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# Assessment of Milk Quality in Skopelos Goats Under Low- and High-Input Farming Systems

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**Abstract**

This study investigated the effect of different farming systems and lactation stages on the physicochemical characteristics, somatic cell count (SCC), and total bacterial count (TBC) of milk from Skopelos goats. This study was conducted over two consecutive lactation periods on two commercial farms in Greece, an extensive system on Skopelos Island and an intensive system in the Attica region, involving 237 goats of shared genetic background, thereby minimizing genetic variability and strengthening the validity of the comparisons between the production systems. Higher milk yields were observed in the extensive system (0.98 vs. 0.85 kg/day), while milk from this system also had a higher protein (3.57% vs. 3.47%; $p < 0.001$) and casein content (2.72% vs. 2.57%; $p < 0.001$), which are traits favorable for cheese production. Fat content peaked during mid-lactation (4.83%; $p < 0.05$) and remained unaffected by the farming system. Lactose declined from early (4.74%) to late lactation (4.42%; $p < 0.001$). Both SCC and TBC were significantly elevated in the extensive system ($p < 0.001$), possibly due to hand milking, environmental exposure, and less-controlled hygiene conditions. These findings highlight a trade-off between the nutritional advantages of extensive systems and challenges related to milk hygiene. A balanced approach, optimizing both quality and sustainability, is recommended.

**Keywords:** goat milk; extensive; intensive; lactation stage; milk composition

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## 1. Introduction

Dairy goats play a crucial role in global milk production, especially in the Mediterranean, where they contribute significantly to local economies and food security [1,2]. Over the past few decades, these sectors have undergone substantial transformations, with a growing emphasis on sustainable and agroecological production systems [3]. In key dairy-producing countries such as Greece, Italy, and Spain, goat farming systems range from small-scale traditional operations to intensive commercial farms, reflecting the diversity of management approaches and economic strategies within the sector [1]. In Greece, dairy goat farming is predominantly characterized by semi-extensive systems adapted to mountainous and semi-mountainous landscapes. These systems are based on traditional grazing practices that optimize the use of natural resources, making them an essential component of sustainable rural development [4].

The Skopelos goat is a local dairy breed mainly reared in the Sporades islands and central Greece, with a population of about 10,000 animals. It is known for its genetic consistency and ability to thrive in harsh, dry environments with limited vegetation and poor-quality grazing lands. Phenotypically, Skopelos goats are small-bodied (68 cm at the withers) but relatively heavy, with adult females averaging 56 kg. They are distinguished by a smooth, glossy coat, predominantly red–brown in color, and both sexes are horned [5].

The growing interest in goat dairy products, particularly cheese, has been influenced by evolving farming practices that impact both the intrinsic and extrinsic characteristics of milk quality, as well as consumer perception [6]. Goat milk has gained popularity due to its unique nutritional profile and potential health benefits. Its composition closely resembles human breast milk, making it a viable alternative for individuals with cow milk allergies [7]. Compared with cow milk, goat milk typically contains higher levels of fat, protein, and ash but less lactose, making it easier to digest for lactose-intolerant individuals [8]. Moreover, it is rich in essential fatty acids, such as omega-3 and conjugated linoleic acid, particularly when goats are raised in pasture-based systems [9]. Additionally, the physicochemical and microbiological properties of goat milk are crucial in determining its suitability for dairy processing and human consumption [10].

Among the key factors affecting milk quality, the farming system plays a significant role. Research indicates that organic and grazing-based systems produce milk with higher levels of unsaturated fatty acids and a lower saturated fat content compared with conventional intensive systems [11]. Additionally, grazing systems have been associated with improved milk composition, including higher fat, protein, and total solids (TSs) contents, as well as enhanced nutritional indices [12]. However, the overall impact of farming systems on milk composition is influenced by management practices, including nutrition, breed, selection, and milking techniques [13–16]. Furthermore, extensive farming systems have been linked to lower rates of intramammary infections compared with intensive systems, although this relationship is not always consistent across different studies [6,17].

While numerous studies have examined the effects of farming systems on milk composition [15,18–21], limited research has investigated the combined influence of farming systems and lactation stage within goats of the same breed, particularly under commercial conditions. Additionally, the genetic relatedness between intensively and extensively raised goats is often overlooked, despite its potential to provide valuable insights into milk quality variations. One of the major innovations of the present study is the inclusion of purebred Skopelos goats certified by the Skopelos Goat Association and sharing the same genetic background. Moreover, several studies have investigated the production traits [22–26] and genetic characteristics [27–30] of the Skopelos breed, including gene polymorphisms and genome-wide variation; however, to our knowledge, no study has evaluated milk quality under both low- and high-input farming systems. In this study, two commercial farms (intensive vs. extensive) were involved, and all goats in the intensive system originated from the extensive farm. This shared genetic background between the two farms reduces genetic variability as a confounding factor, allowing for a more precise evaluation of how farming systems influence milk quality. Another important aspect in this study is the inclusion of only second- and third-lactation-stage animals. The farms were large enough to provide a sufficient number of second- and third-lactation animals for this study, thus further limiting animal variability. Consequently, the objective of this study was to evaluate the combined effects of farming systems (intensive vs. extensive) and lactation stage over two consecutive lactation periods on goat milk quality regarding the chemical and physical characteristics and the somatic cell count (SCC) from two commercial farms rearing the Skopelos goat breed.

## 2. Materials and Methods

### 2.1. Farms and Animals

This study was conducted from February 2022 to August 2023 on two goat farms in Greece: one extensive on the island of Skopelos (latitude 39.09°, longitude 23.73°) and one intensive in the Attica region (latitude 37.95°, longitude 23.95°). The environmental conditions on Skopelos island ranged from 2 °C to 42 °C in temperature and 55% to 74% in relative humidity, while the Attica region experienced temperatures ranging from −3 °C to 44 °C and humidity levels from 61% to 71%. The farms were classified as 'extensive' or 'intensive' based on the differences in input utilization, including farm characteristics, management practices, labor force, and infrastructure.

