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Molecular detection and prevalence assessment of human norovirus: NoV (GI and GII) in *Mugil cephalus* (fish, teleost, Mugilidae) in Dakar, Senegal

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ABSTRACT

Noroviruses (NoV) cause the majority of foodborne gastroenteritis. Consumption of raw or undercooked fish exposes you to this risk. This study evaluates the prevalence of NoV (GI and GII) in *Mugil cephalus* fish in Dakar. Thirty-nine specimens were collected in 2025 in Soumbedioume and Hann Bel-Air. Viral RNA was extracted from organ pools and then analyzed by RT-qPCR in real time. Organs from positive fish were tested individually to study tropism.**:** The overall prevalence was 7.69% (3/39), exclusively in Soumbedioume. The GI genogroup affected two fish (5.13%) and the GII only one (2.56%). The genome of NoV GII was detected only in the gills, with a low viral load (Cq = 37.43). Sex, site, height or weight did not significantly influence the prevalence ($p > 0.05$). This study shows for the first time the presence of human norovirus in the gills of *Mugil cephalus*. It confirms the contamination of the marine environment of human origin in Dakar and calls for strengthening virological surveillance.

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INTRODUCTION

Fish is a major source of animal protein, particularly in Senegal where it accounts for more than 70% of protein intake (Deme, 2018; Thiao *et al.*, 2018). However, the growing trend of eating raw, undercooked or fast-cooked fish (e.g., grilling, carpaccio) increases the risk of exposure to pathogens, including enteric viruses (Filipa-Silva *et al.*, 2021). Noroviruses (NoV), members of the Caliciviridae family, are non-enveloped single-stranded RNA viruses with positive polarity.

They are the leading cause of food- and water-borne epidemic gastroenteritis worldwide, responsible for nearly 685 million annual cases and a considerable economic burden (Bartsch *et al.*, 2016; Capece *et al.*, 2025). Classified into ten genogroups (GI to GX), GI, GII and GIV genogroups infect humans, with a global predominance of GII strains.4 (Vinjé, 2015; Chhabra *et al.*, 2019).

NoV transmission occurs primarily via the fecal-oral route, via the consumption of contaminated water or food, or through direct person-to-person contact (De Graaf *et al.*, 2016). Food can be contaminated at the source, especially seafood, through contact with waters polluted by sewage discharges (Campos and Lees, 2014; La Bella *et al.*, 2017).

Although NoV contamination of bivalve shellfish is well documented (Li *et al.*, 2014; Bosch *et al.*, 2018), data on fish, especially pelagic or demersal fish such as mullets, are scarce (Filipa-Silva *et al.*, 2021; Hennechart-Collette *et al.*, 2023). Fish feeding on detritus or sediment, such as *Mugil cephalus*, living in coastal areas often subject to anthropogenic pollution, could be sentinels or potential vectors of these viruses (Kane, 2014; Machu *et al.*, 2023).

The general objective of this study is to contribute, through molecular analysis, to the understanding of human noroviruses in fish (*Mugil cephalus*) marketed in Dakar, Senegal. Specifically, the study aims to detect human noroviruses of genogroups GI and GII in *M. cephalus* samples using RT-qPCR, determine their prevalence, and investigate their tropism across different target organs and tissues, including the gills, liver, spleen, kidneys, heart, gonads, and muscle/skin.

MATERIALS AND METHODS

Sampling sites and study design

A prospective study targeting human enteric viruses (Norovirus genogroup I [NoV GI] and genogroup II [NoV GII]) in marine fish was conducted from March to November 2025 in Dakar (Senegal). Samples were taken at two major landing points:

1. The fishing wharf of Soumbedioune (14°40'42" N; 17°27'42" W), located on the western cornice of Dakar.
2. The fishing wharf of Hann Bel-Air (14°43'0" N; 17°25'0" W), located on the eastern coast of the Cape Verde peninsula, within the bay of Hann.

The cartographic representation and precise location of these sampling sites were carried out using the QGIS Desktop software (version 3.42.3) (Fig. 1).

