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LIPID CONTENT AND FATTY ACID COMPOSITION OF FRESHWATER MUSSELS (BIVALVIA: UNIONIDAE) FROM THE DICLE RIVER AND AMBAR STREAM, SOUTHEASTERN TÜRKIYE

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ABSTRACT: This study compared total lipid content and fatty acid composition in *Leguminaia wheatleyi* from Ambar Stream and the Dicle River, *Unio elongatulus* from Ambar Stream, and *Unio tigridis* from the Dicle River in southeastern Türkiye. Whole soft tissues were analysed for total lipid content and fatty acid composition by GC-FID; 41 fatty acids were screened. Total lipid content varied markedly among mussel groups, ranging from 0.19% to 2.21% wet weight. Saturated fatty acids were the dominant class in all samples (49.39–76.94% of total identified fatty acids), whereas marked variation among species/locality groups was observed in monounsaturated and polyunsaturated fractions. *Unio elongatulus* showed the highest MUFA (monounsaturated fatty acids) proportion (43.74%), while *U. tigridis* had the highest PUFA (polyunsaturated fatty acids) level (24.94%). In addition, *L. wheatleyi* displayed pronounced locality-associated variation, with the Dicle River population exhibiting higher total lipid content and a more unsaturated profile than the Ambar Stream population. Palmitic acid (C16:0) was the principal saturated fatty acid in all mussel groups, whereas oleic acid (C18:1ω9) was particularly abundant in *U. elongatulus*. These findings indicate substantial biochemical variation among the studied mussel samples and provide new baseline data for future ecological, nutritional, and conservation-oriented studies on unionid mussels in southeastern Türkiye.

KEYWORDS: fatty acids; freshwater mussels; *Leguminaia wheatleyi*; *Unio elongatulus*; *Unio tigridis*

INTRODUCTION

Freshwater mussels (Bivalvia: Unionidae) are important components of inland aquatic ecosystems, and the Eastern Mediterranean is recognised as a key region for their diversity and biogeographic differentiation (DE MOULPIED et al. 2024, VERMA et al. 2025). Recent integrative studies have shown that the regional unionid fauna is more diverse than previously assumed, highlighting the need for further ecological and biochemical characterisation of populations inhabiting major river basins such as the Tigris–Euphrates system (LOPES-LIMA et al. 2021).

Lipid content and fatty acid composition are widely applied biochemical descriptors in mussel research because they provide a useful basis for evaluating tissue composition, nutritional quality, and variation among species and populations from different habitats (EKİN & BAŞHAN 2010, ERSOY & ŞEREFLIŞAN 2010, EKİN et al. 2011, DEMIRTAŞ 2025). In unionid mussels, fatty acid profiles have also been used as indicators of assimilated food sources, and differences in essential fatty acid composition among rivers have been linked to habitat-related variation in nutrition (NEWTON et al. 2013). In Türkiye, earlier studies on *Unio elongatulus* from the Tigris River documented tissue-specific fatty acid profiles and showed that phospholipid and neutral lipid fractions may vary among localities in southeastern Anatolia (EKİN & BAŞHAN 2010, EKİN et al. 2011).

This study aimed to compare total lipid content and fatty acid composition among four freshwater

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mussel species/locality groups from the Dicle River basin, southeastern Türkiye: *Leguminaia wheatleyi* (Lea, 1862) from Ambar Stream and the Dicle River, *Unio elongatulus* C. Pfeiffer, 1825 from Ambar Stream, and *Unio tigridis* Bourguignat, 1852 from the Dicle River. The study was designed primarily as a species/locality-based comparison, rather than as a direct test of habitat effects, because not all species were represented in both habitats. However, the presence of *L. wheatleyi* in both Ambar Stream and the Dicle River allowed a limited within-species comparison between these two localities. These data provide baseline biochemical information for poorly studied unionid mussels in southeastern Türkiye.

