

Epimutations in Developmental Genes Underlie the Onset of Domestication in Farmed European Sea Bass

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The RRBS and RNA-seq data that support the findings of this study have been deposited in the NCBI Gene Expression Omnibus and are available with the following accession codes: GSE104366 for muscle and testis of wild fish and GSE125124 for the rest of NGS libraries.

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Abstract

Domestication of wild animals induces a set of phenotypic characteristics collectively known as the domestication syndrome. However, how this syndrome emerges is still not clear. Recently, the neural crest cell deficit hypothesis proposed that it is generated by a mildly disrupted neural crest cell developmental program, but clear support is lacking due to the difficulties of distinguishing pure domestication effects from preexisting genetic differences between farmed and wild mammals and birds. Here, we use a farmed fish as model to investigate the role of persistent changes in DNA methylation (epimutations) in the process of domestication. We show that early domesticates of sea bass, with no genetic differences with wild counterparts, contain epimutations in tissues with different embryonic origins. About one fifth of epimutations that persist into adulthood are established by the time of gastrulation and affect genes involved in developmental processes that are expressed in embryonic structures, including the neural crest. Some of these genes are differentially expressed in sea bass with lower jaw malformations, a key feature of domestication syndrome. Interestingly, these epimutations significantly overlap with cytosine-to-thymine polymorphisms after 25 years of selective breeding. Furthermore, epimutated genes coincide with genes under positive selection in other domesticates. We argue that the initial stages of domestication include dynamic alterations in DNA methylation of developmental genes that affect the neural crest. Our results indicate a role for epimutations during the beginning of domestication that could be fixed as genetic variants and suggest a conserved molecular process to explain Darwin's domestication syndrome across vertebrates.

Key words: developmental processes, animal domestication, epigenetics, neural crest, domestication syndrome, epimutation, transgenerational effects, glutamate receptors.

Introduction

Domestication lies at the heart of human civilization and involves raising animals in an environment that differs substantially from their natural habitat. Darwin was the first to notice that domesticated animals evolve certain morphological, physiological, and behavioral traits (Darwin 1868), a phenomenon now known as the domestication syndrome (Wilkins et al. 2014). Research into the mechanisms underlying the domesticated phenotypes has traditionally focused on the detection of genes under positive selection in mammalian and avian domesticates, where domestication is mostly pronounced in behavioral traits such as tameness. However, this approach commonly involves interspecies comparisons, since most current domesticates have remained genetically isolated from their wild ancestors for thousands of years. Thus, the processes taking place during the initial stages of domestication, that is, the beginning of human-controlled rearing in a captive farming environment, have remained unclear and their contribution to the acquisition of a domesticated phenotype not well assessed (Wilkins 2017).

The first stages of domestication and adaption to a new environment likely involve epigenetic changes (Belyaev et al. 1981; Trut et al. 2009; Koch et al. 2016; Vogt 2017), that is, epimutations, defined as heritable changes in gene activity due to DNA modification, not mutation, occurring via mitotic transmission of epigenetic marks rather than DNA variants (Oey and Whitelaw 2014). Epigenetic regulatory mechanisms, such as DNA methylation, can respond to environmental change and, at the same time, be stable enough to be maintained throughout lifetime. Recently, there is mounting evidence in both plants and animals showing that epimutations can be transmitted across generations (Skinner et al. 2015; Chamorro-Garcia et al. 2017; Knecht et al. 2017; Leroux et al. 2017; Vogt 2017; Kamstra et al. 2018; Skjærven et al. 2018; Zhang Y-Y et al. 2018). To our knowledge, no studies have specifically addressed the involvement of epigenetic changes established during early development in the first steps of domestication prior to the appearance of major genetic differences. To determine whether such changes underlie the domestication syndrome, we reasoned that fish could provide a model in which to

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investigate the effects of the farming environment. Although the domestication syndrome refers originally to mammals, nevertheless domesticated fish exhibit many characteristics of domestication syndrome comparable to those of mammals, including jaw alterations, abnormal pigmentation, and behavioral changes (see examples in [supplementary fig. 1, Supplementary Material](#) online). Unlike domesticated mammals and birds, however, in fish wild relatives remain easily accessible. Consequently, it should be possible to make comparisons between genetically similar animals.

