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36 **Keywords:** total alkaline proteases; trypsin; chymotrypsin; feed formulation; intestine; fish
37 digestive physiology

38

39 **1. Introduction**

40

41 Digestion is a multi-level complex process that consists of the physico-chemical
42 degradation and absorption of a wide number of organic and inorganic substances ingested by
43 the organism. The key role in the degradation of food items is related to digestive enzymes,
44 which are characterized by their origin (i.e., pancreas, stomach, intestine, food items, symbiotic
45 microbiota among others), substrate specificity (proteins, carbohydrates, lipids, etc), and gut
46 localization (lumen, brush border, intracellular), dependence on pH, cofactors required for
47 activation, etc. As a result, the spectrum of digestive enzymes that could be found in fish gut is
48 very diverse and enables hydrolysis of a wide variety of substrates from food items, facilitating
49 nutrient absorption by the organism. The digestive system of vertebrates is adapted through
50 evolution to maximize nutrient uptake and energy from each available food substrate. Proteins,
51 one of the main substrates obtained by fish from the diet, vary in terms of their molecular weight,
52 size, amino acid composition, solubility, surface hydrophobicity and chemical modifications
53 (i.e., phosphorylation, glycosylation, etc.) among others. For the majority of fish species, trypsin
54 and chymotrypsin are known as the two main alkaline digestive proteases responsible for the
55 initial stage of protein hydrolysis in the intestine of both gastric and agastric fish species. Both
56 proteases are synthesized in the exocrine pancreas and accumulated in non-active zymogen
57 forms (trypsinogen and chymotrypsinogen) and, then they are discharged in the intestinal lumen
58 where enterokinase cleaves a short peptide from trypsinogen converting it to an active form
59 (trypsin). Furthermore, the trypsin autoactivates/activates other molecules of trypsinogen (Kay
60 and Kassell, 1971), chymotrypsinogens (Appel, 1986), procarboxypeptidases A and B (Keller et
61 al., 1958), and several other hydrolases (Williams, 2004). Trypsin and chymotrypsin are
62 characterized by several substrate specificities, cleaving different peptide bonds in proteins and
63 polypeptides; for instance, trypsin predominantly cleaves proteins at the carboxyl side of amino
64 acids like lysine and arginine, except when either is bound to a C-terminal proline, whereas
65 chymotrypsin preferentially cleaves peptide amide bonds at the carboxyl side of aromatic amino
66 acids like tyrosine, tryptophan, and phenylalanine (Heu et al., 1995). Moreover, for different
67 proteases, the most relevant biochemical characteristics affecting protein hydrolysis are the
68 number of cleavage sites and secondary enzyme specificity (i.e., enzyme preferences resulting
69 from neighboring amino acids) that may change from different proteins (Deng et al., 2019).
70 Both of these proteases are found in several isoforms/isoenzymes in fish gut (Heu et al., 1995;
71 Cohen et al., 1981; Chong et al., 2002; Moutou et al., 2004; Rungruangsak-Torrissen et al.,

72 2006). These isoforms/isoenzymes are characterized by different kinetic parameters, optimal pH
73 values and temperature, and other variables and show different stabilities under several
74 physicochemical parameters of the chyme (i.e., pH, temperature, ion concentrations, osmolarity,
75 bile acid composition and concentration, etc.). The synthesis and production of different
76 isoforms/isoenzymes are considered as one of adaptative mechanisms of fish to enhance their
77 digestive capacities under various biotic and abiotic factors such as water temperature, pH, food
78 supply, water salinity, among others (Zhou and Budge, 2011).

79 Both trypsin and chymotrypsin are normally detected in the digestive system of fish at
80 their early life stages (Vega-Orellana et al., 2006; Jimenez-Martinez et al., 2012; Solovyev et al.,
81 2016; Mente et al., 2017). For several fish species, the activity of both proteolytic enzymes may
82 be detected at hatching before the exocrine pancreas has fully completed its morphogenesis
83 (Jimenez-Martinez et al., 2012; Alvarez-González et al., 2008; Mello et al., 2021). Furthermore,
84 both proteases may demonstrate several peaks of activity during fish ontogeny, which are
85 generally correlated to the morphogenesis of the digestive organs (i.e., pancreas, stomach) and/or
86 shifts in the diet. As the ontogeny of digestive enzymes is genetically preprogrammed
87 (Zambonino Infante and Cahu, 2001), their observed peaks of activity at different stages of
88 development are considered to be related to various substrate demands (i.e., proteins,
89 carbohydrates, lipids) based on the capacities of the fish digestive system. In the same time, the
90 above-mentioned changes in proteolytic activity may also be modulated by the inclusion of
91 dietary proteins (Pérez-Jiménez et al., 2009). The effect of dietary proteins on the pancreatic
92 proteolytic enzymes depends on the proteins concentrations and sources (Rodiles et al., 2012;
93 Mente et al., 2017; Abbasi et al., 2020; Fronte et al., 2021), the stage of fish ontogeny (Canada et
94 al., 2017), feeding protocol (Solovyev and Gisbert, 2021), among others.. However, the
95 relationship between dietary crude protein and alkaline protease activities is not always linear.
96 For instance, the level of activity of both trypsin and chymotrypsin in tilapia juveniles
97 (*Oreochromis* sp.) increased when the concentration of crude protein changed from 24 to 35%,
98 whereas the activity of the above-mentioned enzymes decreased when diets contained 42% crude
99 protein (Santos et al., 2020). Similar results were obtained for *Culter mongolicus* fingerlings
100 when the activity of pancreatic proteases was positively modulated by dietary protein inclusion
101 until certain level (Qian et al., 2022).

102 Despite there being no doubt about the critical role of these proteases for protein
103 hydrolysis in fish intestine, the relative input of each enzyme in protein hydrolysis is still unclear
104 and disputable (Moutou et al., 2004; Alvarez-González et al., 2008; Lazo et al., 2007; López-
105 Ramírez et al., 2011). Several different approaches have been applied in order to estimate the
106 relative importance of trypsin and chymotrypsin in protein degradation. In some studies, the

107 direct comparison of activity values between both proteases has been conducted (Moutou et al.,
108 2004; Olatunde and Ogunbiyi, 1977; Jónás et al., 1983; Uscanga et al., 2010). It is well known
109 that under optimal conditions (i.e., pH, temperature, concentration of enzyme activators,
110 substrate concentration, among others), the activity of any digestive enzyme depends on its
111 concentration and turnover number (Bisswanger, 2014). Unfortunately, there is no information
112 about turnover numbers for trypsin and chymotrypsin from the majority of fish species.
113 Moreover, Lazo et al. (2007) mentioned that the direct estimation of the relative contribution of
114 trypsin and chymotrypsin to protein digestion is not possible since different specific substrates
115 are applied in their biochemical spectrophotometric quantification. At the same time, when the
116 activity of any digestive enzyme, for example trypsin or chymotrypsin, is estimated for different
117 fish species, the reaction buffer used for assessing enzyme activity is generally formulated with a
118 “standard” buffer with a fixed level of pH, concentration of ions such as Ca^{2+} (CaCl_2) and Na^+
119 (NaCl), total osmolarity, and some other parameters that may not have been optimized for the
120 target species and the enzyme of interest. The development and use of “universal” protocols for
121 the quantification of trypsin, chymotrypsin or any other digestive enzymes has the limitation that
122 it does not take into account that each enzyme has species-specific functional properties. For
123 instance, trypsins obtained from different fish species may have different optimal pH values,
124 they may be inhibited and/or activated by different concentrations of Na^+ and Ca^{2+} ions, and/or
125 osmolarity levels (Dos Santos et al., 2016; Silva et al., 2011; Liu et al., 2012; Shi et al., 2007;
126 Khangembam et al., 2012). All these factors will affect the activity of the enzyme in different
127 ways by means of changing their activities in unpredictable manner, which make straight-
128 forward comparisons unclear. As a result, activity levels will be obtained with biases that,
129 consequently, may potentially lead to wrong conclusions. In this sense, Yúfera et al. (2018)
130 directly compared the specific activity of trypsin among 15 fish species obtained by different
131 studies and showed that the specific trypsin activity ranged over more than 50-fold among fish
132 species and therefore concluded that direct comparisons of absolute values among species should
133 be very restricted. In order to overcome such limitations, it should be recommended that the
134 functional properties of any targeted enzyme be determined in advance. Unfortunately, such time
135 and resource consuming preliminary studies are ignored in many cases and the activity of
136 enzymes is measured using “standard” protocols; whereas the most accurate way for performing
137 these analyses would be to create, based on a known scheme, species-specific protocols for key
138 digestive enzymes based on their biochemical features. Although conducting this approach may
139 be impossible considering the large diversity in fish species, it seems reasonable that it should be
140 conducted at least for economically valuable species due to the impact that nutrition has on fish
141 growth and performance under farming conditions, or developing alternative approaches to by-

142 pass such preliminary time-consuming studies.

143 Among the different approaches that may be used for properly estimating the relative
144 importance of different enzymes on the digestive processes, the use of specific inhibitors is a
145 conventional and useful procedure. For instance, applying the specific inhibitors for each
146 protease in the hydrolysis of model protein may help to proper understanding their relative input
147 on protein digestion. In this context, several specific synthetic inhibitors, e.g. TLCK (N α -Tosyl-
148 L-lysine chloromethyl ketone hydrochloride) and TPCK (N-p-Tosyl-L-phenylalanine
149 chloromethyl ketone) / ZPCK (N-Carbobenzoxy-L-phenylalanyl-chloromethyl ketone) / CHYM
150 (chymostatin), are normally used in order to inhibit the activity of trypsin and chymotrypsin,
151 respectively (Lazo et al., 2007; Martinez and Serra, 1989; Alarcón et al., 1998; Essed et al.,
152 2002; García-Carreño et al., 2002; Natalia et al., 2004; Sáenz de Rodrigáñez et al., 2005).