MATERIAL AND METHODS

SAMPLE COLLECTION AND PREPARATION

Freshwater mussel specimens were collected from two localities in Diyarbakır Province, southeastern Türkiye, during July and August 2025. The studied material consisted of *Leguminaia wheatleyi* (Lea, 1862) from Ambar Stream and the Dicle River, *Unio elongatulus* C. Pfeiffer, 1825 from Ambar Stream, and *Unio tigridis* Bourguignat, 1852 from the Dicle River. Collection localities, geographic coordinates, sampling dates, approximate numbers of collected individuals, and habitat characteristics are presented in Table 1.

After collection, live mussels were transported to the Laboratory of Energy Systems Engineering, Faculty of Engineering, Şırnak University. Prior to dissection, the specimens were kept in clean, aerated water without food for 24 h to allow depuration of gut contents. The shells were then rinsed with distilled water to remove adhering debris, and the entire soft bodies were removed from the shells. Whole soft tissues were gently blotted dry, weighed, and homogenised. For each species/locality group, three independent pooled biological replicates were prepared, each consisting of homogenised whole soft tissues from approximately 20 individuals. Pooling was used to obtain representative whole-body biochemical profiles for each species/locality group. All samples were maintained under cold conditions during transport and were transferred under a continuous cold chain to the Oxigen Analysis Private Food Control Laboratory (İstanbul, Türkiye) for total lipid and fatty acid analyses. Until analysis, the samples were stored at −20 °C to minimise lipid degradation.

TOTAL LIPID DETERMINATION AND FATTY ACID ANALYSIS

Total lipid content and fatty acid composition were determined at Oxigen Analysis Private Food Control Laboratory (İstanbul, Türkiye), a TÜRKAK-accredited laboratory (AB-0953-T) operating in accordance with TS EN ISO/IEC 17025:2017.

Total lipid content was determined according to TS 1744. Homogenised mussel tissues were subjected to acid-hydrolysis-based solvent extraction, and the extracted lipid fraction was quantified gravimetrically. Results were expressed as percentage of sample mass and reported as mean ± standard deviation (SD) of three replicate analyses.

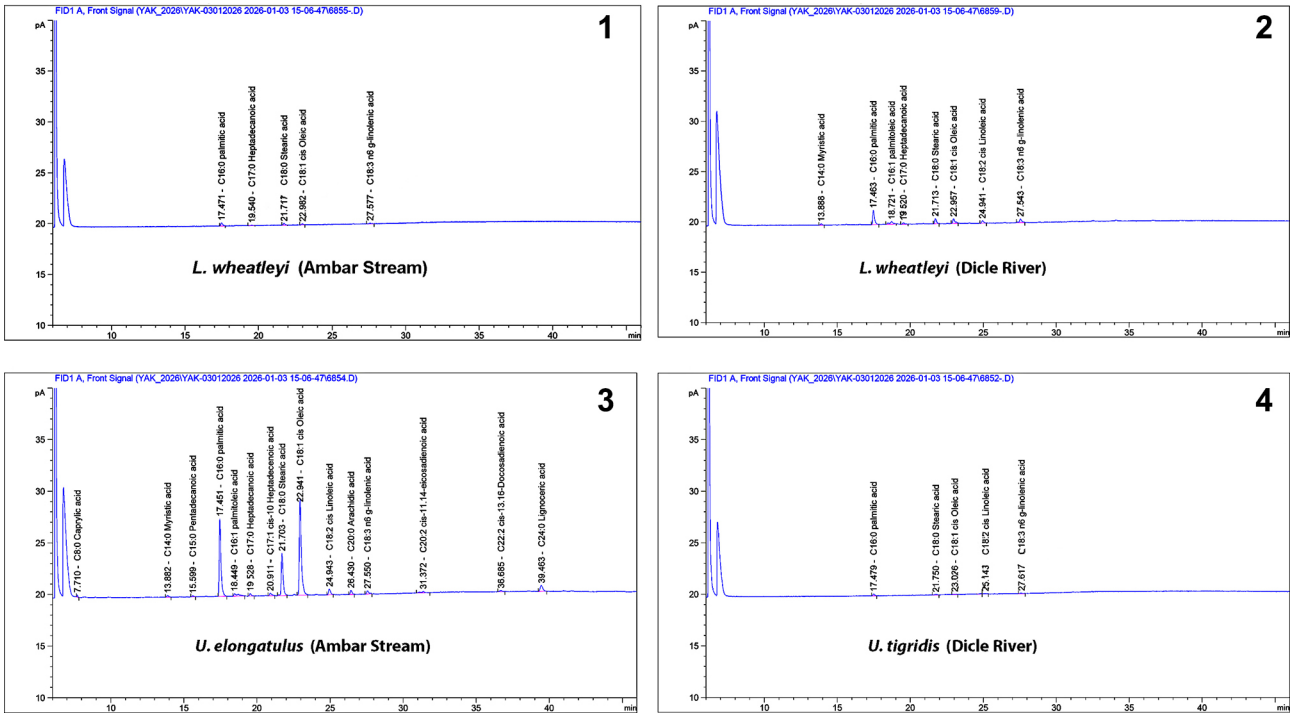
Fatty acid methyl esters (FAMEs) were prepared in accordance with the Turkish Food Codex Olive Oil and Olive-Pomace Oil Analysis Method (2014/53) and TS EN ISO 12966-1 and TS EN ISO 12966-4.

