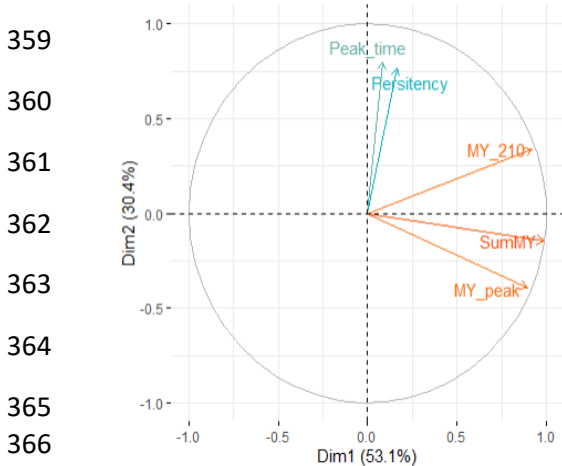
344 For the two data sets, the RMSE averaged $5.0 \% \pm 1.9 \%$ of the average milk yield per
 345 lactation, $2.7 \% \pm 1.0 \%$ of the average body weight per lactation, $3.6 \% \pm 1.6 \%$ of the
 346 average lumbar BCS per lactation and $3.1 \% \pm 1.3 \%$ of the average sternal BCS per
 347 lactation.

348 *Trajectories characterization*

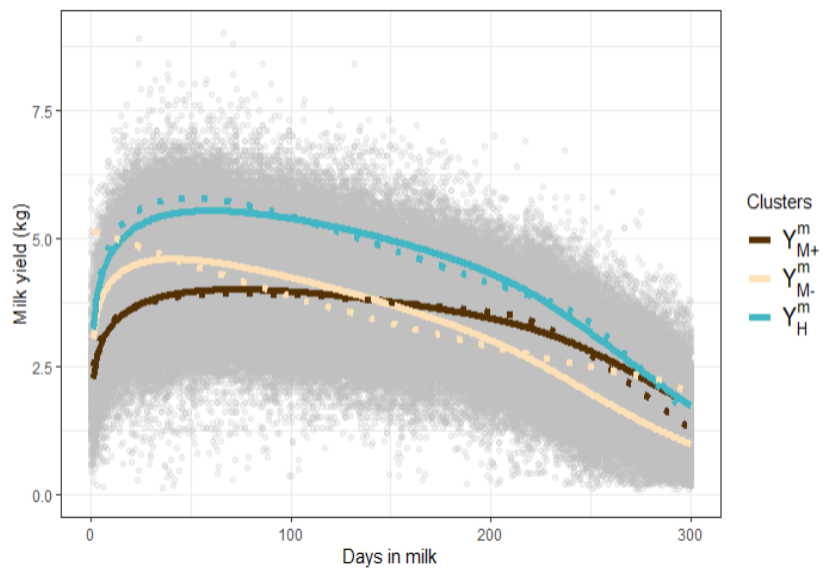
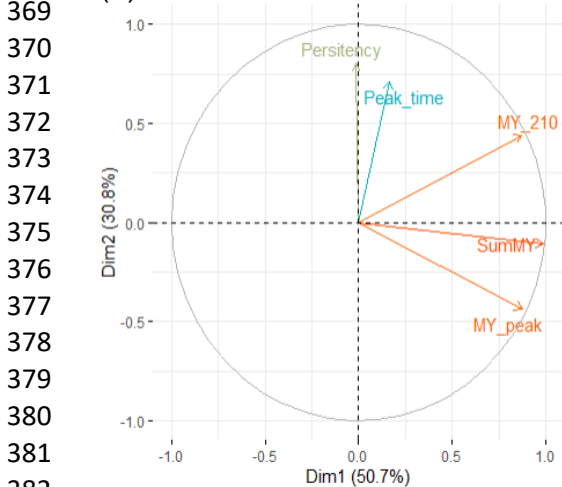
349 Milk yield trajectory

350 The first two principal components (PC) accounted for 83.5 % of the total variance for
 351 primiparous goats and 81.6 % for multiparous goats. The first PC captured the total
 352 amount of milk produced during the lactation and accounted for 53.1 % of the total
 353 variance for primiparous goats and 50.7 % for multiparous goats. The second PC
 354 captured the persistency and peak time of the lactation curve and accounted for 30.4%
 355 of the total variance for primiparous goats and 30.8 % for multiparous goats. Based on
 356 the highest loss of inertia, four clusters were retained for primiparous goats, and three
 357 clusters were kept for multiparous goats (Figure.4).

358 (a) Variables - PCA



368 (b) Variables - PCA



385 **Figure.4** PCA and clusters of milk yield synthetic indicators in primiparous (a) and multiparous (b) goats
 386 with grey points representing raw data, straight lines representing the mean trajectory and dotted lines
 387 representing a paragon trajectory (MY_{peak} = highest milk yield value; MY_{210} = milk yield value at 210 days;
 388 $SumMY$ = sum of daily milk yield values on 250 days; Peak time = time of the highest milk yield value;
 389 $Persistence = (MY_{250} - MY_{150} / MY_{150}) \times 100$; $Y^{P_{L+}}$ = Low milk yield and high persistency profile for
 390 primiparous; $Y^{P_{L-}}$ = Low milk yield and low persistency profile for primiparous; $Y^{P_{M-}}$ = Medium milk yield
 391 and low persistency profile for primiparous; Y^{P_H} = High milk yield and a medium persistency profile for
 392 primiparous; $Y^{m_{M+}}$ = Medium milk yield and high persistency for multiparous; $Y^{m_{M-}}$ = Medium milk yield
 393 and a low persistency for multiparous; Y^{m_H} = High milk yield and a medium persistency for multiparous).

394 Full details for each cluster are given in tables 3a and 3b.

395 Primiparous profiles were characterized by:

- 396 - a group of low persistency profiles with two different total milk production levels
 397 (63.3% of the primiparous): a low-level trajectory ($Y^{P_{L-}}$) that produced 155.6 kg
 398 less over the lactation than a medium-level trajectory ($Y^{P_{M-}}$).
- 399 - a medium persistency profile with the highest total milk production level that
 400 gathered 22.6% of the primiparous (Y^{P_H}).
- 401 - the highest persistency profile with a low total milk production level that gathered
 402 14.1% of the primiparous ($Y^{P_{L+}}$).

403 **Table 3a.** Statistical description of synthetic indicators for MY clusters in primiparous goats.

Indicator	$Y^{P_{L-}}$ ³ n = 273	$Y^{P_{L+}}$ n = 163	$Y^{P_{M-}}$ n = 459	Y^{P_H} n = 262	Pooled SE	p-value ²
SumMY ¹	629.1 ^a	675.5 ^b	784.7 ^c	925.4 ^d	67.2	0.001 ^{***}
MY_{peak}	3.0 ^a	3.0 ^a	3.7 ^b	4.2 ^c	0.4	0.001 ^{***}
MY_{210}	2.1 ^a	2.7 ^b	2.6 ^b	3.4 ^c	0.3	0.001 ^{***}
Peak time	47.4 ^a	106.0 ^b	49.8 ^a	71.4 ^c	26.7	0.001 ^{***}
Persistence	-36.7 ^a	-19.2 ^b	-35.2 ^a	-27.2 ^c	10.9	0.001 ^{***}

^{a-d} Means with superscripts differ significantly by row.

¹ SumMY = sum of daily milk yield values on 250 days; MY_{peak} = highest milk yield value; MY_{210} = milk yield value at 210 days; Peak time = time of the highest milk yield value; Persistence = $(MY_{250} - MY_{150} / MY_{150}) \times 100$

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS (p<0.1), *(p<0.05); and ***(p<0.001).

³ $Y^{P_{L+}}$ = Low milk yield and high persistency profile; $Y^{P_{L-}}$ = Low milk yield and low persistency profile; $Y^{P_{M-}}$ = Medium milk yield and low persistency profile; Y^{P_H} = High milk yield and a medium persistency profile.

404

405 Multiparous profiles were characterized by:

- 406 - a group of medium total milk production levels with two different persistency
 407 (65.4 % of the multiparous): a high persistency trajectory ($Y^{m_{M+}}$) that maintained
 408 20.4 % more the production than a low persistency trajectory ($Y^{m_{M-}}$).
- 409 - the highest total milk production level profile with a medium persistency (Y^{m_H})
 410 that gathered 34.6 % of the population.

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412

413 **Table 3b.** Statistical description of synthetic indicators for MY clusters in multiparous goats.

Indicator	$Y^{m_{M+}}$ ³ n = 741	$Y^{m_{M-}}$ n = 740	Y^{m_H} n = 783	Pooled SE	p-value ²
SumMY ¹	911.4 ^a	940.9 ^b	1,212.4 ^c	111.5	0.001***
MY _{peak}	4.1 ^a	4.7 ^b	5.7 ^c	0.6	0.001***
MY ₂₁₀	3.4 ^a	2.9 ^b	4.1 ^c	0.5	0.001***
Peak time	71.1 ^a	38.1 ^b	58.3 ^c	27.4	0.001***
Persistence	-25.9 ^a	-46.3 ^b	-36.3 ^c	12.4	0.001***

^{a-c} Means with superscripts differ significantly by row.

¹ SumMY = sum of daily milk yield values on 250 days; MY_{peak} = highest milk yield value; MY₂₁₀ = milk yield value at 210 days; Peak time = time of the highest milk yield value; Persistence = $(MY_{250} - MY_{150} / MY_{150}) \times 100$

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS (p<0.1), *(p<0.05); and ***(p≤0.001).

