Journal of Fisheries
Volume 12 Issue 1 April 2024
Peer Reviewed | Open Access

eISSN 2311-3111
pISSN 2311-729X

DOI: https://doi.org/10.17017/j.fish.460

Original Article

Effect of ploidy on growth, fillet composition and colour of large rainbow trout (*Oncorhynchus mykiss*) in the Black Sea

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Manuscript history
Received 22 June 2022 | Accepted 17 February 2023 | Published online 16 March 2024

Citation
Dilara KO (2024) Effect of ploidy on growth, fillet composition and colour of large rainbow trout (*Oncorhynchus mykiss*) in the Black Sea. Journal of Fisheries 12(1): 121202. DOI: 10.17017/j.fish.460

Abstract
The purpose of this study was to determine the growth performance and fillet quality parameters of large rainbow trout (*Oncorhynchus mykiss*) and of different ploidy (diploid-DTS and triploid- TTS) cultured in the Black Sea. This study was carried out in a commercial fish farm in Sinop, Black Sea of Turkey. Triploid groups had a higher weight and a better feed conversion rate than the DTS at the end of the 150-day study. Crude protein and crude fat ratios were respectively higher in the DTS and TTS groups; while ploidy affected the biochemical and fatty acid compositions of the large rainbow trout, it had no effect on the amino acid compositions. The colour of fillets was affected by the crude fat ratio of the fillet. This study indicated that large rainbow trout produced in the Black Sea, regardless of its ploidy, were of high quality, nutritious and healthy for human consumption. Furthermore, it demonstrated yet again that large rainbow trout is of sufficient quality to compete with other salmonid species in the national or international markets.

Keywords: amino acid; biochemical composition; diploid; fatty acid; fillet colour; *Oncorhynchus mykiss*; triploid.

1 | INTRODUCTION

The production of sterile animals is beneficial in aquaculture because it can promote higher growth while reducing the ecological impact of farmed fish escapees (Piferrer *et al.* 2009). Triploidisation is the most widely used method for producing sterile fish on a large scale and it is frequently made with thermal or pressure shock (Piferrer *et al.* 2009). The energy required for sexual maturation and reproduction in diploids can be redirected to larger growth in triploids since triploidy decreases gonad development in general. But the consequences of triploidy on growth, on the other hand, are quite variable and depend on a range of factors, including fish species and environmental conditions. In some cases, triploid growth may be similar (Sacobie *et al.* 2012) or lower than that of diploids (Friars *et al.* 2001).

Triploid fish species may differ in biochemical, fatty acid and amino acid composition and carcass yield, all of which have an immediate influence on market acceptance (Buchtova *et al.* 2004; Poontawee *et al.* 2007; Manor *et al.* 2012; Ribeiro *et al.* 2012). Triploid fish for commercial production has been assessed for a long time (Quillet and Gaingon 1990; Benfey 2001; Dunham 2004). In comparison to other countries, the culture of rainbow trout (*Oncorhynchus mykiss*) in Turkey has been increased rapidly in recent years. In 2020, the total production of rainbow trout in Turkey was 144.182 tons including 126.101 tons from inland waters and 18.182 tons from the Black sea (Anonymous 2020). Especially when compared to previous years, there was an increase of nearly 50% in the production of rainbow trout in the sea (Anonymous 2020). The rationale for this is to capitalise on the fact that rainbow trout, which are raised to varied weight objectives in order to secure new product entry into the

market and compete with imported products, can survive in both fresh and saltwater. Using this advantage of the rainbow trout, the producers preferred to introduce different weight groups to the market, and by increasing the quality of fish diets, they produced the large rainbow trout, under the name Turkish salmon, presented in the national or international markets, which can compete with the Atlantic/Norwegian salmon (*Salmo salar*) in the world market in terms of fillet quality and fillet colour (Keskin *et al.* 2022; Kocatepe *et al.* 2022). As a result, the cultivated large rainbow trout product became more desirable in terms of both appearance and fillet quality. Today, especially with the newly identified potential breeding areas in the Black Sea, a competitive environment has been prepared for the operators who want to produce large rainbow trout. Various studies should be conducted in order to maximise fish production economically and to establish the essential diet kinds and production techniques required by the fish, as well as to pick the most appropriate ones, no studies are available that compared diploid and triploid large rainbow trout weighing above 1 kg in commercial aquaculture in Black Sea in Turkey. It is thought that determining the growth and feed evaluation performance of different ploidy on large rainbow trout, raised under the same conditions, will contribute positively to producers and the fillet quality parameters will be beneficial to consumers. The purpose of this study is to determine the growth performance and fillet quality parameters of diploid and triploid large rainbow trout cultured in the Black Sea.

2 | METHODOLOGY

2.1 Samples Collection

The current study was conducted at a commercial fish farm (SAGUN AQUA) in Sinop, Turkey's southern Black Sea coasts (Demirciköy site: 41°54′44.15′′N 35°10′55.92′′E; 41°54′33.92′′N 35°11′03.42′′E; and 41°54′32.52′′N 35°10′60′′E; 41°54′N 35°10′52.5′′E) for 150 days. The 4 number polyethylene plastic cages with a diameter of 30 m and a depth of 12+1m and dyneema mesh material were used. Triploid (TTS) and diploid (DTS) large rainbow trout (at 2 years old) were taken from Samsun Derbent Dam Lake in Turkey on 15 December 2018 and the study was finished on 15 May 2019 (150 days). The study was scheduled as two groups with two replications 3 kg m^{-3} large rainbow trout were stocked in each net cage in the sea. All of the fish used in the study are female and imported from a French company (Viviers) that produces triploid fish eggs using the hot shock method. In addition, no application was made to determine the triploidy levels. The average initial weight of TTS and DTS large rainbow trout were 1019.50 ± 77.27 g and 817.25 ± 137.10 g respectively. The fish were fed twice a day until satiation, depending on the weather conditions. Fish were killed with a high dose of anesthesia (MS-222, 25–50 mg L^{-1}, Ortuno *et al.* 2002) and randomly sampled (30 fish) at the start and conclusion of the research by Sagun Aqua personnel. Therefore, this manuscript does not need an ethical approval. Cold chain conditions were used to transfer fish and diet samples to the Faculty of Fisheries and Aquaculture, Scientific and Technological Research Center (University of Sinop). In the laboratory, fish were cut into boneless fillets by separating their internal organs and skins; they were kept in a deep freezer (WiseCryo/WUF-D500-80°C) until analysis. During the study, water temperature was the lowest in February 2019 (8.20 ± 0.15°C) and was the highest in May 2019 (14.41 ± 0.26°C; average 5 m 11.02 ± 0.94°C). The average O_2 values were between 10.42 ± 0.20 and 12.91 ± 0.11 mg L^{-1} (average 5 m, 11.76 ± 0.4 mg L^{-1}).

