Review

Mediterranean Aquaculture and Genetic Pollution: A Review Combined with Data from a Fish Farm Evaluating the Ecological Risks of Finfish Escapes

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Abstract: Mediterranean finfish aquaculture is mainly represented by the production of the gilthead sea bream (Sparus aurata) and sea bass (Dicentrarchus labrax) growing in marine cage farms. Despite the numerous benefits of fish farming, the ecological risk potentially caused by fish escapes to the wild populations is occasionally high. In the current study, an integrated review of fish escapes is presented regarding S. aurata and D. labrax escapes and their potential effect on the genetic composition of wild populations. The collected data from the literature are combined and discussed along with recorded escapes in a fish farm located in the Aegean Sea, Greece. According to these records, fish escapes present a generally stable rate, ranging between 0 and 2% in each escape event, which occur 5–8 times per year. Although for other farmed fish species worldwide, the ecological risk may be higher, this risk is probably lower in Mediterranean finfish populations, which are characterized by generally low levels of genetic differentiation. Nevertheless, the risk of genetic introgression still exists. Particularly in sea bream and sea bass farming, genetic structure and differentiation in wild populations seem to be unaffected for now. Nevertheless, suitable management measurements would be a useful strategy to avoid future negative effects of fish escapes. These strategies should be focused on further efforts towards recapture program development, reduced escapees’ survival, and proper legislation. Furthermore, more data on escapees’ survival percentage, their migration pathways, and the way these pathways relate to mortality, the type of escape event, and the season of release would be also valuable.

Keywords: genetic diversity; Mediterranean Sea; mariculture; gilthead sea bream; sea bass; native fish populations

1. Introduction

Although the aquaculture sector represents the fastest-growing industry in the food production field [1], there are still important challenges regarding its sustainable growth. Furthermore, as aquaculture represents one of the solutions to increased food demand, environmental and biodiversity maintenance concerns have to be taken into consideration in order to provide alternative solutions towards sustainable aquaculture expansion.

One of the major challenges that the aquaculture field faces includes finfish escapes that might cause a serious threat to the genetic integrity of wild populations [2]. Although
in some European countries, such as Norway, Scotland, and Ireland, extensive recording of escape accidents (date, size, cause) are obligatory, information from the Mediterranean region is scarce [3], as Mediterranean countries have not established strict requirements or regulations [4]. Available data from insurance companies, responsible for farming businesses, revealed that escapes pose an important factor for economic losses [5–8]. The above statements have been confirmed by Jackson et al. [9], who estimated that the cost due to the escape events is very high in terms of income loss, reaching annually €42.8 million regarding small- and large-scale events in total. At the same time, apart from the economic part, the ecological impact of these escapes on the wild finfish populations is of great importance, in terms of possible genetic pollution. It should be also noted that in countries where aquaculture of non-indigenous species is allowed, an additional problem is the introduction of those non-indigenous species.

Genetic pollution can be defined as the alteration of the genetic structure of a population due to admixture or introgression with another one, of different genetic composition, often caused by farmed fish escapes. Fish escape events are the result of four major causes, which can be categorized as: environmental, organizational, operational, and technical (Table 1) [10]. More specifically, environmental damage may be generated by wind, water currents, visibility, icing, flotsam, or predators. Organizational related failures causing escape events include workload, work practice, competence, as well as procedures and documentation. Furthermore, operational risk influencing factors include failure due to vessel maneuverings at the fish farm or alongside the net cage, during net attachment procedure or equipment installation, net handling, storage along with repair, and fish pump mounting that may cause damages such as holes in fish cages. Finally, the technical category mainly concerns dysfunctions in the electric power supply, equipment of technical state, floater, feed barge mooring, dead collection system, mooring line, sinker tube chain, and bottom weight system condition, as well as in anchor, coupling plate, and sinker tube placement [10].