³ $Y^{m_{M+}}$ = Medium milk yield and high persistency; $Y^{m_{M-}}$ = Medium milk yield and a low persistency; Y^{m_H} = High milk yield and a medium persistency.

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416 For primiparous goats, Pradel's Alpine goats, Grignon's Alpine goats and Grignon's
 417 Saanen goats were more represented in the $Y^{p_{M-}}$ profile. For multiparous goats,
 418 Pradel's Alpine goats were more represented in the Y^{p_H} profile whereas Grignon's
 419 Alpine goats were less represented in this profile. Grignon's Saanen goats were more
 420 represented in the $Y^{m_{M+}}$ profile. See Appendix B section 1 for more details.

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428 **Body weight trajectory**

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430 The first two PC accounted for 77.4% of the total variance for primiparous goats and
 431 79.4% for multiparous goats. The first PC represented the level of body weight at
 432 different times of lactation and accounted for 52.8% of the total variance for
 433 primiparous goats and 56.9% for multiparous goats. The second PC represented the
 434 body weight speed loss in the 30 days after kidding and accounted for 24.7% of the
 435 total variance for primiparous goats and 22.5% for multiparous goats. Three clusters
 436 were retained for each **parity** due to the highest loss of inertia with three clusters
 437 (Figure.5).

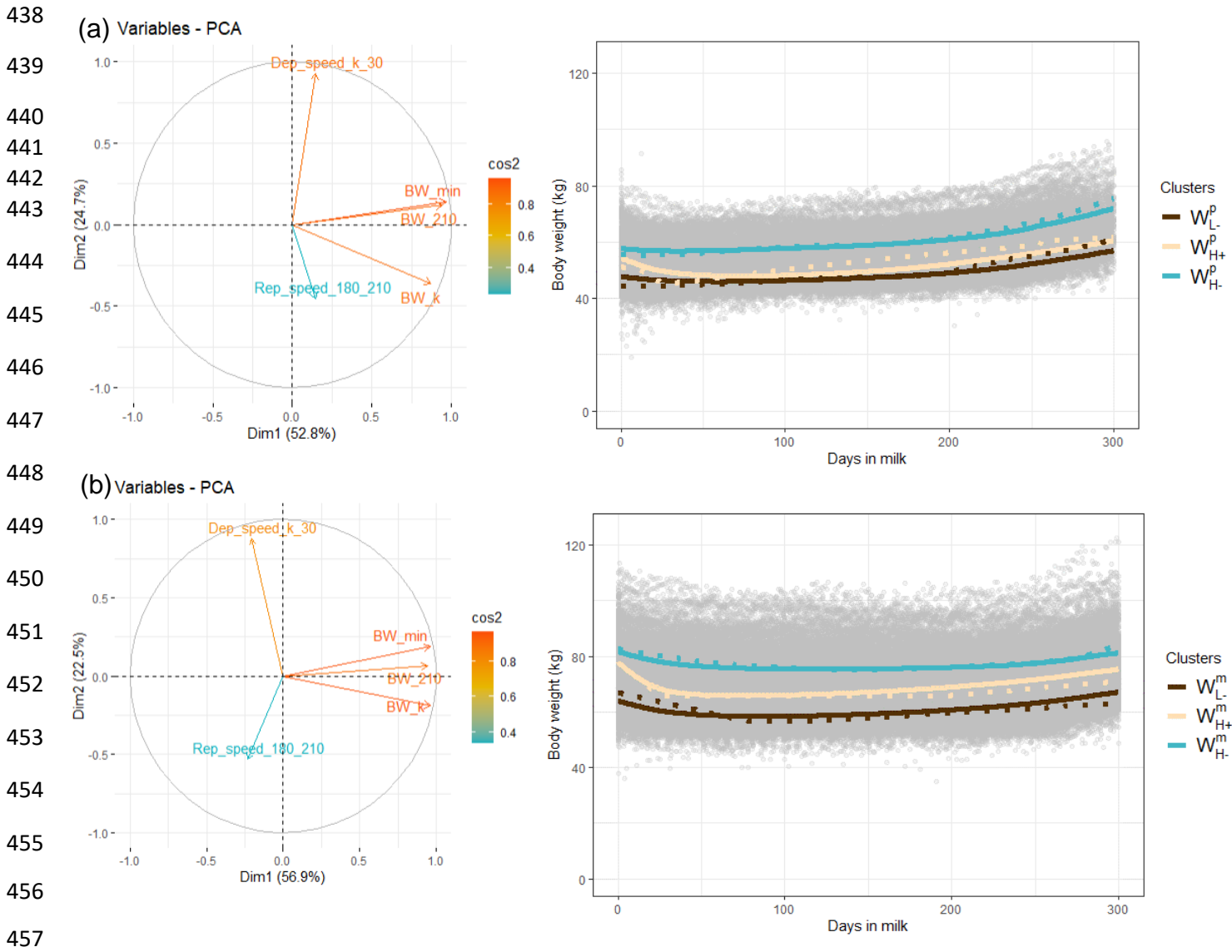


Figure.5 PCA and clusters of body weight synthetic indicators in primiparous (a) and multiparous (b) goats with grey points representing raw data, straight lines representing the mean trajectory and dotted lines a paragon trajectory (BW_k = body weight at kidding; BW_{min} = minimum body weight; BW_{210} = body weight at 210 days; $Dep_speed_{k \rightarrow 30} = (BW_{30} - BW_k) / 30$; $Rep_speed_{180 \rightarrow 210} = (BW_{210} - BW_{180}) / 30$; W_{L-}^p = Low body weight and low depletion profile in primiparous; W_{H+}^p = High body weight and high depletion profile in primiparous; W_{H-}^p = High body weight and low depletion profile in primiparous; W_{L-}^m = Low body weight and low depletion profile in multiparous; W_{H+}^m = High body weight and high depletion profile in multiparous; W_{H-}^m = High body weight and low depletion profile in multiparous).

473 Full details for each cluster are given in tables 4a and 4b.

474 Primiparous profiles were characterized by:

- 475 - a group of low depletion profiles with two different body weight level at kidding
- 476 (68.6% of the primiparous): a low-level trajectory (**W^P_L**) that averaged 10.0 kg
- 477 less at kidding than a high-level trajectory (**W^P_H**). Those profiles had a higher
- 478 BW_{210} than BW_k .
- 479 - the highest depletion profile with a high body weight level at kidding (**W^P_{H+}**) that
- 480 gathered 31.4% of the population. Despite having the highest repletion speed,
- 481 this profile presented a lower BW_{210} than BW_k due to the high level of depletion,
- 482 that is not totally compensated at 210 days of lactation.

483

484 **Table 4a.** Statistical description of synthetic indicators for BW clusters in primiparous goats.

Indicator	W ^P _L ³ n = 418	W ^P _{H+} n = 312	W ^P _{H-} n = 264	Pooled SE	p-value ²
BW _k ¹	47.7 ^a	54.3 ^b	57.7 ^c	4.0	0.001***
BW _{min}	45.2 ^a	47.6 ^b	55.6 ^c	3.5	0.001***
BW ₂₁₀	49.5 ^a	52.9 ^b	61.5 ^c	4.3	0.001***
Dep_speed _{k→30}	-0.05 ^a	-0.17 ^b	-0.03 ^c	0.07	0.001***
Rep_speed _{180→210}	0.04 ^a	0.06 ^b	0.05 ^c	0.03	0.001***

^{a-c} Means with superscripts differ significantly by row.

¹ BW_k = body weight at kidding; BW_{min} = minimum body weight; BW_{210} = body weight at 210 days; $Dep_speed_{k→30} = (BW_{30} - BW_k) / 30$; $Rep_speed_{180→210} = (BW_{210} - BW_{180}) / 30$.

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS ($p < 0.1$), * ($p < 0.05$); and *** ($p < 0.001$).

³ W^P_L = Low body weight and low depletion profile; W^P_{H+} = High body weight and high depletion profile; W^P_{H-} = High body weight and low depletion profile.

485

486 Multiparous profiles were characterized by:

- 487 - a group of low depletion profiles with two different body weight level at kidding
- 488 (73.4 % of the multiparous): a low-level trajectory (**W^m_L**) that averaged 17.6 kg
- 489 less at kidding than a high-level trajectory (**W^m_{H-}**). For these profiles BW_{210} was
- 490 lower than BW_k .
- 491 - the highest depletion profile with a high body weight level at kidding (**W^m_{H+}**) that
- 492 gathered 26.6% of the multiparous. Despite having the highest repletion speed,
- 493 this profile presented a lower BW_{210} than BW_k due to the high level of depletion,
- 494 that is not totally compensated at 210 days of lactation.

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500 **Table 4b.** Statistical description of synthetic indicators for BW clusters in multiparous goats.

Indicator	W ^{m_L} ³ n = 835	W ^{m_{H+}} n = 513	W ^{m_{H-}} n = 583	Pooled SE	p-value ²
BW _k ¹	64.1 ^a	78.1 ^b	81.7 ^c	6.2	0.001***
BW _{min}	57.8 ^a	65.5 ^b	74.2 ^c	5.2	0.001***
BW ₂₁₀	61.1 ^a	69.4 ^b	76.2 ^c	5.4	0.001***
Dep_speed _{k->30}	-0.14 ^a	-0.35 ^b	-0.14 ^a	0.12	0.001***
Rep_speed _{180->210}	0.04 ^a	0.04 ^b	0.01 ^c	0.03	0.001***

^{a-c} Means with superscripts differ significantly by row.