153 Although these inhibitors will decrease the activity of these targeted enzymes, the level of
154 such inhibition could be species-specific (Eshel et al., 1993), and its efficiency will depend on
155 several factors such as the enzyme:inhibitor ratio, mutations or deletions in specific binding site
156 of the enzyme, and/or the fish species considered (Martinez and Serra, 1989, García-Carreño et
157 al., 2002, Natalia et al., 2004, Zhou et al., 1989; Turk et al., 2002). As a result, in many cases the
158 sum of inhibition activities of trypsin and chymotrypsin together is more than 100%. For
159 example, the sum of the percentage of inhibition for trypsin and chymotrypsin by TLCK and
160 TPCK was 129.2% (Natalia et al., 2004), which complicates the proper interpretation of the
161 results with regard to the relative importance of each alkaline protease in the digestive process.

162 Another possible approach to determine the relative importance of these endoproteases is
163 to compare the level of gene expression for each one. It is generally accepted that the higher the
164 gene expression level, the higher is the expected enzyme activity. However, the abundance of
165 gene transcripts is not always correlated to the amount of protein transcribed, since mRNA levels
166 may be post-transcriptionally and/or translationally regulated, or there may even exist protein
167 degradation/turnover. In this sense, the cellular concentrations of proteins correlate with the
168 abundances of their corresponding mRNAs, but not strongly. Some authors have shown a
169 squared Pearson correlation coefficient of ca. 0.40 between protein and mRNA levels, which
170 implies that ~40% of the variation in protein concentration, can be explained by knowing
171 mRNA abundances (Vogel and Marcotte, 2012).

172 Despite the fact that there are various methods for determining the activity of trypsin and
173 chymotrypsin for many economically valuable fish species, and the specific biochemical features
174 of these enzymes are known, the appropriate approach showing the relative inputs of trypsin and
175 chymotrypsin in protein digestion is still needed. This information would help to better
176 understand the digestive capacity of a given species and meet their specific nutritional protein

177 demands that vary during morphological and physiological changes in the digestive system of
178 fish during their ontogeny. This may be of special importance during early life stages of
179 development when acid digestion may not exist or only partially achieved. Thus, understanding
180 the relative inputs of trypsin and chymotrypsin in protein digestion in fish larvae coupled with
181 information associated with fish digestive physiology may be of interest for proper formulation
182 of compound diets in a stage- and species-specific way, since each endoprotease has different
183 cleavage sites.

184 In the present study, for proper understanding of the above-mentioned methodological
185 shortcomings, we have estimated the relative importance of trypsin and chymotrypsin in protein
186 digestion for different fish species based on the correlation analysis among activity levels of
187 trypsin, chymotrypsin, and total alkaline proteases from available literature. In order to achieve
188 this aim, we have put forward two hypotheses: 1) the development of activity of total alkaline
189 proteases during fish ontogeny will be substantially dependent on the activity of trypsin and
190 chymotrypsin as these are the major alkaline proteases when compared to metalloproteases and
191 cysteine proteases that are also detected in fish intestine by inhibitor analyses; and 2) as the role
192 of trypsin or chymotrypsin in protein hydrolysis increases, then there will be a higher level of
193 similarities between trypsin/chymotrypsin and total alkaline proteases activities during fish
194 ontogeny as expressed by means of correlation coefficients.

195

196 **2. Materials and methods**

197

198 Data used in the present study has been retrieved from a bibliographic search using the
199 Dimensions application (<https://app.dimensions.ai/discover/publication> tool). The following key
200 words in different combinations were used for this bibliographic search: “trypsin”,
201 “chymotrypsin”, “alkaline proteases”, “fish”, “larva”, “ontogeny”, and “development”. Retrieved
202 articles were carefully inspected to identify whether they contained the description of the
203 development of ontogenetic activities for trypsin, chymotrypsin, and alkaline proteases. Among
204 the list of consulted articles (85), authors have chosen a total of 21 studies in order to run
205 correlation analysis that included 19 fish species and 2 fish hybrids (raw data may be find in the
206 Supplementary file 1). The rest of the articles were excluded from the analysis because of the
207 dataset for one of proteases (trypsin or chymotrypsin or total alkaline protease activities) was
208 absent. In order to support the obtained results by the correlation analysis, we have chosen 13
209 articles where the inputs for trypsin and chymotrypsin in protein digestion were available by
210 means of using specific protease inhibitors using casein as a protein substrate. Unfortunately, the
211 low number of available data did not allow us to estimate the effect of casein (azo-casein)
212 concentrations (ranged between 0.5-8.0%) on the percentages of inhibition. Thus, we have only

213 shown the concentration of model protein in Table as a supporting information. In addition, we
214 have also provided information about preferable water salinity, rearing, and feeding conditions
215 as well as feeding habits in order to characterize each studied fish species and assumed that these
216 conditions are optimal for studied fish development.

217 When data were not presented in numerical values within tables, activity values for
218 trypsin, chymotrypsin and total alkaline proteases were extracted from graphs to the closest unit
219 from each selected paper of interest. The correlation analysis among activity for trypsin,
220 chymotrypsin, and total alkaline proteases was conducted by means of the Pearson correlation
221 test and a level of significance of $p < 0.10$. Principal Components Analysis (PCA) was calculated
222 based on Pearson correlation coefficients (r values) between trypsin and total alkaline proteases,
223 chymotrypsin and total alkaline proteases, as well as trypsin and chymotrypsin. All calculations
224 were done using PAST v. 3.16 (Hammer et al., 2001) and Microsoft Office Excel.

225

226 **3. Results**

227 **3.1. Correlation analysis between enzyme activities**

228

229 All Pearson correlation coefficients (r) calculated among values for the activities of
230 trypsin, chymotrypsin, and total alkaline proteases during ontogeny of different fish species are
231 given in Figure 1 and Supplementary file Table A.

232

233 Figure 1. Heat map based on r values calculated with Pearson correlation analysis among the
234 activity of trypsin (Tryp), chymotrypsin (Chymo), and total alkaline proteases (TAP) during
235 ontogenetic development of different fish species. Correlation coefficients that were statistically
236 significant ($p < 0.1$) are marked by white asterisks.

Value	Tryp/TAP	Chymo/TAP	Tryp/Chymo	Species (Family)	References
1.00	-0,17	0,61 *	0,02	<i>Centropomus undecimalis</i> (Centropomidae)	(Jimenez-Martinez et al. 2012)
0.25	0,33	0,64 ***	0,16	<i>C. viridis</i> (Centropomidae)	(Hernández-López et al. 2021)
0.00	0,37	0,80 ***	0,50	<i>Argyrosomus regius</i> (Sciaenidae)	(Solovyev et al. 2016)
-0.25	-0,05	0,97 ****	0,10	<i>Archocentrus nigrofasciatus</i> (Cichlidae)	(Mente et al. 2017)
-1.00	-0,08	0,83 ****	0,23	<i>Petenia splendida</i> (Cichlidae)	(Uscanga-Martínez et al. 2011)
	0,26	0,79 ***	0,55 *	<i>Paralichthys californicus</i> (Paralichthyidae)	(Alvarez-González et al. 2006)
	0,59 ***	0,81 ****	0,56 ***	<i>Ocyurus chrysurus</i> (Lutjanidae)	(Ahumada-Hernández et al. 2014)
	0,74 **	0,91 ****	0,91 ****	<i>Atractosteus tropicus</i> (Lepisosteidae)	(Frias-Quintana et al. 2015)
	0,93 ***	0,96 ***	0,83 **	<i>Catla catla</i> (Cyprinidae)	(Rathore et al. 2005)
	0,71 **	0,85 ***	0,72 **	<i>C. catla</i> (Cyprinidae)	(Khangbam et al. 2012)
	0,86 ****	0,92 ***	0,73 ***	<i>Cichlasoma dimerus</i> (Cichlidae)	(Toledo-Solís et al. 2021)
	0,88 **	0,59 ***	0,53 **	<i>C. trimaculatum</i> (Cichlidae)	(Toledo-Solís et al. 2015)
	0,92 ****	0,96 ****	0,98 ****	<i>Cirrhinus mrigala</i> (Cyprinidae)	(Chakrabarti, Rathore 2010)
	0,90 ***	0,97 ****	0,94 ***	<i>Odontesthes bonariensis</i> (Atherinopsidae)	(Pérez Sirkin et al. 2020)
	0,93 ****	0,85 ****	0,82 ****	<i>Hypophthalmichthys molitrix</i> × <i>H. nobilis</i> (Cyprinidae)	(Chakrabarti et al. 2006b)
	0,92 ****	0,85 ****	0,94 ****	<i>Labeo rohita</i> (Cyprinidae)	(Chakrabarti, Rathore 2006a)
	0,97 ****	0,78 ***	0,64 **	<i>Paralabrax maculatofasciatus</i> (Serranidae)	(Alvarez-González et al. 2008)
	0,94 **	0,88 **	0,95 **	<i>Solea solea</i> (Soleidae)	(Clark et al. 1986)
	0,65 ***	-0,01	0,24	<i>C. urophthalmus</i> (Cichlidae)	(López-Ramírez et al. 2011)
	-0,57	-0,22	0,48	<i>Pseudoplatystoma punctifer</i> (Pimelodidae)	(Castro-Ruiz et al. 2019)
	-0,38	-0,49 **	0,03	<i>P. reticulatum</i> (Pimelodidae)	(Mello et al. 2021)
	0,10	-0,32	0,45 *	<i>P. corruscans</i> × <i>P. reticulatum</i> (Pimelodidae)	(Mello et al. 2021)