Gilthead sea bream and European sea bass, are considered the most important Mediterranean finfish aquaculture’s products [11]. A common behavior of gilthead seabream, Sparus aurata (Linnaeus, 1758) (Teleostea: Sparidae), that leads to escape events is net biting when it is agitated from threats or prey [12,13]. On the other hand, European sea bass Dicentrarchus labrax (Linnaeus, 1758) (Teleostea: Moronidae) usually do not exhibit net-biting or induced-escape behavior and are characterized as more opportunistic concerning escape events [14]. Furthermore, wild predator species may cause enlargement of net holes, new sites’ net breakage, and even stress to farmed fish. More specifically, bluefish (Pomatomus saltatrix) (Linnaeus, 1766) [15], Atlantic Bluefin tuna (Thunnus thynnus) (Linnaeus, 1758) [16], swordfish (Xiphias gladius) (Linnaeus, 1758) [17], bottlenose dolphins (Tursiops truncatus) (Montagu, 1821) [18], and monk seals (Monachus monachus) (Hermann, 1779) [19] have been referred to cause such kind of issues.

Turkey is the main producer of sea bass and gilthead sea bream among the Mediterranean countries, with approximately 160,000 tons, followed by Greece with 100,000 tons [20]. Initial intensive aquaculture efforts dated back to the early 1980s, while the industrial level of production was established during mid-1990s [21–23]. Aquaculture development is important for several local economies in the Mediterranean basin; however, the issue of escape events of farmed fish is of major importance for the environmental sustainability and conservation of wild stocks [24]. It should also be pointed out that apart from the main form of escape events mentioned above, recently, another form has raised many concerns. This form is referred to as “escape through spawning” and involves the escape of viable fertilized eggs that are spawned and released from fish under captivity within the fish cages [25]. Keeping this in mind, a clear focus towards escape events should be gained, to avoid negative impacts on the genetic base of wild populations, which at some extent still retain their genetic integrity.
Table 1. Categorization of main factors responsible for finfish escape events.

<table>
<thead>
<tr>
<th>Major Cause Category</th>
<th>Etiological Factor for the Escape Event</th>
</tr>
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<tbody>
<tr>
<td>Environmental</td>
<td>• wind</td>
</tr>
<tr>
<td></td>
<td>• water currents</td>
</tr>
<tr>
<td></td>
<td>• visibility</td>
</tr>
<tr>
<td></td>
<td>• icing</td>
</tr>
<tr>
<td></td>
<td>• flotsam</td>
</tr>
<tr>
<td></td>
<td>• predators</td>
</tr>
<tr>
<td>Organizational failures</td>
<td>• workload</td>
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<tr>
<td></td>
<td>• work practice</td>
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<tr>
<td></td>
<td>• competence</td>
</tr>
<tr>
<td></td>
<td>• procedures and documentation</td>
</tr>
<tr>
<td>Operational risks that may cause</td>
<td>• failure due to vessel maneuverings</td>
</tr>
<tr>
<td>damages such as holes in fish cages</td>
<td>• failure during net attachment procedures or equipment</td>
</tr>
<tr>
<td></td>
<td>installation</td>
</tr>
<tr>
<td></td>
<td>• net handling and storage along with repair</td>
</tr>
<tr>
<td></td>
<td>• fish pump mounting</td>
</tr>
<tr>
<td>Technical</td>
<td>• dysfunctions in the electric power supply</td>
</tr>
<tr>
<td></td>
<td>• dysfunctions in floater and feed barge mooring</td>
</tr>
<tr>
<td></td>
<td>• dead collection system, mooring line, sinker tube</td>
</tr>
<tr>
<td></td>
<td>chain, and bottom weight system condition</td>
</tr>
<tr>
<td></td>
<td>• dysfunctions in anchor, coupling plate, and sinker</td>
</tr>
<tr>
<td></td>
<td>tube placement</td>
</tr>
</tbody>
</table>

Thus, the Mediterranean aquaculture, apart from positive effects on wild fish stocks due to cover of part of the market demand and subsequent overfishing reduction, may also result in detrimental effects on ecological retention [26]. Since the fish which escape from aquaculture units can survive in the wild, compete for food sources, and reproduce with wild individuals, they may pose an important threat to native populations. Among significant threats, inbreeding and subsequent loss of genetic diversity are included [27,28].