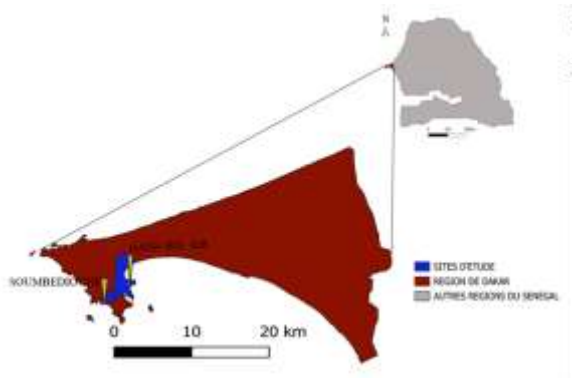


Fig. 1. Sampling sites

Identification and biometrics

First, fish of the *Mugilidae* family belonging to the species *Mugil cephalus* (Fig. 2) were purchased directly from fishermen and dealers at the various landing points (Table 1). The specimens were kept in a cooler and then transported to The Laboratory of General Parasitology.

Subsequently, the identification of the species was confirmed using taxonomic guides (Bellemans *et al.*, 1988).



Fig. 2. Image of a mugilid fish (*Mugil cephalus*)

Table 1. Fish samples used in this study

Species	Disembarkation points	Types of fishery	Number of specimens
Mugil cephalus (Mugilidae)	Soumbedioune	Handcrafted	23
	Hann Bel-Air	Handcrafted	16

Finally, a biometric study was carried out on each fish. Two types of characters were taken into account: metric characters (length measurements) and weight characters (weighed).

The metric characters were measured using an ichthyometer:

1. Total length (Lt): the distance between the anterior end of the snout and the end of the longest ray of the caudal fin.
2. Fork length (Lf): distance between the tip of the muzzle and the hollow of the caudal fork (end of the median rays).
3. Standard length (Lst): the distance from the anterior end of the snout to the articular fold of the caudal fin.
4. Weight characteristics were measured using an electronic scale (Denver Instrument):
5. Total weight (Pt): weight of the whole animal.
6. Eviscerated weight (Pe): weight of the animal after removal of the internal organs (viscera and gonads).

Organ collection and sample preparation

Each fish was dissected using dissection tools under aseptic conditions. Samples from seven target organs were taken: heart, gills, liver, spleen, kidneys, gonads, and a skin/muscle composite. They were introduced individually into 15 mL conical tubes with blue caps, previously coded to avoid cross-contamination or confusion. For initial screening, a pool was formed for each fish by grinding together a fragment of each of the seven organs, generating a total of 39 organ pools. These pools were stored in 1.5 mL Eppendorf tubes at -20 °C until the nucleic acids were extracted.

Viral RNA extraction

At the laboratory of the virology center of the Pasteur Institute of Dakar (IPD), the samples from frozen pools were resuspended in virus transport and preservation medium (VTM/VPM Viral Transport/Preservative Medium). After vortex homogenization, the QIAamp Viral RNA Mini Kit (QIAGEN, Valencia, CA, USA) was used to extract the viral RNA. The total RNA was isolated from 200 µL of supernatant, according to the manufacturer's instructions, then eluted in 60 µL of elution buffer and stored at -20 °C until use.

Table 2. Primers and probes used for the detection of GI and GII noroviruses

Primers/Probes	Meaning	Sequences	Positions	Size
NoVGI_5291-F	+	5'-CGCTGGATGCGNTTCCAT-3'	5291 to 5310	18 N
NoVGI_5376-R	-	5'-CCTTAGACGCCATCATCATTAC-3'	5376 to 5357	23 N
NoVGI_5321-P	+	5'- 6FAM-TGGACAGGAGYCGCRATCT—BHQ-3'	5321 to 5340	20 N
NoVGII_5012-F	+	5'-ATGTTCAGRTGGATGAGRTTCTCWGA-3'	5012 to 5031	26 N
NoVGII_5080-R	-	5'-TCGACGCCATCTTCATTCACA-3'	5080 to 5061	21 N
NoVGII_5042-P	+	5'- 6FAM-AGCQCGTGGGAGGGCGATCG—BHQ-3'	5042 to 5060	20 N

NB: The probes were marked in 5' with the fluorochrome 6-FAM and in 3' with a Black Hole Quencher (BHQ) extinguisher.