237

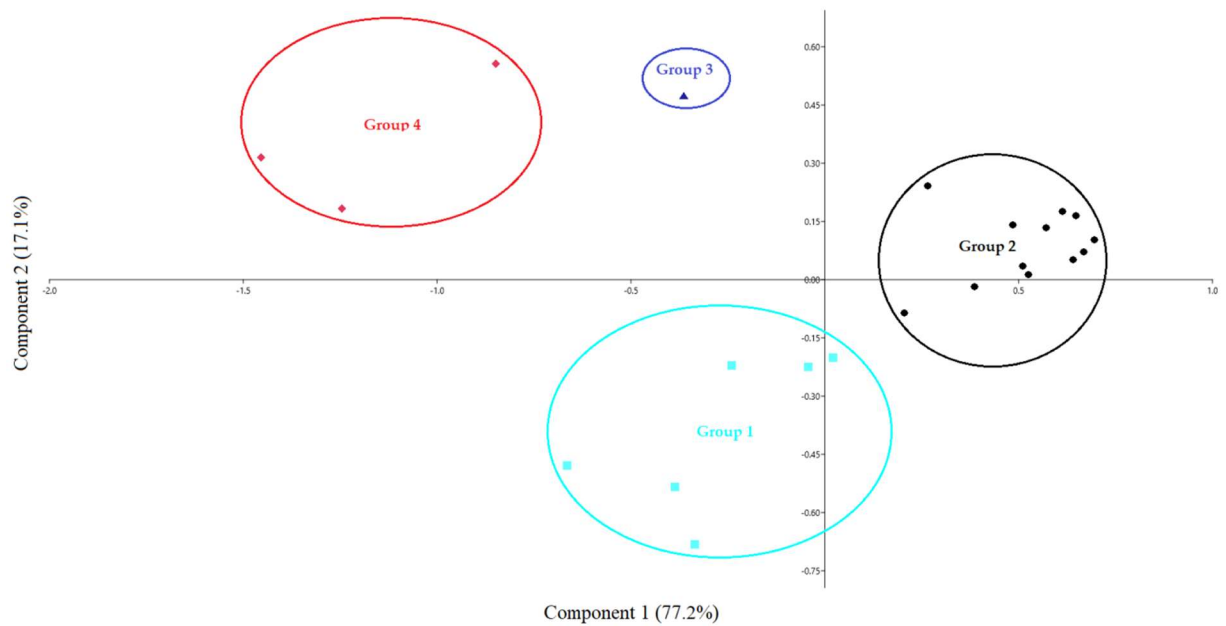
238 Tryp – trypsin, Chymo – chymotrypsin, TAP – total alkaline proteases. The asterisks denote
 239 **** $p < 0.001$, *** $p < 0.01$, ** $p < 0.05$, * $p < 0.10$.

240

241 Based on the similarity and correlation ($-1 < r > 1$) of the correlation coefficients and
 242 Principal Components Analysis (PCA), four groups of fish were identified (Figure 2). These
 243 groups are described as follow: 1) high positive significant correlation ($r = 0.61 - 0.97$)
 244 between the activity of chymotrypsin and total alkaline proteases (6 species – 28.6%); 2) high
 245 positive significant correlation between the activity of trypsin ($r = 0.59 - 0.97$),
 246 chymotrypsin ($r = 0.78 - 0.97$), and total alkaline proteases (10 species and 1 hybrid species –
 247 52.4%); 3) high positive significant correlation ($r = 0.65$) between the activity of trypsin and
 248 total alkaline proteases (1 species – 4.8%); and 4) negative correlation between trypsin ($r = -0.38$
 249 – -0.57), chymotrypsin ($r = -0.22 - -0.49$), and total alkaline proteases (2 species and 1 hybrid
 250 species – 14.3%).

251

252 Figure 2. Principal Components Analysis (PCA) based on correlation coefficients
 253 between trypsin and total alkaline proteases, chymotrypsin and total alkaline proteases, trypsin
 254 and chymotrypsin.



255

256

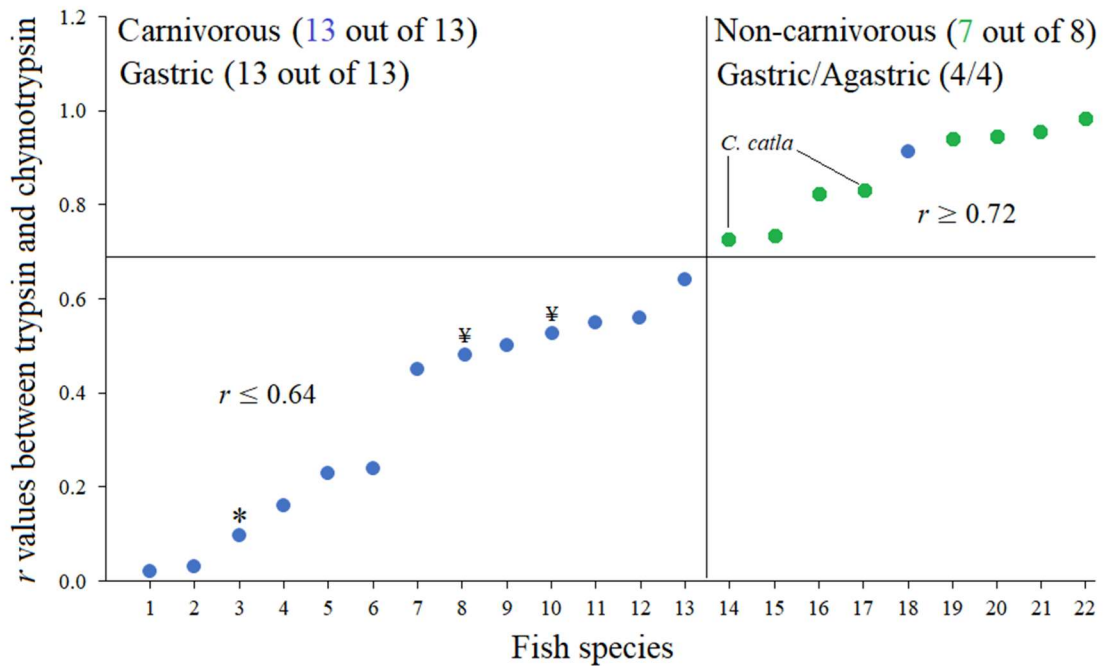
257 It is of special relevance that all six species with high inputs of only chymotrypsin (group
 258 1) and trypsin activities (group 3) regarding comparison to total alkaline proteases belonged to
 259 gastric fish species with predominated carnivorous feeding habits. However, all fish species from
 260 group 2 for which the effect of both enzymes (trypsin and chymotrypsin) on the activity of total
 261 alkaline proteases was significant and similar, belonged to both gastric and agastric species,
 262 which were characterized by different feeding habits (carnivorous, zooplanktivorous,
 263 benthivorous, herbivorous, and omnivorous). The group 4 characterized by negative
 264 correlation among studied proteases only included Amazonian carnivorous-omnivorous
 265 catfishes (Supplementary file 2 - Table A).

266 The correlation between trypsin and chymotrypsin activities was positive for all
 267 studied fishes. In 38.1% of the cases (7 species and 1 hybrid), the correlation was irrelevant
 268 and low or moderate ($r = 0.02-0.48$) whereas in 61.9% of the cases (12 species and 1 hybrid),
 269 the correlation between the activity of both proteases was high ($r = 0.50-0.98$). It has to be
 270 noted that the r values between trypsin and chymotrypsin were lower for gastric carnivorous
 271 fishes ($r = 0.02-0.64$, mean $r = 0.35$) with one exception, the tropical gar (*A. tropicus*) ($r = 0.91$),
 272 while Pearson correlation values for non-carnivorous fishes (6 species and 1 hybrids) were
 273 higher ($r = 0.73-0.98$, mean $r = 0.88$) (Figure 3).

274

275

276 Figure 3. Pearson correlation (r values) between trypsin and chymotrypsin for studied fish
 277 species.



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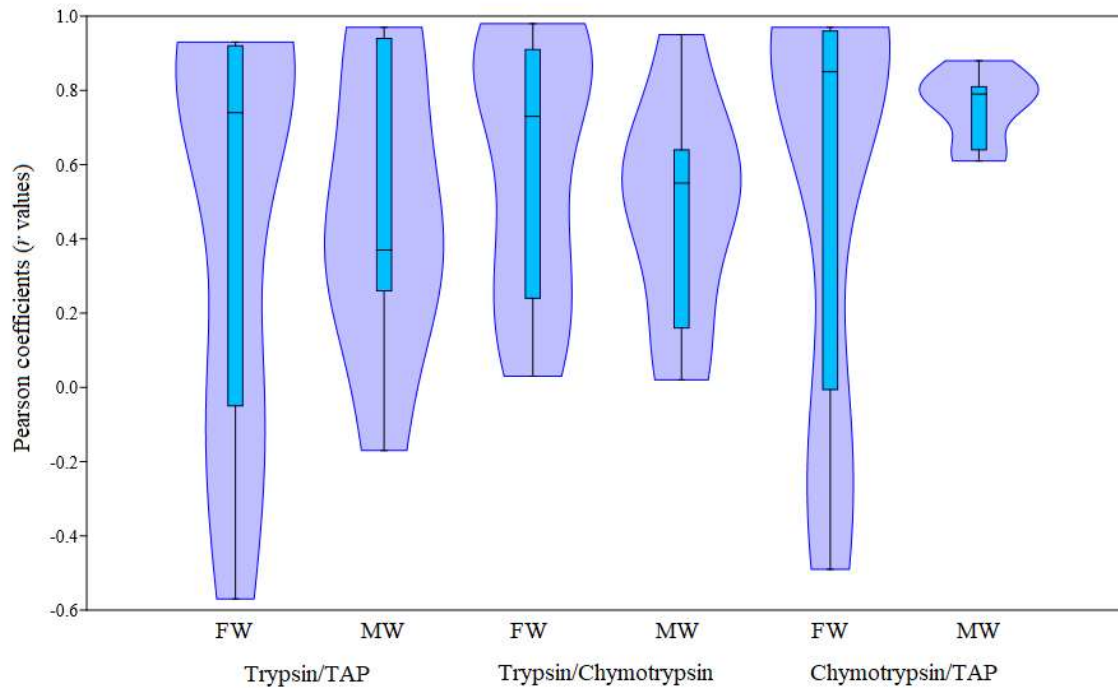
279 1. *Centropomus undecimalis*, 2. *Pseudoplatystoma reticulatum*, 3. *Archocentrus nigrofasciatus*,
 280 4. *C. viridis*, 5. *Petenia splendida*, 6. *Cichlasoma urophthalmus*, 7. *P. corruscans* × *P.*
 281 *reticulatum*, 8. *P. punctifer*, 9. *Argyrosomus regius*, 10. *C. trimaculatum*, 11. *Paralichthys*
 282 *californicus*, 12. *Ocyurus chrysurus*, 13. *Paralabrax maculatofasciatus*, 14. *Catla catla*
 283 (Khangembam et al., 2017), 15. *C. dimerus*, 16. *Hypophthalmichthys molitrix* × *H. nobilis*, 17. *C.*
 284 *catla* (Rathore et al., 2005), 18. *Atractosteus tropicus*, 19. *Odontesthes bonariensis*, 20. *Labeo*
 285 *rohita*, 21. *Solea solea*, 22. *Cirrhinus mrigala*; Blue circle – carnivorous species, green circle –
 286 non-carnivorous species. * – carnivorous-benthivorous, ¥ – carnivorous-omnivorous.