¹ BW_k = body weight at kidding; BW_{min} = minimum body weight; BW₂₁₀ = body weight at 210 days; Dep_speed_{k->30} = (BW₃₀ - BW_k)/30; Rep_speed_{180->210} = (BW₂₁₀ - BW₁₈₀) / 30.

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS (p<0.1), *(p<0.05); and ***(p≤0.001).

³ W^{m_L} = Low body weight and low depletion profile; W^{m_{H+}} = High body weight and high depletion profile; W^{m_{H-}} = High body weight and low depletion profile.

501

502 For primiparous goats, Pradel's Alpine goats were more represented in the W^{p_{L-}} and
 503 W^{p_{H+}} profiles. Grignon's Alpine goats were more represented in the W^{p_{L-}} profile.
 504 Grignon's Saanen goats were more represented in the W^{p_{H-}} profile. For multiparous
 505 goats, Pradel's Alpine goats and Grignon's Alpine goats were more represented in the
 506 W^{m_{L-}} profile. Grignon's Saanen goats were more represented in the W^{m_{H-}} profile. See
 507 Appendix B section 2 for more details.

508

509 Body condition score trajectory

510

511 For lumbar and sternal body condition score, clusters were built all parities together.
 512 For lumbar body condition score (BCS_L), the first two PC accounted for 75.8% of the
 513 total variance. The first PC represented levels of lumbar score at different times of the
 514 lactation (BCS_{Lmin} and BCS_{Lk}) and accounted for 46.9% of the total variance. The
 515 second PC represented the lumbar BCS speed loss in the 30 days after kidding and
 516 accounted for 28.9% of the total variance. Three clusters were retained due to the
 517 highest loss of inertia with three clusters. For sternal body condition score (BCS_S),
 518 the first two PC represented 78.6% of the total variance. The first PC represented
 519 levels of sternal score at different times of the lactation (BCS_{Smin} and BCS_{S210}) and
 520 accounted for 50.7% of the total variance. The second PC represented the sternal BCS
 521 speed loss in the 30 days after kidding and accounted for 27.9% of the total variance.
 522 Three clusters were retained due to the highest loss of inertia with three clusters
 523 (Figure.6).

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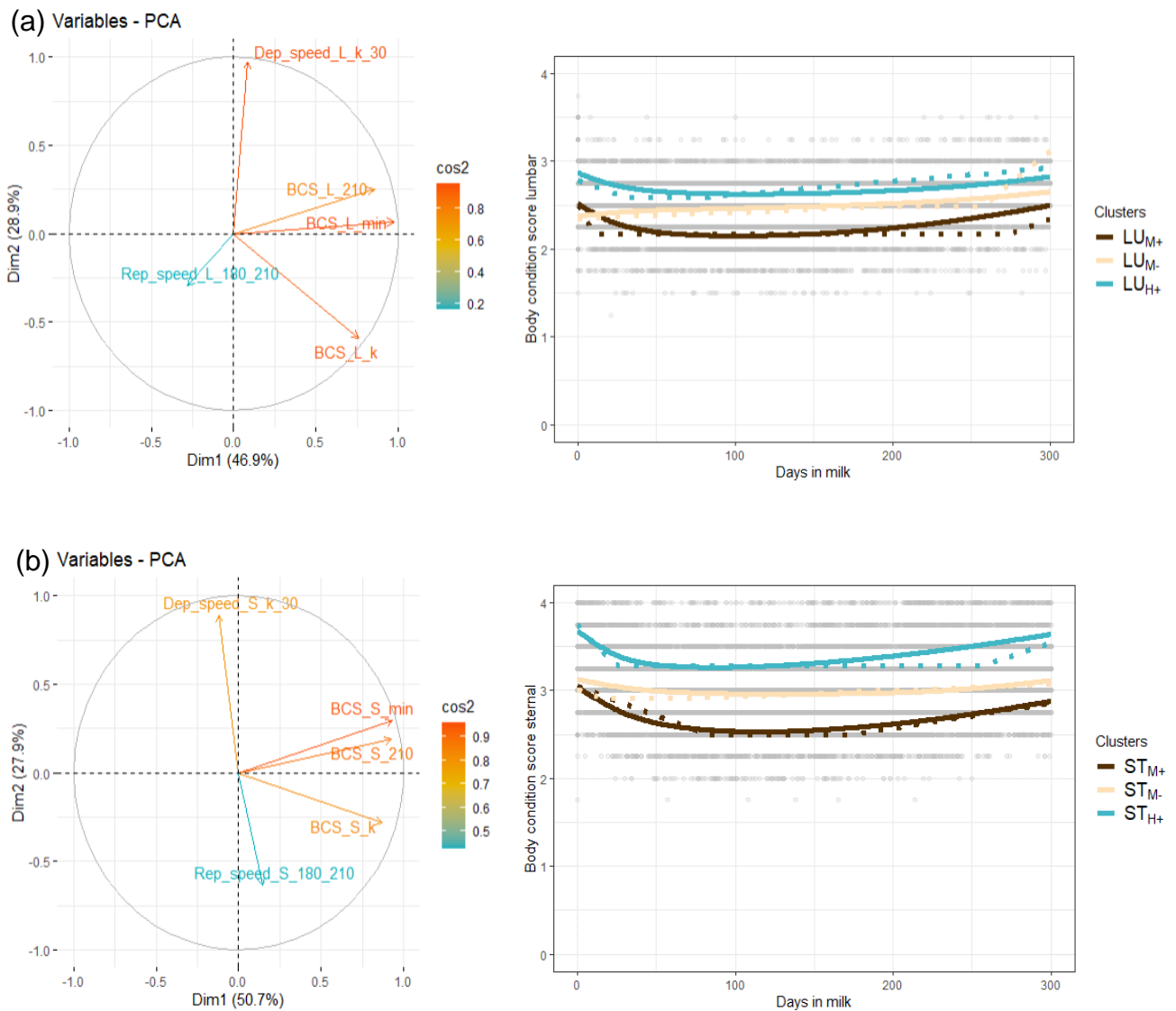


Figure.6 PCA and clusters of lumbar (a) and sternal (b) body condition score synthetic indicators with grey points representing raw data, straight lines representing the mean trajectory and dotted lines a paragon trajectory (BCS_{L_k} = lumbar BCS at kidding; BCS_{L_{min}} = minimum lumbar BCS; BCS_{L₂₁₀} = lumbar BCS at 210 days; Dep_speed_{L_k→30} = (BCS_{L₃₀} - BCS_{L_k}) / 30; Rep_speed_{L₁₈₀→210} = (BCS_{L₂₁₀} - BCS_{L₁₈₀}) / 30; BCS_{S_k} = sternal BCS at kidding; BCS_{S_{min}} = minimum sternal BCS; BCS_{S₂₁₀} = sternal BCS at 210 days; Dep_speed_{S_k→30} = (BCS_{S₃₀} - BCS_{S_k}) / 30; Rep_speed_{S₁₈₀→210} = (BCS_{S₂₁₀} - BCS_{S₁₈₀}) / 30; LU_{M+} = Medium lumbar body condition score and depletion profile; LU_{M-} = Medium lumbar body condition score and low depletion profile; LU_{H+} = High lumbar body condition score and depletion profile; ST_{M+} = Medium sternal body condition score and depletion profile; ST_{M-} = Medium sternal body condition score and low depletion profile; ST_{H+} = High sternal body condition score and depletion profile).

562 Full details for each cluster are given in tables 5 and 6.

563 Lumbar BCS profiles were characterized by:

- 564 - a group of depletion profiles with two different lumbar BCS level at kidding (68.7
565 % of the population): a medium level trajectory (**LU_{M+}**) that averaged 0.4 points
566 less at kidding than a high-level trajectory (**LU_{H+}**). LU_{M+} profile presented the
567 highest repletion speed and the lowest minimum lumbar BCS value.
- 568 - the lowest depletion profile with a medium lumbar BCS level at kidding that
569 gathered 31.3% of the population (**LU_{M-}**). LU_{M-} profile presented the same
570 repletion speed than LU_{H+}.

572 **Table 5.** Statistical description of synthetic indicators for lumbar BCS clusters in goats.

573

Indicator	LU _{M+} ³ n = 437	LU _{M-} n = 459	LU _{H+} n= 572	Pooled SE	p-value ²
BCS_L _k ¹	2.5 ^a	2.4 ^b	2.9 ^c	0.2	0.001***
BCS_L _{min}	2.1 ^a	2.3 ^b	2.6 ^c	0.2	0.001***
BCS_L ₂₁₀	2.3 ^a	2.5 ^b	2.7 ^c	0.2	0.001***
Dep_speed_L _{k->30}	-0.009 ^a	0.002 ^b	-0.006 ^c	0.005	0.001***
Rep_speed_L _{180->210}	0.002 ^a	0.001 ^b	0.001 ^b	0.001	0.001***

^{a-c} Means with superscripts differ significantly by row.

¹ BCS_L_k = lumbar BCS at kidding; BCS_L_{min} = minimum lumbar BCS; BCS_L₂₁₀ = lumbar BCS at 210 days; Dep_speed_L_{k->30} = (BCS_L₃₀ - BCS_L_k) / 30; Rep_speed_L_{180->210} = (BCS_L₂₁₀ - BCS_L₁₈₀) / 30

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS (p<0.1), *(p<0.05); and ***(p≤0.001).