Detection of noroviruses by RT-qPCR

The search for noroviruses (NoV GI and GII) was performed by real-time RT-PCR. The specific primers and probes used (Table 2) target the highly conserved junction area of open reading frames 1 and 2 (ORF1/ORF2), according to the protocols of the U.S. CDC (Centers for Disease Control and Prevention, 2009).

Amplifications were performed using the AgPath-ID™ One-Step RT-PCR Kit (Thermo Fisher Scientific, USA). The final reaction volume of 25 µL per sample consisted of: 5 µL of PCR-grade water, 0.5 µL of each primer, 0.5 µL of probe, 12.5 µL of 2X RT-PCR buffer, 1 µL of 25X RT-PCR enzyme mix, and 5 µL of template RNA.

After brief centrifugation, the PCR plate was placed in a CFX96™ real-time PCR thermal cycler (Bio-Rad). The thermal programme consisted of reverse transcription at 50°C for 30 minutes, initial denaturation at 95°C for 10 minutes, and 40 amplification cycles comprising denaturation at 95°C for 15 seconds and annealing/extension at 55°C for 30 seconds. Positive and negative controls were included in each run to validate the results. A sample was considered positive when its amplification curve showed a clear exponential phase that crossed the detection threshold above background fluorescence.

Norovirus tropism

For specimens with a positive pool, samples from each organ were analyzed individually to investigate tropism. The previously described methodology (grinding, viral RNA extraction and amplification by RT-qPCR in sections I.3, I.4 and I.5) was applied for the detection of noroviruses in the remaining target tissues.

Statistical analysis

Prevalence was calculated as the percentage of positive fish among the total number examined. Associations between prevalence and variables (site, sex, size/weight class) were assessed using the exact Fisher test, with a significance level of $p < 0.05$. Analyses were performed with R software (version 4.4.0) and figures with Excel software.

RESULTS

Characteristics of the fish population studied

Of the 39 specimens of *Mugil cephalus* examined, 22 were females (56.4%) and 17 were males (43.6%), resulting in a sex ratio (M/F) of 0.77. Of these specimens, 23 fish (59.0%) were from Soumbedioune and 16 (41.0%) were from Hann Bel-Air. The mean total length was 288.9 ± 34.7 mm (range: 250-400 mm) and the mean total weight was 236.2 ± 77.9 g (range: 100-500 g). The majority of fish (64.1%) were in the size class [250-300 mm [(Fig. 3) and 43.6% were in the weight class [200-300 g [(Fig. 4).