Water temperature and oxygen were measured using the HANNA multiparameter device (HANNA HI9829, UK). The diets were made by BioMar SAGUN (Aydın-Turkey), a commercial diet manufacturer, using a closed diet formula for large rainbow trout. In pursuant to the manufacturer's diet label, the biochemical composition of the diets is shown in Supplementary Data 1. The feeds used in the study were of two different sizes; the fish were given 4.5 mm feed in the dam lakes and 6 mm feed were given in the sea. The biochemical, amino and fatty acid compositions of the diets are given in Table 1. Crude protein (CP) and crude fat (CF) values of initial and final diets were 46.28 ± 0.22 – 41.71 ± 0.56% and 19.47 ± 0.05 – 23.96 ± 0.68% respectively.

Growth, diet use and biometric data were calculated following Jobling (2003). The biochemical analyses of the diet, liver and fillets samples were evaluated following AOAC (1995). Amino acid and fatty acid analyses of diets and fillets were carried out at the Sinop University Scientific Research and Application Center (SUBITAM). All biochemical analysis in fish fillets were based on wet samples and used in triplicates. For fatty acid analyses, the fillet and diet samples were converted to methyl esters by derivatisation of fat samples in a gas chromatography device (Thermo Scientific Trace 1310). For this purpose, 0.25 g of the extracted oil was removed and 4 ml of heptane and 0.4 ml of 2N KOH were added. The mixture was stirred in a vortex for 2 min and then centrifuged at 5000 rpm for 5 min. After centrifugation, 1.5 – 2 ml of the heptane phase was collected and transferred to glass tubes for GC/MS analysis. Injection of samples into the device was carried out with an automatic sampler (Autosampler AI 1310). Samples were analysed by Thermo Scientific ISQ LT (model GC/MS). For this analysis, Trace Gold TG-WaxMS capillary column (Thermo Scientific code: 26088-1540) with a film thickness of 0.25 µm and 60 m length was used. The injection block temperature was set to 240°C, and the column temperature was increased from 100°C to 240°C in the temperature programme. Helium gas (1 ml min^{-1}) was used as a carrier gas at constant flow

and 1:20 split ratio was applied. The MS unit (ISQ LT) was used in electron ionisation mode. Fatty acids were defined by comparing the standard FAME mixture of 37 components based on the arrival times.

TABLE 1 The biochemical, amino and fatty acid compositions of the diets.

Parameters	Initial diet	Final diet
Biochemical composition (%)		
Crude protein	46.28 ± 0.22	41.71 ± 0.56
Crude fat	19.47 ± 0.05	23.96 ± 0.68
Crude ash	8.33 ± 0.17	9.57 ± 0.33
Dry matter	91.36 ± 0.05	92.64 ± 0.24
Amino acid composition (g / 100 g)		
Alanine	2.43 ± 0.01	1.97 ± 0.01
Aspartic acid	4.95 ± 0.01	4.04 ± 0.01
Methionine	0.91 ± 0.01	1.03 ± 0.01
Glutamic acid	5.89 ± 0.01	5.10 ± 0.01
Phenilalanine	1.85 ± 0.01	1.65 ± 0.01
Lysine	3.79 ± 0.01	2.67 ± 0.01
Histidine	0.96 ± 0.01	0.91 ± 0.01
Tyrosine	1.07 ± 0.04	0.91 ± 0.01
Glysine	2.34 ± 0.01	1.98 ± 0.01
Valine	1.95 ± 0.01	1.58 ± 0.01
Leucine	2.97 ± 0.01	2.69 ± 0.02
Isoleucine	1.26 ± 0.01	1.03 ± 0.01
Threonine	1.79 ± 0.01	1.52 ± 0.01
Serine	2.40 ± 0.02	1.95 ± 0.01
Proline	2.32 ± 0.01	2.00 ± 0.01
Ornitine	0.02 ± 0.01	0.02 ± 0.01
Cystine	0.19 ± 0.01	0.17 ± 0.01
Arginine	2.69 ± 0.01	2.24 ± 0.01
ΣEAA	18.15 ± 0.03	15.30 ± 0.02
ΣSEAA	3.65 ± 0.01	3.15 ± 0.01
ΣNEAA	21.60 ± 0.02	18.12 ± 0.02
Fatty acid composition (%)		
C12:0	0.11 ± 0.01	0.08 ± 0.01
C13:0	0.02 ± 0.01	0.02 ± 0.01
C14:0	3.56 ± 0.02	3.78 ± 0.01
C15:0	0.34 ± 0.01	0.38 ± 0.01
C16:0	11.16 ± 0.08	10.61 ± 0.09
C17:0	0.34 ± 0.01	0.34 ± 0.01
C18:0	4.65 ± 0.07	3.96 ± 0.01
C20:0	0.88 ± 0.01	1.05 ± 0.01
C21:0	0.04 ± 0.01	0.02 ± 0.01
C22:0	0.42 ± 0.01	1.12 ± 0.01
C23:0	0.07 ± 0.01	0.07 ± 0.01
C24:0	0.40 ± 0.01	0.48 ± 0.0
C14:1	0.18 ± 0.01	0.19 ± 0.01
C15:1	0.05 ± 0.01	0.06 ± 0.01
C16:1	0.29 ± 0.01	0.33 ± 0.01
C17:1	0.27 ± 0.01	0.32 ± 0.01
C18:1n-9c	25.16 ± 0.12	23.91 ± 0.11
C18:1n-9t	4.15 ± 0.02	2.83 ± 0.57
C20:1n-9c	5.85 ± 0.01	6.26 ± 0.05
C22:1n-9	4.93 ± 0.01	5.32 ± 0.04
C24:1	1.01 ± 0.03	1.18 ± 0.02
C18:2n-6t	0.29 ± 0.01	0.35 ± 0.01
C18:2n-6c	13.84 ± 0.06	13.45 ± 0.09
C18:3n-3	7.59 ± 0.01	8.71 ± 0.09
C18:3n-6	0.25 ± 0.01	0.28 ± 0.01
C20:2	1.99 ± 0.01	2.25±0.02
C20:3n-3	0.01 ± 0.01	0.02 ± 0.01
C20:3n-6	0.44 ± 0.01	0.51 ± 0.01
C20:4n:6	0.53 ± 0.01	0.62 ± 0.03
C20:5n-3	4.85 ± 0.02	5.05 ± 0.01
C22:2	0.21 ± 0.01	0.25 ± 0.01
C22:6n-3	6.09 ± 0.01	6.17 ± 0.06
ΣSFA	21.97 ± 0.18	21.91 ± 0.12
ΣMUFA	41.88 ± 0.13	40.40 ± 0.47
ΣPUFA	36.10 ± 0.08	37.65 ± 0.38

∑SFA = C12:0 + C13:0 + C14:0 + C15:0 + C16:0 + C17:0 + C18:0 + C20:0 + C21:0 + C22:0 + C23:0 + C24:0; ∑MUFA = C14:1 + C15:1 + C16:1 + C17:1 + C18:1n-9c + C18:1n-9t + C20:1n-9c + C22:1n-9 + C24:1; ∑PUFA = C18:2n-6t + C18:2n-6c + C18:3n-3 + C18:3n-6 + C20:2 + C22:2 + C20:3n-6 + C20:5n-3 + C20:4n-6 + C22:6n-3; essential amino acids (EAA) = Histidine + Lysine + Phenylalnine + Methitonine + Threonine + Leucine + Isoleucine + Valine + Arginine; semi-essential amino acids (SEAA) = Histidine + Arginine; non-essential amino acids (NEAA)= Alanine + Aspartic acid + Glutamic acid + Tyrosine + Glicine + Serine + Proline.