287

288 The correlation between chymotrypsin and total alkaline proteases activities was
 289 positive for all studied marine fishes with r values that ranged from 0.61 to 0.88. In the same
 290 time, for freshwater fishes the r values between chymotrypsin and total alkaline proteases
 291 activities were widely ranged ($r = -0.49 - 0.97$). Correlations between trypsin and total
 292 alkaline proteases as well as trypsin and chymotrypsin activities were similar between studied
 293 marine and freshwater fishes (Figure 4).

294

295 Figure 4. Pearson correlation (r values) between chymotrypsin/total alkaline proteases
 296 (TAP), trypsin/chymotrypsin, and trypsin/total alkaline proteases for studied marine and
 297 freshwater fishes. Abbreviations: MW: marine fish species, FW, freshwater fish species.



298
299
300
301

3.2. Specific inhibitor analysis

302 The relative input of trypsin and chymotrypsin in the hydrolysis of proteins as estimated
303 by specific inhibitors like TLCK and TPCK/ZPCK/CHYM, respectively is presented in Table X.
304 Based on similarity of percentages of inhibition activity, three fish groups were identified as
305 follows: 1) high percentage of trypsin inhibition (*B. orbignyanus* and *C. viridis* – 13.3%); 2) high
306 percentage of chymotrypsin inhibition (*D. dentex*, *T. thynnus*, and *M. chrysops* × *saxatilis* –
307 20%); 3) similar percentage of trypsin and chymotrypsin inhibition (all other fishes not included
in groups 1 and 2 – 66.7%).

308 **Table X.** The effect of the specific synthetic inhibitors on trypsin and chymotrypsin activities in
309 the gut of different fish species. In all cases, TLCK and TPCK were used as the specific
310 inhibitors for trypsin and chymotrypsin activity, respectively, when additionally, other inhibitors
311 (ZPCK and CHYM) for chymotrypsin were used, they were indicated in parenthesis. The data
312 are expressed as mean ± SE.

Species (Family)	Percent of inhibited activity		Model protein	References
	Trypsin	Chymotrypsin		
Common dentex <i>Dentex dentex</i> (Linnaeus, 1758) (Sparidae)	6.0 ± 4.7%	26.2 ± 8.9% (TPCK) 40.5 ± 7.5% (CHYM) 36.1 ± 7.5% (ZPCK)	0.5% casein	(Alarcón et al., 1998)
Gilthead seabream <i>Sparus aurata</i> (Linnaeus, 1758) (Sparidae)	16.8 ± 2.7%	19.5 ± 7.3% (TPCK) 45.4 ± 6.7% (CHYM) 26.2 ± 5.4% (ZPCK)	0.5% casein	(Alarcón et al., 1998)
Atlantic bluefin tuna <i>Thunnus thynnus</i> (Linnaeus, 1758) (Scombridae)	7.0%	29.0% (TPCK) 32.0% (ZPCK)	0.5% casein	(Essed et al., 2002)
Red drum <i>Sciaenops ocellatus</i> (Linnaeus, 1766) (Sciaenidae)	26%	30% (TPCK)	2.0% azo-casein	(Lazo et al., 2007)
<i>Hypophthalmichthys molitrix</i> × <i>nobilis</i> (Cyprinidae)	45.1-55.5%	35.8-48.2% (TPCK)	1.0% azo-casein	(Chakrabarti et al., 2006b)
<i>Labeo rohita</i> (Cyprinidae)	41.1-52.4%	28.0-44.5% (TPCK)	1.0% azo-casein	(Chakrabarti et al., 2006a)
European anchovy	96.0%	98.0%	8.0% casein	(Martinez and Serra, 1989)

<i>Engraulis encrasicolus</i> (Linnaeus, 1758) (Engraulidae)				
<i>Atractosteus tropicus</i> (Lepisosteidae) Blue discus	7.2%	9.4%	1.0% casein	(Guerrero-Zárate et al., 2014)
<i>Symphysodon aequifasciatus</i> (Pellegrin, 1904) (Cichlidae)	46.4 ± 5.3%	39.7 ± 6.8%	1.0% casein	(Chong et al., 2002)
Senegalese sole <i>Solea senegalensis</i> (Kaup, 1858) (Soleidae)	35.6-41.5%	4.3-6.0% (TPCK) 28.7-29.4% (ZPCK)	0.5% casein	(Sáenz de Rodrigáñez et al., 2005)
Asian bony tongue <i>Scleropages formosus</i> (Müller & Schlegel, 1840) (Osteoglossidae)	71.5 ± 3.5%	57.7 ± 2.8%	1.0% azo-casein	(Natalia et al., 2004)
<i>Brycon orbignyanus</i> (Valenciennes, 1850) (Bryconidae)	52.0 ± 2.0%	3.0 ± 0.2%	1.5% azo-casein	(García-Carreño et al., 2002)
<i>Centropomus viridis</i> (Centropomidae)	69.8%	9.0%	1.0% casein	(Hernández-López et al., 2021)
European seabass <i>Dicentrarchus labrax</i> (Linnaeus, 1758) (Moronidae)	≈ 38%	≈ 48%	0.95% casein	(Eshel et al., 1993)
White bass x striped bass <i>Morone chrysops</i> (Rafinesque, 1820) x <i>M. saxatilis</i> (Walbaum, 1792) (Moronidae)	≈ 20%	≈ 37%	0.95% casein	(Eshel et al., 1993)

313 4. Discussion

314 The relative importance of trypsin and chymotrypsin in alkaline protein digestion may
315 change during fish ontogeny (López-Ramírez et al., 2011), whereas it also depends on rearing
316 and feeding conditions (Rungruangsak-Torrissen et al., 2006). Jónás et al. (1983) have shown
317 that the activity of trypsin was about four times higher in comparison to the activity of
318 chymotrypsin in the intestine of sheatfish (*Silurus glanis* Linnaeus, 1758), whereas in Nile tilapia
319 (*Oreochromis niloticus* Linnaeus, 1758) the activity of chymotrypsin was two times higher than
320 the activity of trypsin. As it was mentioned above, the estimation of inputs of both trypsin and
321 chymotrypsin in protein digestion using the direct comparison of their activity levels between
322 each other is unreliable. This approach requires information about turnover numbers based on
323 analysis of the purified enzymes as well as the specific optimal activity conditions (pH, ion
324 concentrations, osmolarity, etc.). Unfortunately, this information is only available in a very
325 reduced number of species (Heu et al., 1995; Jónás et al., 1983; Hinsui et al., 2006). Moreover,
326 the quality of enzyme purification depends on the applied protocol, and consequently, it also
327 affects the turnover number (Hinsui et al., 2006; Barkia et al., 2010; Stefansson et al., 2010). But
328 even if all these required biochemical characteristics were determined, the different enzyme
329 specific substrates applied would not allow for a direct comparison between both endoproteases
330 (Lazo et al., 2007).

331 The use of enzyme inhibitors is another approach for the characterization of contribution
332 of trypsin and chymotrypsin activity to protein digestion (Heu et al., 1995; Alarcón et al., 1998).
333 As different inhibitors have different inhibitory mechanisms and there may exist several
334 inhibition constants for the same enzyme (Ferguson et al., 2022), the degree of enzyme inhibition
335 activity may also change in a significant way (Chong et al., 2002; Guerrero-Zárate et al., 2014).
336 This fact has significantly restricted the determination of the input of different enzymes in the

337 general digestive process. However, based on the analysis of the inhibitory effects of specific
338 inhibitors in trypsin and chymotrypsin in fish gut from the literature, relatively high inputs were
339 noted for both proteases as described in Table. On one hand, the significant role of trypsin in
340 protein hydrolysis in fish intestine is not surprising, since trypsin may digest a number of
341 different proteins in fish diets and also activates other pancreatic proteases. On other hand, the
342 inhibition efficiency depends largely on different digestive variables, as well as on the inhibitor
343 considered. In the present study, we have not used data based on the use of soybean trypsin
344 inhibitor (SBTI), because it has been shown that this inhibitor affects the activity of both trypsin
345 and chymotrypsin (Martinez and Serra, 1989). Except for two fish species belonging to the group
346 1 (*B. orbigyanus* and *C. viridis*; Table? Figure 1), we did not find that the input of trypsin
347 activity was significant when considered alone. At the same time, the input of chymotrypsin
348 activity alone in casein digestion was found to be significant only for *D. dentex*, *T. thynnus*, and
349 *M. chrysops* × *M. saxatilis* (group 2; Table). For the majority of considered fish species, both
350 proteases showed a significant contribution in protein digestion (group 3; Table). This result is in
351 agreement with our correlation analysis that also showed that the majority of fish species had
352 significant inputs for both trypsin and chymotrypsin activities in protein digestion (Figure 1 and
353 2; Supplementary file raw data). One of the main limitations of the application of the inhibitory
354 analysis as a tool for determination of inputs of protease activities in protein digestion is the
355 different specificity of inhibitors to target enzymes. For instance, the percentage of inhibition in
356 chymotrypsin activity was significantly different when TPCK (4.3-6.0%) or ZPCK (28.7-29.4%)
357 inhibitors were used (Sáenz de Rodrigáñez et al., 2005). Thus, depending on the inhibitor
358 considered, the reader may get misleading conclusions depending on the study consulted. In this
359 sense, if only TPCK was used as a specific chymotrypsin inhibitor, the reader may conclude that
360 the input of chymotrypsin in casein digestion is no more than 6.0% for *S. senegalensis*, whereas
361 when another specific inhibitor (ZPCK) was used for such analyses, chymotrypsin contribution
362 ranged from 28.7 to 29.4%, values that were similar to those observed for trypsin (35.6–41.5%)
363 (Sáenz de Rodrigáñez et al., 2005).