A total of 237 goats were randomly selected for the study, including 132 from an extensive farming system and 105 from an intensive farming system. The sample sizes were designed to ensure the follow-up of at least 100 animals per system throughout the prospective study. All goats were in either their second or third lactation, with equal representation of lactation stages between farming systems to ensure balanced comparisons. This grouping reflects standard practices on commercial farms for managing feeding and milking. Additionally, goats were balanced by body weight (BW) and had similar parturition dates to minimize variability due to differences in lactation onset.

The goats belonged to the Skopelos breed, an indigenous Greek breed known for its adaptation to dry and hot climates. The annual milk yield for the Skopelos breed ranges from 250 to 450 kg per 210-day lactation, with prolificacy ranging from 1.2 to 1.6 kids per doe. Genetic relatedness existed between the animals on both farms, as all goats in the intensive farming system originated from the Skopelos farm, having been purchased three years prior to the start of the study.

Extensively reared goats were kept indoors at night in permanent sheds with ventilation openings, adequate floor space per animal, and floors that can absorb humidity and rainwater. Milking was performed by hand without prior udder preparation or teat disinfection. The goats grazed on natural grasslands and shrublands, and fed on typical endemic plants for the northwestern Aegean islands [31] and cultivated oat pastures. During the winter period, when pasture quality declined, the goats were supplemented with 0.5 to 1.0 kg/day of concentrated feed pellets (barley, corn, soybean meal, and a vitamin/mineral premix). In addition, 0.0 to 0.5 kg/day of alfalfa hay was offered depending on the condition and availability of natural forage. The goats continued to graze throughout the year; however, supplementary feeding was necessary in winter to compensate for the reduced nutritional value of the pasture. As pasture conditions improved in the spring and early summer, supplementation was gradually reduced, with concentrate offered at approximately 0.5 kg per day, while roughage needs were primarily met through grazing. In contrast, the intensively reared goats had no access to grazing and were kept in a permanent, well-ventilated barn with a controlled temperature and humidity, and straw bedding on the floor. These goats were fed 1.0 to 1.2 kg per day of commercial concentrated feed mixtures (including vitamin and mineral feed supplements) formulated specifically for dairy goats and 0.9 to 1.8 kg per day of alfalfa hay. The intensive farm was equipped with a 2 × 24 parallel milking parlor and ample feed storage facilities. The parlor was regularly cleaned and well maintained to ensure hygienic conditions. Standard milking hygiene protocols were followed, including udder preparation using a wet towel followed by a dried towel before milking. In both systems, feeding strategies were developed based on the farmers' experience (both farms are multiyear commercial enterprises with vast experience in managing this particular breed) and in collaboration with animal scientists, ensuring that the nutritional needs of the goats were met to support maximum milk yield and maintain an appropriate body condition score (BCS). This study was approved by

the Research and Ethics Committee of the Aristotle University of Thessaloniki, Greece (Approval No. 277235/2020).

### 2.2. Milk Sample Collection

Milk samples were collected during the morning milking (am_MY) from the same individual goats across two consecutive lactation periods. In each lactation period, sampling began in February, approximately 80 days postpartum, and continued at 45-day intervals until the end of the lactation in August, following ICAR recommendations [32].

Each sampling corresponded to a specific lactation stage (LS), which was divided into four stages as follows: the first stage (days in milk, (DIM), approximately (approx.) 80 days), the second stage (DIM approx. 125 days), the third stage (DIM approx. 170 days), and the fourth stage (DIM approx. 215 days). To ensure accuracy and consistency, this process was carried out by trained personnel, including animal scientists and veterinarians.

Milk samples were collected in 50 mL screw-capped flasks, cooled to 4–6 °C with ice packs, and transported to the laboratory in isothermal containers for analysis within 24 h. Over the two lactation periods, a total of 1828 milk samples from the two farms were collected and analyzed for chemical composition (fat, protein, lactose, and total solids (TSs) and casein (Cas) content), physical characteristics (pH, electrical conductivity (EC), refractive index (RI), and Brix value), SCC, and total bacterial count (TBC). Milk samples were analyzed within 24 h after their collection. To preserve the milk samples for TBC analysis, sodium azide (0.01 g/100 mL; Merck KGaA, Darmstadt, Germany) was added as a preservative.

### 2.3. Milk Chemical Composition, Milk Physical Properties, SCC, and TBC

The milk samples were allowed to reach room temperature and then placed in a heated water bath. After that, they were thoroughly mixed by gently inverting the sample container multiple times, ensuring no frothing occurred.

Chemical composition analysis was conducted using the Foss MilkoScan FT-plus fully automatic milk FTIR analyser (Foss Electric A/S, Hillerød, Denmark) following the ISO/IDF method [33]. Milk pH was measured with a portable pH/conductivity meter SG23-FIELD-KIT2 (51302602) (Mettler Toledo, Schwerzenbach, Switzerland) using an electrode equipped with a built-in temperature sensor (pH InLab® Expert-Go-ISM (IP67), 1.8 m cable, Schwerzenbach, Switzerland). The pH meter was calibrated using standard pH 4.0 and 7.0 buffer solutions, following the manufacturer's guidelines. The EC of the milk samples was also assessed with a pH/conductivity meter SG23-FIELD-KIT2 (51302602) (Mettler Toledo, Schwerzenbach, Switzerland) and an In-Lab®738-ISM (IP67), 1.8 m cable, electrode, which was calibrated with buffer solutions of 147 µS/cm, 1413 µS/cm, and 12.88 mS/cm. The RI and Brix values were measured using a digital hand-held refractometer PAL-BX.RI (ATAGO Co., Ltd, Tokyo, Japan) set to 20 °C. SCC and TBC were determined using a Fossomatic 5000 instrument and a BactoScan FC150 analyzer, respectively, developed by Foss Electric (Hillerød, Denmark).

### 2.4. Statistical Analysis

To explore the relationships among milk quality indicators, composition traits, and production parameters, both Principal Component Analysis (PCA) and Pearson's correlation analysis were employed. PCA was performed using the FactoMineR and factoextra packages in R Core Team (2024) [34] to reduce dimensionality and visualize variable groupings [35,36]. In parallel, a Pearson's correlation matrix was computed using the cor() function in R and visualized as a heatmap using the corrplot package [37]. This analysis provided a more direct and statistically interpretable view of inter-variable relationships,

with correlation coefficients (r values) ranging from –1 (perfect negative correlation) to +1 (perfect positive correlation).