Table 1. Sampling localities and habitat characteristics of the studied freshwater mussels from Diyarbakır, southeastern Türkiye

Species	Province	Locality	Coordinates	Collection date	Approximate number of specimens	Habitat characteristics
Leguminaia wheatleyi	Diyarbakır	Ambar Stream	38°17'32.8"N, 40°27'43.8"E	July 2025	~80	Clear water; moderate algal growth; low flow velocity; water depth approximately 1–1.5 m.
Leguminaia wheatleyi	Diyarbakır	Dicle River	37°58'07.9"N, 40°14'41.6"E	August 2025	~70	Muddy, particulate substrate; turbid irrigation water; water depth approximately 2–3 m.
Unio elongatulus	Diyarbakır	Ambar Stream	38°17'32.8"N, 40°27'43.8"E	July 2025	~70	Clear water; moderate algal growth; low flow velocity; water depth approximately 1–1.5 m.
Unio tigridis	Diyarbakır	Dicle River	37°58'07.9"N, 40°14'41.6"E	August 2025	~90	Muddy, particulate substrate; turbid irrigation water; water depth approximately 2–3 m.

Briefly, approximately 0.2 g of extracted lipid was mixed with 4 mL heptane and 0.4 mL 2 M methanolic potassium hydroxide, vortexed for about 20 s, and allowed to separate into phases. The upper phase was collected with a syringe, filtered through a 0.45 µm membrane filter into a vial, and injected into the gas chromatography system.

FAME analysis was performed using an Agilent 7820A gas chromatograph equipped with a flame ionisation detector (GC-FID) and an HP-88 capillary column (100 m × 0.250 mm i.d., 0.20 µm film thickness). The oven temperature was programmed from 60 °C (held for 5 min) to 140 °C at 10 °C/min (held for 5 min), then increased to 240 °C at 4 °C/min and held for 15 min. The injector and detector temperatures were set at 260 °C and 280 °C, respectively. Samples were injected manually (1 µL; split ratio 1:30), and helium was used as the carrier gas at a flow rate of 1 mL/min. Fatty acids were identified by comparison of retention times with those of authentic FAME standards and quantified by relative peak area normalisation using Hewlett-Packard ChemStation software. Results were expressed as percentages of total identified fatty acids and reported as mean ± SD of three replicate analyses. A representative GC-FID chromatogram of FAMEs obtained from whole-soft-tissue lipid extracts is shown in Figs 1–4. A total of 41 fatty acids were screened, and the major detected components are presented in the Results and Tables 2 & 3.



Figs 1–4. Representative GC-FID chromatograms of fatty acid methyl esters (FAMEs) obtained from total lipid extracts of whole soft tissues of the studied freshwater mussels from the Dicle River basin, southeastern Türkiye: 1 – *Leguminaia wheatleyi* from Ambar Stream; 2 – *L. wheatleyi* from the Dicle River; 3 – *Unio elongatulus* from Ambar Stream; 4 – *U. tigridis* from the Dicle River. The x-axis represents retention time (min), and the y-axis represents detector response/signal intensity (pA). Major peaks are labelled with their retention times and corresponding fatty acid names