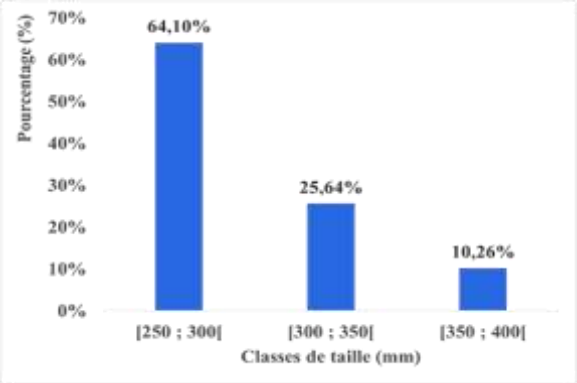


Fig. 3. Distribution of fish according to size classes

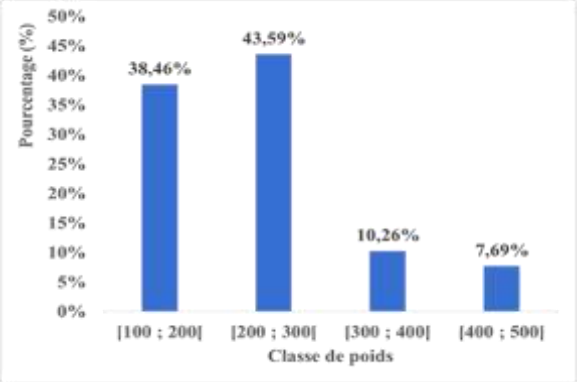


Fig. 4. Distribution of fish according to weight classes

Detection and overall prevalence of noroviruses

RT-qPCR analysis of the 39 organ pools revealed the presence of norovirus RNA in three samples, for an overall prevalence of 7.7% (3/39). All positive fish specimens were from the Soumbedioune site, corresponding to a prevalence of 13.0% (3/23) at this site. No fish from Hann Bel-Air were positive (0/16) (Fig. 5). The difference in prevalence between the two sites was not statistically significant ($p = 0.25$).

In terms of genogroups, two organ pools were positive for NoV GI (Cq= 36.32 and 36.74) and one pool for NoV GII (Cq= 38.08) corresponding to prevalences of 5.1% and 2.6%, respectively (Fig. 6). The difference in prevalence between genogroups was significant (p= 0.0001).

Prevalence by fish characteristics

No significant association was found between norovirus prevalence and fish sex (males = 11.76% vs. females = 4.54%; p = 0.57), size class (p = 0.28; Fig. 7) or weight class (p = 0.90; Fig. 8). The highest prevalences were observed in fish belonging to the size class [300-350 mm[(20%) and weight class [200-300 g[(11.76%)].