Before PCA, the dataset was standardized (mean-centered and scaled to unit variance) to ensure comparability among variables with different units. The eigenvalues and screen plots were examined to determine the number of significant principal components, with components retaining eigenvalues greater than 1 considered for interpretation (Kaiser's criterion). Individual samples were color-coded in the PCA scatterplot to explore the potential differences between farming systems (extensive vs. intensive), with confidence ellipses representing group variability. Following the PCA, cluster analysis was conducted to further explore the patterns and groupings in the milk trait data, beyond the dimensions captured by PCA. This method allows the identification of natural groupings without predefined categories. Statistical analyses were performed in R, and results were considered significant at $\alpha = 0.05$.

The effect of farming system, lactation stage, year on am_milk yield (am_MY), and milk quality traits, accounting for random variability among individual animals, was assessed with the following linear mixed-effects model (1); each trait was analyzed separately as follows:

$$Y_{ijkl} = \mu + FS_i + LS_j + Y_k + (LS_j \times Y_k)\, FS_i + A_m + e_{ijkm} \quad (1)$$

where $Y_{ijkl}$ denotes the dependent variable (am_MY, chemical composition, physical properties, SSC, and TBC); $\mu$ the overall mean; $FS_i$ the fixed effect of farming system (i = 1–2); $LS_j$ the fixed effect of the LS (j = 1–4); $Y_k$ the fixed effect of the year (k = 1–2); ($LS_j$ x $Y_k$) the interaction effects of LS and year within each farming system ($FS_i$); $A_m$ the random effects of the animal within farming system; and $e_{ijkm}$ the residual error associated with observation ijkm. The model was fitted using the linear mixed-effects (lmer()) function from the lme4 package [38] in R. Fixed effects included farm, lactation stage (each sampling corresponded to a specific lactation stage), year of sampling, and the interaction effects of year and lactation stage within the farming system, while animals were included as a random effect to account for repeated measures and inter-individual variability. Model assumptions were assessed by inspecting residual plots, ensuring normality and homoscedasticity. Model significance was evaluated using likelihood ratio tests, and estimated marginal means were obtained using the emmeans package [39] for post hoc comparisons. SCC and TBC data were log-transformed to normalize their distributions prior to statistical analysis.

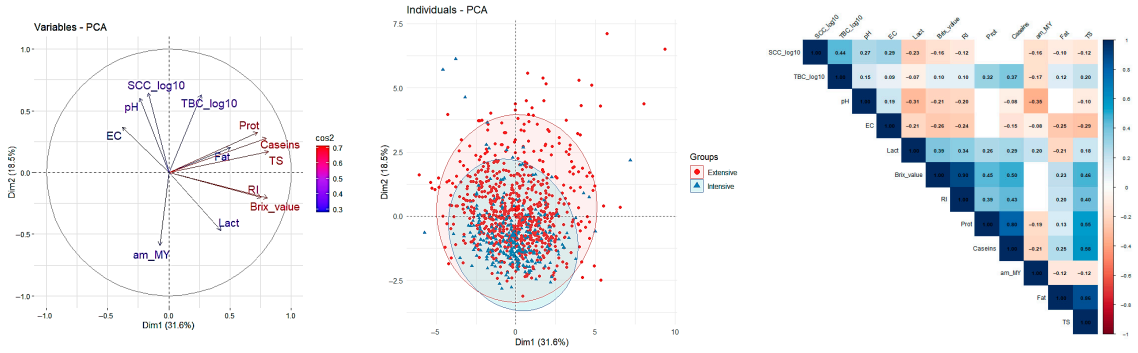
## 3. Results

### *3.1. Principal Component Analysis (PCA)*

Principal Component Analysis (PCA) was performed to investigate the relationships among the physicochemical, SCC, and TBC parameters of goat milk and to evaluate the differences between extensive and intensive farming systems. The first two principal components (Dim1 and Dim2) explained 31.6% and 18.5% of the total variance, respectively, effectively summarizing the main sources of variation in the dataset. The remaining principal components (Dim3 and beyond) explained a relatively small proportion of the total variability, each contributing to a minor extent to the overall variation in the dataset.

The PCA biplot (Figure 1a) provides insights into the relationships between the milk quality parameters. The angles between these variables serve as indicators of correlation; specifically, a smaller angle signifies a strong positive correlation, while variables that point in opposite directions indicate a negative relationship. In this analysis, SCC_log10, TBC_log10, and EC are closely aligned, suggesting a strong positive correlation among these variables. Conversely, milk composition traits, including fat, protein, and total solids (TSs), show a different directional contribution, highlighting their influence on a separate

component of variability. The cos2 values, represented by the color gradient, indicate how well each variable is explained by Dim1 and Dim2.




(**a**) (**b**) (**c**)

**Figure 1.** Principal component analysis (PCA) of milk composition in relation to farming systems (extensive and intensive) (**a**) Represents the correlation between milk traits through a PCA plot. (**b**) Displays the distribution of individual samples across the two principal components, with the extensive and intensive systems color-coded. cos2 values, represented by the color gradient, indicate how well each variable is explained by Dim1 and Dim2. (**c**) Heatmap of Pearson's correlation coefficients among milk quality, composition, and production traits. Correlation values are displayed only in cells where the relationships are statistically significant ($p < 0.05$). Blank cells indicate non-significant correlations. The color scale represents the strength and direction of the correlation, with blue tones indicating positive correlations and red tones indicating negative correlations.

The PCA individual plot (Figure 1b) visualizes the distribution of milk samples, with each point representing an individual sample, classified by the farming system (extensive vs. intensive). Each point represents a milk sample, and the grouping is indicated by color-coded markers (red for extensive and blue for intensive). The confidence ellipses (95% confidence interval) surrounding each group illustrate the variation within each system, showing how individual samples are distributed along the first two principal components. The overlap of extensive and intensive samples suggests no clear distinction between the extensive and intensive samples based on the first two principal components alone. However, the confidence ellipses indicate that intensive samples are slightly more clustered, while extensive samples show greater dispersion along Dim1; this implies that milk from extensive systems exhibits greater compositional variability, potentially due to dietary differences or seasonal variations in grazing conditions.