Table 2. Total lipid content and fatty acid class distribution (% wet weight) of the studied freshwater mussels

Parameter (%)	*L. wheatleyi* (Ambar Stream)	*L. wheatleyi* (Dicle River)	*U. elongatulus* (Ambar Stream)	*U. tigridis* (Dicle River)
Total lipid	0.85 ± 0.03^{a}	1.92 ± 0.05^{b}	2.21 ± 0.06^{c}	0.19 ± 0.02^{d}
SFA	0.65 ± 0.02^{a}	1.03 ± 0.03^{b}	1.12 ± 0.03^{c}	0.09 ± 0.01^{d}
UFA	0.20 ± 0.02^{a}	0.89 ± 0.03^{b}	1.09 ± 0.03^{c}	0.10 ± 0.01^{d}
MUFA	0.10 ± 0.01^{a}	0.52 ± 0.02^{b}	0.97 ± 0.03^{c}	0.03 ± 0.01^{d}
PUFA	0.10 ± 0.01^{a}	0.37 ± 0.01^{b}	0.12 ± 0.01^{a}	0.07 ± 0.01^{c}

SFA – saturated fatty acids; UFA – unsaturated fatty acids; MUFA – monounsaturated fatty acids; PUFA – polyunsaturated fatty acids. Values are expressed as percentage of wet weight (% ww). UFA represents the sum of MUFA and PUFA. Different superscript letters within the same row indicate statistically significant differences among groups according to one-way ANOVA followed by Tukey's post hoc test ($p < 0.05$)

Table 3. Fatty acid composition (% of total identified fatty acids) of the studied freshwater mussels from Ambar Stream and the Dicle River system

Fatty acids	*L. wheatleyi* (Ambar Stream)	*L. wheatleyi* (Dicle River)	*U. elongatulus* (Ambar Stream)	*U. tigridis* (Dicle River)
C8:0	nd	nd	0.38 ± 0.02	nd
C14:0	nd	3.02 ± 0.09[a]	0.65 ± 0.03[b]	nd
C15:0	nd	nd	0.38 ± 0.02	nd
C16:0	43.59 ± 0.82[a]	34.37 ± 0.71[b]	27.71 ± 0.66[c]	32.47 ± 0.69[d]
C16:1ω7	nd	13.53 ± 0.32[a]	2.33 ± 0.08[b]	nd
C17:0	8.65 ± 0.21[a]	4.00 ± 0.12[b]	0.89 ± 0.04[c]	nd
C17:1ω7	nd	nd	1.08 ± 0.04	nd
C18:0	24.70 ± 0.58[a]	12.50 ± 0.29[b]	15.95 ± 0.37[c]	16.92 ± 0.41[c]
C18:1ω9	12.09 ± 0.28[a]	13.68 ± 0.31[a]	40.33 ± 0.78[b]	25.67 ± 0.54[c]
C18:2ω6	nd	7.14 ± 0.18[a]	2.42 ± 0.08[b]	11.61 ± 0.27[c]
C18:3ω6	10.98 ± 0.25[a]	11.77 ± 0.28[a]	1.58 ± 0.05[b]	13.33 ± 0.31[c]
C20:0	nd	nd	1.57 ± 0.05	nd
C20:2ω6	nd	nd	1.03 ± 0.04	nd
C22:2ω6	nd	nd	0.53 ± 0.02	nd
C24:0	nd	nd	3.18 ± 0.09	nd
∑SFA	76.94 ± 0.96[a]	53.89 ± 0.85[b]	50.71 ± 0.81[c]	49.39 ± 0.77[c]
∑MUFA	12.09 ± 0.28[a]	27.21 ± 0.56[b]	43.74 ± 0.82[c]	25.67 ± 0.54[b]
∑PUFA	10.98 ± 0.25[a]	18.91 ± 0.42[b]	5.56 ± 0.17[c]	24.94 ± 0.49[d]

SFA – saturated fatty acids; MUFA – monounsaturated fatty acids; PUFA – polyunsaturated fatty acids; nd – not detected. Values are expressed as % of total fatty acids (mean ± SD, n = 3). Different superscript letters within the same row indicate statistically significant differences among groups according to one-way ANOVA followed by Tukey's post hoc test ($p < 0.05$)

STATISTICAL ANALYSIS

Data are presented as mean ± SD. Statistical analyses were performed using SPSS version 16.0. Differences in total lipid content and fatty acid composition among species/locality groups were evaluated by one-way analysis of variance (ANOVA), followed by Tukey's post hoc test where appropriate. Each species/locality group was analysed in three independent replicates. Statistical significance was accepted at $p \leq 0.05$.