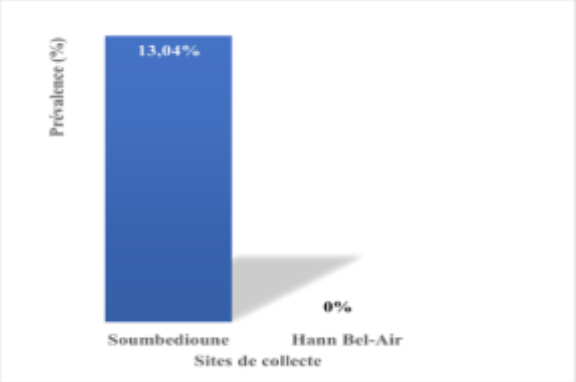


Fig. 5. Prevalence of noroviruses as a function sites

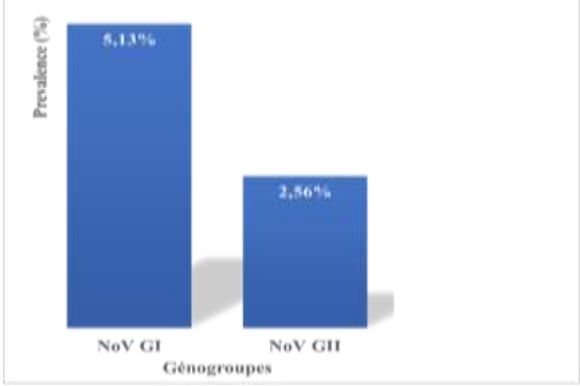


Fig. 6. Prevalence of genogroups of the norovirus

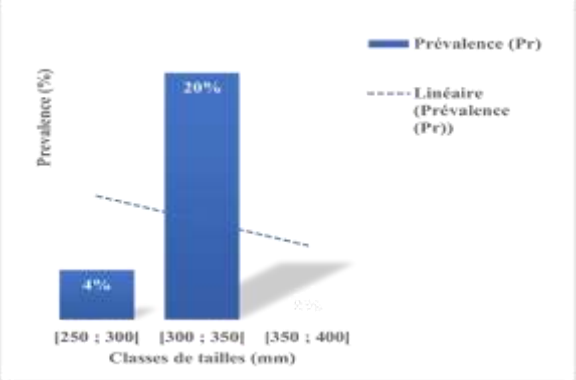


Fig. 7. Norovirus prevalence by size classes

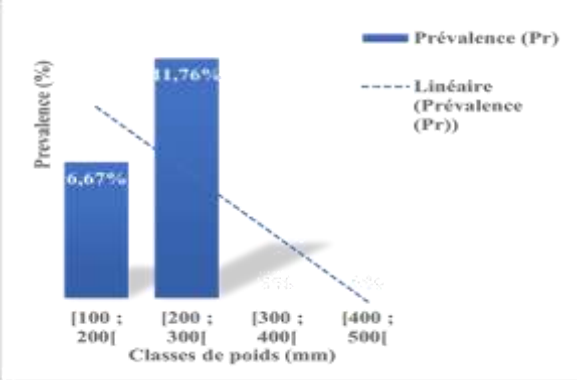


Fig. 8. Norovirus prevalence by weight classes

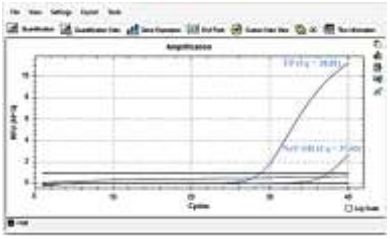


Fig. 9. Norovirus (NoV GII) detection by RTq-PCR in gills (M5)

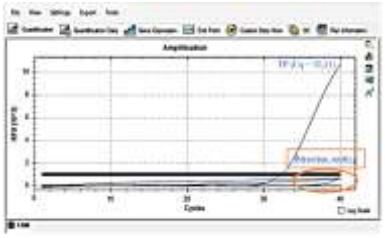


Fig. 10. Detection of GI norovirus by RTq-PCR in organs (M19)

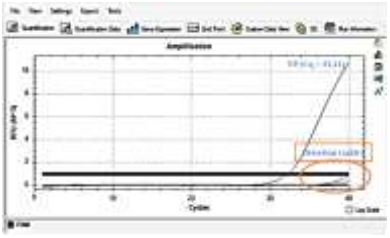


Fig. 11. Detection of GI norovirus by RTq-PCR in organs (M11)

Norovirus tropism in organs

Individual analysis of the 21 organ samples (7 organs × 3 positive individuals) allowed locating the viral RNA. The RNA of NoV GII was detected specifically in the gills of one specimen (M5), with a Cq of 37.43 (Fig. 9). No detections were obtained for the other organs of this fish. Similarly, no significant amplification was observed for the organs of the two NoV GI positive fish pools (M19 and M11). Although a low late amplification was noted for the latter as the 40th cycle approached, it suggests a viral load below the robust detection limit (Fig. 10 and 11).

DISCUSSION

Mugil cephalus is a catadromous and benthic fish, which lives mainly in shallow coastal waters, estuaries

and lagoons. It feeds by filtering mud, surface sediment and organic detritus. The fact that 13% of mullets are positive in Soumbedioune is perfectly explained by their mode of nutrition. Noroviruses released into wastewater (via the Gueule Tapee canal in Soumbedioune) (Kane, 2014; Machu *et al.*, 2023) tend to adsorb to suspended particles and to sediment. By digging through the polluted sediment for food, the mullet ingests and mechanically accumulates viruses.

The lack of detection at Hann Bel-Air, although known for its intense industrial and domestic pollution, may have meant that the mullets caught at Hann came from areas further from the coast (sectors less impacted by direct discharges at the time of fishing), or the hydrodynamic configuration of the Bay of Hann favours a different dispersion of viruses in the sediments compared to the more closed/direct configuration of the Soumbedioume channel (Kluser *et al.*, 2006).

The demographic characterization of the 39 specimens of *Mugil cephalus* revealed a sex ratio of 0.77 in favor of females. This predominance of females is frequently observed in *Mugilidae* during specific phases of their life cycle, in particular during spawning migrations or due to the selectivity of artisanal fishing gear in Soumbedioune and Hann Bel-Air (Fall *et al.*, 1997; Sarr *et al.*, 2012).