Correlation coefficients were calculated and are shown in Figure 1c. Among the compositional traits, a particularly strong correlation was found between fat and TSs (r = 0.86), as well as between protein and caseins (r = 0.80), reflecting their shared biochemical basis and consistent contribution to overall milk solids. Similarly, the Brix value, which serves as a rapid estimation method for milk solids, showed a strong positive association with TSs (r = 0.86), fat (r = 0.50) and protein (r = 0.45), supporting its use as a proxy for compositional richness. Furthermore, lactose was moderately positively correlated with the Brix value (r = 0.39) and protein (r = 0.26) but negatively associated with SCC_log10 (r = −0.23), which may reflect compromised udder health affecting sugar synthesis.

The distribution of milk traits and farming systems by clusters are presented in Figure 2. Cluster 2 exhibited the highest concentrations of key milk components, including fat (5.09%), protein (3.95%), lactose (4.62%), and total solids (13.7%). However, this cluster was also characterized by elevated levels of SCC (SCClog = 6.20) and TBC (TBClog = 2.78), reflecting a trade-off between richer milk composition and increased indicators of udder health challenges. Cluster 3 showed intermediate values for most traits, while cluster 1 had

the lowest average levels across most milk quality indicators. In terms of farming system distribution (Figure 2b), cluster 2 was predominantly composed of samples from extensive systems (93.62%), whereas cluster 3 had a more balanced representation (61.58% extensive, 38.42% intensive).

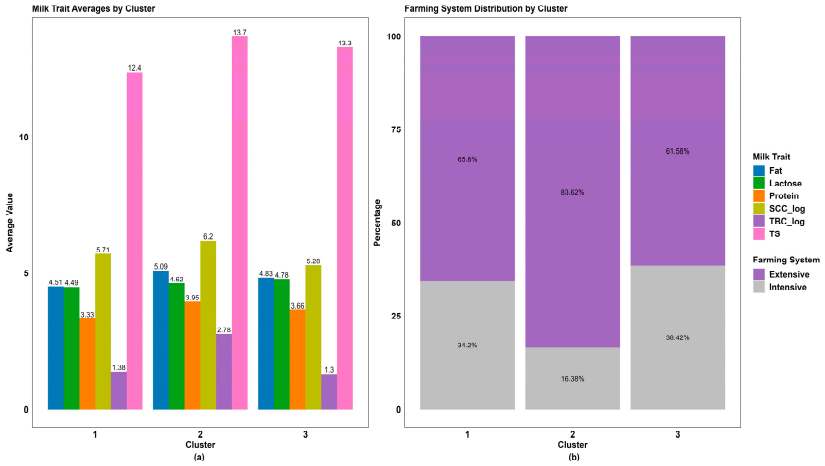



**Figure 2.** (**a**) Distribution of milk traits across clusters; (**b**) Distribution of farming systems across clusters.

Cluster 1 also included mostly extensive system samples (75.8%) but with a higher proportion of intensive farms (24.2%) compared with cluster 2. These findings indicate an association between farming system and milk composition, with extensive systems linked to higher milk solids but also higher SCC and TBC levels, underscoring a compromise between milk quality and udder health that should be considered in management decisions.

### *3.2. Effect of Farming System and Lactation Stage on Milk Yield and Composition Across the Two Lactation Periods*

The results from the linear mixed-effects model examining the effects of the farming system on morning milk yield (am_MY) and milk composition indicate that only certain parameters were significantly affected (Figure 3). Specifically, am_MY was significantly higher in the intensive system (0.98 kg/day) compared with the extensive system (0.85 kg/day) ($p < 0.01$).

In contrast, protein content was significantly higher in the extensive system (3.57%) than in the intensive system (3.47%) ($p < 0.001$), and similar results were observed for Cas content (2.72% vs. 2.57%, $p < 0.001$). However, no significant differences were found between farming systems for fat (4.76% vs. 4.75%) or lactose content (4.58% vs. 4.57%), indicating that farming conditions did not influence these components.

Regarding the effect of the LS (Figure 4), a highly significant impact was observed on all analyzed milk parameters ($p < 0.001$). Specifically, the average milk yield (am_MY) peaked during the first LS (1.05 kg/day) and then declined progressively through the second (0.96 kg/day), third (1.01 kg/day), and fourth stages (0.67 kg/day). Fat content (Figure 4b) increased slightly but significantly in the second LS (4.83%), while values in the first, third, and fourth stages remained relatively stable (4.69–4.78%; $p < 0.05$). Protein content was highest in early lactation (3.58%) and showed a marked decrease by the third (3.43%) and fourth LSs (3.51%) ($p < 0.001$). Lactose followed a similar downward trend, dropping from 4.74% in the first LS to 4.42% in late lactation ($p < 0.001$). Both TSs and casein content were significantly influenced by LS, with concentrations highest during early lactation and consistently declining across later stages ($p < 0.001$), highlighting the dynamic nature of milk composition over time.