Amino acid analyses of diet and fish fillets were performed using the Jasem LC-MS/MS amino acid assay kit. The concentration of the target amino acids was determined using the electrospray ionization (ESI)-based multiple reaction monitoring (MRM) mode. 0.5g sample was taken into a glass vial with a screw cap and 4ml of reagent-2 was added, and then, a hydrolysis reaction was performed at 110°C for 24 -hr. The hydrolysate was centrifuged for 5 min at 4000rpm when it reached room temperature. Then, 100µl of the supernatant was transferred to a vial and completed to 1ml with distilled water. This dilution procedure was repeated one more time to yield 800-fold diluted hydrolysate of the sample. 50µl of the diluted hydrolysate was transferred to a sample vial and 50µl of internal standard mixture with isotope-labeled and 700µl of reagent-1 was added, respectively, and then, the mixture was vortexed for 5s. All samples were prepared according to the above procedures and injected into the LC-MS/MS system where the amounts of amino acids were read.

The colour values of skin and fillet of DTS and TTS were assessed using Minolta Chroma Meter, standardized to white plate as a reference before each measurement

(standard values for white plate L*=91.97; a*=−1.4; b*=2.0, Standard C2-22326). L*, a* and b* values represent lightness, redness and yellowness, respectively. The Hue is a descriptor of what is generally understood to be the true colour, and the chroma (C*) is the intensity or degree of saturation of the colour. The angle of Hue and C* was calculated using a* and b* values (Kestin and Warriss 2001):

$C^*=\sqrt{a^{*2}+b^{*2}}$ and $Hue = \arctan(b^*/a^*)$

Colour measurement of fillet and skin of DTS and TTS was done from three locations: 1st location: between the behind of the operculum; 2nd location: under of the dorsal fin; and 3rd location: front of the caudal fin. Colour differences (ΔE) were calculated by using the equation of Özcan (2008): (ΔE) =√(L*1-L*2)2 + (a*1-a*2)2 + (b*1-b*2)2L*1: Initial measuring, L*2: Final measuring; a*1: Initial measuring, a*2: Final measuring; b*1: Initial measuring, b*2: Final measuring.

The data were reported as average values with standard error (SE). The IBM SPSS 21 statistics package application was used for statistical analysis. Shapiro–Wilk normality and Levene's tests were used to determining the data's normality and equality of variance. The significance of the differences in the data was determined using oneway ANOVA, followed by Tukey's procedure for multiple comparisons.

3 | RESULTS

Feed consumption amounts (FC) and feed conversion rates (FCR) were higher in DTS. The statistical difference between the protein efficiency ratio (PER) values of the experimental groups was not significant. Condition factor (K) decreased in DTS and increased in TTS at the end of the study. Viserosomatic index (VSI) values decreased in both groups at the end of the experiment and the difference between the groups was not significant. Although the hepatosomatic index (HSI) value of the TTS was higher than the DTS at the initial, the HSI value of both groups decreased at the end of the study, and the HSI value of the TTS was lower than the DTS. The carcass yield (CR) value was higher in TTS, but the statistical difference between the carcass yield values of the experimental groups was not significant.

TABLE 2 Growth performance, biometric index, feed efficiency and biochemical composition of DTS and TTS.

Parameters	DTS		TTS	
	Initial	Final	Initial	Final
Weight (g)	817.25±137.10	3209.13±205.59	1019.50±77.27	3756.72±175.76
K[1]	1.70±0.09	1.52±0.06^{a}	1.41±0.06	1.52±0.03^{a}
VSI (%)[2]	18.46±0.40	16.22±0.98^{a}	17.87±0.66	15.17±0.90^{a}
HSI (%)[3]	1.39±0.27	1.24±0.10^{b}	1.65±0.09	0.90±0.05^{a}
GSI (%)[4]	1.55±0.04	0.33±0.04	-	0.02±0.01
CY (%)[5]	47.18±0.47	51.64±1.96^{a}	49.74±1.29	52.48±0.93^{a}
CP (%)[6]	22.05±0.22^{b}	21.50±0.59^{ay}	21.60±0.33^{b}	15.92±0.15^{ax}
CF (%)[7]	8.67±0.92^{a}	17.29±0.51^{bx}	5.73±0.60^{a}	27.92±1.22^{by}
CA (%)[8]	2.68±0.04^{a}	3.28±0.19^{by}	2.93±0.07^{a}	2.85±0.14^{ax}
DM (%)[9]	32.97±0.71^{a}	41.56±0.08^{bx}	28.31±0.36^{a}	50.21±1.02^{by}
SR (%)[10]	82.15±1.68^{a}		83.88±0.97^{b}	
Weight gain (g)	2391.88±211.22^{b}		2737.22±143.78^{a}	
Weight gain (%)	388.84±105.57^{b}		276.98±23.47^{a}	
SGR (%)[11]	0.97±0.13^{b}		0.88±0.04^{a}	
TGR (%)[12]	0.34±0.01^{a}		0.33±0.04^{a}	
FC (kg/fish)[13]	4.22±0.25^{a}		4.17±0.37^{a}	
FCR[14]	1.76±0.07^{b}		1.52±0.09^{a}	
PER[15]	0.57±0.19^{a}		0.56±0.06^{a}	

The each value means mean ± standard error. Values expressed with different exponential letters on the same line are statistically different from each other ($p < 0.05$). $^{a, b}$: The differences between the means with different letters on the same line within the group are statistically significant ($p < 0.05$). $^{x, y}$: The differences between the means with different letters on the same line between the groups are statistically significant ($p < 0.05$). [1]K = condition factor, [2]VSI = viserosomatic index, [3]HSI = hepatosomatic index, [4]GSI = gonadosomatic index, [5]CY = carcass yield, [6]CP = crude protein, [7]CF = crude fat, [8]CA = crude ash, [9]DM = dry matter, [10]SR = survival rate, [11]SGR = specific growth rate, [12]TGR = thermal growth rate, [13]FC = Feed consumption, [14]FCR = feed conversion ratio, [15]PER = protein efficiency ratio.

The biochemical compositions of the DTS and TTS fillets are given Table 2. Crude protein (CP) values of DTS (22.05 ± 0.22 and 21.50 ± 0.59%; $p < 0.05$) and TTS (21.60 ± 0.33 and 15.92 ± 0.15%; $p < 0.05$) fillets decreased in the final. When CP values in the final were compared, the CP value in DTS fillets (21.50 ± 0.59%) was higher than the

TTS fillets (15.92 ± 0.15%) ($p < 0.05$). The CF values of DTS (8.67 ± 0.92 and 17.29 ± 0.51%) and TTS (5.73 ± 0.60 and 27.92 ± 1.22%) fillets increased in the final for both groups and the statistical difference was significant ($p < 0.05$). When the final CF values were compared, TTS fillets (27.92 ± 1.22%) contained more fat than DTS fillets (17.29 ± 0.51%) ($p < 0.05$). The CA values increased in DTS fillets and decreased in TTS fillets in the final. The statistical difference between the dry matter (DM) values of DTS (41.56 ± 0.08%) and TTS (50.21 ± 1.02%) fillets in the final was significant ($p < 0.05$).