Regarding the size structure, the average total length obtained (288.9 ± 34.7 mm) as well as the dominance of the class [250-300 mm [indicate that the majority of individuals captured are adults that have reached their size of first sexual maturity, generally estimated between 15 cm and 46 cm depending on the species Albaret and Legendre, 1985 and McDonough *et al.*, 2005. This result suggests that sampling targets a fraction of the population that has already potentially participated in the renewal of the stock.

However, the absence of large individuals (maximum length of 400 mm) compared to the historical maximum size of the species (sometimes greater than 500 mm) could reflect the impact of sustained fishing pressure on the small coast and the Cape Verde peninsula.

This study reports for the first time the molecular detection of the human norovirus (NoV) genome in the fish *Mugil cephalus* in Senegal, with an overall prevalence of 7.69%. As noroviruses do not replicate in these fish, they act as passive hosts or bioaccumulators. Their presence is therefore a clear indicator of human-induced fecal contamination of the marine environment.

Although noroviruses are considered host-specific viruses, recent studies have shown their ability to replicate asymptomatically in zebrafish models (Van Dycke *et al.*, 2019) and to be detected in fish tissues (Filipa-Silva *et al.*, 2021). Our discovery reinforces the hypothesis that fish, especially demersal filter-feeding species like mullets, could act as mechanical vectors or transient reservoirs for these viruses, accumulating viral particles from water.

The prevalence observed here is significantly higher than that reported in a similar study in Portugal (0.31%). This disparity could be explained by higher levels of fecal pollution in the coastal marine environment of Dakar, in particular due to the discharge of untreated sewage, as described near the Soumbedioune site.

The analysis also shows a statistically significant predominance ($p = 0.0001$) of the GI genogroup (5.13%) compared to the GII (2.56%). This profile reverses the trend observed in human clinical infections (gastroenteritis), where the GII (especially the GII.4 genotype) is largely prevalent worldwide (Chhabra *et al.*, 2019; de Rougemont, 2019). However, our results are consistent with data from the literature on aquatic environments and shellfish, which often highlight preferential bioaccumulation and greater stability of the GI. This genogroup is known to be more resistant to environmental factors and wastewater treatment than the GII (de Rougemont, 2019). Thus, the high proportion of GIs in our sampling suggests chronic and persistent

environmental contamination, rather than a recent acute human epidemic (which would have resulted in an overrepresentation of GII).

The location in the gills (NoV GII) could be explained by the fact that the gills are in direct contact with water and act as a filter. The detection of GII only in the gills (Cq 37,43) reinforces the idea of external contamination or recent passive ingestion/filtration of polluted water, rather than systemic distribution.

As for the paradox of positive GI/negative organ pools, this could be due to several, first, the initial viral loads were extremely low (Cq > 36). During the individual analysis, the amount of RNA present in the single organ extracts was probably just below the sensitivity limit of our RT-qPCR kit. The viral RNA, which is very fragile, may have undergone suboptimal degradation between the time of the pool analysis and the individual analysis (freeze/thaw cycles). Finally, some fish organs (liver, viscera) contain strong polymerase inhibitors that can delay Cq or block amplification if not perfectly removed during individual extraction.

It should be noted, however, that even if viral loads appear to be low, the presence of GI and GII norovirus in Soumbedioune fish poses a potential food safety risk to consumers (especially if undercooked or cross-contaminated during handling).

The lack of a significant correlation with sex, height or weight suggests that the risk of contamination is more related to environmental exposure than to the intrinsic biological characteristics of the fish. Nevertheless, the trend towards a higher prevalence in fish of intermediate size/weight may reflect the feeding habits of juveniles of *M. cephalus*, which feed closer to coastal bottoms and sediments where viruses can accumulate (Farrugio, 1975).