364 According to our correlation analysis, we demonstrated that the inputs of both trypsin and
365 chymotrypsin in the activity of total alkaline proteases had a similar importance in terms of
366 protein digestion as *r* values indicated for half of the studied fish species (10 out 19 species and 2
367 hybrids, group 2 in Figure 1 and 2 and Supplementary file Table A). In addition, we have also
368 found a good agreement in data obtained from different studies (Rathore et al., 2005 and
369 Khangembam et al., 2017), but for the same fish species (*C. catla*) that confirmed the
370 reproducibility of our obtained results. High inputs of both trypsin and chymotrypsin in the
371 activity of total alkaline proteases is also consistent with data from inhibitor analyses that

372 showed the similar and high percentages of inhibition for both proteases for the following
373 species: *E. encrasicolus* (Martinez and Serra, 1989), *S. aequifasciata* (Chong et al., 2002), *H.*
374 *molitrix* × *H. nobilis* (Chakrabarti et al., 2006b), and *S. ocellatus* (Lazo et al., 2007).
375 Unexpectedly, only for *C. urophthalmus* was there shown a high positive significant
376 relationship between activity of total alkaline proteases and trypsin ($r = 0.65$; $p < 0.01$) and
377 slightly negative, but not significant, relationship between the activity of chymotrypsin and
378 total alkaline proteases ($r = -0.006$ at $p = 0.98$) (group 3; Figure 1 and 2 and Supplementary file
379 Table A). Moreover, six fish species (28.6%) showed a significant contribution only for
380 chymotrypsin activity in protein digestion (group 1; Figure 1 and 2 and Supplementary file Table
381 A). This observation was also partially supported by data from enzyme inhibitor analyses, since
382 for several species like *T. thynnus* (Essed et al., 2002), *D. dentex*, and *S. aurata* (Alarcón et al.,
383 1998) the percentage of chymotrypsin activity inhibited was higher when compared to that of
384 trypsin. We may assume that the significant prevalence of trypsin or chymotrypsin alone in
385 protein hydrolysis in fish intestine is less common among fishes when compared to fish species
386 for which both proteases have relatively high activity levels. Unfortunately, we could not extend
387 these analyses, since there were only three fish species (*C. viridis*, *A. tropicus*, and *L. rohita*),
388 one hybrid (*H. molitrix* × *H. nobilis*), and one genus (*Solea*) for which the data of correlation and
389 inhibitory analyses were available, which highlights the importance of conducting species-
390 specific studies on the proper characterization of digestive enzymes. In case of *C. viridis*,
391 chymotrypsin showed a significant contribution in the activity of total alkaline proteases between
392 1 and 40 DAH ($r = 0.64$, $p = 0.003$; Supplementary file table A), whereas on the contrary, the
393 results based on the inhibitory analysis for the same species demonstrated a higher input of
394 trypsin than chymotrypsin activity at 55 DAH (69.8% by 9.0%, respectively; Table) (Hernández-
395 López et al., 2021). However, it is important to mention that data from this study may not be
396 directly comparable, since the correlation analysis was computed with the integrated results
397 based on ontogeny data (1-40 DAH), whereas data from the inhibitor analysis was taken only
398 from one age point at the juvenile stage (55 DAH). It also needs to be mentioned that at 55 DAH,
399 the relative importance of studied proteases could be changed due to physiological alterations or
400 changes in diets (fish were only fed by a compound dry diet after 35 DAH). For instance, the
401 percentage of inhibited trypsin and chymotrypsin activities changed during ontogeny in the
402 hybrid *H. molitrix* × *H. nobilis* (Chakrabarti et al., 2006b) and *S. ocellatus* (Applebaum et al.,
403 2001). Moreover, using only one specific inhibitor for chymotrypsin may lead to
404 underestimation of chymotrypsin input in protein digestion for this species as it has been shown
405 for *S. aurata* (Alarcón et al., 1998) and *S. senegalensis* (Sáenz de Rodrigáñez et al., 2005). For
406 the other four cases (*H. molitrix* × *H. nobilis*, *A. tropicus*, *L. rohita*, and *Solea* spp.), the results

407 obtained by correlation and inhibitory analyses were in agreement. Such good concordance in
408 results obtained by two different approaches demonstrated that inhibitory analysis is a suitable
409 approach when specific inhibitors are correctly targeted towards selected enzymes. But this
410 assumption needs to be supported by additional approaches, because in the case of *D. dentex* we
411 were not able to establish whether the real trypsin input was only of 6%, or because of the
412 inhibitor in use being unable to inhibit trypsin. Unexpectedly, for three Amazonian catfishes we
413 have found a negative relationships between total alkaline proteases and both trypsin and
414 chymotrypsin (group 4; Supplementary file Table A). It means that the total alkaline protease
415 activity was mainly due to cysteine- or/and metallo-proteases. The cysteine-proteases are
416 believed to have low importance for protein digestion in the intestinal lumen of fish due to the
417 percent of inhibition that was registered was very weak for different fish species (Dimes et al.,
418 1994; Izvekova and Solovyev, 2016). It has been shown, based on inhibitory analyses, that the
419 input of metallo-proteases is relatively low and does not exceed 10% (Lazo et al., 2007;
420 Chakrabarti et al., 2006a) but, for example, for *S. aurata* the input of metallo-proteases was
421 similar with trypsin and chymotrypsin (Alarcón et al., 1998).

422 **5. Conclusions**

423 These results indicate that arriving at conclusions about the digestive capacity of fish may
424 vary depending on the methodological (correlation analysis and/or inhibitor analysis) and stage
425 of development considered (mainly based on inhibitor analysis). Moreover, correlation analysis
426 as shown in this meta-analysis, may be used as an integrative biomarker and has demonstrated
427 the relative importance of trypsin, or chymotrypsin, or both of them for the proper assessment of
428 digestive capacity at early life stages of fish, as well as a tool for the proper formulation of
429 compound feeds for fish species of interest. Theoretically, this approach is also appropriate for
430 estimation of relative inputs of trypsin and chymotrypsin in any experiments where series of
431 digestive enzyme activity measurements are enough for running correlation analyses. As the
432 bonds cleaved by trypsin and chymotrypsin in proteins and polypeptides are distinct, inclusion of
433 appropriate components in fish diet will potentially increase the feed efficiency.