3.1 Amino acid composition

The amino acid compositions of the DTS and TTS fillets are given Table 3. While glutamic acid, aspartic acid, lysine, alanine and leucine were the highest amino acid in DTS fillets, glutamic acid, aspartic acid, lysine were the highest amino acid in TTS fillets at initial and final. All amino acid values, except valine, isoleucine, tyrosine, and glycine, in DTS fillets, decreased considering to initial. In TTS fillets, all amino acid values except methionine, phenylalanine and tyrosine increased in the final period.

TABLE 3 Amino acid composition of DTS and TTS fillets (g $100g^{-1}$).

Amino Acids	DTS		TTS	
	Initial	Final	Initial	Final
Alanine	$1.35±0.01^{b}$	$1.26±0.01^{ax}$	$1.15±0.01^{a}$	$1.24±0.01^{bx}$
Aspartic Acid	$2.40±0.01^{b}$	$1.68±0.01^{ax}$	$1.78±0.01^{a}$	$2.12±0.01^{by}$
Methinonine	$0.58±0.01^{b}$	$0.51±0.01^{ax}$	$0.52±0.01^{b}$	$0.48±0.01^{ax}$
Glutamic Acid	$2.64±0.01^{b}$	$2.29±0.01^{ax}$	$2.19±0.01^{a}$	$2.31±0.01^{bx}$
Phenylalanine	$0.77±0.01^{b}$	$0.66±0.01^{ax}$	0.68±0.01	$0.68±0.01^{ax}$
Lysine	$1.76±0.01^{b}$	$1.67±0.01^{ax}$	$1.64±0.01^{a}$	$1.96±0.01^{by}$
Histidine	$0.58±0.01^{b}$	$0.49±0.01^{ax}$	$0.46±0.01^{a}$	$0.58±0.01^{by}$
Tyrosine	$0.54±0.01^{a}$	$0.55±0.01^{ay}$	$0.52±0.01^{a}$	$0.49±0.01^{ax}$
Glysine	$1.14±0.01^{b}$	$0.79±0.01^{ax}$	$0.47±0.01^{a}$	$0.75±0.01^{bx}$
Valine	$0.64±0.01^{a}$	$0.64±0.01^{ax}$	$0.58±0.01^{a}$	$0.60±0.01^{ax}$
Leucine	$1.33±0.01^{b}$	$1.17±0.01^{ax}$	$1.17±0.01^{a}$	$1.23±0.01^{by}$
Isoleucine	$0.39±0.01^{a}$	$0.39±0.01^{ax}$	$0.34±0.01^{a}$	$0.34±0.01^{ax}$
Threonine	$0.79±0.01^{b}$	$0.70±0.01^{ax}$	$0.65±0.01^{a}$	$0.69±0.01^{bx}$
Serine	$0.84±0.01^{a}$	$0.82±0.01^{ax}$	$0.79±0.01^{a}$	$0.82±0.01^{ax}$
Proline	$0.73±0.01^{b}$	$0.64±0.01^{ax}$	$0.65±0.01^{a}$	$0.68±0.01^{ax}$
Ornithine	$0.15±0.01^{a}$	$0.14±0.01^{ax}$	$0.16±0.01^{a}$	$0.19±0.01^{ay}$
Cystine	$0.13±0.01^{a}$	$0.11±0.01^{ax}$	$0.14±0.01^{a}$	$0.14±0.01^{ax}$
Arginine	$1.01±0.01^{a}$	$0.99±0.01^{ax}$	$0.92±0.01^{a}$	$0.99±0.01^{bx}$
TAA	17.77±0.01	$15.49±0.01^{ax}$	$14.79±0.01^{a}$	$16.27±0.01^{by}$
ΣEAA	$7.85±0.01^{b}$	$7.21±0.01^{ax}$	$6.96±0.01^{a}$	$7.54±0.01^{by}$
ΣSEAA	$1.59±0.01^{b}$	$1.48±0.01^{ax}$	$1.38±0.01^{a}$	$1.57±0.01^{by}$
ΣNEAA	$9.92±0.01^{b}$	$8.28±0.01^{ax}$	$7.84±0.01^{a}$	$8.74±0.01^{by}$
EAA/NEAA	$0.79±0.01^{a}$	$0.87±0.01^{bx}$	$0.89±0.01^{a}$	$0.86±0.01^{ax}$
ΣBcAA	$2.36±0.01^{b}$	$2.20±0.01^{ax}$	$2.09±0.01^{a}$	$2.17±0.01^{bx}$
ΣSAA	$0.71±0.01^{b}$	$0.62±0.01^{ax}$	$0.66±0.01^{b}$	$0.62±0.01^{ax}$
ΣArAA	$1.31±0.01^{b}$	$1.21±0.01^{ax}$	$1.20±0.01^{a}$	$1.17±0.01^{ax}$
ΣBAA	$3.35±0.01^{b}$	$3.15±0.01^{ax}$	$3.02±0.01^{a}$	$3.53±0.01^{by}$
ΣAAA	$5.04±0.01^{b}$	$3.97±0.01^{ax}$	$3.96±0.01^{a}$	$4.43±0.01^{by}$
EAAI	$0.89±0.01^{a}$	$0.86±0.01^{ax}$	$0.84±0.01^{a}$	$0.88±0.01^{by}$

The each value means mean ± standard error. Values expressed with different exponential letters on the same line are statistically different from each other ($p < 0.05$). $^{a, b}$: The differences between the means with different letters on the same line within the group are statistically significant ($p < 0.05$). $^{x, y}$: The differences between the means with different letters on the same line between the groups are statistically significant ($p < 0.05$). Essential Amino Acids (EAA) = Histidine + Lysine + Phenylalanine + Methitonine+ Threonine + Leucine + Isoleucine + Valine + Arginine; Semi-Essential Amino Acids (SEAA) = Histidine + Arginine; Non-Essential Amino Acids (NEAA) = Alanine + Aspartic acid+ Glutamic acid+ Tyrosine + Glicine + Serine + Proline; Branched-chain amino acid (BcAA) = Leucine+ Isoleucine + Valine; Sulfur-containing amino acids (SAA) = Cystine + Methinonine; Aromatic amino acids (ArAA) = Phenylalanine + Tyrosine; Basic (alcaline) amino acids (BAA) = Lysine + Arginine + Histidine; Acidic amino acids (AAA) = Aspartikc acid + Glutamic acid

When the final amino acid values of DTS and TTS fillets were compared, alanine, methionine, tyrosine, glycine, valine, isoleucine and threonine values in DTS; aspartic acid, glutamic acid, phenylalanine, lysine, histidine, leucine, proline, ornithine and cystine values were higher in TTS fillets. Serine and arginine values were similar in both large rainbow trouts groups. As a result of the statistical analysis between the amino acid values of TTS and DTS fillets, the differences between aspartic acid, lysine, histidine, tyrosine, leucine and ornithine values were significant ($p < 0.05$). Total amino acid (TAA) value was more in TTS fillets ($p < 0.05$). The ΣEAA, ΣSEAA and ΣNEAA values were lower in DTS fillets than in TTS fillets, and the statistical difference between groups was significant ($p < 0.05$). The EAA/NEAA ratio was higher in DTS fillets and the EAAI value was higher in TTS fillets.