RESULTS

Total lipid contents are presented in Table 2. Fatty acid composition was determined by GC-FID analysis. A total of 41 fatty acids, ranging from short-chain to very long-chain compounds (C4:0–C24:0), were screened, and the major detected components are presented in Table 3.

Total lipid content differed markedly among the studied mussel samples, being highest in *Unio elongatulus* from Ambar Stream (2.21% ww) and lowest in *U. tigridis* from the Dicle River (0.19% ww) (Table 2). *Leguminaia wheatleyi* also showed clear locality-related variation, with the Dicle River population displaying substantially higher total lipid content than the Ambar Stream population (1.92 vs. 0.85% ww) (Table 2). In absolute terms, SFA (Saturated Fatty Acids) constituted the major lipid fraction in all groups, whereas UFA (Unsaturated Fatty Acids) was especially high in *U. elongatulus* (1.09% ww) and in *L. wheatleyi* from the Dicle River (0.89% ww) (Table 2).

The fatty acid profiles were dominated by a limited number of major components. Palmitic acid (C16:0) was the principal saturated fatty acid in all samples, ranging from 27.71% in *U. elongatulus* to 43.59% in *L. wheatleyi* from Ambar Stream. Stearic acid (C18:0) was also abundant, particularly in *L. wheatleyi* from Ambar Stream (24.70%) (Table 3). Among unsaturated fatty acids, oleic acid (C18:1ω9) was the dominant MUFA and reached its highest proportion in *U. elongatulus* (40.33%), whereas C18:2ω6 and C18:3ω6 were the main PUFA components, especially in *U. tigridis* (11.61% and 13.33%, respectively) (Table 3).

On a relative basis, ∑SFA was the dominant fatty acid class in all mussel groups, most strongly in *L. wheatleyi* from Ambar Stream (76.94%), indicating the most saturated profile among the samples. In contrast, *U. elongatulus* was characterised by the highest ∑MUFA proportion (43.74%), while *U. tigridis* had the highest relative ∑PUFA content (24.94%). The

Dicle River population of *L. wheatleyi* was intermediate but clearly more unsaturated than the Ambar Stream population, with markedly higher ∑MUFA and ∑PUFA proportions (27.21% and 18.91%, respectively) (Table 3).

A pronounced within-species difference was evident in *L. wheatleyi*. Compared with specimens from Ambar Stream, the Dicle River population had higher total lipid content and a more unsaturated fatty acid profile, mainly associated with the appearance or increase of C16:1ω7 (13.53%), C18:2ω6 (7.14%), and a higher overall contribution of unsaturated fatty acids (Table 3). Overall, the results indicate substantial variation in lipid quantity and fatty acid composition among the studied species/locality groups. Total lipid content differed significantly among groups ($p < 0.05$). The two populations of *L. wheatleyi* also differed significantly in total lipid content and in the relative proportions of major fatty acid classes ($p < 0.05$).

DISCUSSION

The present study revealed marked variation in total lipid content and fatty acid composition among freshwater mussels from the Dicle River basin. Total lipid content ranged from 0.19% ww in *Unio tigridis* from the Dicle River to 2.21% ww in *U. elongatulus* from Ambar Stream, while *Leguminaia wheatleyi* showed a clear locality-related difference between Ambar Stream and the Dicle River (0.85 vs. 1.92% ww), indicating that both species identity and sampling locality were associated with biochemical variation in the studied material. This interpretation is consistent with previous unionid studies showing that biochemical metrics may differ substantially among rivers and localities, and that fatty acid composition in *Unio elongatulus* can vary among populations from southeastern Anatolia (Ekin et al. 2011, Newton et al. 2013). A comparable regional pattern was also reported for other freshwater mussels from the Tigris River, in which C16:0, C18:0, C16:1ω7, C18:1ω9, C18:2ω6, and C20:4ω6 were identified as dominant fatty acids in different lipid classes of total body lipids, further supporting the view that major interspecific and locality-associated biochemical differences are common in inland unionids from southeastern Türkiye (Ekin et al. 2012).