The European sea bass (*Dicentrarchus labrax*) is one of the main farmed species in all Mediterranean regions but selective breeding is not widespread. Thus, although some farms have carried out breeding for several generations others still rely on wild-caught fish for broodstock. A previous study identified genomic regions under positive selection in sea bass obtained from two independent Mediterranean hatcheries that had been carrying out selective breeding for 25 years ([Bertolini et al. 2016](#)). To confirm that sea bass would be a suitable model for analysis of epigenetic changes during domestication, we compared genes under positive selection in this species with those found in mammalian and avian domesticates ([Carneiro et al. 2014](#); [Montague et al. 2014](#); [Schubert et al. 2014](#); [Kukekova et al. 2018](#); [Pendleton et al. 2018](#); [Zhang Z et al. 2018](#)) ([supplementary fig. 2 and supplementary data set 1, Supplementary Material](#) online). We found several genes in common, among them genes coding for glutamate receptors, which are found under positive selection in all the domesticates examined ([O'Rourke and Boeckx 2018](#)). This, along with the observation that farmed sea bass also shares some of the characteristics of the domestication syndrome, for example, changes in morphology ([Arechavala-Lopez et al. 2012](#)), jaw malformation ([Babbucci et al. 2016](#)), indicates that this species constitutes a suitable model to study the first steps of domestication in vertebrates.

Results and Discussion

Early Domesticates Differ in DNA Methylation from Wild Fish

To identify the underlying epigenetic processes operating during the early stages of domestication, we first compared wild and early domesticates of sea bass exhibiting no genetic differences, as confirmed by a low fixation index (mean $F_{ST} = 0.0085$) ([supplementary fig. 3, Supplementary Material](#) online; see Materials and Methods). Early domesticates were the offspring of a cross between a 3-year-old unselected broodstock that were hatchery raised for no more than one generation. We sampled adult tissues derived from all three embryonic layers—brain (ectoderm), muscle and testis (mesoderm), and liver (endoderm)—and analyzed DNA methylation by reduced representation bisulfite sequencing (RRBS). We chose to perform RRBS that effectively enriches for the informative parts of the genome, instead of whole genome bisulfite sequencing (WGBS), which produces 70–80% of uninformative reads for CpG dinucleotide methylation ([Ziller et al. 2013](#)). RRBS libraries were sequenced at an average 47-fold coverage per sample using 3 replicates per group and per tissue, that is,

12 samples for wild fish and 12 samples for early domesticates (technical details and data quality in [supplementary table 1 and supplementary fig. 4, Supplementary Material](#) online).

Differentially methylated regions (DMRs) were defined as having more than 15% methylation differences (False Discovery Rate, $FDR < 0.05$) to reassure biologically meaningful results, between wild and early domesticates, kept under the same environmental conditions of temperature and photoperiod. DMRs were present in all four tissues examined and had a genome-wide distribution ([fig. 1A and B](#)). DMRs were preferentially located (z -score = 2.92, P value = 0.0023) inside gene bodies or within 5-kb upstream of the transcription start site or downstream of the transcription termination site ([supplementary fig. 5a, Supplementary Material](#) online) and overlapping CpG islands and/or shores (mean unique DMRs, 53.53%; [supplementary fig. 5b, Supplementary Material](#) online). Compared with wild fish, the number of hypomethylated DMRs in early domesticates (210 in brain, 476 in muscle, 275 in testis, and 52 in liver) was higher than the number of hypermethylated DMRs (148 in brain, 160 in muscle, 82 in testis, and 37 in liver; Fisher's exact test for count data, odds ratio = 0.42, P value $< 2.2 \times 10^{-16}$, [supplementary fig. 5c, Supplementary Material](#) online). The possibility that a fraction of the methylation differences may have a genetic basis cannot be excluded. However, considering the low F_{ST} between wild and early domesticates, a value even below the lowest value of the genetic differentiation of natural populations ($F_{ST} = 0.011$) ([Loukovitis et al. 2015](#)), the influence of the genetic background to epimutations can be considered minimal.