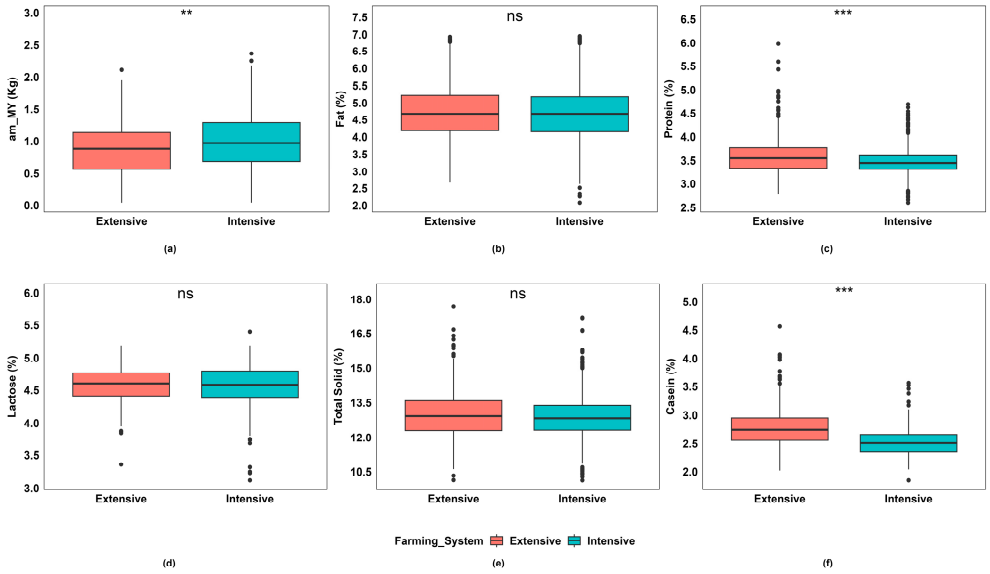



**Figure 3.** Effect of farming system (extensive vs. intensive) on milk yield and chemical composition. (**a**) milk yield; (**b**) fat; (**c**) protein; (**d**) lactose; (**e**) total solids; (**f**) caseins. Significance levels: ns = not significant ($p \geq 0.05$); ** = $p < 0.01$; *** = $p < 0.001$.

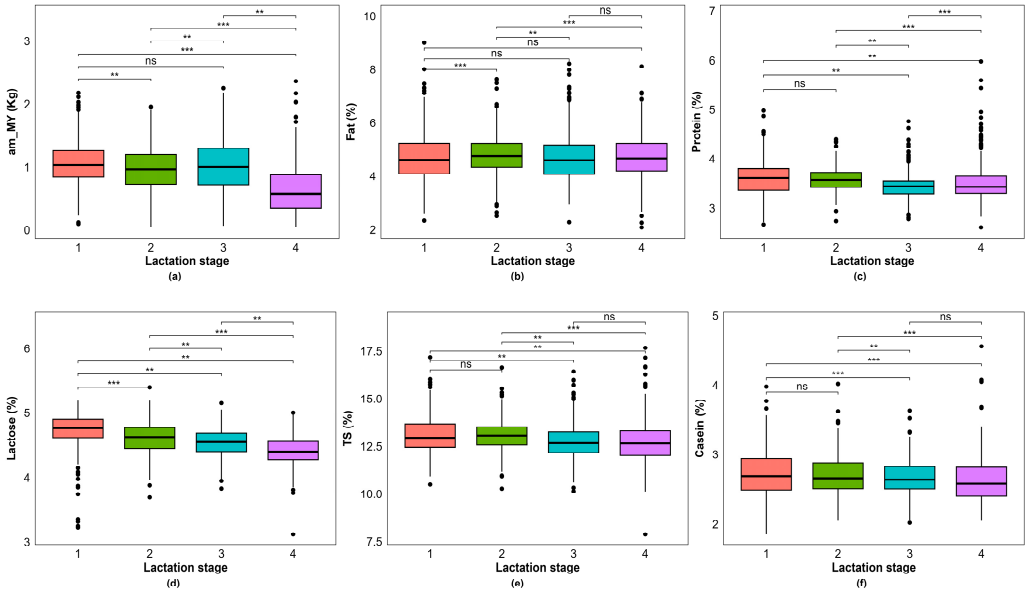



**Figure 4.** Effect of the lactation stage on milk yield and chemical composition. (**a**) am_milk yield; (**b**) fat; (**c**) protein; (**d**) lactose; (**e**) total solids; (**f**) caseins. Significance levels: ns = not significant ($p \geq 0.05$); ** = $p < 0.01$; *** = $p < 0.001$.

Significant interactions were also observed between the year and LS within each farming system. Figure 5 highlights the differences in milk composition at specific LSs between the two years within each system. In the extensive system, am_ MY (Figure 5a) exhibited a significant decline ($p < 0.001$) across LSs, with the highest production recorded in the first LS (1.09 kg in 2022, 0.99 kg in 2023) and the lowest in the fourth LS (0.34 kg in 2022, 0.61 kg in 2023). When comparing lactation curves between the two years, no significant difference was observed in the first LS. However, in the second and third LSs, 2023 showed significantly lower yields compared twitho 2022, followed by an improvement in the fourth LS in 2023 ($p < 0.001$).