3.2 Fatty acid composition

The fatty acid composition of the DTS and TTS fillets are given in Table 4. In the study, C14:0, C16:0, C17:0 and C18:0 values were high in DTS, C15:0, C20:0, C21:0, C22:0, C23: 0 and C24:0 values were higher in TTS fillets. Among the SFAs in DTS and TTS fillets, only the statistical difference between C18:0 and C20:0 values was significant ($p < 0.05$). In MUFAs of DTS and TTS fillets, C17:1, C20:1n-9c and C22:1n-9 values were higher in DTS, C14:1, C18:1n-9c, C18:1n-9t and C24:1 were higher in TTS fillets. In the final, EPA value of DTS fillets decreased, EPA value of TTS fillets increased and EPA value of TTS fillets was higher than DTS fillets ($p < 0.05$). DHA values of fillets decreased in the final of both groups ($p < 0.05$). In the final fillets, ΣSFA and ΣPUFA values were higher in the DTS, and ΣMUFA values were higher in the TTS ($p < 0.05$). The statistical difference between EPA/DHA ratios of DTS and TTS fillets was significant ($p < 0.05$).

TABLE 4 Fatty acid composition of DTS and TTS fillets (%).

Fatty acid	DTS		TTS	
	Initial	Final	Initial	Final
C12:0	0.08±0.01^{a}	0.07±0.01^{ax}	0.05±0.01^{a}	0.07±0.01^{ax}
C13:0	0.02±0.01^{a}	0.02±0.01^{ax}	0.01±0.01^{a}	0.02±0.01^{ax}
C14:0	3.47±0.04^{b}	3.27±0.01^{ax}	2.69±0.01^{a}	3.26±0.04^{bx}
C15:0	0.41±0.01^{a}	0.38±0.01^{bx}	0.32±0.01^{a}	0.39±0.01^{bx}
C16:0	12.7±0.04^{b}	11.4±0.04^{ax}	11.0±0.02^{a}	11.4±0.15^{bx}
C17:0	0.45±0.01^{a}	0.40±0.01^{ax}	0.36±0.01^{a}	0.37±0.01^{ax}
C18:0	7.29±0.13^{a}	7.65±0.05^{by}	6.26±0.02^{a}	7.21±0.06^{bx}
C20:0	0.92±0.02^{b}	0.77±0.01^{ax}	0.72±0.01^{a}	0.86±0.01^{by}
C21:0	0.02±0.01^{a}	0.01±0.01^{ax}	0.02±0.01^{a}	0.02±0.01^{ax}
C22:0	0.59±0.01^{b}	0.46±0.01^{ax}	0.40±0.01^{a}	0.51±0.01^{bx}
C23:0	0.06±0.01^{a}	0.06±0.01^{ax}	0.05±0.01^{a}	0.07±0.01^{ax}
C24:0	0.34±0.01^{b}	0.29±0.01^{ax}	0.30±0.01^{a}	0.32±0.01^{ax}
ΣSFA	26.4±0.20^{b}	24.8±0.10^{ay}	22.1±0.04^{a}	24.5±0.25^{bx}
C14:1	0.20±0.01^{a}	0.18±0.01^{ax}	0.13±0.01^{a}	0.19±0.01^{bx}
C15:1	0.06±0.01^{a}	0.06±0.01^{ax}	0.04±0.01^{a}	0.06±0.01^{ax}
C16:1	0.41±0.01^{a}	0.41±0.01^{ax}	0.31±0.01^{a}	0.41±0.01^{bx}
C17:1	0.45±0.01^{a}	0.49±0.01^{ax}	0.33±0.01^{a}	0.45±0.01^{bx}
C18:1n-9c	20.6±0.12^{a}	23.9±0.70^{bx}	21.7±0.09^{a}	25.9±0.09^{by}
C18:1n-9t	3.04±0.09^{b}	2.52±0.28^{ax}	3.48±0.02^{b}	2.69±0.02^{ay}
C20:1n-9c	1.25±0.01^{a}	1.23±0.01^{ay}	5.95±0.01^{b}	1.18±0.01^{ax}
C22:1n-9	4.11±0.03^{a}	4.60±0.06^{by}	4.10±0.03^{a}	4.55±0.02^{bx}
C24:1	1.23±0.06^{b}	1.13±0.02^{ax}	1.20±0.02^{a}	1.29±0.01^{by}
ΣMUFA	31.3±0.14^{a}	34.5±0.40^{bx}	37.2±0.07^{b}	36.7±0.08^{ay}
C18:2n-6t	0.46±0.01^{a}	0.43±0.01^{ax}	0.34±0.01^{a}	0.43±0.01^{bx}
C18:2n-6c	14.7±0.08^{b}	14.5±0.14^{ay}	14.3±0.01^{b}	13.2±0.03^{ax}
C18:3n-3	6.30±0.04^{a}	6.91±0.05^{by}	6.35±0.01^{a}	6.82±0.02^{bx}
C18:3n-6	0.71±0.01^{a}	0.70±0.01^{ax}	0.61±0.01^{a}	0.69±0.01^{bx}
C20:2	3.14±0.01^{a}	3.32±0.03^{bx}	3.40±0.01^{b}	3.31±0.02^{ax}
C20:3n-3	1.50±0.01^{a}	1.67±0.02^{by}	1.46±0.01^{a}	1.47±0.01^{ax}
C20:3n-6	0.35±0.01^{a}	0.33±0.01^{ax}	0.32±0.01^{a}	0.39±0.01^{by}
C20:4n-6	1.37±0.03^{a}	2.01±0.02^{by}	1.77±0.01^{b}	1.41±0.34^{ax}
C20:5n-3	4.45±0.01^{b}	3.71±0.03^{ax}	3.29±0.01^{a}	3.93±0.04^{by}
C22:2	0.03±0.01^{a}	0.03±0.01^{ax}	0.09±0.01^{a}	0.06±0.03^{ax}
C22:6n-3	9.27±0.02^{b}	7.41±0.07^{ay}	8.68±0.01^{b}	7.06±0.02^{ax}
ΣPUFA	42.3±0.06^{b}	41.0±0.35^{ay}	40.6±0.06^{b}	38.8±0.30^{ax}
ΣOmega-3	21.5±0.02^{b}	19.6±0.17^{ay}	19.8±0.03^{b}	19.3±0.07^{ax}
ΣOmega-6	17.6±0.05^{a}	18.0±0.16^{by}	17.3±0.02^{b}	16.1±0.30^{ax}
ΣOmega-9	29.0±0.23^{a}	32.3±0.39^{bx}	35.2±0.07^{b}	34.3±0.07^{ay}
n3/n6	1.22±0.01^{b}	1.10±0.01^{ax}	1.14±0.01^{a}	1.20±0.01^{by}
n6/n3	0.82±0.01^{a}	0.91±0.01^{by}	0.87±0.01^{a}	0.84±0.01^{ax}
EPA/DHA	0.48±0.01^{a}	0.50±0.01^{ax}	0.38±0.01^{a}	0.56±0.01^{by}
EPA+DHA	13.7±0.02^{b}	11.1±0.10^{ay}	12.0±0.03^{b}	11.0±0.05^{ax}
AI	0.38±0.01^{a}	0.34±0.01^{ay}	0.29±0.01^{a}	0.28±0.01^{ax}
TI	0.26±0.01^{a}	0.26±0.01^{ax}	0.23±0.01^{a}	0.24±0.01^{ax}
PUFA/SFA	1.60±0.01^{a}	1.66±0.01^{ay}	1.83±0.01^{b}	1.58±0.01^{ax}
H/H	3.14±0.02^{a}	3.54±0.03^{bx}	3.66±0.01^{b}	3.55±0.06^{ax}