Independent assessment of DNA methylation levels was carried out by multiplex bisulfite sequencing (MBS) ([Anastasiadi, Vandeputte, et al. 2018](#)), targeting the detected DMRs of six genes ([supplementary fig. 6, Supplementary Material](#) online). MBS results fully validated our genome-wide approach with RRBS (Pearson's correlation coefficient $\rho = 0.89$, P value $< 2 \times 10^{-16}$; [supplementary fig. 6, Supplementary Material](#) online). In the muscle of hatchery-reared versus wild salmon, DMRs were found in the gene body or regulatory regions of 52 genes ([Le Luyer et al. 2017](#)). Fifteen genes of the sea bass showed similarities to the genes affected in salmon and these included five protocadherins (*pcdh18* and *fat3*), three dual specificity phosphatases and one homeobox protein ([supplementary data set 2, Supplementary Material](#) online). Protocadherins and homeobox genes have also been found differentially methylated between wild and hatchery-reared steelhead trout ([Gavery et al. 2018](#)). Thus, DNA methylation differences between wild and domesticated fish are not exclusive to the sea bass.

To gain insight into the functions of the genes with DMRs, we performed enrichment tests for the associated Gene Ontology (GO) terms. The most significantly enriched biological processes GO terms were related to developmental process (GO:0032502), such as anatomical structure development (GO:0048856) and regulation of embryonic development (GO:0045995). Among the developmental processes affected by the farming environment, a large portion was associated with the nervous system and neural crest cell

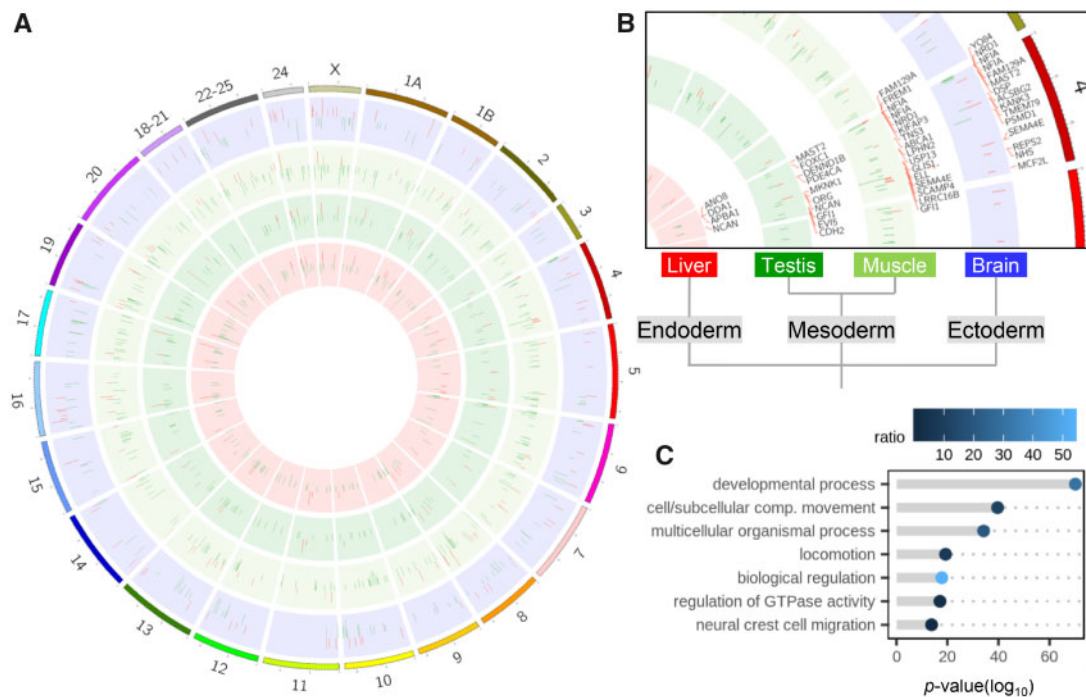


FIG. 1. DNA methylation changes in early domesticated versus wild European sea bass. (A) Genome-wide distribution of DMRs; red, hypermethylation; green, hypomethylation. (B) Details of annotated genes on chromosome 4 containing DMRs in tissues derived from the ectoderm (brain; blue), paraxial mesoderm (muscle; light green), intermediate mesoderm (testis; green), and endoderm (liver; red). (C) GO term enrichment of genes that contain DMRs. The length of the bar indicates the \log_{10} -transformed P value of the enrichment and the color scale indicates the amount (in percent) of genes associated with the specific GO term as compared with the total number of genes with DMRs.