³LU_{M+} = Medium lumbar body condition score and depletion profile; LU_{M-} = Medium lumbar body condition score and low depletion profile; LU_{H+} = High lumbar body condition score and depletion profile

574

575 Sternal BCS profiles were characterized by:

- 576 - a group of depletion profiles with two different sternal BCS level at kidding (56.5
577 % of the population): a medium-level trajectory (**ST_{M+}**) that averaged 0.7 points
578 less at kidding than a high-level trajectory (**ST_{H+}**). ST_{M+} profile presented the
579 lowest minimum sternal BCS. These profiles presented the highest and the
580 same repletion speed.
- 581 - the lowest depletion profile with a medium sternal BCS level at kidding that
582 gathered 43.5 % of the population (**ST_{M-}**). ST_{M-} profile presented the lowest
583 repletion speed.

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590 **Table 6.** Statistical description synthetic indicators for sternal BCS clusters in goats.

591

Indicator	ST _{M+} ³ n = 489	ST _{M-} n = 708	ST _{H+} n = 433	Pooled SE	p-value ²
BCS_S _k ¹	3.0 ^a	3.1 ^b	3.7 ^c	0.2	0.001***
BCS_S _{min}	2.5 ^a	2.9 ^b	3.2 ^c	0.2	0.001***
BCS_S ₂₁₀	2.6 ^a	3.0 ^b	3.4 ^c	0.2	0.001***
Dep_speed_S _{k→30}	-0.010 ^a	-0.003 ^b	-0.010 ^a	0.006	0.001***
Rep_speed_S _{180→210}	0.0020 ^a	0.0004 ^b	0.0020 ^a	0.001	0.001***

^{a-c} Means with superscripts differ significantly by row.

¹ BCS_S_k = sternal BCS at kidding; BCS_S_{min} = minimum sternal BCS; BCS_S₂₁₀ = sternal BCS at 210 days; Dep_speed_S_{k→30} = (BCS_S₃₀ - BCS_S_k) / 30; Rep_speed_S_{180→210} = (BCS_S₂₁₀ - BCS_S₁₈₀) / 30.

² p-value resulting from Tukey's test assessing the significance of differences between profiles for each variable. NS (p<0.1), *(p<0.05); and ***(p≤0.001).

³ ST_{M+} =Medium sternal body condition score and depletion profile; ST_{M-} =Medium sternal body condition score and low depletion profile; ST_{H+} =High sternal body condition score and depletion profile

592 For lumbar BCS, Pradel's Alpine goats were more represented in the LU_{H+} profile
 593 whereas Grignon's Alpine goats were more represented in the LU_{M-} profile. Grignon's
 594 Saanen goats were more represented in the LU_{M-} profile. Primiparous represented
 595 between 30 % to 38 % of the population in each profile for lumbar BCS. For sternal
 596 BCS, Pradel's Alpine goats were more represented in the ST_{M-} profile whereas
 597 Grignon's Alpine goats were more represented in the ST_{H+} profile. Grignon's Saanen
 598 goats were more represented in the ST_{H+} profile. Primiparous represented between 30
 599 % to 35 % of the population in each profile for sternal BCS. See Appendix B section 3
 600 for more details.

601

602 *Diversity of phenotypic trajectories at lactation scale*

603 *Associations between milk yield and body weight trajectories*

604

605 In this section, only the association between MY and BW is presented. For primiparous,
 606 the association between MY and BW profiles is shown in Table 7a. The Chi² test was
 607 significant (P<0.001) with a Cramer's V of 0.17. The association Y^{P_{M-}} with W^{P_{L-}} gathered
 608 the highest proportion of goats with 17.8 % of the population followed by the
 609 associations Y^{P_{L-}} with W^{P_{L-}} and Y^{P_{M-}} with W^{P_{H+}} with 13.9 % of the population. The
 610 association Y^{P_{L+}} with W^{P_{H+}} gathered the lowest proportion of goats with 2.8 % of the
 611 population. The remain 51.6% of the population was almost equally distributed
 612 between profiles.

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618 **Table 7a.** Contingency table displaying the frequency of individual primiparous goats affected to MY
 619 and BW profile clusters (see section 2 for clustering methodology).

Milk yield profile	Body weight profile						Total	
	$W^{p_{L-}2}$		$W^{p_{H+}}$		$W^{p_{H-}}$		n	%
	n	% ¹	n	%	n	%		
$Y^{p_{L-}2}$	124	13.9	45	5.0	43	4.8	212	23.7
$Y^{p_{L+}}$	44	4.9	25	2.8	44	4.9	113	12.7
$Y^{p_{M-}}$	159	17.8	124	13.9	77	8.6	360	40.3
$Y^{p_{H}}$	60	6.7	86	9.6	62	6.9	208	23.3
Total	387	43.3	280	31.4	226	25.3	893	100.0

¹ % = proportion of goats among the 893 primiparous goats.

² $Y^{p_{L+}}$ = Low milk yield and high persistency profile; $Y^{p_{L-}}$ = Low milk yield and low persistency profile; $Y^{p_{M-}}$ = Medium milk yield and low persistency profile; $Y^{p_{H}}$ = High milk yield and a medium persistency profile; $W^{p_{L-}}$ = Low body weight and low depletion profile; $W^{p_{H+}}$ = High body weight and high depletion profile; $W^{p_{H-}}$ = High body weight and low depletion profile.

620

621 For multiparous, the association between MY and BW profiles is shown in Table 7b.
 622 The Chi² test was significant (P<0.001) with a Cramer's V of 0.17. The association
 623 $Y^{m_{M+}}$ with $W^{m_{L-}}$ gathered the highest proportion of goats with 18.6% of the population.
 624 The association $Y^{m_{M+}}$ with $W^{m_{H+}}$ gathered the lowest proportion of goats with 5.6 % of
 625 the population. The remain 75.8 % of the population was almost equally distributed
 626 between profiles.

627 **Table 7b.** Contingency table displaying the frequency of individual multiparous goats affected to MY
 628 and BW profile clusters (see section 2 for clustering methodology).

Milk yield profile	Body weight profile						Total	
	$W^{m_{L-}2}$		$W^{m_{H+}}$		$W^{m_{H-}}$		n	%
	n	% ¹	n	%	n	%		
$Y^{m_{M+}2}$	313	18.6	95	5.6	145	8.6	553	32.8
$Y^{m_{M-}}$	242	14.4	166	9.9	140	8.3	548	32.5
$Y^{m_{H}}$	169	10.0	200	11.9	215	12.8	584	34.7
Total	724	43.0	461	27.4	500	29.7	1,685	100.0

¹ % = proportion of goats among the 1,685 multiparous goats.

² $Y^{m_{M+}}$ = Medium milk yield and high persistency; $Y^{m_{M-}}$ = Medium milk yield and a low persistency; $Y^{m_{H}}$ = High milk yield and a medium persistency; $W^{m_{L-}}$ = Low body weight and low depletion profile; $W^{m_{H+}}$ = High body weight and high depletion profile; $W^{m_{H-}}$ = High body weight and low depletion profile.

629

630 The conclusions were the same for the associations between MY and lumbar BCS and
 631 for the associations between MY and sternal BCS (see Appendix C section 1 and 2).

632

633

634 *Associations between body weight and sternal BCS trajectories*

635

636 In this section, only the association between BW and sternal BCS is presented. For
 637 primiparous, the association between BW and sternal BCS profiles is shown in Table
 638 8a. The Chi² test was significant (P<0.001) with a Cramer’s V of 0.25. The
 639 association W^p_{L-} with ST_{M+} and W^p_{H+} with ST_{M-} gathered the highest proportion of goats
 640 with 18.8 % of the population followed by the association W^p_{L-} with ST_{M-} with 17.9 %
 641 of the population. The association W^p_{H-} with ST_{M+} gathered the lowest proportion of
 642 goats with 1.6 % of the population. The remain 42.9 % of the population was almost
 643 equally distributed between profiles.

644 **Table 8a.** Contingency table displaying the frequency of individual primiparous lactations affected
 645 to BW and sternal BCS profile clusters (see section 2 for clustering methodology).

Body weight profile	Sternal BCS profile						Total	
	ST _{M+} ²		ST _{M-}		ST _{H+}		n	%
	n	% ¹	n	%	n	%	n	%
W ^p _{L-} ²	84	18.8	80	17.9	24	5.4	188	42.0
W ^p _{H+}	75	16.7	84	18.8	29	6.5	188	42.0
W ^p _{H-}	7	1.6	29	6.5	36	8.0	72	16.0
Total	166	37.1	193	43.1	89	19.9	448	100.0

¹ % = proportion of goats among the 448 primiparous goats.

²W^p_{L-} = Low body weight and low depletion profile; W^p_{H+}= High body weight and high depletion profile;
 W^p_{H-}= High body weight and low depletion profile; ST_{M+} =Medium sternal body condition score and
 depletion profile; ST_{M-} =Medium sternal body condition score and low depletion profile; ST_{H+} =High
 sternal body condition score and depletion profile.