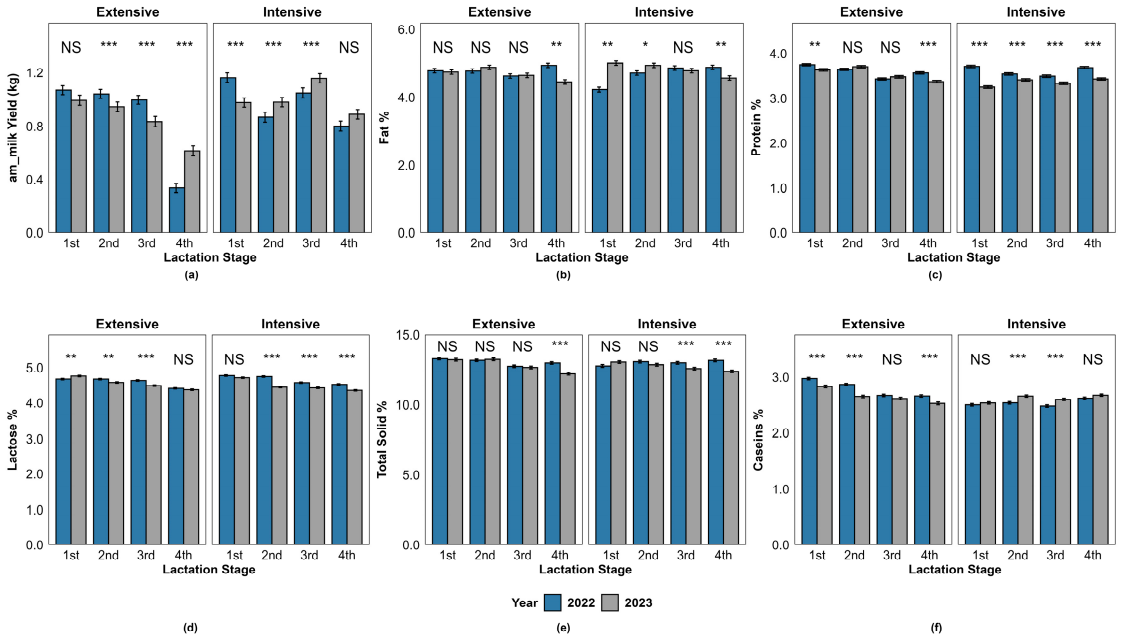



**Figure 5.** Chemical composition of milk across the four LSs within farming systems (extensive and intensive) over the two years (2022 and 2023). (**a**) am_milk yield; (**b**) fat; (**c**) protein; (**d**) lactose; (**e**) total solids; (**f**) caseins. Within each farming system and milk trait, means were compared across lactation stages. Significance levels: NS = not significant ($p \geq 0.05$); * = $p < 0.05$; ** = $p < 0.01$; *** = $p < 0.001$.

In the intensive system, milk yield was consistently higher in 2023 across the second, third, and fourth LSs ($p < 0.001$), suggesting improved productivity over time. However, the fluctuations observed between the years seemed to diminish in the fourth LS, where the differences became less pronounced.

In both farming systems, fat content remained relatively consistent across most lactation stages (Figure 5b). In the extensive system, no significant year effect was observed during the first and third LSs, while lower fat percentages in 2023 were recorded in the fourth LS ($p < 0.01$). In the intensive system, significant year-to-year differences were found in the first, second, and fourth LSs ($p < 0.01$), whereas no year effect was detected in the third LS.

Protein content was significantly affected by the year across all lactation stages in both farming systems ($p < 0.001$). In the extensive system, protein levels declined progressively as lactation advanced, decreasing from 3.75% in the first LS of 2022 to 3.56% in the fourth LS. A similar trend was observed in 2023, with values dropping from 3.63% to 3.36%. In the intensive system, protein content started at 3.71% in the first LS of 2022, declining to 3.24% in 2023. A further reduction was evident in the second LS, with values dropping from 3.54% in 2022 to 3.40% in 2023. However, in contrast to the early lactation stages, protein levels stabilized or increased slightly in the third and fourth LSs. In particular, the fourth LS in 2022 showed an increase of 0.19%, while in 2023 it rose by 0.09% from the third LS, suggesting a potential compensatory effect in late lactation ($p < 0.001$) (Figure 5c).

Lactose content showed a greater sensitivity to year × LS interactions, followed by a consistent downward curve, corresponding with the decline in milk yield (Figure 5d). Regarding TSs (Figure 5e), a gradual decline was observed as lactation progressed, with the extensive system consistently showing slightly higher values than the intensive system across all stages. While both systems followed a similar downward trend, no significant year-to-year differences were observed during the early lactation stages (first and second

LSs). The differences between years became more noticeable only in later stages, but the overall pattern of decline remained consistent across systems and years.

Casein levels (Figure 5f) in the extensive system declined progressively as lactation advanced. A significantly lower casein content was observed in 2023 compared with 2022 during the first, second, and fourth LSs ($p < 0.001$). In contrast, the intensive system exhibited more fluctuation in casein levels across the lactation stages rather than a steady decline. Despite this variability, significant year effects were still detected in the second and third LSs ($p < 0.001$), with higher casein concentrations recorded in 2023.

### 3.3. Effect of Farming System, Year, and LS on Milk Physical Properties, SCC, and TBC

Table 1 presents the physical properties, SCC, and TBC of goat milk under different farming systems (extensive vs. intensive), years (2022 vs. 2023), and LSs (first–fourth LS). The pH values remained stable across farming systems and years, with no significant differences observed ($p > 0.05$). However, LS had a highly significant effect ($p < 0.001$), with the highest pH recorded during the fourth LS (6.75), while the other stages exhibited consistent values (6.65–6.66).

**Table 1.** Effect of farming system and lactation stage on physical properties, SCC, and TBC of milk across the two years.

| | Farming System | | | Year | | | Lactation Stage | | | | | Significance | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Variable** | **E[1] *n* = 919** | **I[2] *n* = 909** | **SED[3]FS** | **2022 n = 938** | **2023 n = 890** | **SED[3]Y** | **1st *n* = 458** | **2nd *n* = 472** | **3rd *n* = 450** | **4th *n* = 448** | **SED[3]LS** | **FS** | **Y** | **LS** | **Y × LS** |
| pH | 6.67 | 6.680 | 0.004 | 6.680 | 6.670 | 0.005 | 6.65 [a] | 6.660 [a] | 6.650 [a] | 6.750 [b] | 0.007 | NS | NS | *** | NS |
| EC (mS/cm) | 5.77 [a] | 5.740 [b] | 0.020 | 5.770 | 5.740 | 0.020 | 5.73 [a] | 5.700 [a] | 5.880 [b] | 5.720 [a] | 0.037 | *** | NS | * | NS |
| RI | 1.348 | 1.349 | 0.001 | 1.349 | 1.348 | 0.001 | 1.349 [a] | 1.349 [a] | 1.348 [a] | 1.347 [b] | 0.001 | NS | NS | *** | NS |
| Brix (°Bx) | 10.51 [a] | 10.110 [b] | 0.043 | 10.510 | 10.260 | 0.003 | 10.72 [a] | 10.44 [b] | 10.23 [c] | 9.860 [d] | 0.061 | ** | NS | *** | NS |
| log10 SCC/mL | 5.687 [a] | 5.504 [b] | 0.024 | 5.487 [a] | 5.705 [b] | 0.020 | 5.529 [a] | 5.439 [b] | 5.623 [c] | 5.792 [d] | 0.028 | *** | * | *** | NS |
| log10 TBC (cfu/mL) | 1.592 [a] | 1.285 [b] | 0.032 | 1.450 | 1.448 | 0.026 | 1.704 [a] | 1.238 [b] | 1.391 [c] | 1.449 [c] | 0.037 | *** | NS | *** | NS |

[1] E = Extensive; [2] I = Intensive; [3] Standard error of the difference among means; within a row and a model effect, means without a common superscript (a, b, c, d) differ at $p < 0.05$; * = $p < 0.05$; ** = $p < 0.01$; *** = $p < 0.001$. NS = non-significant; EC = Electrical Conductivity; RI = Refractive Index; SCC = Somatic Cell Count; TBC = Total Bacterial Count.