434 **Author contributions**

435 Conceptualization, M.S. and E.G.; Data Curation, M.S. and E.G.; Formal Analysis, M.S.,
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437 Methodology, M.S., and E.G.; Resources, M.S., E.K., and E.G.; Writing—Original Draft, M.S.,
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445 The authors declare that they have no known competing financial interests or personal
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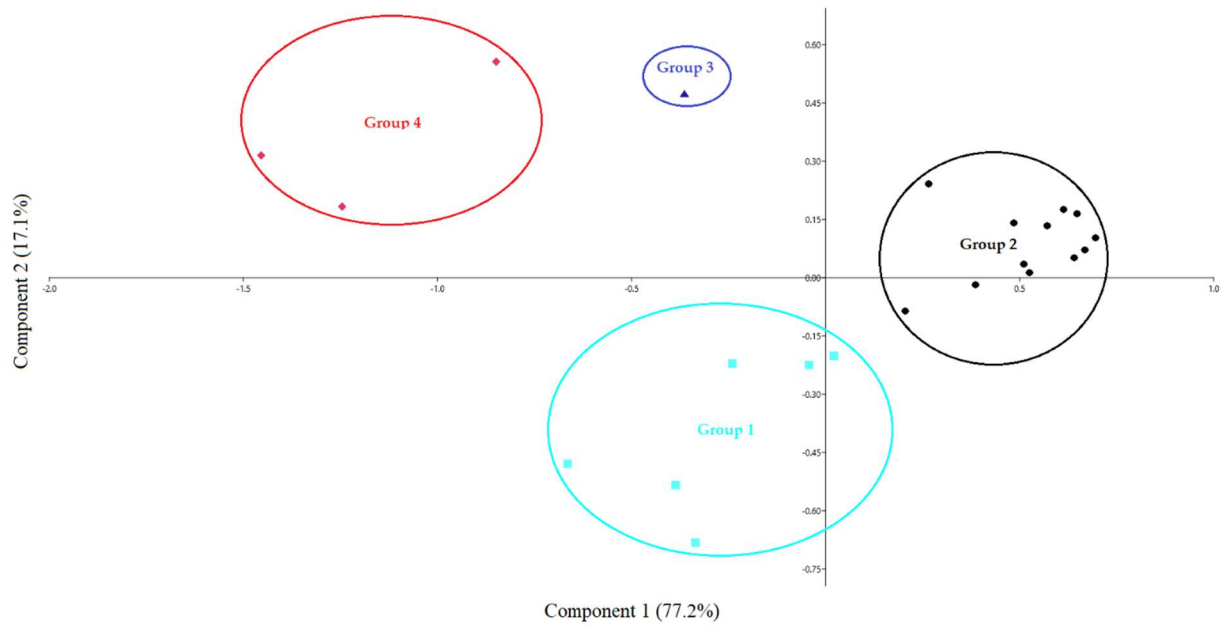
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Value	Tryp/TAP	Chymo/TAP	Tryp/Chymo	Species (Family)	References
1.00					
0.25					
0.00					
-0.25					
-1.00					
Group 1	-0.17	0.61 *	0.02	<i>Centropomus undecimalis</i> (Centropomidae)	(Jimenez-Martinez et al. 2012)
	0.33	0.64 ***	0.16	<i>C. viridis</i> (Centropomidae)	(Hernández-López et al. 2021)
	0.37	0.80 ***	0.50	<i>Argyrosomus regius</i> (Sciaenidae)	(Solovyev et al. 2016)
	-0.05	0.97 ****	0.10	<i>Archocentrus nigrofasciatus</i> (Cichlidae)	(Mente et al. 2017)
	-0.08	0.83 ****	0.23	<i>Petenia splendida</i> (Cichlidae)	(Uscanga-Martínez et al. 2011)
	0.26	0.79 ***	0.55 *	<i>Paralichthys californicus</i> (Paralichthyidae)	(Alvarez-González et al. 2006)
	0.59 ***	0.81 ****	0.56 ***	<i>Ocyurus chrysurus</i> (Lutjanidae)	(Ahumada-Hernández et al. 2014)
	0.74 **	0.91 ****	0.91 ****	<i>Atractosteus tropicus</i> (Lepisosteidae)	(Frias-Quintana et al. 2015)
	0.93 ***	0.96 ***	0.83 **	<i>Catla catla</i> (Cyprinidae)	(Rathore et al. 2005)
	0.71 **	0.85 ***	0.72 **	<i>C. catla</i> (Cyprinidae)	(Khangembam et al. 2012)
	0.86 ****	0.92 ***	0.73 ***	<i>Cichlasoma dimerus</i> (Cichlidae)	(Toledo-Solis et al. 2021)
Group 2	0.88 **	0.59 ***	0.53 **	<i>C. trimaculatum</i> (Cichlidae)	(Toledo-Solis et al. 2015)
	0.92 ****	0.96 ****	0.98 ****	<i>Cirrhinus mrigala</i> (Cyprinidae)	(Chakrabarti, Rathore 2010)
	0.90 ***	0.97 ****	0.94 ***	<i>Odontesthes bonariensis</i> (Atherinopsidae)	(Pérez Sirkin et al. 2020)
	0.93 ****	0.85 ****	0.82 ****	<i>Hypophthalmichthys molitrix</i> × <i>H. nobilis</i> (Cyprinidae)	(Chakrabarti et al. 2006b)
	0.92 ****	0.85 ****	0.94 ****	<i>Labeo rohita</i> (Cyprinidae)	(Chakrabarti, Rathore 2006a)
	0.97 ****	0.78 ***	0.64 **	<i>Paralabrax maculatofasciatus</i> (Serranidae)	(Alvarez-González et al. 2008)
	0.94 **	0.88 **	0.95 **	<i>Solea solea</i> (Soleidae)	(Clark et al. 1986)
Group 3	0.65 ***	-0.01	0.24	<i>C. urophthalmus</i> (Cichlidae)	(López-Ramírez et al. 2011)
	-0.57	-0.22	0.48	<i>Pseudoplatystoma punctifer</i> (Pimelodidae)	(Castro-Ruiz et al. 2019)
Group 4	-0.38	-0.49 **	0.03	<i>P. reticulatum</i> (Pimelodidae)	(Mello et al. 2021)
	0.10	-0.32	0.45 *	<i>P. corruscans</i> × <i>P. reticulatum</i> (Pimelodidae)	(Mello et al. 2021)

Fig. 1. Heat map based on r values calculated with Pearson correlation analysis among the activity of trypsin (Tryp), chymotrypsin (Chymo), and total alkaline proteases (TAP) during ontogenetic development of different fish species. Correlation coefficients that were statistically significant ($p < 0.1$) are marked by white asterisks. Tryp – trypsin, Chymo – chymotrypsin, TAP – total alkaline proteases. The asterisks denote **** $p < 0.001$, *** $p < 0.01$, ** $p < 0.05$, * $p < 0.10$.



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Fig. 2. Principal Components Analysis (PCA) based on correlation coefficients between trypsin and total alkaline proteases, chymotrypsin and total alkaline proteases, trypsin and chymotrypsin.

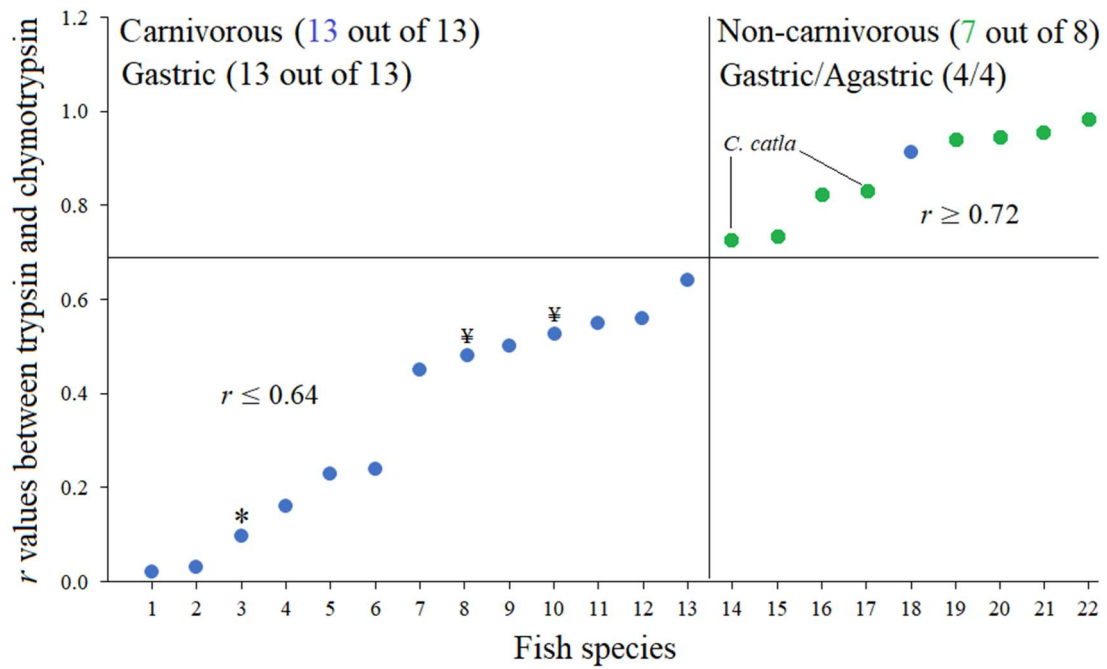
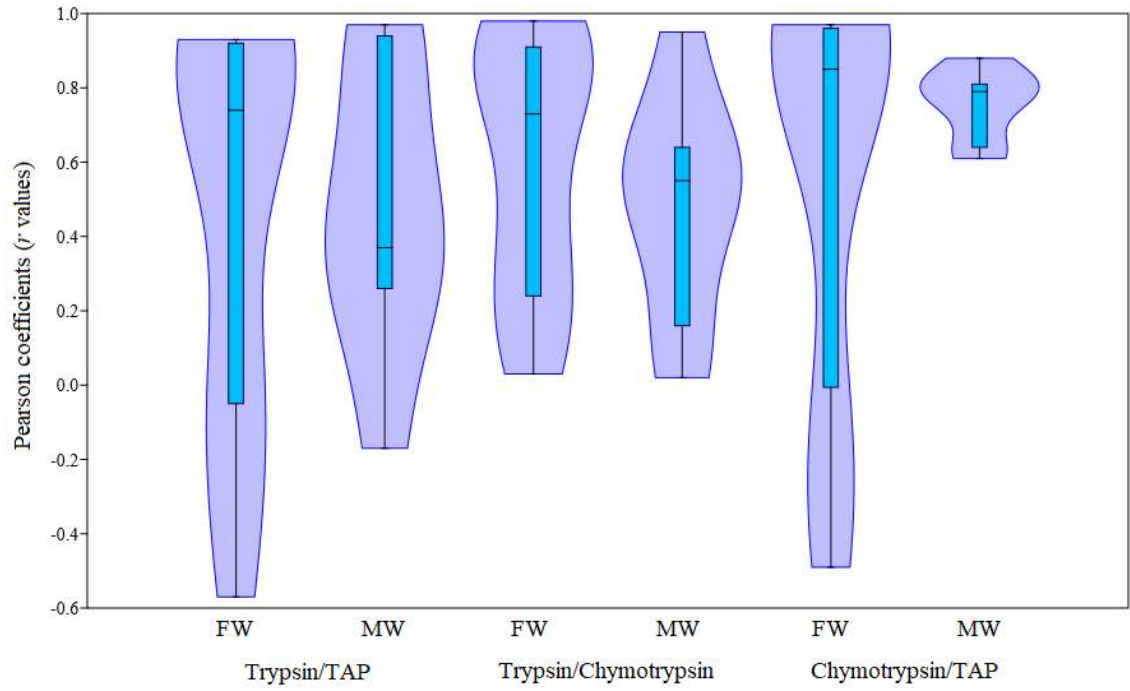


Fig. 3. Pearson correlationship (r values) between trypsin and chymotrypsin for studied fish species. 1. *Centropomus undecimalis* (Jimenez-Martinez et al., 2012), 2. *Pseudoplatystoma reticulatum* (Mello et al., 2021), 3. *Archocentrus nigrofasciatus* (Mente et al., 2017), 4. *C. viridis* (Hernández-López et al., 2021), 5. *Petenia splendida* (Uscanga-Martínez et al., 2011), 6. *Cichlasoma urophthalmus* (López-Ramírez et al., 2011), 7. *P. corruscans* × *P. reticulatum* (Mello et al., 2021), 8. *P. punctifer* (Castro-Ruiz et al., 2019), 9. *Argyrosomus regius* (Solovyev et al., 2016), 10. *C. trimaculatum* (Toledo-Solís et al., 2015), 11. *Paralichthys californicus* (Alvarez-González et al., 2006), 12. *Ocyurus chrysurus* (Ahumada-Hernández et al., 2014), 13. *Paralabrax maculatofasciatus* (Alvarez-González et al., 2008), 14. *Catla catla* (Khangembam et al., 2017), 15. *C. dimerus* (Toledo-Solís et al., 2021; Toledo-Solís et al., 2021), 16. *Hypophthalmichthys molitrix* × *H. nobilis* (Chakrabarti et al., 2006b), 17. *C. catla* (Rathore et al., 2005), 18. *Atractosteus tropicus* (Frias-Quintana et al., 2015), 19. *Odontesthes bonariensis* (Pérez Sirkin et al., 2020), 20. *Labeo rohita* (Chakrabarti et al., 2006a), 21. *Solea solea* (Clark et al., 1986), 22. *Cirrhinus mrigala* (Chakrabarti and Rathore, 2010); Blue circle – generally carnivorous species, green circle – generally non-carnivorous species.