The main scope of this review was to report the most relevant information on the potential environmental risks of sea bream and sea bass escape events as well as their consequences on wild fish populations from a genetic pollution point of view in the Mediterranean basin. Together with the literature review, data from a sea bream farm located in the Evoikos Gulf (Western Aegean Sea) were collected and analyzed, to enrich the scarce information existing about escape events in Greek fish farms. The present work aims at operating as a reference for future decision making concerning sustainable aquaculture management.

2. Evidence for Aquaculture Driven Evolution?

Animal domestication process refers to a situation where the domesticated organisms have been adapted to both captivity conditions and human presence [29]. Usually, this process takes time and many generations and is a never-ending phenomenon [30]. During the domestication process, the animals remaining in captivity undergo changes at the genetic level compared to their wild ancestors. These changes occur progressively, usually at a very slow pace, whereas from a certain moment, animals may be considered domesticated. However, the time point when an animal changes from wild to domesticated is unclear and in most cases a subjective and arbitrary decision [29].

Unlike most terrestrial animals whose domestication process started thousands of years ago [31], the domestication of aquatic organisms represents a rather recent phenomenon [32]; most aquaculture species are considered to be in their early stages [33].
Although farming efforts for some species [e.g., *C. caprio*; *Carassius gibelio* (Bloch, 1782)] are dated back to 8000 years ago, the vast majority of these have begun during the previous century [34]. As it can be drawn from the above, aquaculture is a recent developing sector, and as a result, there are knowledge gaps regarding the genetic status of most farmed fish and their domestication stage [35].

In respect of its definition, domestication modifies the genetic composition of the animals’ population gene pools that are under captivity intending to create more productive and efficient individuals. This process takes time and effort to meet the food demands of the growing human population. Thus, the success of the growth and sustainability of the aquaculture sector in the future will partly rely on the successful domestication process of fish species [28,36]. Consequently, domestication has the potential to be a fundamental tool towards sustainable aquaculture development as it can lead to increased production of the farmed species, preferably to the native ones. Aquaculture development is of major importance to be focused on native species as these species may exhibit better adaptation towards socioeconomic and environmental issues [1].

To clarify the domestication stages in fish species, Teletchea and Fontaine [37] proposed a new concept for fish classification based on the human control scale over the life cycle of cultured species. Out of the species listed in the Food and Agriculture Organization (FAO), around 100 could be considered globally domesticated [33,35,38]. However, although the number of farmed fish worldwide faced a sharp increase during the last three decades, approximately 80% of fish aquaculture production is attributed to the 20 main fish species [38]. The most widely cultured and domesticated fish species in Europe, in terms of production in descending order, are the Atlantic salmon (*S. salar*), the rainbow trout (*O. mykiss*), the gilthead sea bream (*S. aurata*), the European sea bass (*D. labrax*), the common carp (*C. caprio*), and the turbot (*Psetta maxima*) (Linnaeus, 1758) [39]. However, the “domesticated” characterization is not a stable situation, as these populations are under continuous selective pressure (both natural and artificial). Further, continuous evolution is the result of the altered environmental conditions occurring that individuals cope with under captivity [40]. Furthermore, cultured fish are often being released both intentionally and accidentally in the wild, a process called “feralization”, which means re-adaptation to the natural environment [41]. It should be noted though that re-introduction in the natural environment does not necessarily cause feralization. It is worth noting that feralization is categorized as by some authors among the main problems of the aquaculture industry at a global scale [40]. Further, release of fish from aquaculture into the wild has the risk of pathogen spread [41].