Regarding EC, the values ranged from 5.70 to 5.88 mS/cm, with no significant differences between farming systems or years ($p > 0.05$). However, EC was significantly influenced by the LS ($p < 0.05$), with the highest value recorded during the third LS (5.88 mS/cm) and the lowest in the second LS (5.70 mS/cm).

Similar observations were found for the RI values, with no significant effects of farming system or year ($p > 0.05$). RI decreased slightly but significantly ($p < 0.001$) from the first (1.349) to the fourth LS (1.347). In contrast, the Brix values were influenced by both farming system ($p < 0.01$) and LS ($p < 0.001$). The extensive system had slightly higher Brix values (10.51°Bx) compared with the intensive system (10.74°Bx). Across LSs, the Brix values decreased progressively, with the highest value recorded in the first LS (10.11°Bx) and the lowest in the fourth stage (9.86°Bx).

The results for SCC (Table 1) indicated significant differences between farming system, year, and LS. The extensive farming system (5.687 log10 SCC/mL) showed significantly higher SCC values compared with the intensive system (5.504 log10 SCC/mL) ($p < 0.001$). The SCC values were also significantly influenced by year ($p < 0.05$), with the 2023 data (5.705 log10 SCC/mL) being higher than the 2022 data (5.487 log10 SCC/mL). Across LSs, SCC progressively increased from the second stage (5.439 log10 SCC/mL) to the fourth stage (5.792 log10 SCC/mL), with the fourth stage showing the highest value ($p < 0.001$). For TBC, significant differences were observed between farming systems and LSs (Table 1).

The extensive farming system had a higher bacterial count (1.592 log10 cfu/mL) compared with the intensive system (1.285 log10 cfu/mL) ($p < 0.001$). Across LSs, TBC was significantly affected ($p < 0.001$), with the highest count recorded during the first stage (1.704 log10 cfu/mL) and the lowest in the second stage (1.238 log10 cfu/mL).

## 4. Discussion

This study evaluated the combined effects of farming systems (intensive vs. extensive) and LS across two lactation periods on the chemical and physical characteristics and SCC of Skopelos goat milk derived from two commercial farms. To the best of our knowledge, there are no previous studies comparing these effects in commercial dairy goat farms with the same genetic background under different farming systems. This study demonstrated that milk yields are consistently higher in the intensive farming system. These results are in agreement with those reported in other breeds, including Italian local goat breeds [40] and Baladi goats [41], indicating that a controlled environment, as is often the case in intensive farming systems, improves productivity in dairy goats. In addition to the farming system, the LS significantly affects milk yields. Milk output gradually declines from the beginning to the end of lactation with a relatively fast reduction towards the end. As lactation progresses, the decline in mammary gland synthesis efficiency leads to a reduction in milk yield. As observed in our study, am_MY decreases by 30% and 36% in the third and fourth LSs, respectively, compared with the first stage. The farming system in this study did not influence the fat content of the milk. These results are in agreement with Morand-Fehr et al. [42] who reported that grazing-based systems do not significantly affect fat content and Goetsch et al. [43] who noted that in goats with moderate to low milk production potential, such as the Skopelos breed, farming systems have a relatively minor influence on fat content. Regardless of the farming system, LS significantly affects the fat content of milk with the higher values occurring during mid-lactation. This peak coincides with the spring season, where goats in the extensive farming system have access to fresh, high-quality pasture, while those in the intensive system benefit from the higher availability and lower prices of alfalfa [44]. Protein content was significantly higher in the extensive system compared with the intensive system. This suggests that grazing may enhance the nutritional profile of milk, and particularly its protein fraction, as observed in another study [45]. This supports the idea that while intensive farming maximizes milk volume, extensive systems may enhance milk protein content, which is particularly valuable for cheese production and dairy product formulation, as demonstrated in Skopelos goat milk by Kotsiou et al. [46].

Lactation stage also influences the protein content of milk, with lower values during mid-lactation. Similar findings have also been reported with higher productivity breeds such as the Alpine and Nubian breeds [47]. Caseins are the predominant proteins in milk, accounting for approximately 80% of total milk proteins [48]. Caseins play a crucial role in calcium transport and absorption and they are a precursor for bioactive peptides, which have various potential health benefits [49]. Additionally, caseins are fundamental in cheese manufacturing, affecting both cheese yield and texture. They are the major proteins involved in coagulation during renneting [46]. In this study, the Cas content was similarly affected by farming system and LS as total protein level. Goats in the extensive system produced milk with higher Cas levels (2.72%) than those from the intensive system (2.57%). These findings are consistent with the results of Inglingstad et al. [50] who studied Norwegian dairy goats under grazing. Cas content was also affected by LS with higher levels in early and mid-lactation compared with later stages. These findings are in agreement with previous studies [51], suggesting that early lactation supports higher casein synthesis, which gradually decreases as lactation progresses due to metabolic shifts

prioritizing energy and lipid production over protein synthesis. The lactose content of milk is not affected by farming systems but significantly and consistently declines during lactation. The decrease in lactose content during lactation has been previously attributed to changes in prolactin activity. While prolactin plays a crucial role in stimulating lactose synthesis by enhancing the activity of enzymes involved in its production, its regulatory effects may decline as lactation progresses [52]; this, combined with the increasing metabolic demand for lipid synthesis and energy production in the mammary gland, may contribute to the observed reduction in lactose concentration over time [53]. Farming systems do not affect TSs in milk. However, as is the case with protein and lactose content, TSs decrease progressively during lactation.