(NCC) migration (GO:0001755; [fig. 1C](#); full list of genes with DMRs in [supplementary data set 3, Supplementary Material online](#), and list of GO term enrichment in [supplementary data set 4, Supplementary Material online](#)). Genes that are responsible for NCC migration during early development are not necessarily expressed in differentiated, adult tissues. Thus, differences found in adults suggest that these genes became epimutated by the farming environment at the time they were expressed in the early domesticates.

Gene Expression Is Altered in Early Domesticates

It has been shown that just one generation of domestication can heritably alter gene expression ([Christie et al. 2016](#)). The possible effects of DNA methylation differences on gene expression in early domesticated sea bass were investigated by RNA sequencing (see quality of RNA-seq data in [supplementary fig. 7, Supplementary Material online](#), and RNA-seq statistics in [supplementary table 2, Supplementary Material online](#)). The number of differentially expressed genes (DEGs; P adjusted < 0.05 and absolute \log_2 fold change > 1 ; [supplementary fig. 8, Supplementary Material online](#)) ranged from 248 in the testis to 2,416 in the liver, with an approximately equal number of upregulated and downregulated genes in early domesticates versus wild sea bass (see full list of DEGs in [supplementary data set 5, Supplementary Material online](#)). RNA-seq results were validated by qPCR in four genes (Pearson's correlation coefficient $\rho = 0.60$, P value = 0.00016; [supplementary fig. 9, Supplementary Material online](#)). Overall, DEGs were related to the defense response,

including regulation of cytokine production and immune system process ([supplementary fig. 10a, Supplementary Material online](#); see a full list of GO terms enriched in [supplementary data set 6, Supplementary Material online](#)). The number of DEGs that also contained DMRs was between 5 (testis) and 28 (muscle) ([supplementary fig. 10b–e, Supplementary Material online](#)). This low number is likely due to differences in the temporal and spatial expression of these genes, which should be affected during development rather than in adulthood, since most DMRs were found in developmental genes ([fig. 1C](#)). Changes in the expression of stress- and immune-related genes have been previously reported in farmed fish ([Tymchuk et al. 2009](#); [Bicskei et al. 2016](#); [Wellenreuther et al. 2019](#)). Therefore, our gene expression results are consistent with the phenotypic responses to the farming environment observed in other fish species.

DNA Methylation Changes in Developmental Genes Are Established during Gastrulation

The observation that DMRs were mostly found in development-related genes led us to hypothesize that the farming environment induces epimutations during early development, and that these are responsible for mild developmental deficits that are maintained through adulthood. Therefore, it was necessary to discriminate between epimutations present in adult tissues from those established already during early development, which have more potential for long-term effects since they are more persistent and may propagate consistently in a variety of differentiated tissues,