Gilthead sea bream’s genetic structure and domestication level are less studied in comparison with other important reared fish such as salmon and trout [42]. While gilthead sea bream aquaculture started during the 1970s [39], its domestication process is dated one decade later, during the 1980s [43]. As of 2008, the first genetic improvement program was established and implemented through selective breeding schemes [44]. A few years later, in 2012, eight breeding companies conducted selective breeding programs for gilthead sea bream. Four of them, located in Greece, produced more than 80% of the juveniles among all breeding companies [45]. Further, as reported, most of these breeding companies performed family-based selection with only one of them performing mass selection. Desirable features on which selection was based were growth performance, morphology product quality, disease resistance, and feed efficiency [45].

### 3. Population Genetic Structure of the Main Farmed Mediterranean Marine Fish Species, *S. aurata* and *D. labrax*

One of the most important parameters for the management of cultured species is their genetic composition, which may provide information regarding the potential interactions of cultured and wild populations [46]. Regarding gilthead sea bream’s genetics, inferences so far are occasionally contradictory, and a consistent scenario has not been provided yet. For instance, data provided from previous surveys are contradictory, since some of
them propose strong population subdivision and genetic differentiation among them [47], whereas others exhibited lower values [48] or complete absence of genetic structure among geographically distant wild populations based on microsatellite markers [49,50]. On the other hand, there are studies that report some levels but always weak genetic differentiation or genetic subdivision [51–54].

Limited research was carried out on the effects of domestication on the genetic profile of the species. However, in most cases, when wild and farmed fish were examined, populations were distinct from each other [49,55,56]. From the first large-scale population genetic analysis carried out on six wild and five farmed populations based on 16 allozyme, 6 microsatellite, and mitochondrial DNA markers, the results revealed lower levels of genetic variability in farmed populations in comparison to the wild ones. The observed genetic divergence was attributed to genetic drift [49]. Likewise, Loukovitis et al. [55] and Polovina et al. [56] recorded distinct genetic makeup among farmed and wild populations distributed in the Mediterranean Sea. In a study by Karaiskou et al. [50], absence of genetic differentiation was observed among wild sea bream populations, while for farmed individuals, distinct groups were evident within the same farm but from different cages. In a more recent study, eight microsatellites were analyzed to assess the genetic structure between farmed and wild populations of sea bream from the Adriatic Sea revealing low levels of differentiation [52].

Thus, when genetic differentiation between farmed and wild populations is present, genetic tools may be particularly useful towards the determination of fish escape events from farming units. For instance, the incidence of escapees in the Adriatic Sea was also confirmed by Šegvić-Bubić et al. [57], who examined nine microsatellite markers in combination with 19 morphological characteristics and confirmed the spatial distribution of escaped gilthead sea bream individuals near the farms. Therefore, one of the most intriguing questions that arises is the evaluation of the extent to which the genetic integrity of Mediterranean finfish has been compromised. In a recent wide study, Gkagkavouzis et al. [58] used a robust genome-wide distributed single-nucleotide polymorphism (SNP) set to analyze five cultured populations originating from Greek aquaculture companies and 23 wild populations from the Mediterranean basin, unveiling a genetic panel that can be used for distinguishing wild and farmed individuals as well as signs of parallel divergent selection in some farmed gilthead sea bream populations. Interestingly, as can be drawn from the above, there is evidence for aquaculture-driven evolution due to intra-population domestication selection or alternatively genetic drift [58].

Evidence for genetic structure or population subdivision was obtained from: three distinct geographic populations on the Spanish coast [54], four distinct populations sampled across the European Atlantic coast [53], three populations collected from the Adriatic Sea [36], two populations sampled from two Tyrrenian coastal lagoons [59], and another three within the Western Mediterranean Sea [51]. Most of the above studies were based on microsatellites and mitochondrial markers. On the other hand, an extensive study conducted on wild gilthead sea bream sampled from 23 locations within the Mediterranean Sea and Atlantic Ocean using 1159 genome-wide SNP markers suggested subtle subdivision into three distinct groups: Atlantic, West, and East Mediterranean [60].