646

647 For multiparous, the association between BW and sternal BCS profiles is shown in
 648 Table 8b. The Chi² test was significant (P<0.001) with a Cramer’s V of 0.18. The
 649 association W^m_{L-} with ST_{M-} gathered the highest proportion of goats with 18.6 % of the
 650 population followed by the association W^m_{L-} with ST_{M+} with 14.2 % of the population.
 651 The association W^m_{H-} with ST_{M+} gathered the lowest proportion of goats with 2.8 % of
 652 the population. The remain 64.4 % of the population was almost equally distributed
 653 between profiles.

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661 **Table 8b.** Contingency table displaying the frequency of individual multiparous lactations affected to
 662 BW and BCS sternal profile clusters (see section 2 for clustering methodology).

	Sternal BCS profile						Total	
	ST _{M+} ²		ST _{M-}		ST _{H+}		n	%
Body weight profile	n	% ¹	n	%	n	%		
W ^m _{L-} ²	139	14.2	182	18.6	74	7.6	395	40.5
W ^m _{H+}	120	12.3	132	13.5	93	9.5	345	35.3
W ^m _{H-}	27	2.8	115	11.8	94	9.6	236	24.2
Total	286	29.3	429	44.0	261	26.7	976	100.0

¹ % = proportion of goats among the 976 multiparous goats.

²W^m_{L-} = Low body weight and low depletion profile; W^m_{H+} = High body weight and high depletion profile; W^m_{H-} = High body weight and low depletion profile; ST_{M+} = Medium sternal body condition score and depletion profile; ST_{M-} = Medium sternal body condition score and low depletion profile; ST_{H+} = High sternal body condition score and depletion profile.

663

664 The conclusions were the same for the associations between BW and lumbar BCS
 665 (see Appendix C section 3).

666 *Association between lumbar and sternal BCS trajectories*

667

668 For primiparous, the association between lumbar and sternal BCS profiles is shown in
 669 Table 9a. The Chi² test was significant (P<0.001) with a Cramer's V of 0.27. The
 670 association LU_{M+} with ST_{M+} gathered the highest proportion of goats with 21.4 % of the
 671 population followed by the association LU_{H+} with ST_{M-} with 19.5 % of goats. The
 672 association LU_{M-} with ST_{M+} gathered the lowest proportion of goats with 6.7 % of the
 673 population. The remain 52.4 % of the population was almost equally distributed
 674 between profiles.

675 **Table 9a.** Contingency table displaying the frequency of individual primiparous lactations affected to
 676 BCS lumbar and BCS sternal profile clusters (see section 2 for clustering methodology).

	Sternal BCS profile						Total	
	ST _{M+} ²		ST _{M-}		ST _{H+}		n	%
Lumbar BCS profile	n	% ¹	n	%	n	%		
LU _{M+} ²	80	21.4	31	8.3	28	7.5	139	37.2
LU _{M-}	25	6.7	51	13.6	30	8.0	106	28.3
LU _{H+}	27	7.2	73	19.5	29	7.8	129	34.5
Total	132	35.3	155	41.4	87	23.3	374	100.0

¹ % = proportion of goats among the 374 primiparous goats.

²LU_{M-} = Medium lumbar body condition score and low depletion profile; LU_{H+} = High lumbar body condition score and depletion profile; ST_{M+} = Medium sternal body condition score and depletion profile; ST_{M-} = Medium sternal body condition score and low depletion profile; ST_{H+} = High sternal body condition score and depletion profile.

677

678 For multiparous, the association between lumbar and sternal BCS profiles is shown in
679 Table 9b. The Chi² test was significant (P<0.001) with a Cramer’s V of 0.35. The
680 association LU_{M+} with ST_{M+} gathered the highest proportion of goats with 20.0 % of the
681 population followed by the association LU_{H+} with ST_{M-} with 18.6 % of goats. The
682 association LU_{M+} with ST_{H+} gathered the lowest proportion of goats with 4.1 % of the
683 population. The remain 57.3 % of the population was almost equally distributed
684 between profiles.

685 **Table 9b.** Contingency table displaying the frequency of individual multiparous lactations affected to
686 lumbar and sternal BCS profile clusters (see section 2 for clustering methodology).

	Sternal BCS profile						Total	
	ST _{M+} ²		ST _{M-}		ST _{H+}		n	%
Lumbar BCS profile	n	% ¹	n	%	n	%	n	%
LU _{M+} ²	148	20.0	52	7.0	30	4.1	230	31.1
LU _{M-}	59	8.0	108	14.6	45	6.1	212	28.6
LU _{H+}	36	4.9	138	18.6	124	16.8	298	40.3
Total	243	32.8	298	40.3	199	26.9	740	100.0

¹ % = proportion of goats among the 740 multiparous goats.

² LU_{M-} = Medium lumbar body condition score and low depletion profile; LU_{H+} = High lumbar body condition score and depletion profile; ST_{M+} =Medium sternal body condition score and depletion profile; ST_{M-} = Medium sternal body condition score and low depletion profile; ST_{H+} =High sternal body condition score and depletion profile.

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702 Diversity of phenotypic trajectories at lifetime scale

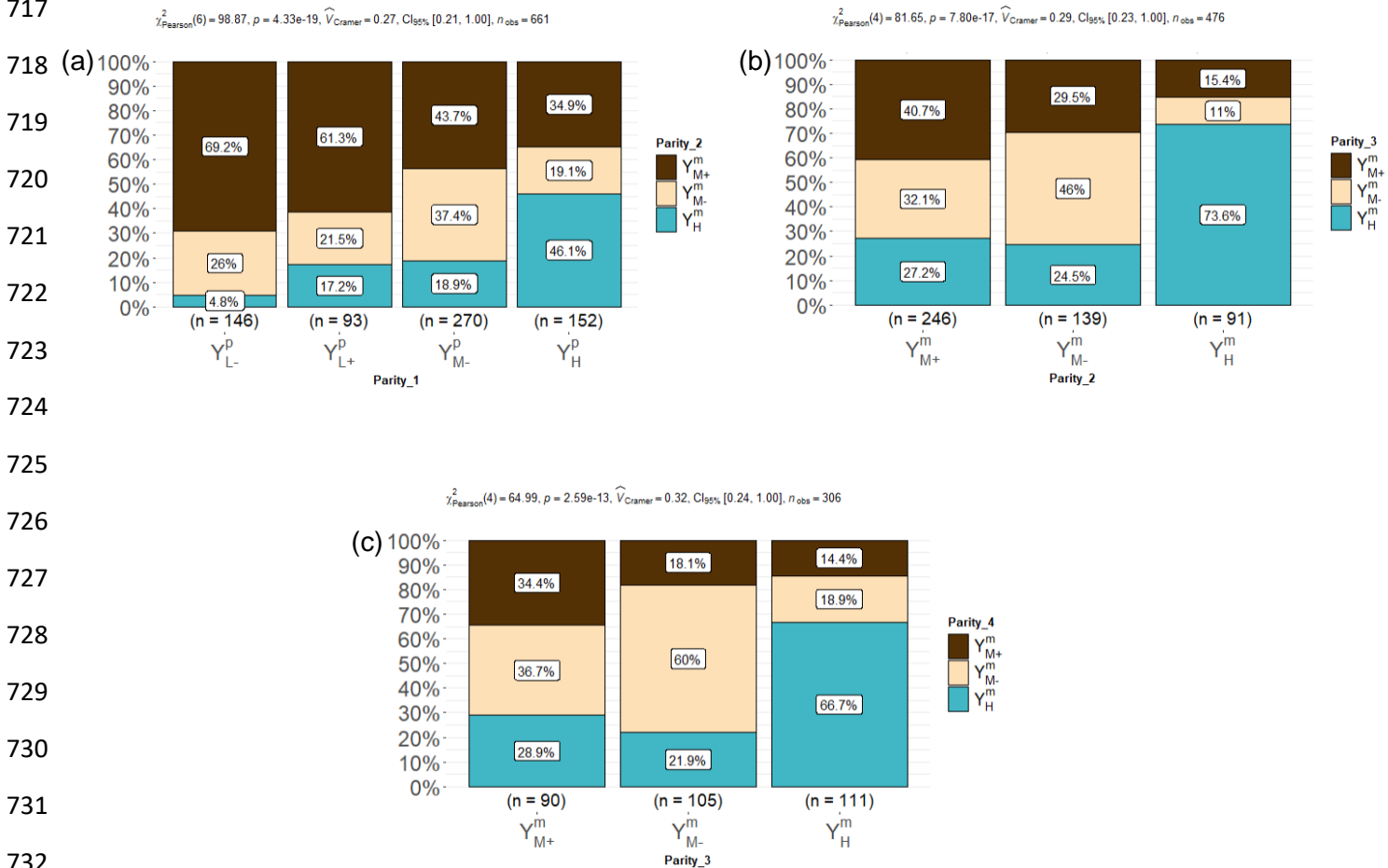
703

704 Milk yield trajectories throughout parities

705

706 Individual lactation transition in MY trajectories between successive lactations is shown
 707 in Figure.7. Between parity 1 to 4, the Chi² test was significant (P<0.001) with a
 708 Cramer's V ranging from 0.27 to 0.32. For primiparous, almost half of the goats in the
 709 Y^{P_H} profile remained the most productive ones in parity 2 (Y^{m_H}), while the other half
 710 switched to other profiles. More than half of the goats in the two lowest productive
 711 profiles (Y^{P_{L-}} and Y^{P_{L+}}) switched to the Y^{m_{M+}} profile. Goats in the Y^{P_{M+}} profile were
 712 almost equally distributed between the profiles in parity 2. For multiparous, more than
 713 two third of the goats in the Y^{m_H} profile remained in this profile in successive lactations.
 714 The proportion of goats that remained in the Y^{m_{M-}} profile in successive lactations
 715 increased with parity. Goats in the Y^{m_{M+}} profile were almost equally distributed between
 716 profiles in successive lactations.