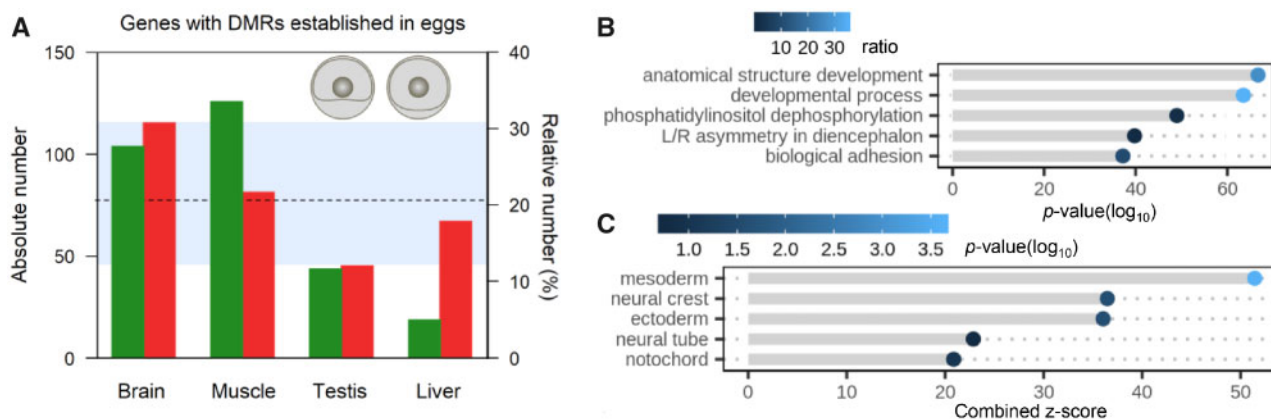


Fig. 2. Epimutations established during early development. (A) Absolute (green) and relative (red) number of genes with DMRs established during gastrulation, the latter shown as a percentage of the total number of genes with DMRs in adults. The dotted line indicates the mean of the relative number and the shaded area includes the range. (B) GO term enrichment of genes that contain DMRs. The most significantly enriched GO terms, related to development, are ranked according to the decreasing order of $-\log_{10}$ -transformed P value of the enrichment and colored according to the percentage of genes that contain DMRs and that are members of each GO category. (C) Enrichment of tissues where the genes with DMRs are expressed. The most significantly enriched tissues are ranked according to the combined z-score as calculated by the Enrichr tool and colored according to the $-\log_{10}$ -transformed adjusted P value of the enrichment.

including the germ line (Faulk and Dolinoy 2011). Since epimutations of the latter type may affect directly the germ line, they are likely more susceptible to be involved in transgenerational effects. Even if the extent to which DNA modifications can be inherited through meiotic divisions is still under debate, several cases of environmentally induced epimutations even in somatic tissues have been reported in the last years to be transgenerationally transmitted (Knecht et al. 2017; Leroux et al. 2017; Kamstra et al. 2018; Norouzitallab et al. 2019). In fish, additionally and in contrast to the situation in mammals, there seems to be little or no epigenetic reprogramming after fertilization, providing further means for transgenerational epigenetic inheritance since epigenetic marks present in the genome of the sperm or of the eggs would not have been reprogrammed or “erased” in the genome of the zygote (Jiang et al. 2013; Potok et al. 2013). Even though the detailed mechanisms of soma-to-germline transfer of epigenetic patterns remain mostly an unresolved question, recent studies point to possible ways of soma-to-germline transfer of information (Cossetti et al. 2014; Devanapally et al. 2015; Eaton et al. 2015; Reilly et al. 2016), including mediation by exosomes, circulating double-stranded RNAs, and transposable elements (Devanapally et al. 2015; Sharma 2017; Danchin et al. 2019; Norouzitallab et al. 2019; Perez and Lehner 2019).

To determine whether epimutations were indeed established during early development, we therefore collected hatchery-reared sea bass embryos at 60–90% epiboly (~30-h postfertilization), when the embryo remains a homogeneous cell mass and sequenced three RRBS libraries (see Principal Component Analysis in supplementary fig. 11, Supplementary Material online). This sampling point was chosen to allow enough time for epimutations to accumulate due to the farming environment, but not long enough for tissue- or organ-specific epimutations to have arisen. In this way, we also removed all noise due to differences in the

environment (food, habitat, etc.) of early domesticates and wild fish. An average of 20.6% of loci harboring DMRs in adult tissues had similar levels of methylation already present in the embryos (defined as no more than $\pm 10\%$ differences in at least 50% of the CpGs within the DMRs), with a minimum of 12.1% in the testis and a maximum of 30.8% in the brain (fig. 2A). Thus, roughly one fifth of the DMRs present in adult tissues of farmed fish were already established within the first ~30 h of life. Significantly, despite eliminating on average ~80% of the DMRs present in adults after filtering, developmental processes (GO:0032502) such as anatomical structure development (GO:0048856) were still the most enriched terms (fig. 2B; see a full list of genes with DMRs established in embryos in supplementary data set 7, Supplementary Material online, and a list of GO terms enriched in supplementary data set 8, Supplementary Material online). More specifically, pathway analysis (Reactome database 2016) showed that these genes participate in several aspects of extracellular matrix (ECM) organization (e.g., nonintegrin membrane–ECM interactions, laminin and integrin cell-surface interactions, and collagen degradation), as well as glutamate binding, adrenoceptors and synaptic plasticity (supplementary table 3, Supplementary Material online). Interestingly, genes harboring epimutations early in development are predominantly expressed in the mesoderm, the neural crest and the ectoderm (adjusted P value < 0.05) or similar structures, such as the neural tube and the notochord (fig. 2C; full list in supplementary table 4, Supplementary Material online). Taken together, these results suggest that the first steps in domestication involve epimutations established in genes related to developmental processes and expressed in the embryonic germ layers, including the neural crest.