In general, gilthead sea bream Mediterranean populations are characterized by low genetic differentiation, by the means of FST, throughout the basin (Table 2). Even when comparing wild gilthead sea bream populations from the Atlantic Ocean and the Mediterranean Sea, genetic differentiation is at similarly low levels (FST = 0.036) [49,51]. Most of these inferences are based on various types of markers and allozyme loci, but mostly microsatellites (Table 2). Nevertheless, microsatellite markers sometimes present technical drawbacks such as null alleles or allelic dropouts [61], leading to difficulties in result analysis and interpretation. As a result, in some cases, important differences regarding genetic diversity may be missed or underestimated [62]. On the other hand, studies that apply both simple sequence repeats (SSRs) and SNP markers on many samples may lead to more robust results. Maroso et al. [60] studied 958 wild gilthead sea breams from 23 locations within
the Mediterranean Sea and Atlantic Ocean genotyped at 1159 genome-wide SNP markers by restriction-site associated DNA (RAD) sequencing. Neutral marker analyses identified weak subdivisions into three genetic clusters: Atlantic, West, and East Mediterranean, while the latter group could be further subdivided into an Ionian/Adriatic and an Aegean group. In general, \( F_{ST} \) values were low (average \( F_{ST} = 0.0031 \)) with a trend of increased values in the Atlantic Ocean compared to the Mediterranean Sea [60].

**Table 2.** Indicative genetic differentiation (\( F_{ST} \)) of gilthead sea bream populations.

<table>
<thead>
<tr>
<th>Location of Populations</th>
<th>( F_{ST} )</th>
<th>Markers Used</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Central Mediterranean</td>
<td>0.093</td>
<td>Allozymes</td>
<td>Ben Slimen et al. [63]</td>
</tr>
<tr>
<td>Western Mediterranean</td>
<td>0.069</td>
<td>Microsatellites—RAPDs</td>
<td>Chaoui et al. [47]</td>
</tr>
<tr>
<td>Central Mediterranean</td>
<td>0.017</td>
<td>Microsatellites</td>
<td>Franchini et al. [64]</td>
</tr>
<tr>
<td>Italian coasts</td>
<td>0.007</td>
<td>Microsatellites</td>
<td>Franchini et al. [64]</td>
</tr>
<tr>
<td>Greece (Aegean vs. Ionian Sea)</td>
<td>0.002</td>
<td>Microsatellites</td>
<td>Gkagkavouzis et al. [48]</td>
</tr>
<tr>
<td>Adriatic</td>
<td>0.033</td>
<td>Microsatellites</td>
<td>Šegvić-Bubić et al. [52]</td>
</tr>
<tr>
<td>Atlantic</td>
<td>0.068</td>
<td>Microsatellites—EST—mtDNA dloop</td>
<td>Cossia et al. [53]</td>
</tr>
</tbody>
</table>

In 2021, an SNP array tool was developed by Peñaloza et al. [65] and designed for both species (European sea bass and gilthead sea bream). This tool, called MedFish array, was designed using individuals from 27 populations of gilthead sea bream and from 24 populations of European sea bass that were collected throughout the species distribution. More specifically, MedFish includes about 30 K markers for sea bream and about 30 K markers for sea bass [65]. Overall, SNP arrays represent high-throughput genotyping methods that may result in more robust assumptions in population structure and genetic variability assessment. The MedFish tool was utilized for the investigation of population structure in a large sample size of wild and farmed populations of sea bream and sea bass throughout the Mediterranean Sea, including three wild sea bream populations from the Atlantic Ocean as well [66]. According to the results, it was revealed that the degree of genetic differentiation among wild sea bream populations was generally low. Indicatively, the majority of pairwise \( F_{st} \) comparisons were lower than 0.05. Furthermore, the differentiation between Mediterranean and Atlantic populations was confirmed; however, the data neither support the genetic structure among Mediterranean populations nor the genetic distinction of wild in comparison to farmed populations [66], unlike the previous study by Maroso et al. [60] who distinguished the genetic clusters of wild populations.