The each value means mean ± standard error. Values expressed with different exponential letters on the same line are statistically different from each other ($p < 0.05$). $^{a, b}$: The differences between the means with different letters on the same line within the group are statistically significant ($p < 0.05$). $^{x, y}$: The differences between the means with different letters on the same line between the groups are statistically significant ($p < 0.05$). ∑Omega-3 = C18:3n-3 + C20:3n-3 + C20:5n-3 + C22:5n-3 + C22:6n-3; ∑Omega-6 = C18:2n-6t + C18:2n-6c + C18:3n-6 + C20:4n-6 + C20:3n-6; ∑Omega-9 = C18:1n-9c + C18:1n-9t + C20:1n-9c + C22:1n-9; Atherogenicity Index (AI) = [(C12:0 + (4 × C14:0) + C16:0)] / (MUFA + Omega-3 + Omega-6); Thrombogenicity Index (TI) = (C14:0 + C16:0 + C18:0) / [(0.5 × MUFA) + (0.5 × Omega-6) + (3 × Omega-3) + (Omega-3/Omega-6)]; Hypocholesteroemic / Hypercholesterolemic ratio (H/H) = (C18:1n-9 + C18:2n-6 + C18:3n-3 + C20:4n-6 + C20:5n-3 + C22:6n-3) /(C14:0 + C16:0).

3.3 Colour parameters

In the study, the colour parameters of the skins of DTS and TTS were also measured, they are given in a Supplementary Data 3. The average L*, a*, b*, C* and Hue values in the skins of DTS in initial and final were 70.76 ±

2.62 – 73.11 ± 3.47, -0.58 ± 0.11 – 0.84 ± 0.39, 1.50 ± 0.52 – 3.35 ± 0.49, 2.29 ± 0.35 – 3.88 ± 0.46 and –0.57 ± 0.17 – 0.06 ± 0.30 respectively. The average L*, a*, b*, C* and Hue values of the initial and final TTS skins were 73.68 ± 205 – 92.49 ± 0.77, 0.28 ± 0.33 – 0.52 ± 0.22, 5.64 ± 0.68 – 2.72 ± 0.29, 5.94 ± 0.62 – 2.96 ± 0.27 and –0.17 ± 0.31 – 0.15 ± 0.30 respectively. The L*, a*, b*, C*, Hue and ΔE values of DTS and TTS fillets are given Table 5.

TABLE 5 The L*, a*, b*, C* and Hue values of DTS and TTS fillets.

	DTS		TTS	
	Initial	**Final**	**Initial**	**Final**
1st location (behind the operculum)				
L*	60.1 ± 0.91^{b1}	44.7 ± 1.27^{ax1}	53.9 ± 1.14^{b3}	47.7 ± 1.63^{ay2}
a*	8.7 ± 0.28^{a1}	17.6 ± 0.89^{by2}	6.4 ± 0.57^{a1}	14.9 ± 0.40^{bx2}
b*	13.1 ± 0.41^{a2}	22.0 ± 2.99^{by3}	7.9 ± 0.57^{a1}	19.4 ± 1.11^{bx3}
C*	15.7 ± 0.47^{a1}	28.3 ± 1.49^{by3}	10.2 ± 0.78^{a2}	24.6 ± 1.01^{bx2}
Hue	1.0 ± 0.01^{b1}	0.9 ± 0.02^{ax2}	0.9 ± 0.02^{a2}	0.9 ± 0.02^{ax3}
ΔE	19.91		15.67	
2nd location (Under the dorsal fin)				
L*	61.4 ± 0.76^{b2}	45.1 ± 1.22^{ax2}	51.5 ± 0.53^{b1}	46.7 ± 1.45^{ax1}
a*	8.2 ± 0.35^{a1}	13.7 ± 0.02^{bx1}	6.0 ± 0.58^{a1}	14.0 ± 0.43^{bx1}
b*	12.3 ± 0.41^{a1}	17.2 ± 1.31^{by1}	7.9 ± 0.44^{a1}	16.8 ± 0.73^{bx1}
C*	15.7 ± 0.47^{a1}	22.1 ± 1.40^{by1}	9.9 ± 0.67^{a1}	21.9 ± 0.75^{bx1}
Hue	0.98 ± 0.01^{b1}	0.89 ± 0.02^{ax2}	0.93 ± 0.03^{b3}	0.87 ± 0.02^{ax2}
ΔE	17.95		12.92	
3rd location (Front of the caudal fin)				
L*	60.8 ± 1.00^{b1}	49.4 ± 1.84^{ay3}	52.3 ± 1.04^{b2}	46.2 ± 1.53^{ax1}
a*	9.0 ± 0.48^{a1}	17.2 ± 1.13^{bx2}	9.7 ± 0.87^{a2}	18.0 ± 1.11^{bx3}
b*	12.3 ± 0.74^{a1}	18.8 ± 1.37^{bx2}	10.4 ± 1.08^{a2}	18.9 ± 1.18^{bx2}
C*	15.3 ± 0.82^{a1}	25.5 ± 1.73^{bx2}	14.4 ± 1.20^{a3}	26.1 ± 1.55^{bx3}
Hue	1.0 ± 0.02^{b1}	0.8 ± 0.02^{ax1}	0.8 ± 0.66^{a1}	0.8 ± 0.02^{ax1}
ΔE	15.47		13.31	

Each value represents the mean ±standard error. Values expressed with different exponential letters on the same line are statistically different from each other ($p < 0.05$). ^{a,b}: The differences between the means with different letters on the same line within the group are statistically significant ($p < 0.05$). ^{x,y}: The differences between the means with different letters on the same line between the groups are statistically significant ($p < 0.05$). ^{1,2,3}: the differences between the means with different letters in the same column in different regions are statistically significant ($p < 0.05$).

When the L* values of DTS and TTS fillets were compared in the final, the TTS came to the fore in the 1st and 2nd measurement regions, and the DTS in the 3rd measurement region. The difference between 1st and 3rd measurement L* values of TTS and DTS fillets was significant ($p < 0.05$), but the statistical difference between the L* values in the 2nd measurement regions was not significant. The a* values were high in DTS fillets in 1st measurement region, and in TTS fillets in the 2nd and 3rd measurement regions. The statistical difference between the a* values determined in the 1st measurement regions of the fillets of TTS and DTS was significant ($p < 0.05$). The b* values of the fillets were prominent in the DTS in the 1st and 2nd measurement regions ($p < 0.05$), while the 3rd measurement regions were similar values. The C* value was high in the 1st and 2nd measurement regions of DTS fillets, and the 3rd measurement region in TTS fillets. The statistical difference between the Hue values of the TTS and DTS fillets in final was not significant.