During NCC migration, cells separate from the surrounding tissues. This process, called delamination, requires the excretion of integrins, laminins and collagens such as the ones detected in this study (supplementary table 3,

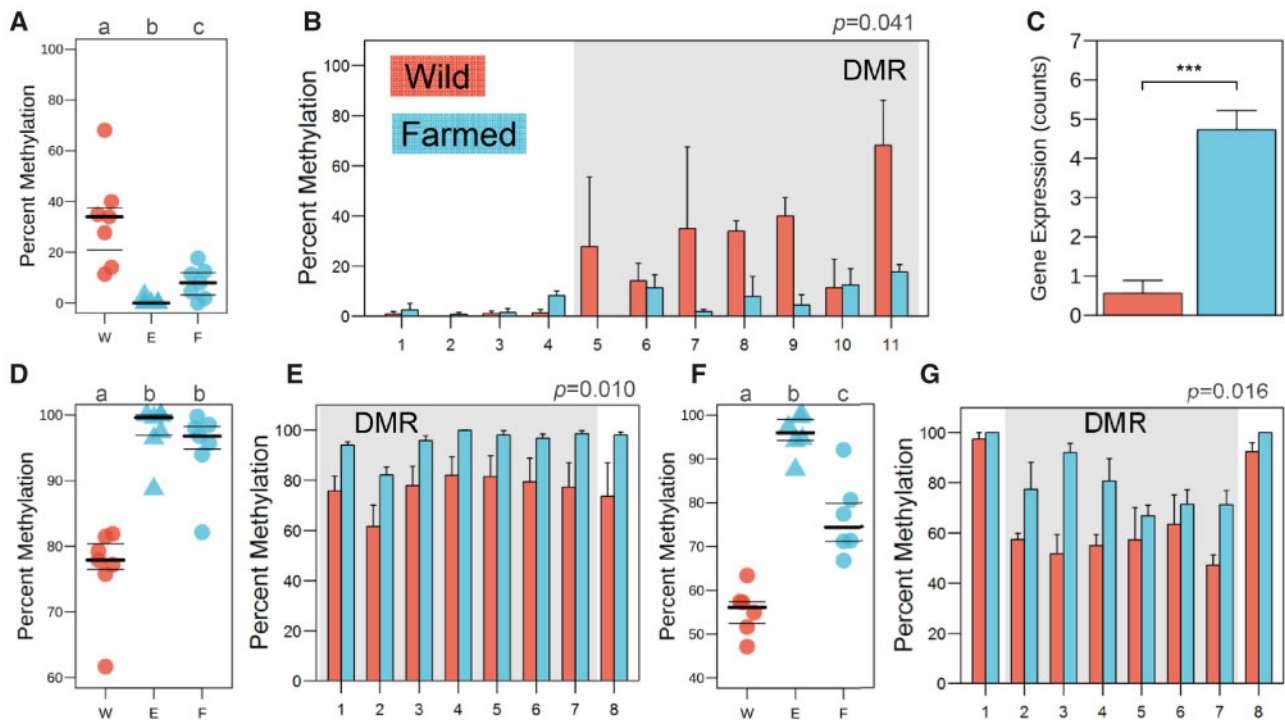


Fig. 3. Influence of the farming environment on genes interacting with the ECM and neurotransmitters. Distribution of CpG methylation in wild (red, W) and farmed (blue) sea bass during gastrulation (E) and in adult tissues (F) inside the DMRs of *adamts9* (A), *col18a1* (D), and *gria4a* (F). Mean methylation of CpGs around the DMRs of *adamts9* in muscle (B), *col18a1* in testis (E), and *gria4a* in brain (G). Differential gene expression of *adamts9* is also shown (C). The extent of DMRs is highlighted with gray shading and the CpGs are arbitrarily numbered. Differences in expression are shown with the following equivalence: ****P* adjusted <0.001.