The overall fatty acid pattern observed here was dominated by a limited number of major components, particularly palmitic acid (C16:0), stearic acid (C18:0), and oleic acid (C18:1ω9). Palmitic acid was the dominant fatty acid in all samples (27.71–43.59%), stearic acid was consistently important (12.50–24.70%), and oleic acid reached its highest proportion in *U. elongatulus* (40.33%) (Table 3). This general pattern agrees with earlier work on *U. elongatulus* from southeastern Anatolia, where C16:0, C16:1ω7, C18:1ω9, C18:2ω6, and C20:4ω6 were reported as predominant fatty acids in whole-tissue lipid fractions (Ekin & Başhan 2009, Ekin et al. 2011). Although the earlier study analysed phospholipid and neutral lipid fractions rather than total lipid alone, the recurrence of C16:0 and C18:1ω9 among the main components supports the view that the present profile is consistent with previously reported regional unionid patterns (Ekin et al. 2011). This interpretation is also supported by Ekin & Başhan (2010), who found that C16:0, C16:1ω7, C18:1ω9, C20:1ω9, C20:4ω6, and C20:5ω3 were the predominant fatty acids in selected tissues and whole-body samples of *U. elongatulus* from the Tigris River, with C16:1ω7 (27.6%) and C16:0 (23.6%) being the most abundant constituents in the whole-body analysis. Although that study included tissue-specific comparisons, its whole-body results reinforce the regional predominance of a restricted set of major fatty acids in freshwater unionids (Ekin & Başhan 2010).

Class-level fatty acid distributions also differed substantially among the studied mussels. SFA was highest in *L. wheatleyi* from Ambar Stream (76.94%), MUFA was highest in *U. elongatulus* (43.74%), and relative PUFA was highest in *U. tigridis* (24.94%) (Table 3). Within *L. wheatleyi*, mussels from the Dicle River had markedly lower SFA and higher MUFA and PUFA proportions than those from Ambar Stream (53.89% vs. 76.94% SFA; 27.21% vs. 12.09% MUFA; 18.91% vs. 10.98% PUFA) (Table 3). These differences should be interpreted cautiously, but they are compatible with previous evidence that mussel lipid composition may vary with environmental conditions and food availability, and that locality-based variation can be pronounced even when the same broad fatty acid classes are present (Ekin et al. 2011, Newton et al. 2013). The two habitats examined in the present study also differed visibly in environmental character, with Ambar Stream described as a clear, low-flow habitat with moderate algal growth and the Dicle River as a more turbid, muddy habitat, which provides a plausible ecological context for the observed biochemical divergence without implying a single confirmed mechanism. More specifically, these habitat differences may influence the quantity and biochemical quality of available food resources, including suspended particulate organic matter, sediment-associated detritus, algae, and bacterial material. Variation in turbidity, flow regime, sediment structure, nutrient availability, and local primary production may alter the organic particles filtered or

ingested by mussels and may therefore be reflected in their lipid content and SFA/MUFA/PUFA balance. This interpretation is consistent with previous evidence that food resources, algal community structure, bacterial and detrital inputs, and river-specific habitat conditions can influence fatty acid composition in freshwater mussels (Newton et al. 2013, Bartsch et al. 2017). However, because seston quality, phytoplankton composition, sediment organic matter, nutrient concentrations, and physicochemical parameters were not directly quantified in the present study, these environmental factors should be regarded as plausible explanatory drivers rather than confirmed causal mechanisms. In addition, Ekin et al. (2012) reported that Σω6/Σω3 ratios were high in all lipid fractions of two freshwater mussel species from the Tigris River and that the relative proportions of ΣSFA, ΣMUFA, and ΣPUFA differed among lipid classes, highlighting the biochemical flexibility of freshwater mussels in the same river system (Ekin et al. 2012).