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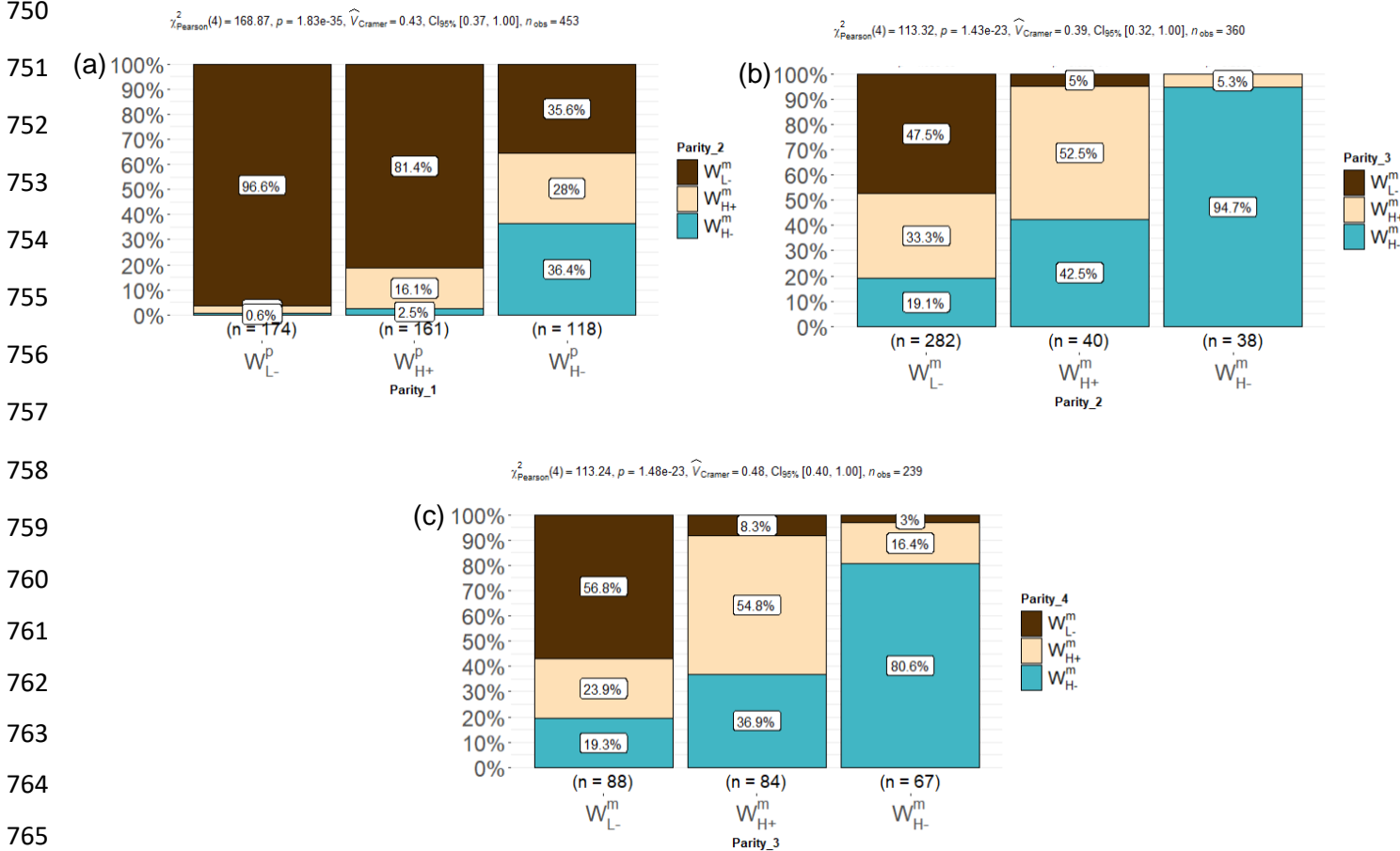
733 **Figure .7** Barplots displaying the frequency of goats affected to a MY cluster between (a) parity 1 and
 734 2, (b) parity 2 and 3 , (c) parity 3 and 4 (Y^{P_{L+}}= Low milk yield and high persistency profile for primiparous;
 735 Y^{P_{L-}}= Low milk yield and low persistency profile for primiparous; Y^{P_{M-}} = Medium milk yield and low
 736 persistency profile for primiparous; Y^{P_H} = High milk yield and a medium persistency profile for
 737 primiparous; Y^{m_{M+}} = Medium milk yield and high persistency for multiparous; Y^{m_{M-}} = Medium milk yield
 738 and a low persistency for multiparous; Y^{m_H} = High milk yield and a medium persistency for multiparous).

739 Body weight trajectories throughout parities

740

741 Individual lactation transition in BW trajectories between successive lactations is
 742 shown in Figure.8. Between parity 1 and 4, the Chi² test was significant (P<0.001) with
 743 a Cramer's V ranging from 0.41 to 0.44. For primiparous, goats in the W^p_{H-} profile
 744 switched profiles in parity 2. More than 80% of the goats in the W^p_{H+} and in the W^p_{L-}
 745 profiles switched to the W^m_{L-} profile in parity 2. For multiparous, more than two third of
 746 the goats in the W^m_{H-} profile remained in this profile in successive lactations. Half of
 747 the goats in the W^m_{H+} profile remained in this profile while the other half switched
 748 profiles in successive lactations. Half of the goats in the W^m_{L-} profile remained in this
 749 profile while the other half switched profiles in successive lactations.

750



767 **Figure .8** Barplots displaying the frequency of goats affected to a BW cluster between (a) parity 1 and
 768 2, (b) parity 2 and 3 , (c) parity 3 and 4 (W_{L-}^p = Low body weight and low depletion profile; W_{H+}^p = High
 769 body weight and high depletion profile; W_{H-}^p = High body weight and low depletion profile; W_{L-}^m = Low
 770 body weight and low depletion profile; W_{H+}^m = High body weight and high depletion profile; W_{H-}^m = High
 771 body weight and low depletion profile).

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775 Body condition trajectories throughout parities

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777 Only sternal BCS is presented here. Individual lactation transition in sternal BCS
 778 trajectories between successive lactations is shown in Figure.9. Between parity 1 and
 779 4, Chi² test was significant (P<0.001) with a Cramer's V ranging from 0.35 to 0.49. For
 780 primiparous, more than half of the goats in the three profiles remained in their profile
 781 in parity 2, while the other part switched to other profiles. For multiparous, more than
 782 three quarters of the goats in the ST_{H+} profile remained in this profile in successive
 783 lactations, while the other part switched to other profiles. More than half of the goats in
 784 the ST_{M+} and ST_{M-} profile remained in their profile in successive lactations, while the
 785 other part switched to other profiles.

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$\chi^2_{\text{Pearson}}(4) = 51.10, p = 2.12e-10, \hat{V}_{\text{Cramer}} = 0.35, \text{CI}_{95\%} [0.25, 1.00], n_{\text{obs}} = 197$

$\chi^2_{\text{Pearson}}(4) = 53.68, p = 6.15e-11, \hat{V}_{\text{Cramer}} = 0.41, \text{CI}_{95\%} [0.30, 1.00], n_{\text{obs}} = 148$

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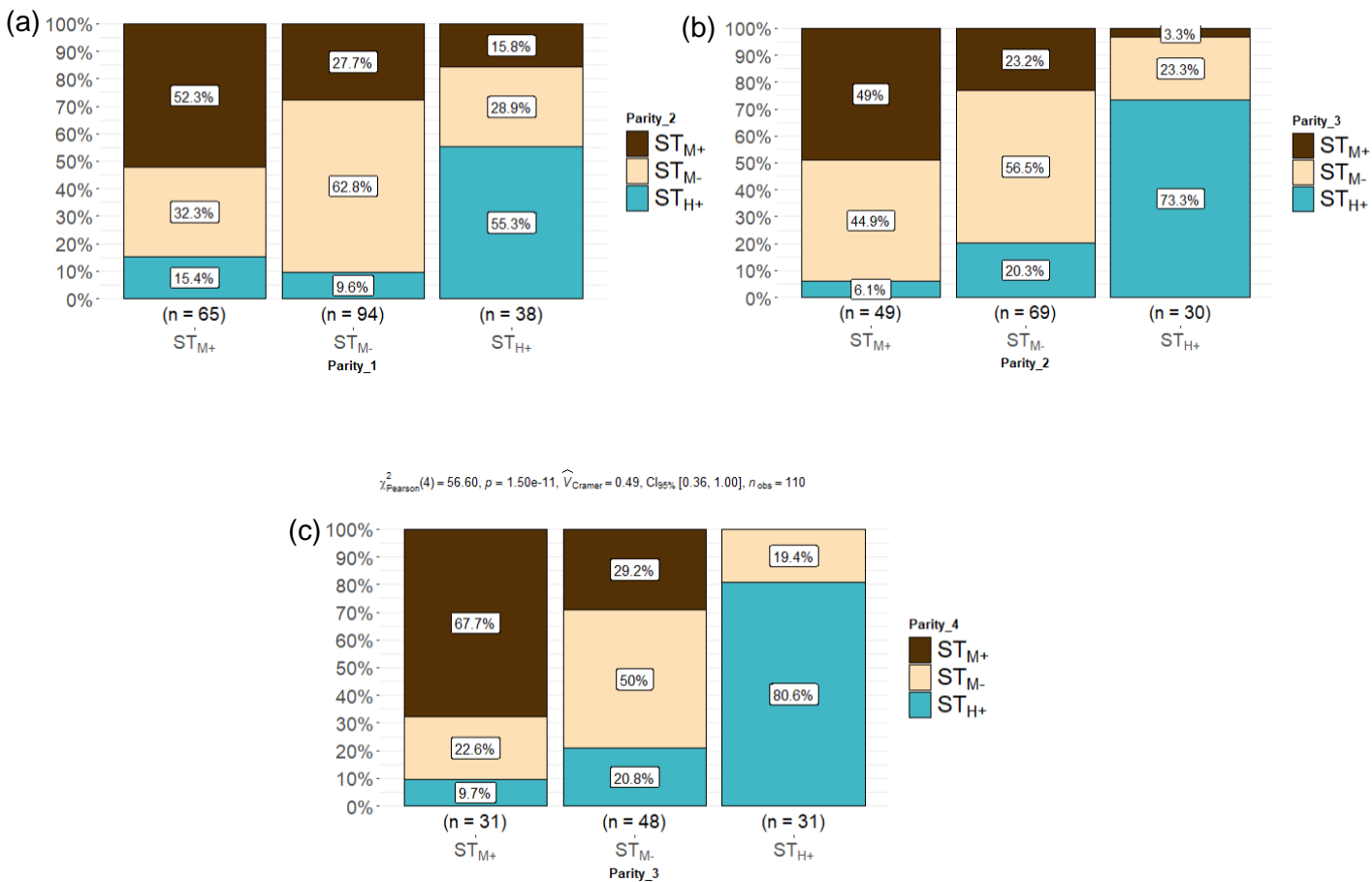