*D. labrax* genetics indicate similar patterns to *S. aurata*, characterized by a low degree of differentiation [66]. Further, previous data support the existence of slight genetic differentiation among sea bass wild populations in the Mediterranean basin [67–73]. Among the above studies, two of them [71,72] proposed differentiated clusters in contrast with the study by Villanueva et al. [66] where a gradual change was observed when moving from east to west. More specifically, a low level of differentiation was exhibited among sea bass populations originating from eastern and western Mediterranean [66] with an accordingly significant level of gene flow.

Concerning wild and farmed populations, Greek-farmed individuals have been found to be significantly distinct in comparison to the wild ones [56]. This phenomenon was attributed mainly to three possible explanations. Firstly, the geographic origin of the wild and farmed individuals was different. Secondly, the samples may originate from common locations, but the farmed individuals retained only a small amount of the genetic profile. Lastly, the artificial selection and continuous breeding programs led to distinct genetic structure of the farmed individuals. However, the same study showed that this was not the case for Spanish samples, since wild and farmed samples are grouped into a single cluster [56]. The existence of genetic differentiation among wild and farmed European sea bass has also been observed by Brown et al. [74] and Villanueva et al. [66]. This was probably due to the heterogeneous nature of the *D. labrax* aquaculture, which has been implied to be generated from many origins [66]. The information regarding genetic
differentiation between wild and farmed populations is of paramount importance not only for breeding programs in order to create a base population but for investigation of the introgression level if existing.

In summary, although contradictory results occasionally exist regarding the differentiation among wild *S. aurata* populations, in most cases, the degree of differentiation among them remains low. The above observation demonstrates the existence of a considerable level of gene flow among wild populations potentially enhanced by the escape events from fish cages. Nevertheless, clear genetic differentiation was observed when wild and farmed *D. labrax* populations were studied. Although selection schemes are used in fish farms towards improvement of growth rate and other desirable traits [28], an important observation is that the heterozygosity (HE) levels among farmed populations were only slightly lower than the ones among wild populations, probably reflecting the care taken in breeding schemes by the farm owners to maintain genetic diversity.

4. Sea Bream Escapes—A Case Report in Evoikos Gulf, Central Greece

Fish farm employees are in general aware of the problem of fish escapes. For instance, determination of escapes from a 3-year survey through questionnaire collection from six countries, i.e., Ireland, UK, Norway, Spain, Greece, and Malta, as well as some information derived from the Norwegian Fisheries Directorate and the Scottish Aquaculture Research Forum, resulted to $9 \times 10^9$ finfish escapees, recorded from 242 escape events [9]. Gilthead sea bream escapes exhibited the highest percentage of escapes reaching 76.7% (6,846,100 out of 8,922,863 total fish escapees). Of the 6,846,100 sea bream escapees, two of them were counted for 1.9 and 3.8 million escapees. In Greece, 15 sea bream and 9 sea bass escape events were recorded over this 3-year period [9]. However, there is a gap in knowledge regarding more recent data on Greek aquaculture.

A detailed assessment was conducted at the Evoikos Gulf fish farm, located in the Western Aegean, Central Greece. The farm, representing a typical medium to large aquaculture unit, reared sea bream and sea bass from 2016 to 2021. The assessment focused on the reasons behind escapes, the net holes in the fish cages (Figure 1), and the corresponding number of escapes. During the examined period, 37 escape events were recorded in total (Figure 2). Escape events were attributed to several reasons, including environmental reasons such as adverse weather conditions, sea turtles that apparently caused damage to the materials of the fish cages, or due to technical reasons during transfer (Figure 3a). Furthermore, according to the number of escaped fish, the events were categorized into low (0–500 escapes), medium (500–1000 escapes), and high (>1000 escapes) density (Figure 3b).