4 | DISCUSSION

4.1 Growth performance, biometric index, feed efficiency and biochemical composition

Aquaculture in Turkey has gained speed in recent years, paralleling technical and economic progress, and export numbers are growing on a daily basis. The large rainbow trout culture has taken place in the world market under the name of "Turkish salmon" in recent years, and it is predicted that the Black Sea will be used in this potential productively for many years with its production technology and market opportunities. The growth performance and fillet quality characteristics of cultured diploid (DTS) and triploid (TTS) large rainbow trout in net cages in the Black Sea (Sinop) were assessed and compared in this study. In the study, the average water temperature and dissolved oxygen values were 11.02 ± 0.94°C and 11.76 ± 0.40 mg L^{-1} respectively. Temperature and dissolved oxygen levels in the production area varied between those stated in the literature for rainbow trout they did not have a negative effect on their growth performance and biochemical values (Aral *et al*. 1996; Kaya Öztürk *et al.* 2019).

In the study, survival rates (SR) of DTS and TTS were similar. Previous research with diploid and triploid fish found that SR of fish in identical culture conditions may be the same (Wang *et al.* 2015), and triploid fish SR falls when the optimum culture parameters for fish were altered (Oppedal *et al*. 2003). The similar SR of DTS and TTS cultured in Black Sea can be explained by the fact that environmental water parameters are suitable for these fish.

At the end of the 150-day study, the average weights of DTS and TTS were 3209.13 ± 205.59 and 3756.72 ± 175.76 g respectively. While TTS gained more weight than DTS in the final, DTS outperformed TTS in terms of proportional weight increase (%), specific (SGR), and thermal growth rates (TGR). Triploid *Salmo salar*, rainbow trout, and *Oncorhynchus masou* outperform diploids in studies conducted by Carter *et al*. (1994), Sheehan *et al.* (1999), Oppedal *et al*. (2003) and Wang *et al*. (2015). TTS had a lower SGR than DTS, which is consistent with earlier research (Frias *et al*. 2001; Fraser *et al*. 2013; Taylor *et al*. 2013). Nonetheless, it was shown in several research that triploid fish do not always have a greater

development performance (Cal *et al*. 2006; Maxime 2008; Piferrer *et al*. 2009; Sacobie *et al*. 2012; Ghaeni *et al*. 2013; Domingues *et al*. 2019). According to studies, life phases (Leclercq *et al.* 2011), fish age (Cotte *et al*. 2002), culture strategy (Fraser *et al*. 2012) and gender (Taylor *et al*. 2013) can influence on these growth performances. The reason for the differences in growth performance of the said TTS and DTS can be explained by the fact that the energy that diploid fish spare for gonadal growth is devoted to somatic growth due to the sterility of triploid fish

Feed consumption per fish in the study was 4.22 and 4.17 kg fish^{-1} in DTS and TDS, respectively. The feed conversion rate (FCR) in TDS is better than DTS. Under suitable environmental conditions, Sambraus *et al*. (2018) found that ploidy had no influence on FCR in *S. salar*. Triploid *S. salar* and *O. masou* exhibited a reduced FCR, according to Fraser *et al*. (2012) and Wang *et al.* (2015). TTS was shown to be more effective in converting feed to weight in the current study and the findings were consistent with the previous studies.

At the end of the study, the condition factor (*K*) decreased in DTS and increased in TTS. Previous research found that the K values of triploid salmonids, particularly those grown in the sea, are lower than those of diploid salmonids (Leclercq *et al*. 2011; Taylor *et al.* 2015; Fjelldal *et al*. 2016; Smedley *et al*. 2016; Sambraus *et al*. 2018). The data relating to the *K* determined in the study were compatible with the literature. With this result, it is thought that TTS can have as good condition as DTS with a suitable culture medium and good feeding conditions for fish.

Despite the fact that there have been few papers comparing the biochemical makeup of triploid and diploid fish, the results differ. In the current study, crude protein (CP) and ash (CA) content of DTS fillets and crude fat (CF) and dry matter (DM) content of TTS were high. Manor *et al*. (2014) reported that CF in triploid rainbow trout and CP in diploid rainbow trout were high. CP and CF values of diploid and triploid rainbow trout were consistent with this study (Manor *et al*. 2014). Wang *et al*. (2015) noticed no change in the biochemical parameters of diploid and triploid fish. Studies reporting higher CP ratios of triploids and higher CF ratios of diploids have been reported in the literature in disagreement with our findings (Wang and Han 2017; Cai *et al*. 2021). Poontawee *et al*. (2007) reported that ploidy had no influence on fish biochemical composition, particularly CP levels. Shearer (1994) and Ignatz *et al*. (2020) in their study correlated temperature, lipid intake and protein:lipid in the diet. Given these findings, the fact that the TTS in this study had more CF and less CP than the DTS while ingesting the same diet and being cultivated in the same environment shows the ploidy impact. Furthermore, independent of ploidy, the biochemical composition values of large rainbow trout were shown to be enough quality for human consumption (Xiang *et al*. 2006; Liu *et al*. 2008; Wang *et al*. 2015; Wang and Han 2017).

4.2 Amino acid composition

While alanine, methionine, tyrosine, glycine valine, isoleucine, and threonine were higher DTS fillets, aspartic acid, glutamic acid, phenylalanine, lysine, histidine, leucine, proline, ornithine and cystine were higher TTS fillets. Buchthova *et al*. (2005) reported that some amino acids determined in triploid *Tinca tinca* showed significant differences, whereas Kızak *et al*. (2013) noticed that the amino acid composition in diploid and triploid *S. trutta fario* fillets was similar. However, Wang *et al*. (2015) determined that there was no difference in amino acid values in diploid and triploid *O. masou* fillet. The aspartic acid, lysine, histidine, tyrosine, leucine and ornithine values of TTS and DTS fillets were significant differences.

4.3 Fatty acid composition

The total SFA in DTS fillets decreased in the final while increasing in TTS fillets, in this study. SFA levels in diploid fish were identified to decrease throughout sexual development in several studies (Manor *et al*. 2012; Riberio *et al.* 2012; Cleveland *et al*. 2017). The most SFAs in the current study were C16:0 and C18:0, MUFAs C18:1 and C22:1. In studies with salmonid species determined that higher amounts of C16:0, C18:0 from SFAs, and C16:1 and C18:1 from MUFAs (Haliloğlu *et al*. 2004; Wang *et al*. 2015). This difference in MUFAs between the aforementioned studies can be explained in two ways: first, C16:1 is one of the main features of freshwater fish, but although trout is a freshwater fish, the study was conducted in seawater, and second, the amount of C22:1 used in diet was high, and the same fatty acid was as same as in fish fillets. TTS fillets contained higher MUFA and C18:1-9c was lower in the DTS, similar to the results reported elsewhere (do Nascimento *et al.* 2017). Even Riberio *et al*. (2012) revealed that MUFA and C18:1-9c moved from the muscles to the eggs during this phase; furthermore, Henderson *et al*. (1984) reported that fish need C18:1-9c to spawn. Unfortunately, although the fatty acid composition of the gonads was not performed in this study, it is thought that the difference in the amount of MUFA and C18:1-9c in the study is due to the expenditure on gonad development in DTS. Sissener (2018) reported that C18:1n-9, C18:2n-6 and C18:3n-3 fatty acids in fish fillet would increase with vegetable oils added to fish diets, thus, this increase in C18:3n-3, an omega-3 fatty acid, has been reported to decrease EPA and DHA levels (Reksten *et al.* 2022). Along with these literatures, the reason for the high C18:1n-9, C18:2n-6 and C18:3n-3 fatty acids in both groups in the current study can be explained by the effect of the vegetable oils added to the fish diets on the fillet fatty acid composition. The EPA value of TTS fillets was higher than the DTS fillets. According to Cleveland et