Figure .9 Barplots displaying the frequency of goats affected to a sternal BCS cluster between (a) parity 1 and 2, (b) parity 2 and 3 and (c) parity 3 and 4 (ST_{M+} =Medium sternal body condition score and depletion profile; ST_{M-} =Medium sternal body condition score and low depletion profile; ST_{H+} = High sternal body condition score and depletion profile).

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808

809 **Discussion**

810 *Trajectories were consistent with existing knowledge in dairy goats.*

811 The first objective of this work was to characterize the diversity of phenotypic
812 trajectories (MY, BW, BCS) at the lactation scale.

813 *Milk yield trajectories*

814 For MY trajectories we found four profiles for primiparous goats and three profiles for
815 multiparous goats. Parity played a strong effect on the scale of the lactation curve.
816 Primiparous presented lower milk level over the lactation than multiparous goats
817 (Gipson and Grossman, 1990). Parity also played on the shape of the lactation. For all
818 parities, some profiles presented the same shape characterized by a low persistency
819 with different milk production levels (Y^{pL-} , Y^{pM-} , Y^{mM-}). These profiles were similar to the
820 mean curve or the cluster 2 observed by Arnal et al., (2018) over the French dairy
821 goats population. For primiparous, one profile presented a low level of milk with the
822 highest persistency over the whole population (Y^{pL+}) which is consistent with
823 observations made by Gipson and Grossman, (1990) where persistency was the
824 highest in primiparous goats and decreased with increasing parity. This can be
825 explained by a lower level of development of the mammary gland (Safayi et al., 2010).
826 This shape of lactation curve was also observed in the study led by Arnal et al., (2018).
827 However, persistency and milk yield are not always negatively correlated because for
828 all parities we observed that the highest productives profiles were not the lowest
829 persistent ones they presented a medium persistency (Y^{pH} , Y^{mH}). This result is close to
830 what Arnal et al., (2018) observed with their highest productive profile with a high
831 persistency. With genetic improvement goats are more able to maintain milk production
832 after the peak. Breed didn't play a strong role in the scale and the shape of lactation
833 curves. For primiparous, Alpine and Saanen goats were more represented in the Y^{pM-}
834 profile because it was the largest profile. For multiparous, Saanen were more
835 represented in the Y^{mM+} profile. This is not consistent with study made by Gipson and
836 Grossman, (1990), who showed that breed played a role on the scale of the lactation
837 curve because Saanen are more productive than Alpine goats (Arnal et al., 2018; Rupp
838 et al., 2011). This lack of breed effect is probably linked to the fact that Alpine goats
839 and Saanen goats for Grignon farm did not differ in terms of milk production level (not
840 shown in the results).

841 *Body weight trajectories*

842 For BW trajectories we found three profiles for primiparous and multiparous goats.
843 Parity and breed played a strong role on the scale of BW trajectories. First for parity,
844 primiparous goats were lighter than multiparous goats. For all parities, we found low
845 depletion profiles (W^{pL-} , W^{mL-} , W^{pH-} , W^{mH-}) and high depletion profiles (W^{pH+} , W^{mH+}). Low
846 depletion profiles presented the same shape but differed in terms of level. Only the
847 high depletion profiles were different in terms of shape than the other profiles.
848 However, the depletion speed was lower in primiparous goats than multiparous goats.
849 Indeed, for primiparous, the variation between kidding and the minimum of BW
850 averaged 3.7 kg while for multiparous this variation averaged 8.3 kg. These results are
851 consistent with what Sauviant et al., (2012) saw when they modelled the BW trajectory
852 by parity. They observed that primiparous were lighter and lost less BW (4.0 kg on

853 average) than multiparous goats (7.3 kg on average) . To our knowledge, few works
854 were done to characterize BW trajectories in dairy goats. Our work can be compared
855 to the study lead by Macé et al., (2019) in meat sheep. They analyzed BW longitudinal
856 data in 1146 ewes to characterize trajectories on multiple production cycles. Most of
857 their trajectories had the same shape but differed in terms of level. Moreover, for
858 primiparous, goats in the $W^{P_{L-}}$ and $W^{P_{H-}}$ profiles had lower level of BW_k than BW_{210}
859 while goats in the $W^{P_{H+}}$ profile had lower values for BW_{210} than BW_k . These
860 observations made for $W^{P_{L-}}$ and $W^{P_{H-}}$ profiles could reflect animals that are still growing
861 whereas $W^{P_{H+}}$ profile could reflect more mature animals. For multiparous and for all
862 profiles BW_k was higher to BW at the end of lactation. BW is easy to measure on farm
863 to monitor animals especially to quantify energy balance (Thorup et al., 2012).
864 However, BW measures include digestive content, growth, gravid uterus and body
865 reserves. So, only BW measures are not enough to quantify body reserves variations.
866 It needs to be analyzed with BCS to better understand body reserves dynamics. Finally
867 for breed, Saanen goats were represented in the high-level trajectories for all parities
868 ($W^{P_{H-}}$, W^{m_H}) which is consistent with observations made by (Sauvant et al., 2012).

869 *Body condition score trajectories*

870 For lumbar and sternal BCS we found three profiles for all parities. First for all parities,
871 we found high depletion profiles for lumbar (LU_{M+} , LU_{H+}) and sternal (ST_{M+} , ST_{H+}) BCS.
872 Then, we found low depletion profiles for lumbar (LU_{M-}) and sternal (ST_{M-}) BCS. High
873 depletion profiles presented the same shape but differed in terms of level. Only the low
874 depletion profiles were different in terms of shape. These results are also consistent
875 with what Macé et al., (2019) observed with their BCS trajectories. They had the same
876 shape but differed in terms of level. Moreover, for the high depletion profiles the
877 variation between kidding and the minimum of BCS averaged 0.4 points for LU_{M+} , 0.3
878 points for LU_{H+} and 0.5 points for ST_{M+} and ST_{H+} . Our values and especially for sternal
879 BCS are lower but close to those observed in the French feeding system. Indeed, they
880 observed an average of 0.75 points variation between kidding and the peak of lactation
881 for sternal BCS (Inra, 2018). Parity did not played a strong role in BCS trajectories.
882 Indeed, primiparous represented a third of the whole population in each cluster. Breed
883 did not palyed a strong role in BCS trajectories. We just observed for BCS a farm effect
884 because Grignon's Alpine and Saanen goats were more represented in the LU_{M-} and
885 ST_{H+} . This observation could be explained by different factors such as a human effect
886 in the BCS evaluation, differences in herd management or a random distribution linked
887 to the clustering approach.