CONCLUSION

This study reports for the first time in Senegal, the molecular detection of the human norovirus (*NoV*) genome in the mullet *Mugil cephalus*, with an overall prevalence of 7.69%. As a catadromous, benthic and detritivorous species, *M. cephalus* has proven to be an excellent bioindicator of human-induced fecal contamination of the coastal ecosystem of the Cape Verde peninsula. The high prevalence of positivity observed at the Soumbedioune site (13%) is explained by the adsorption of viruses on suspended solids from the Gueule Tapee canal and their sedimentation, resulting in direct mechanical bioaccumulation during fish nutrition.

From a virological point of view, the reversal of the usual human clinical profile in favour of the GI genogroup (5.13% compared to 2.56% for the GII) highlights the greater environmental stability of the GI in the face of marine treatments and physicochemical factors. This result demonstrates that the Dakar coastline is subject to chronic and persistent environmental pollution rather than acute and epidemic contamination in the short term. Although the low viral loads (Cq > 36) and the gill location of the GII confirm a role as a passive host or transient reservoir rather than a systemic infection, the presence of these pathogens in commercial-sized fish poses a concrete health risk for local populations, particularly in the event of undercooking or cross-contamination.

Finally, the demographic characterization reveals a highly anthropized population. While the majority of the specimens caught are mature adults that have potentially participated in the renewal of the stock (average length of 288.9 ± 34.7 mm), the total absence of large individuals (> 400 mm) compared to historical data for the species testifies to sustained fishing pressure on the Petite Côte and the Cape Verde peninsula. These results underline the urgency of improving the management of urban domestic effluents in Dakar and of setting up regular microbiological monitoring of artisanal fishery products in order to reconcile the conservation of fishery resources and food safety.

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REFERENCES

Albaret JJ, Legendre M. 1985. Biology and ecology of Mugilidae in the Ebrié lagoon (Côte d'Ivoire): Potential interest for aquaculture. Cahiers ORSTOM, Série Hydrobiologie **18(4)**, 281–303.

Bartsch SM, Lopman BA, Ozawa S, Hall AJ, Lee BY. 2016. Global economic burden of norovirus gastroenteritis. PLOS ONE **11(4)**, e0151219. DOI: 10.1371/journal.pone.0151219

Bellemans M, Sagna A, Fischer W, Scialabba N. 1988. FAO species identification sheet for fishing purposes. Guide to the Fisheries Resources of Senegal and the Gambia (Marine and Brackish Water Species). Rome, Italy, 227 p.

Bosch A, Gkogka E, Le Guyader FS, Loisy-Hamon F, Lee A, van Lieshout L, Marthi B, Myrmel M, Sansom A, Schultz AC, Winkler A, Zuber S, Phister T. 2018. Foodborne viruses: Detection, risk assessment, and control options in food processing. International Journal of Food Microbiology **285**, 110–128.
DOI: 10.1016/j.ijfoodmicro.2018.06.001

Campos CJA, Lees DN. 2014. Environmental transmission of human noroviruses in shellfish waters. Applied and Environmental Microbiology **80(12)**, 3552–3561. DOI: 10.1128/AEM.04188-13

Capece G, Tobin EH, Gignac E. 2025. Norovirus. StatPearls Publishing, Treasure Island, Florida. Available online

Chhabra P, de Graaf M, Parra GI, Chan MC-W, Green K, Martella V, Wang Q, White PA, Katayama K, Vennema H, Koopmans MPG, Vinj J. 2019. Updated classification of norovirus genogroups and genotypes. The Journal of General Virology **100(10)**, 1393–1406.
DOI: 10.1099/jgv.0.001318

De Graaf M, Van Beek J, Koopmans MPG. 2016. Human norovirus transmission and evolution in a changing world. Nature Reviews Microbiology **14(7)**, 421–433.
DOI: 10.1038/nrmicro.2016.48

de Rougemont A. 2019. Norovirus: Infectious diarrhea in adults and children. French Society of Microbiology **172**, 10 p. Available online

Deme EB. 2018. Co-management and sustainable participatory dynamics of Senegalese artisanal fisheries: Potentialities and limits in the context of crisis in the Senegalese fisheries sector. Geography thesis, University of Clermont Auvergne, Clermont-Ferrand, France, 327 p.