Figure 1. Sea cage damages allowing fish escapes in sea bream aquaculture from Evoikos Gulf.
transfer (Figure 3a). Furthermore, according to the number of escaped fish, the events were categorized into low (0–500 escapes), medium (500–1000 escapes), and high (>1000 escapes) density (Figure 3b).

Figure 2. Total reared fish before escape event, % percentage of escaped fish to the total reared fish, and estimation of the fish number in each escape event in Evoikos marine fish farm.

Figure 3. (a) Reasons to which escape events have been attributed and (b) density of the escape events.

It should be mentioned that the majority of the highest number of escapes was observed in 2020 when 13 escape events took place, with most of them included in the low category. These events may have been affected by the pandemic outbreak that took place during this year and specifically by the reduced operational work of the employees. It can be assumed that farm operations and management of escapes has not improved in
these years as the number of escapes does not exhibit a downward trend for the next years recorded (Figure 2).

Furthermore, it should be highlighted that the range of fish loss percentage varied from 0 to 2% at the farm level, with only six cases overlapping 2%, representing thus a generally stable rate that could be reduced with appropriate management strategies. Additionally, it should be noted that during these years, fish numbers exhibited fluctuations in the Evoikos fish farm, with the lowest and the highest number being recorded in 2018 (33,952) and 2016 (163,235), respectively (Figure 2).

To sum up, from the data collected from the fish farm in Evoikos during 2016–2021, no stable trend regarding the fish escape events in each year was recorded, a fact considered to be expected, since they are mostly caused by casual accidents. However, the number of fish escapes exhibited a fluctuation between 500 and 1500 individuals/case of incidents.

5. Consequences and Proposed Strategies for Risk Reduction of Fish Escapes

Escape events are recorded every year, representing a serious issue for the aquaculture industry. However, there is a difficulty in mitigating these events. It is worth noting that domestic-reared individuals exhibit a reduced capacity to avoid and compete with the predators as well as to survive in the wild in comparison with the wild conspecific individuals [75].

Sea bass escapees seem to be able to establish self-reproducing populations and reach maturity in the wild in non-native ecosystems as well as to compete with native species for food sources [76,77]. Additionally, diet shifts towards a natural diet [78], as well as rapid dispersion after escape [79], were observed in meagre (*Argyrosomus regius*) (Asso, 1801) and in sea bass [80], although it seems that aquaculture escapees might need some time to adapt to the native-wild environments. Furthermore, sea bass escapees from all-size classes including some egg-bearing females and juveniles were caught in Cypriot waters [74], whereas high mortalities of escapees have been occasionally observed [81].

Regarding *S. aurata* escapees, evidence showed that they got used to the natural prey of the species one week after the escape event, although a high mortality rate was recorded (>60%). However, some individuals in the first case [82] and (>70%) of escapees in the second case [83] remained near farm facilities for long periods. Furthermore, although exhibiting a dispersal ability of around 20 km, sea bream escapees were mostly recaptured near fish farms [84]. In comparison with escaped sea bass, sea breams seem to need a shorter adaptation period in the natural environment [80]. Furthermore, the high mortality of initial sea bream escapees is supported by many studies [80,82,85].

Despite the biological factors related to the risk from escapes, management strategies are needed to mitigate the effect of the phenomenon. Continuous monitoring and sampling for evaluation of genetic introgression from escapees is crucial, however it may be complicated for the farms on their own. On the other hand, specific infrastructure, such as the use of copper-alloy mesh materials and nets could represent a promising practice for reducing the density or even eliminating the escape events [86]. This practice has been proven beneficial for several other aspects of aquaculture including mitigation of biofouling, leading to better economic performance of the farms [87].

6. Conclusions

As aquaculture represents the fastest-growing food production industry, the sustainable development of this sector should be a priority. Although gilthead sea bream is ranked among the most highly produced species, there are many questions regarding its domestication level from an evolutionary adaptation point of view [42]. It should be emphasized, however, that there is evidence for an aquaculture-induced evolution pattern [36]. Domestication has the potential to be a fundamental tool towards sustainable aquaculture development as it can lead to increased production of the farmed species, preferably native ones. The development of aquaculture practices regarding native species is of major importance as they can exhibit better adaptation towards socioeconomic and environmental
issues [35]. However, there is a risk of genetic introgression with wild populations that does not exist when farmed species are non-native.