In the present study, milk pH ranged from 6.65 to 6.75, with no significant differences across farming systems or years, similarly to what has been previously reported in other studies [16,54–56]. The pH remained stable during early and mid-lactation. However, a significant pH increase was observed at the end of lactation similarly to what has been reported by Fox et al. [57]. The EC in milk is influenced by the presence and concentration of electrically charged ions, including sodium ($Na^+$), potassium ($K^+$), chloride ($Cl^-$), and calcium ($Ca^{2+}$) [58]. These ions are crucial in determining the milk's ability to conduct electrical current, making EC a useful parameter for evaluating milk composition and udder health. The PCA (Figure 1a, Table 1) demonstrated that the variations in SCC and TBC were reflected in the EC values, indicating that milk with a higher bacterial and SCC content also tends to have increased EC, likely due to udder inflammation and compromised milk quality. Since SCC and TBC are key indicators of udder health, their influence on EC suggests that monitoring conductivity alongside these parameters provides a comprehensive assessment of milk quality, and EC is a commonly used parameter for detecting subclinical mastitis [10,59,60], while the refractive index and Brix values offer insights into the TSs content of milk [61]. Using these physical parameters as rapid assessment point-of-service tools could enhance monitoring practices, facilitating the early detection of health issues and milk quality optimization.

SCC and TBC are key indicators of milk quality, udder health, and hygiene practices [62,63]. The results of this study indicate that both SCC and TBC were significantly higher in the extensive farming system compared with the intensive system (Table 1), findings which are in agreement with other studies [12,15]. These elevated levels may be partially attributed to hand milking, which is more susceptible to contamination, as well as generally less-controlled milking environments. It is also well established that non-infectious factors, such as management practices, significantly influence SCC and TBC levels in goats [43,64–66]. High SCC values are commonly associated with subclinical mastitis and reduced milk shelf life, while elevated TBC can compromise milk safety and restrict marketability due to regulatory limits.

The lactation stage also had a strong and consistent effect on milk quality. SCC progressively increased from the first to the fourth stage ($p < 0.001$), likely reflecting cumulative stress on the mammary gland, a factor known to elevate SCC levels [43,62,65,67]. TBC was highest during early lactation, possibly due to the presence of colostrum residues and/or a greater susceptibility to contamination. This may also be influenced by environmental factors such as rainfall and high humidity, particularly since the first LS occurred in February, a month typically associated with elevated humidity levels.

In addition to the LS, regional environmental differences between the farming systems may have influenced SCC and TBC outcomes. In the extensive system, goats grazed outdoors throughout the year and were exposed to greater temperature fluctuations and higher ambient humidity, particularly during winter and early spring, which may have contributed to increased microbial contamination and udder stress. In contrast, in the inten-

sive farming system, animals were housed indoors, where the temperature and humidity were more controlled and stable. This controlled environment likely contributes to better udder health and lower bacterial contamination, as it reduces environmental exposure.

Although environmental data were used descriptively to characterize the study regions, they were not included as covariates in the statistical analysis. Future studies could benefit from integrating environmental variables (e.g., temperature, humidity, and rainfall) into statistical models to better assess their impact on SCC and TBC. This would allow for a clearer distinction between the effects of management practices and environmental stressors and could help identify periods of increased risk that require targeted hygiene interventions, particularly in extensive systems.

In the analysis of farming systems, significant interactions were observed between year and lactation stage (LS), showing how these factors are interrelated. In the extensive system, milk yield, protein, and lactose decreased as lactation progresses, while fat content increased. These trends remain consistent across both years, suggesting that extensive farming results in a predictable milk composition over time, though individual goats may vary, as seen in the PCA. These results are consistent with the findings by Idamokoro et al. [18] in Nguni goats, Manousidis et al. [68] in goats grazing Mediterranean woody rangelands, and Paschino et al. [67] in goats reared in extensive farms. In the intensive system, milk yield and composition vary across the years, suggesting that factors such as management practices, diet, and feeding regimes influence milk composition [16,20,55,69,70]. The PCA supports this by showing a tighter cluster for intensive farming, indicating greater control over milk traits. This suggests that while intensive farming supports higher production, maintaining a consistent milk composition requires careful management.

## 5. Conclusions

This study confirms established findings that intensive farming systems, through controlled feeding and management, consistently achieve higher milk yields compared with extensive systems. However, it also reinforces that milk from extensive, pasture-based systems tends to have a superior protein and casein content, which is valuable for cheese production and the quality of dairy products. The influence of lactation stage on milk composition and udder health parameters was evident in both systems, highlighting the importance of monitoring throughout lactation. Importantly, our work provides novel insights by comparing these effects within a single breed that shares a common genetic background, thereby minimizing confounding factors and strengthening the validity of the comparison. Additionally, the environmental and management factors inherent to each farming system contributed to the differences in milk quality and somatic cell and bacterial counts, emphasizing that hygiene and udder health remain key challenges in extensive systems. Future research integrating environmental variables and management interventions could help optimize milk quality and animal health across production systems. Overall, this study supports a balanced approach, recognizing the trade-offs between productivity and milk quality, which can guide sustainable dairy goat farming strategies tailored to specific production goals.

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**Institutional Review Board Statement:** The animal studies were approved by the Research and Ethics Committee of the Aristotle University of Thessaloniki, Greece (No 277235/2020). The collection of milk samples during milking is not within the context of relevant EU legislation for animal experimentations (Directive 86/609/EC) and are routinely performed on a farm to identify milk quality. The animals were handled by trained personnel.

**Informed Consent Statement:** Informed consent was acquired from all the farmers involved in this study.

**Data Availability Statement:** The original contributions presented in the study are included in the article; further inquiries can be directed to the corresponding author.

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## Abbreviations

The following abbreviations are used in this manuscript:

| | |
|---|---|
| DIM | Days in milk |
| PCA | Principal component analysis |
| am_MY | Am milk yield |
| LS | Lactation stage |
| TS | Total Solid |
| CAS | Total Casein |
| EC | Electrical Conductivity |
| RI | Refractive Index |
| SCC | Somatic Cell Count |
| TBC | Total Bacterial Count |
| BCS | Body Condition Score |

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