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Fig. 4. A Violin plot for Pearson correlation (r values) between chymotrypsin/total alkaline proteases (TAP), trypsin/chymotrypsin, and trypsin/total alkaline proteases for studied marine and freshwater fishes. Abbreviations: MW: marine fish species, FW, freshwater fish species. Box plots designate mean, standart error, and 95% confidence interval of the data.

- 1 *Centropomus undecimalis* Jimenez-Martinez et al. 2012
Digestive enzymes activities during early ontogeny in common snook (*Centropomus undecimalis*)
Fish Physiol. Biochem. 38 (2), 441–454

Enzymatic activity	DAH*								
	0	1	4	5	7	12	30	34	36
Trypsin	0,033	0,035	0,037	0,037	0,05	0,052	0,033	0,028	0,029
Chymotrypsin	1	1	2,3	2,5	2,6	2,6	3,92	3,5	2
Total alkaline proteases	1230	1234,2	3461,5	2100	393,4	6729	5990	6000	5800

DAH* - day after hatching

- 2 *Centropomus viridis* Hernández-López et al. 2021
Characterization of digestive enzymes during early ontogeny of white snook (*Centropomus viridis*)
Aqua culture. 535, 736399

Enzymatic activity	DAH																		
	1	3	5	7	9	11	13	15	17	19	21	23	25	27	29	31	33	35	40
Trypsin	18	14	5	10	8	14	11	8	9	13	15	18,5	15	22	12	13	10	23	17
Chymotrypsin	5	29	10,5	8	2	8	53	17	9	10	8	15	12	28	11	13	12,5	15	24
Total alkaline proteases	10	11	7	12	6	12	17	11	10	10	9	12	5	13	11,5	12,5	5,5	11	17

- 3 *Argyrosomus regius* Solovyev et al. 2016
Morphological and functional description of the development of the digestive system in meagre
Aqua culture. 464, 381–391

Enzymatic activity	DAH									
	1	5	9	12	20	25	30	38	45	50
Trypsin	0,1	2,2	0,3	0,48	1,1	1,3	0,28	0,5	0,08	0,48
Chymotrypsin	0,11	0,24	0,22	0,1	0,13	0,052	0,02	0,02	0,03	0,01
Total alkaline proteases	0,01	2,1	3,8	0,3	1,1	1,2	0,2	0,3	0,01	0,3

- 4 *Archocentrus nigrofasciatus* Mente et al. 2017
Digestive enzyme activity during initial ontogeny and after feeding diets with different protein sources in zebra cichlid, *Archocentrus nigrofasciatus*
J. World Aquac. Soc. 48 (5), 831–848

Enzymatic activity	DAH								
	0	3	7	10	16	23	26	30	
Trypsin	0,051	0,1	0,08	0,1	0,082	0,075	0,052	0,048	0,036
Chymotrypsin	0,8	1	1,5	1,7	2,57	2	1,55	1,95	1,5
Total alkaline proteases	0,004	0,006	0,02	0,025	0,047	0,038	0,028	0,03	0,027

- 5 *Patenia splendida* Uscanga et al. 2011
Changes in digestive enzyme activity during initial ontogeny of bay snook *Patenia splendida*
Fish Physiol. Biochem. 37 (3), 667–680

Enzymatic activity	DAH																		
	0	2	4	9	11	12	14	16	18	21	24	26	30	32	36	39	42	44	60
Trypsin	0	1	1	0	1	0	0	1	2	2,5	2,5	36	17	8	10	7	18	40	300
Chymotrypsin	0	0	0	30	50	40	10	12	38	2	40	160	420	295	320	200	210	260	190
Total alkaline proteases	0	0	0	30	50	25	20	19	25	20	25	40	170	140	160	55	25	30	20

- 6 *Paralichthys californicus* Alvarez-González et al. 2006
Development of digestive enzymes in California halibut *Paralichthys californicus* larvae
Fish Physiol. Biochem. 31, 83–93

Enzymatic activity	DAH										
	0	1	3	4	5	8	12	15	18	25	30
Trypsin	4	3,5	2	5,4	8	6,5	4	4,4	5	4	3,8
Chymotrypsin	0	0	210	290	300	220	180	190	240	130	20
Total alkaline proteases	0	0,2	3,98	4	4,45	2,2	2,4	3,95	3,9	4,45	2,2

- 7 *Ocyurus chrysurus* Ahumada-Hernández et al. 2014
Changes of digestive enzymatic activity on yellowtail snapper (*Ocyurus chrysurus*) during initial ontogeny
Int. J. Biol. 6 (4), 110–118

Enzymatic activity	DAH																				
	1	2	3	4	5	7	8	10	12	15	17	19	21	22	26	28	30	32	34	38	42
Trypsin	0	0,1	0	0	20	210	220	300	0	190	400	100	390	370	210	490	410	620	350	210	780

Chymotrypsin	0	0	0	0	0,2	0	4	2	0	2	17	17	5	11	9	18	4,5	19	6	2	5
Total alkaline proteases	0	2	0	0	6	20	18	18	40	50	230	360	60	200	230	590	190	500	210	410	220

- 8 *Atractosteus tropicus* Frias-Quintana et al. 2015
Development of digestive tract and enzyme activities during early ontogeny of the tropical gar *Atractosteus tropicus*
Fish Physiol Biochem. 41 (5), 1075–1091

Enzymatic activity	DAH								
	0	4	5	6	9	15	20	25	32
Trypsin	0	0	0,01	0,008	0,01	0,01	0,034	0,055	0,062
Chymotrypsin	0,9	0,6	0,8	0,8	0,7	1,2	1,7	1,7	3
Total alkaline proteases	0,9	0,8	0,5	0,85	0,6	0,6	1,3	1,2	5,1

- 9 *Catla catla* Rathore et al. 2005
Digestive enzyme patterns and evaluation of protease classes in *Catla catla* (Family: Cyprinidae) during early developmental stages
Comp. Biochem. Physiol. B. 142 (1), 98–106

Enzymatic activity	DAH					
	4	12	20	22	24	34
Trypsin	53,55	12,03	34,85	33,56	64,92	118,07
Chymotrypsin	57,63	250	497,3	549,4	984,58	1500
Total alkaline proteases	286,96	240	450	527,67	1100,18	2200

- 10 *Catla catla* Khangembam et al. 2017
Effect of cortisol and triiodothyronine bath treatments on the digestive enzyme profile and growth of *Catla catla* larvae during ontogenic development
Aquac. Res. 48 (5), 2173–2185

Enzymatic activity	DAH										
	5	8	11	14	17	20	23	26	29	32	35
Trypsin	20	18	50	25	27	90	18	50	110	100	110
Chymotrypsin	10	50	30	40	70	75	120	130	200	420	250
Total alkaline proteases	50	70	90	100	100	90	100	120	500	1700	2100

- 11 *Cichlasoma dimerus* Toledo-Solis et al. 2021
Changes in digestive enzyme activities during the early ontogeny of the South American cichlid (*Cichlasoma dimerus*)
Fish Physiol. Biochem. 47 (4), 1211–1227

Enzymatic activity	DAH										
	0	1	3	6	9	11	13	15	17	19	21
Trypsin	0	0	0	0	0	0	0,05	0,07	0,15	0,11	0,14
Chymotrypsin	0	0	0	0,26	0,02	0,14	0,31	0,305	0,31	0,29	0,26
Total alkaline proteases	0	0	0,25	60	10	24	50	75	90	85	80

- 12 *Cichlasoma trimaculatum* Toledo-Solis et al. 2015
Changes on digestive enzymes during initial ontogeny in the three-spot cichlid *Cichlasoma trimaculatum*
Fish Physiol Biochem. 41 (1), 267–279

Enzymatic activity	DAH																			
	0	1	3	6	9	11	13	15	17	19	21	24	27	30	33	36	39	42	45	60
Trypsin	0	0	0,05	0,1	0,2	0,15	0,25	1,6	1,7	1,3	0,8	0,45	0,65	0,2	0,27	0,25	0,27	0,3	0,29	0,2
Chymotrypsin	0	0,03	0	0,31	0,5	0,48	0,75	0,77	0,78	0,76	0,7	0,72	0,775	0,79	0,773	0,725	0,795	0,795	0,35	0,19
Total alkaline proteases	0	0	0	0,13	0,15	0,14	0,13	0,27	0,46	0,33	0,21	0,215	0,3	0,07	0,05	0,06	0,09	0,11	0,07	0,05