Fall M, Kpatcha KP, Diebakate C, Faye N, Toguebaye BS. 1997. Observations on myxosporidia (Myxozoa) of the genus *Myxobolus* parasites of *Mugil cephalus* (Pisces, Teleostei) from Senegal. Parasite **4(2)**, 173–180.
DOI: 10.1051/parasite/1997042173

Farrugio H. 1975. The mullets (teleost fishes) of Tunisia: Distribution and fisheries, contribution to their systematics and biology. Doctoral thesis, University of Science and Technology of Languedoc (USTL), Montpellier, France, 201 p.

Filipa-Silva A, Nunes M, Parreira R, Barreto Crespo MT. 2021. Development of a tetraplex qPCR for the molecular identification and quantification of human enteric viruses, NoV and HAV, in fish samples. Microorganisms **9(6)**, 1149.
DOI: 10.3390/microorganisms9061149

Hennechart-Collette C, Dehan O, Fraisse A, Martin-Latil S, Perelle S. 2023. Development of an extraction method to detect hepatitis A virus, hepatitis E virus, and noroviruses in fish products. Microorganisms **11(3)**, 624.
DOI: 10.3390/microorganisms11030624

Kane A. 2014. Global Programme of Action for the Protection of the Marine Environment from Land-based Activities: The Case of Senegal. Progress Report on the Assessment of Marine Pollution from Senegalese Land-Based Activities, 51 p.

Kluser S, Richard J-P, Giuliani G, De Bono A, Peduzzi P. 2006. Illegal oil discharge in European seas. Environment Alert Bulletin 7, 4 p.

La Bella G, Martella V, Basanisi MG, Nobili G, Terio V, La Salandra G. 2017. Food-borne viruses in shellfish: Investigation on norovirus and HAV presence in Apulia (SE Italy). Food and Environmental Virology **9(2)**, 179–186.
DOI: 10.1007/s12560-016-9273-1

Li D, Stals A, Tang Q-J, Uyttendaele M. 2014. Detection of noroviruses in shellfish and semiprocessed fishery products from a Belgian seafood company. Journal of Food Protection **77(8)**, 1342–1347.
DOI: 10.4315/0362-028X.JFP-14-016

Machu E, Brochier T, Capet X, Ndoya S, Ba IS, Descroix L. 2023. Chapter 2. Pollution in a liquid world: Sources, fate and consequences for marine spatial planning in Senegal. In: Marine Spatial Planning in the Tropical Atlantic: From a Tower of Babel to the Organization of a Collective Intelligence. IRD Éditions, Montpellier. DOI: 10.4000/books.irdeditions.44554

McDonough CJ, Roumillat WA, Wenner CA. 2005. Sexual differentiation and gonad development in striped mullet (*Mugil cephalus*) from South Carolina estuaries. Fishery Bulletin **103(4)**, 601–619.

Sarr SM, Kabre JAT, Diadhiou H. 2012. Age and growth of *Mugil cephalus* (Linnaeus, 1758, Mugilidae) in the Senegal River estuary. International Journal of Biological and Chemical Sciences 6(5).

Thiao D, Leport J, Ndiaye B, Mbaye A. 2018. Need for adaptive solutions to food vulnerability induced by fish scarcity and unaffordability in Senegal. Aquatic Living Resources **31**, 25.
DOI: 10.1051/alr/2018009

Van Dycke J, Ny A, Conceição-Neto N, Maes J, Hosmillo M, Cuvry A, Goodfellow I, Nogueira TC, Verbeken E, Matthijnssens J, de Witte P, Neyts J, Rocha-Pereira J. 2019. A robust human norovirus replication model in zebrafish larvae. PLOS Pathogens **15(9)**, e1008009.
DOI: 10.1371/journal.ppat.1008009

Vinjé J. 2015. Advances in laboratory methods for detection and typing of norovirus. Journal of Clinical Microbiology **53(2)**, 373–381.
DOI: 10.1128/JCM.01535-14