The prominence of C18:2ω6 and C18:3ω6 in some samples is also notable. In the present material, C18:2ω6 and C18:3ω6 were especially elevated in *U. tigridis* (11.61% and 13.33%, respectively), and both components were also substantial in *L. wheatleyi* from the Dicle River (7.14% and 11.77%, respectively) (Table 3). In earlier work on *U. elongatulus*, C18:2ω6 was likewise reported among the predominant fatty acids, and the authors noted that some PUFA components are likely to be of exogenous origin rather than synthesised de novo in high amounts by the animals themselves (Ekin et al. 2011). More broadly, unionid studies have shown that mussels may contain the same general fatty acid types across rivers while differing considerably in essential fatty acid composition among habitats, suggesting that fatty acid profiles can reflect habitat-related nutritional differences (Newton et al. 2013). Because the present study did not directly quantify suspended food particles, algae, bacteria, or sediment-associated organic matter, these PUFA differences are best described as habitat-associated rather than directly attributed to a specific dietary source. A related comparison can be made with *U. tigridis* from Lake Gölbaşı, where lipid content was reported as 0.96% and the species was characterised as nutritionally valuable due to its fatty acid composition, although that study was based on muscle tissue and therefore is not directly equivalent to the whole-soft-tissue approach used here (Şereflişan & Altun 2018).

This cautious interpretation is further supported by experimental work showing that nutrient and sediment loading can alter algal community composition and food quality available to freshwater mussels, thereby influencing tissue fatty acid composition and growth (Bartsch et al. 2017). In that study, green algae were more abundant at riverine sites, cyanobacteria were more abundant at lacustrine sites, and reduced juvenile growth was observed when cyanobacteria exceeded 9% of the total phytoplankton biovolume (Bartsch et al. 2017). The same study also emphasised that essential fatty acids are produced by autotrophs and bacteria, reinforcing the idea that mussel fatty acid profiles may be influenced by assimilated food resources (Bartsch et al. 2017). Nevertheless, because that work focused on juvenile mussels and foot tissue rather than homogenised whole soft tissues, it is most appropriate here as mechanistic support rather than as a direct quantitative comparison with the present results.

Comparison with previous Turkish studies also indicates that interspecific differences in total lipid level are not unusual in freshwater mussels. Ersoy & Şereflişan (2010) reported total lipid contents of 2.55% in *Unio terminalis* and 1.05% in *Potomida littoralis* based on edible parts, demonstrating that appreciable variation among freshwater mussel taxa can occur even within broadly similar inland environments. In that context, the present values of 2.21% in *U. elongatulus*, 1.92% in *L. wheatleyi* from the Dicle River, 0.85% in *L. wheatleyi* from Ambar Stream, and 0.19% in *U. tigridis* (Table 3) indicate a comparably wide biochemical range among the studied mussels. These differences should not be overinterpreted, but they support the conclusion that both taxon and locality are relevant descriptors of lipid variability in freshwater unionids from southeastern Türkiye (Ersoy & Şereflişan 2010, Newton et al. 2013). Seasonal evidence from *Unio crassus* in the Aras River further suggests that fatty acid composition and total fat levels can vary over time, with the total average fat content reported to be about 1.5% and several major SFA and unsaturated fatty acids showing seasonal shifts between spring-summer and autumn-winter periods (Arslan et al. 2019). This temporal component should be kept in mind when comparing absolute lipid values across studies.

Overall, the present study shows that freshwater mussels from the Dicle River basin share the regional unionid tendency toward dominance by a restricted set of major fatty acids, while also displaying marked differences in total lipid content and in SFA/MUFA/PUFA balance among species and localities. The most notable patterns were the high total lipid and MUFA proportions in *U. elongatulus*, the strongly saturated profile of *L. wheatleyi* from Ambar Stream, the more unsaturated profile of *L. wheatleyi* from the Dicle River, and the relatively PUFA-rich profile of *U. tigridis*. Taken together, these findings provide new comparative biochemical data for freshwater mussels in southeastern Türkiye and support the use of fatty acid composition as a useful descriptor of locality- and species-associated variation in inland unionids (Ekin et al. 2011, Newton et al. 2013).

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