Supplementary Material online). For example, ADAMTS9, a matrix metalloproteinase whose function is conserved in vertebrates (Christian et al. 2013; Desanlis et al. 2018), is hypomethylated in embryos of early domesticated sea bass (fig. 3A) and this is maintained in adult muscle (fig. 3B), resulting in higher *adamts9* expression levels (fig. 3C). Interestingly, homologs of ADAMTS9 are under positive selection in several domesticates, including rabbit (Carneiro et al. 2014), fox (Kukekova et al. 2018), and duck (Zhang Z et al. 2018). Collagens are also under positive selection in the genomes of rabbit (Carneiro et al. 2014), dog (Pendleton et al. 2018), fox (Kukekova et al. 2018), and horse (Schubert et al. 2014), and we found in sea bass domesticates that *col18a1a* contained a hypermethylated DMR in the testis (fig. 3E), with methylation patterns established already during gastrulation (fig. 3D). Another collagen, *col14a1a*, contained a hypermethylated DMR in the brain (supplementary fig. 12a, Supplementary Material online). The protocadherin γ -*a11-like*, which also belongs to a gene family involved in delamination, was found to carry a DMR in liver (supplementary fig. 12b, Supplementary Material online). This is consistent with previous work showing that cadherins and protocadherins are under positive selection in cat (Montague et al. 2014), dog (Pendleton et al. 2018), and duck (Zhang Z et al. 2018) and exhibit DMRs in hatchery-reared salmon (Le Luyer et al. 2017). DMRs in early domesticates versus wild sea bass were also observed for *phldb1* in brain (supplementary fig. 12c, Supplementary Material online), *foxc1* in testis (supplementary fig. 12d, Supplementary Material online) and *mapk8a* in

muscle (supplementary fig. 12e, Supplementary Material online). The finding that many genes with epimutations established early in development are similar to genes under positive selection in domesticates from a range of species, and that these are also linked to processes of NCC migration, suggests that our observations in sea bass could reflect a general process underlying the onset of the domestication syndrome.

Members of the glutamate receptor family deserve particular attention because they have been found under positive selection in the genomes of all domesticated species studied without exception (O'Rourke and Boeckx 2018), and including the sea bass after 25 years of selective breeding (Bertolini et al. 2016) (supplementary fig. 2, Supplementary Material online). In this study, the ionotropic glutamate receptor *gria4a* contained a hypermethylated DMR (fig. 3G) in the brain of early domesticated sea bass and displayed similar methylation patterns during gastrulation (fig. 3F). Likewise, another glutamate receptor, *grik4*, exhibited a hypermethylated DMR in the muscle (supplementary data set S7, Supplementary Material online). In addition, the expression of *grik5* was downregulated in the testis and liver of early domesticated sea bass, and the same pattern was observed for *grm2*, a glutamate metabotropic receptor in the liver (supplementary data set S5, Supplementary Material online). Among the most easily recognizable features of domestication syndrome are changes in the nozzle and associated jaw deformities. This can be explained in the NCC-deficit hypothesis by the fact that the craniofacial bones, including the jaws

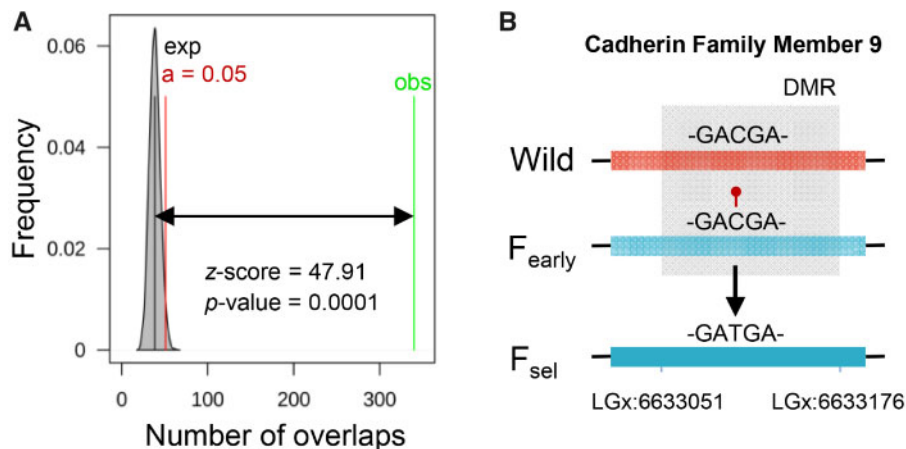


FIG. 4. Epimutations as a consequence of the farming environment associate with genetic changes in the sea bass after 25 years of domestication. (A) DMCs in early domesticate versus wild sea bass overlap with on-the-spot SNPs in two sea bass populations after 25 years of selective breeding (Bertolini et al. 2016). The number of overlaps of the two genomic sites is shown and tested via permutations. The shaded grey area shows the number of overlaps of randomized regions with the mean represented by the black bar. The green line represents the actual number of overlaps of SNPs with DMCs and the double arrow its distance from the significance limit in red. The significance of the association is indicated by the z-score and the P value. (B) Schematic representation inside the DMR of cadherin family member 9 of a CpG in wild sea bass that was found hypermethylated (red lollipop) in early domesticates (F_{early}) and converted into a TG after 25 years of selective breeding (F_{sel}).