Although the marine environment seems to have no distinct boundaries in combination with the extended gene flow existing in marine species with pelagic larvae, population genetic structure has been observed in several marine animal populations. The above observation was also confirmed for gilthead sea bream as a subtle genetic structure was detected, as proposed by recent genetic analyses [e.g., 60]. However, the results are contradictory with more extended research in this field needed. Generally, the $F_{ST}$ levels in sea bream studies seem to be lower than those observed in other marine species. Genetic differentiation has been observed between Atlantic and Mediterranean sea bream populations, while low levels of differentiation have been observed among basins. The low differentiation levels within the basins represent an observation that can be expected, keeping in mind the long period of larval duration of sea bream (>30 days). Therefore, escape events are not exclusively the reason for the limited genetic structure within basins and fronts, as the differentiation among wild populations inhabiting these areas seems to remain stable. They also create the risk of introgression of farmed populations that have lower genetic diversity and may reduce adaptation and fitness of local wild populations. Studies providing evidence for genetic structure and differentiation among wild and farmed $S. aurata$ populations shed light on unanswered biological questions as they represent a pivotal step towards the management of this species which represent the subject of extended aquaculture production.

Escape events represent a common phenomenon in all aquaculture sites established in open pens. Despite all the efforts to mitigate this phenomenon, these events are still recurrent and will probably continue to occur, due to many failure types during their operation and the exacerbation of extreme weather events associated with climate change. Few attempts regarding recapturing of escaped fish after large-scale escape events have been successful [85,88]. However, some major questions remain unanswered. Despite the large quantity of studies that have been conducted mainly on cod, Atlantic salmon, and rainbow trout, there is a gap in knowledge regarding other important farmed species such as sea bass and sea bream. Especially regarding sea bream, a lack of unequivocal documentation exists, referring to the biological and ecological consequences (productivity, distribution, mortality, abundance, fitness success, resilience, life-history profiles) of introgression to the wild populations. Additionally, there is a lack of information regarding the post-escape behavior and recapture success of fish involved in mass escapes (>10,000 fish).

Contrariwise to the escape events’ expected effects, genetic differentiation among basins regarding sea bream seems to remain stable. However, the farmed escapes, as well as their offspring, pose a major environmental threat and can cause important evolutionary changes in wild individuals in the future [89]. As such, further efforts for escapees’ survival reduction in the wild, recapture programs’ establishment, and proper legislation in farming industries should be implemented for escapees’ number reduction [88]. However, even a modest survival rate after an escape event might entail negative ecological consequences for wild populations [89].

In conclusion, escape events represent a major threat, both ecological and economic. Particularly in sea bream as well as sea bass farming, interestingly, genetic structure and differentiation among wild populations seem to be unaffected (low but significant) from the so-far escape events. Thus, as indicated by (a) the small percentages of fish escaped in both our case (Evoikos farm) and other ones reviewed, (b) the undoubtful low levels of population genetic differentiation regardless of the escape events, and (c) the physiological behavior of the species (e.g., long pelagic phase, difficulties in the survival of escaped fish and even mortalities), it can be concluded that escape events represent a risk implying numerous ecological impacts caused by farmed finfish, including seabream and seabass [90]. Nevertheless, since omitting such ecological risks is a responsibility of the aquaculture companies, suitable management measurements in Mediterranean countries with many farmed fish escapes would be a useful strategy to avoid future negative events. These
measurements and strategies should be focused on further efforts for recapture programs' development, reduced escapees' survival, and proper legislation together with more data on escapees' survival percentage, their migration pathways, and the way these pathways relate to mortality, the location, their growth stage, the type of escape event, and the season of release.


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**References**