888 *A great diversity of associations among biological functions*

889 The second objective of this work was to assess the diversity of associations between
890 the different phenotypic trajectories. We investigated whether one phenotypic
891 trajectory could be explained by another. At the lactation scale, the χ^2 test was
892 significant for associations, the Cramer's V showed weak to moderate values (globally
893 less than 0.4) (Kotrlik et al., 2011). This absence of strong associations between MY,
894 BW and BCS trajectories throughout lactation suggests that a great diversity of energy
895 partitioning strategies exists between these biological functions. Assessing
896 associations between MY, BW and BCS was well-studied in dairy cows. Some studies

897 showed a positive correlation between pre-calving BCS and milk production (Roche et
898 al., 2007; Waltner et al., 1993) whereas other studies didn't find any relationship
899 between pre-calving BCS and milk yield (Garnsworthy and Jones, 1987; Garnsworthy
900 and Topps, 1982). More recently, Ollion et al., (2016) assessed the diversity of trade-
901 offs between milk production, body reserves and reproduction in early lactation dairy
902 cows. They showed four different trade-off profiles according to a priority given to a
903 biological function. All these approaches considered correlations between traits at one
904 time point and not at the whole lactation scale. Moreover, these performance traits
905 were evaluated at the beginning of the lactation where cows exhibited a negative
906 energy balance allowing energy partitioning in favor of milk over body reserves.
907 Another possible explanation for the lack of associations we found is that trade-off
908 between life functions, and therefore correlations between traits, are well expressed
909 when the environment is perturbed (Blanc et al., 2006; Friggens et al., 2017). Our data
910 came from two experimental farm where we can assume that animals are well
911 managed and not so perturbed. Finally, the diversity of associations in our study could
912 be explained by the fact that goats are more flexible animals in terms of energy
913 partitioning and have greater adaptive capacities than other ruminants (Silanikove,
914 2000). On the one hand, this diversity of biological profiles can be seen as a potential
915 resource to improve farming system resilience (Dumont et al., 2020). On the other
916 hand, this diversity raises questions about feeding systems that assumed a
917 relationship between a BW trajectory and a MY trajectory to quantify body reserves
918 contribution in terms of energy to goat's requirements (Inra, 2018). These findings
919 question management strategies that are based on average animal profiles. A
920 perspective can be to adapt management strategies to the diversity of individual
921 profiles in terms of phenotypic trajectory and then better match animal's requirements.

922 The final objective of this work was to assess the diversity of trajectory at the lifetime
923 scale. For each phenotypic trait, the Chi^2 test was significant. Cramer's V showed lower
924 values for MY than BW and BCS suggesting stronger associations for BW and BCS.
925 For MY trajectories, we saw for primiparous that almost half of the goats in the Y^{P_H}
926 remained in this profile in parity 2, while the lowest productive goats ($Y^{P_{L-}}$ and $Y^{P_{L+}}$)
927 switched profile in parity 2. For multiparous, we observed a pattern of cluster
928 membership with two third of the goats in the Y^{M_H} profile remaining in this profile in
929 successive lactations. Usually, milk production increased from first to fourth parity and
930 after the fourth parity level of milk production decreased (Arnal et al., 2018). However,
931 with genetic improvement we can make the hypothesis that some goats can reach their
932 milk potential earlier. Goats that stayed in the highest productive profiles could be
933 animals that have reached their milk potential. Goats that are changing profiles could
934 be the ones that have not already reached their potential. For BW trajectories across
935 parities, we saw that for primiparous most of the goats in the $W^{P_{L-}}$ remained in the
936 lowest BW profile ($W^{m_{L-}}$) in parity 2, while $W^{P_{H+}}$ switched to the $W^{m_{L-}}$ profile. Goats in
937 the $W^{P_{H+}}$ presented the highest depletion speed so there were not able to recover from
938 the intense depletion and remained in the lowest profile in parity 2. For multiparous,
939 we also observed a pattern of cluster membership with more than three quarters of the
940 in the $W^{m_{H-}}$ profile remaining in this profile in successive lactations. Half of the goats in
941 the $W^{m_{L-}}$ remained in this profile in successive lactations. For sternal BCS trajectories
942 across parities, we saw that for primiparous more than half of the goats in the three

943 profiles remained in their profile in parity 2. For multiparous, we observed that three
944 quarters of the goats in the ST_{H+} profile remained in this profile in successive lactations.
945 More than half of the goats in the ST_{M+} and ST_{M-} remained in their profile in successive
946 lactations. These observations on BW and BCS over successive lactations, is
947 consistent with what Macé et al., (2019) observed in meat sheep. They observed one-
948 third up to half of ewes that remained in the same trajectory during successive cycles.
949 They supposed that changes in profile distribution could be linked to litter size that can
950 play a role in body weight depletion. These results highlighted the importance of the
951 lifetime approach to better understand potential changes in priorities among functions
952 and see how an early lifetime performance can impact the whole productive lifespan
953 (Puillet and Martin, 2017). Lifetime and longevity approaches are more and more
954 studied because in France from 1991 to 2011, the female productive life decreased by
955 346 days which led to an average productive lifespan of 2.7 years per goat (Palhière
956 et al., 2018) which increases replacement costs.

957 *A methodology to analyze trade-off between phenotypic trajectories with*
958 *heterogeneous data frequency*

959 This methodology was built to analyze trade-off between phenotypic trajectories based
960 on longitudinal data with different frequencies. We used models adapted to data
961 frequency to better characterize our trajectories. However, this approach implied to
962 create synthetic indicators to have the same baseline for phenotypic trajectories
963 characterized by different models. For MY trajectories, synthetic indicators were simple
964 to find because we used common indicators to summarize a lactation curve with level
965 and dynamic indicators such as the MY_{peak} , Peak time and Persistency. However, for
966 BW and BCS some indicators could be improved such as the repletion speed. Indeed,
967 as we wanted to understand trade-off between MY, BW and BCS, it raised a question
968 of the moment in the lactation to look at to be able to capture only body reserves
969 repletion without considering gestation effect. With a heterogeneity of frequencies, it is
970 difficult to use the same models to capture phenotypic trajectories. Differences in
971 frequencies could lead to use simple models with parameters that are not always
972 biologically meaningful. Or it can lead to use more complex models that deal with
973 problems identifiability of parameters. It is important to find a way to use biologically
974 meaningful parameters from different models as inputs for a clustering approach. This
975 approach with parameters will help to summarize the phenotypic trajectories without
976 considering synthetic indicators.

977 *Further development and potential use of on-farm record for managing animal*

978 With development of automatic device, more frequent data for MY or BW are available.
979 Some authors developed methods to characterize new indicators such as deviation of
980 milk production from a theoretical potential production (Ben Abdelkrim et al., 2020;
981 Adriaens et al., 2021; Poppe et al., 2020). Identifying deviation of MY or BW could
982 reflect animals with diseases, metabolic disorders. In our study, we used specific
983 models that captured perturbation from a theoretical unperturbed trajectory. To
984 characterize trajectories, we only focused on unperturbed curves which represented
985 the potential trajectory that an animal could have on a non-perturbed environment. So,
986 we can imagine an improvement of the approach by looking at perturbations. With

987 unperturbed MY and BW trajectories we saw a diversity of associations but if we
988 consider perturbations, we may find out common perturbations on MY and BW
989 perturbed trajectories. This approach was done in dairy cows where they identified
990 common perturbations in MY and BW (Ben Abdelkrim et al., 2021). Using perturbations
991 in a trajectory analysis could help select animals that best cope with their environment.

992 Data acquisition for BCS is more complicated in dairy goats. Manual BCS evaluation
993 provided satisfactory results but still a subjective method depending on the operator
994 (Lerch et al., 2021). Recent studies showed that new methods such as 3-dimension
995 imaging showed not satisfactory estimators of body composition and further
996 developments may help to develop a robust phenotyping tool (Lerch et al., 2021). For
997 all parities, BCS trajectories were well discriminated one month after kidding and
998 stayed constant on the whole lactation. This observation suggests that BCS measures
999 frequency can be reduced to key periods (kidding period, two months before breeding
1000 period, dry-off). This paper is the first step of a study that will include reproduction
1001 success in the analysis. Including reproduction outcome will help to predict the
1002 reproductive success according to trajectories for a given lactation. This analysis will
1003 be conducted also on the lifetime scale to look for potential unfavorable profiles. These
1004 further analyses will clarify this diversity of phenotypic trajectories and will provide
1005 metrics to better manage risky animals in terms of reproduction failure (e.g., finding the
1006 best periods to monitor risky animals). In the dairy goat sector, extended lactations
1007 became an alternative farming management to reduce culling and give another chance
1008 for a goat to reproduce. Being able to early decide for reproduction management, can
1009 make farmers save money and increase sustainability (Adriaens et al., 2020).

1010 **Conclusion**

1011

1012 With a multi-scale approach on MY, BW and BCS time-series data, it was possible to
1013 characterize the diversity of associations between phenotypic trajectories, related to
1014 milk production and the use of body reserves. The diversity of association at the
1015 lactation scale suggests a diversity of energy partitioning strategies for all goats which
1016 can provide good adaptive response to environmental perturbations. Our results
1017 challenge mainstream management strategies that are based on average animal
1018 profiles. Rather, considering diversity of performance profiles can be a way to better
1019 adapt to individuals or groups of individuals to improve their robustness. At the lifetime
1020 scale, change between profiles are more pronounced for primiparous goats while a
1021 pattern of cluster membership appears for multiparous goats. Indeed, more than two
1022 third of the highest profiles for each phenotypic trajectories remained in these
1023 trajectories in successive lactations. To further identify some profiles or combination of
1024 profiles that are at risk of culling, a first perspective of this study is to combine
1025 reproduction performance with MY, BCS and BW trajectories and then provide metrics
1026 to better manage animals at risk of reproductive failure.

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1030 **Appendices**

1031 Appendices are deposited on Zenodo with this following doi : [10.5281/zenodo.10090604](https://doi.org/10.5281/zenodo.10090604)

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1033

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1040 **Data, scripts, code, and supplementary information availability**

1041 Data and scripts/code are deposited on Recherche Data Gouv with this following doi
1042 : <https://doi.org/10.57745/C1XPQ2>

1043 **Conflict of interest disclosure**

1044 The authors declare that they comply with the PCI rule of having no financial conflicts
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1049 **References**

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