- 13 *Cirrhinus mrigala* Chakrabarti and Rathore 2010
Ontogenic changes in the digestive enzyme patterns and characterization of proteases in Indian major carp *Cirrhinus mrigala*
Aquac. Nutr. 16 (6), 569–581

Enzymatic activity	DAH															
	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34
Trypsin	20	10	10	10	15	30	90	100	240	250	510	730	620	590	510	500
Chymotrypsin	0	0	0	0	0	200	1500	1600	2000	3000	4000	7000	6900	6800	6100	5600
Total alkaline proteases	0	0	10	70	100	800	820	1010	1050	1700	2000	2980	3900	3800	4000	4250

- 14 *Odontesthes bonariensis* Pérez Sirkin et al. 2020
Digestive enzyme activities during pejerrey (*Odontesthes bonariensis*) ontogeny
Aquaculture. 524 (6), 735151

Enzymatic activity	WPH**						
	1	2	3	4	5	7	9
Trypsin	17,76	15	16	12	13,55	57,18	23,84

WPH** - weeks post hatching

Chymotrypsin	10	0	20	30	500	1724	454
Total alkaline proteases	10	5	20	30	1000	3000	1500

- 15 *Hypophthalmichthys molitrix* × *H. nobilis* Chakrabarti et al. 2006b
Functional changes in digestive enzymes and characterization of proteases of silver carp (male) and bighead carp (female) hybrid...
Aquaculture. 253, 694–702

Enzymatic activity	DAH															
	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34
Trypsin	10	12	28	21	22	23	23	30	31	25	38	43	50	70	59	
Chymotrypsin	0	0	0	18	20	25	26	55	210	430	430	380	410	400	530	500
Total alkaline proteases	0	10	20	70	80	70	80	80	130	180	220	290	580	610	780	500

- 16 *Labeo rohita* Chakrabarti et al. 2006a
Study of digestive enzyme activities and partial characterization of digestive proteases in a freshwater teleost, Labeo rohita, during early ontogeny
Aquac. Nutr. 12 (1), 35–43

Enzymatic activity	DAH															
	4	6	8	10	12	14	16	18	20	22	24	26	28	30	32	34
Trypsin	20	15	0	0	5	10	15	50	55	100	180	160	165	270	300	350
Chymotrypsin	0	0	0	10	15	30	35	70	250	260	500	770	760	730	950	1750
Total alkaline proteases	0	10	0	50	70	110	220	220	500	800	970	1200	1270	1580	1210	1270

- 17 *Paralabrax maculatofasciatus* Alvarez-González et al. (2008)
Development of digestive enzyme activity in larvae of spotted sand bass *Paralabrax maculatofasciatus*. 1. Biochemical analysis.
Fish Physiol. Biochem. 34 (4), 373–384

Enzymatic activity	DAH												
	0	1	2	3	4	5	7	9	12	15	18	25	30
Trypsin	0,5	1	0,6	1,8	1,75	1	0,8	3,9	10	8	8,5	2	1,5
Chymotrypsin	140	150	135	330	250	300	340	370	339	375	360	210	170
Total alkaline proteases	1	0	2	15	17	9	10	27	50	42	45	7	3

- 18 *Solea solea* Clark et al. 1986
Protease development in dover sole [*Solea solea* (L.)]
Aquaculture. 53 (3-4), 253–262

Enzymatic activity	Days				
	24	49	80	200	Adult
Trypsin	1,76	3	8	10	14
Chymotrypsin	11,3	15	21	39	42
Total alkaline proteases	0,5	2	2,3	2,8	4,5

- 19 *Cichlasoma urophthalmus* López-Ramírez et al. 2011
Development of digestive enzymes in larvae of Mayan cichlid *Cichlasoma urophthalmus*
Fish Physiol. Biochem. 37 (1), 197–208

Enzymatic activity	DAH																		
	0	2	6	8	11	12	14	18	20	22	24	28	30	32	34	38	42	45	60
Trypsin	0	0	0,00001	0,00002	0,00003	0,00018	0,0001	0,00008	0,00022	0,00026	0,0006	0,0003	0,00024	0,00021	0,00018	0,0002	0,00023	0,0004	0,00016
Chymotrypsin	0,001	0,003	0	0,001	0,0018	0,0063	0,0056	0,0058	0,0054	0,008	0,0078	0,0076	0,0056	0,011	0,0054	0,0045	0,058	0,0078	0,0024
Total alkaline proteases	0	0	0	0	10	87	90	72	74	89	95	80	74	80	85	28	20	66	28

- 20 *Pseudoplatystoma punctifer* Castro-Ruiz et al. 2019
Ontogeny of the digestive enzyme activity of the Amazonian pimelodid catfish *Pseudoplatystoma punctifer* (Castelnao, 1855)
Aquaculture. 504, 210–218

Enzymatic activity	DAH						
	0	4	12	17	20	25	27
Trypsin	0,007	0,0055	0,005	0,0075	0,0065	0,009	0,011
Chymotrypsin	0,22	0,06	0,07	0,1	0,12	0,1	0,17
Total alkaline proteases	0,78	0,76	1,5	0,2	0,18	0,4	0,38

- 21 *Pseudoplatystoma reticulatum* Mello et al. 2021
Ontogeny of the digestive system and the profile of proteases in larvae of cachara (*Pseudoplatystoma reticulatum* Siluriformes: Pimelodidae) and its hybrid (*Pseudoplatystoma corruscans* x *Pseudoplatystoma reticulatum*)
J. Fish Biol. 99 (3), 1135–1139

Enzymatic activity	Hours						DAH											
	0	8	13	24	32	40	2	3	4	5	6	7	8	9	10	15	20	25
Trypsin	0,025	0,022	0,03	0,031	0,035	0,026	0,024	0,022	0,023	0,024	0,03	0,02	0,024	0,019	0,024	0,024	0,024	0,023

Chymotrypsin	0,038	0,04	0,015	0,022	0,022	0,021	0,027	0,013	0,015	0,02	0,012	0,02	0,019	0,01	0,012	0,011	0,015	0,019
Total alkaline proteases	1,8	1,6	0,2	1,9	2,1	3	4	6	10	20	15	17	18	90	130	70	50	91

22 *P. corruscans* × *P. reticulatum*

Mello et al. 2021

Ontogeny of the digestive system and the profile of proteases in larvae of cachara (*Pseudoplatystoma reticulatum* Siluriformes: Pimelodidae) and its hybrid (*Pseudoplatystoma corruscans* x *Pseudoplatystoma reticulatum*)
 J. Fish Biol. 99 (3), 1135–1139

Enzymatic activity	Hours						DAH											
	0	8	13	24	32	40	2	3	4	5	6	7	8	9	10	15	20	25
Trypsin	0,025	0,027	0,024	0,028	0,042	0,035	0,024	0,022	0,023	0,04	0,025	0,019	0,023	0,025	0,024	0,025	0,0245	0,04
Chymotrypsin	0,015	0,023	0,015	0,024	0,03	0,027	0,028	0,013	0,019	0,012	0,012	0,011	0,014	0,015	0,011	0,019	0,01	0,019
Total alkaline proteases	0,9	0,9	0,2	1,9	2,2	3,5	3,9	5,5	12	30	12	25	23	140	130	120	110	170

Pearson correlation analysis (r and p -values) among the activity of trypsin (Try), chymotrypsin (Chy), and total alkaline proteases (AP) ($p < 0.1$) are in bold type and marked by red during ontogenetic development of different fish species. P -values are above, r values are below

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,96	0,66
Chymotrypsin	0,02		0,083
Total alkaline proteases	-0,17	0,61	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,51	0,17
Chymotrypsin	0,16		0,003
Total alkaline proteases	0,33	0,64	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,14	0,29
Chymotrypsin	0,50		0,006
Total alkaline proteases	0,37	0,80	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,81	0,90
Chymotrypsin	0,10		0,00002
Total alkaline proteases	-0,05	0,97	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,34	0,76
Chymotrypsin	0,23		1,15E-05
Total alkaline proteases	-0,08	0,83	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,08	0,43
Chymotrypsin	0,55		0,003
Total alkaline proteases	0,26	0,79	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,008	0,005
Chymotrypsin	0,56		7,06E-06
Total alkaline proteases	0,59	0,81	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,0007	0,02
Chymotrypsin	0,91		0,0007
Total alkaline proteases	0,74	0,91	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,04	0,006
Chymotrypsin	0,83		0,002
Total alkaline proteases	0,93	0,96	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,012	0,014
Chymotrypsin	0,72		0,001
Total alkaline proteases	0,71	0,85	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,01	0,0007
Chymotrypsin	0,72		7,08E-05
Total alkaline proteases	0,86	0,92	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,02	2,47E-07
Chymotrypsin	0,53		0,0065
Total alkaline proteases	0,88	0,59	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		2,56E-11	5,82E-07
Chymotrypsin	0,98		2,57E-09
Alkaline proteases	0,92	0,96	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,002	0,005
Chymotrypsin	0,94		0,0002
Total alkaline proteases	0,90	0,97	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,0001	1,18E-07
Chymotrypsin	0,82		3,83E-05
Total alkaline proteases	0,93	0,84	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		4,06E-08	6,19E-07
Chymotrypsin	0,94		3,56E-05
Total alkaline proteases	0,92	0,85	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,02	6,90E-08
Chymotrypsin	0,64		0,002
Total alkaline proteases	0,97	0,78	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,015	0,019
Chymotrypsin	0,95		0,046
Total alkaline proteases	0,94	0,88	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,32	0,003
Chymotrypsin	0,24		0,98
Total alkaline proteases	0,65	-0,006	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,28	0,18
Chymotrypsin	0,48		0,63
Total alkaline proteases	-0,57	-0,22	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,91	0,12
Chymotrypsin	0,03		0,039
Total alkaline proteases	-0,38	-0,49	

	Trypsin	Chymotrypsin	Total alkaline proteases
Trypsin		0,06	0,71

Chymotrypsin	0,45		0,20
Total alkaline proteases	0,10	-0,32	