al. (2017), ploidy in fish altered fatty acids, and the EPA value in triploid fish was higher than the diploid fish. The n-3 PUFAs (C18:3n-6, C20:3n-3 and C20:5n-3) were higher in DTS, particularly DHA, and these findings were similar to those of Ribero *et al*. (2012). According to clinical studies, EPA and DHA fatty acids have a crucial role in the prevention of cardiovascular disorders, particularly in human health (Zimmer *et al*. 2000). This study demonstrated that the EPA and DHA levels in large rainbow trout are safe for human consumption. Maintaining high amounts of n-3 and n-6 PUFAs in farmed fish, as well as assuring high nutritional value requirements, are major concerns for producers. Therefore, suitable raw materials must be chosen to raise the n-3 PUFA contents of diets while maintaining the n-6 PUFA levels. In the current study, regardless of ploidy, the fact that large rainbow trout has low omega-6 fatty acids compared to many other foods was reflected in the omega-3/omega-6 ratio of both groups. The omega-3/omega-6 value in the study is similar to the data obtained by Reksten *et al.* (2022) with *S. salar,* it proved how nutritious the fillet quality of large rainbow trout is.

The atherogenicity (AI) and thrombogenicity index (TI) are indices used in the assessment of cardiovascular diseases that indicate the link between saturated and unsaturated fatty acids (Ghaeni *et al.* 2013). Łuczynska *et al.* (2017) reported in their study that AI and TI values should not be more than 1.00 for human health. The hypocholesterolemic/hypercholesterolemic index expresses the fatty acid ratio based on (H/H) cholesterol metabolism; foods with high H/H index values (>3) are thought to be more advantageous to human health (Fernandes *et al.* 2014). In the literature studies, no study was found comparing the AI, TI and H/H values of triploid and diploid fish. But, in a study conducted in large rainbow trout in the Black Sea, AI, TI and H/H values were determined as 0.24, 0.24 and 3.87 respectively (Kaya Öztürk *et al.* 2019). The AI, TI and H/H values of large rainbow trout in this study are similar to the values given in the literature (Devadowsaon *et al*. 2016; Kaya Öztürk *et al.* 2019) and are at appropriate values for human health.

3.4 Colour parameters

Fillet colour in salmonids is an important quality parameter that gives these fish a distinctive image and depends on the amount of carotene in fish diets, the source and amount of fat (Regost *et al.* 2004), pigment types (Lerfall *et al.* 2016a, 2016b). According to Regost *et al.* (2001), the C* value in fillets rose as the fat content of the diets increased. Enien and Skrede (1998) showed that raising the fat level in fillets enhanced the a* and b* values; Nickell and Bromage (1998) reported that increasing the fat content in diets from 8% to 27% raised the L* value. In the study, the average L* value was higher in TTS fillets, average a*, b*, C*, and Hue values were higher in DTS fillets. In the literature that reported high L*, a* and b* levels in different ploidy types (Poontawee *et al.* 2007; Taylor *et al.* 2013; Lerfall *et al.* 2017). The CF ratio of the diets used in the study increased from 19.6% to 23.96% in the final and the diet manufacturers declared that they added astaxanthin at the rate of 50 mg kg^{-1} to both the initial and final diets. However, in the final, L* values of both ploidy types decreased and a*, b* and C* values increased. While these results were inconsistent with the study of Nickell and Bromage (1998), they were similar to the results of Regost *et al.* (2001) and Enien and Skrede (1998). A positive relationship between the high-fat content of fish and fillet colour (Nickell and Bromage 1998, Enien *et al*. 1999; Marty-Mahe *et al.* 2004; Lefevre *et al.* 2015) and the relationship between the fat content of fillets and L* is usually due to fish diets (Regost *et al.* 2001; Marty-Mahe *et al.* 2004). The relationship between the a* and b* values of fillets and their fat content is still debated. In different studies, the increased fat level and a* and b* values in fillets of brown trout and Atlantic salmon fed with high-energy and fat-containing diets are parallel to each other (Enien and Skrede 1998; Marty-Mahe *et al.* 2004), however, it did not affect Hue values (Enien *et al.* 1999). According to Lefevre *et al.* (2015), the influence of ploidy on the colour of fish fillets is still uncertain, with fish size having a bigger effect than ploidy. While the L* values of the serving weight (250 – 350 g) triploid rainbow trout were higher (Werner *et al.* 2008), there was no such difference in rainbow trout of 900g and above (Choubert *et al.* 1997). L* values were lower in triploid rainbow trout and Atlantic salmon, over 2 kg reported by Poontawee *et al.* (2007) and Bjørnevik *et al.* (2004). These studies were similar to the present study. In the study, L*, a*, b*, C* and Hue values were different for both groups according to the measurement regions. Although it is not the subject of the study, it is known that the fat content of fish fillets differs regionally (Zhu *et al.* 2014). Therefore, in relation to the above literatures, although they are fed with diets containing the same amount of astaxanthin, the regional differences in L*, a*, b*, C* and Hue values in DTS and TTS are thought to be due to the fillet fat content.

As a consequence, when the growth performance and fillet quality parameters of TTS and DTS were evaluated over a 150-day period, TTS showed greater growth performance and a lower feed conversion rate than DTS. The DTS and TTS were cultivated under the same condition (same environmental parameters, diets, and age) and showed a ploidy influence, particularly on biochemical and fatty acid composition. Fish size and diet had an effect on the amino acid compositions of both ploidy species. There was no ploidy effect on the colour of fish fillet. With this paper, without the ploidy difference between DTS and TTS produced in the Black Sea, it is of good quality, nutritious, and healthful for human consumption,

proving the existence of "large rainbow trout" that can compete with Atlantic salmon in the national or world-wide market.

ACKNOWLEDGEMENTS
Author thanks Sagun Aquaculture Company in Sinop for providing the experimental fish and feed samples. This work was financially supported by Sinop University Scientific Research Coordination Unit (Grant ID: SÜF-1901-21-004).

ETHICAL APPROVAL
The fish were sampled by the operating personnel while they were harvested, therefore this manuscript does not need an ethical approval.

CONFLICT OF INTEREST
The author declares no conflict of interest.

DATA AVAILABILITY STATEMENT
The data that support the findings of this study are available on request from the corresponding author.

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