(upper maxilla and mandibula), are derived from the neural crest, whereas other bones are mesodermal in origin (Wilkins et al. 2014). In this context, it is interesting to note that glutamate receptors were also found differentially expressed in the lower jaw of European sea bass with mandibular prognathism (Babbucci et al. 2016).

Epimutations Associate with Genetic Variants after Generations of Rearing in Captivity

Experimental evidence in Atlantic salmon (*Salmo salar*) and delta smelt (*Hypomesus transpacificus*) suggest the possibility of rapid genetic adaptation to captivity (Finger et al. 2018; Horreo et al. 2018). It has been argued that epimutations, particularly DNA methylation changes, can eventually become permanently integrated into the genome by promoting mutation of methylated CpGs or through the generation of copy number variants or genome instability (Skinner et al. 2015; Vogt 2017). Indeed, it is well accepted that methylated cytosines tend to mutate 10–50 times faster than unmethylated ones (Chen et al. 2014; He et al. 2015). However, the role of epimutations in rapid genetic adaptation had not been shown.

To test whether differential methylation due to early domestication is correlated with genetic variants and could therefore be genetically assimilated after several generations, we performed association analysis of genomic regions. We found that differentially methylated cytosines (DMCs) of early domesticates associated ~ 10 times more than expected by chance (z -score = 47.91, P value = 0.0001, 10,000 permutations) with cytosine-to-thymine (C-T) single-nucleotide polymorphisms (SNPs) in two independent populations of sea bass after 25 years of selective breeding (Bertolini et al. 2016) (fig. 4A). This occurred, for example, in cadherin family member 9 (fig. 4B). These results do not provide a causal link between epigenetic and genetic changes and it could be

possible that they represent only a correlation and a case of convergent evolution. Although we cannot exclude this possibility, our results conform to previous studies regarding the high mutability of methylated CpGs (Chen et al. 2014; He et al. 2015; Skinner et al. 2015) to highlight a significant non-random association of genomic sites. A recent study in domesticated chickens and their closest ancestors found that DNA methylation, depending on its levels and interindividual variability, can lead to biases toward SNPs or copy number variation mutations, promoting genomic specificity or flexibility, respectively (Pétille et al. 2019). Thus, these and our results suggest that epimutations occurring during the early stages of domestication can become integrated into the genome as genetic changes after just several generations.

Conclusions

Recent research to elucidate the process of domestication has heavily relied on comparative genomics (Wilkins 2017). This is due to the complexity of the study of the domestication, which combines a polygenic basis, on one hand, with the “conditions of living,” according to Darwin, on the other. Domestication results in widespread common phenotypic characteristics (Darwin 1868; Wilkins 2017). Here, we not only used comparative genomics but integrated epigenomic and transcriptomic data of adult early domesticates and during gastrulation and made comparisons with their closest wild counterparts. One experimental aspect that we could not address concerns the epigenetic patterns of farmed fish reared in the wild environment. However, this would involve releasing freshly fertilized eggs from farmed progenitors into the ocean and recapturing the same fish when adults, which is an essentially impossible experiment in a fish like the sea bass. Likewise, functional experiments involving for example, knocking-down specific genes among the ones discussed in this study or the DNA-methyltransferases, for example, would

likely result in a drastically affected phenotype. Such type of strong effects would not provide reliable answers because the domestication syndrome is, by definition, thought to rise from mild developmental deficits, not strong ones. In vivo hybridization experiments of gene expression could be employed for specific phenotypic traits, such as the jaw deformities, whereas gene methylation editing technology could be used to functionally test the impact of few specific genes identified here. However, this technology is not yet applicable to marine fish with small pelagic eggs. Therefore, in this context, our design and data should be considered a good empirical demonstration of the role of epigenetic processes in the rise of the domesticated phenotype. The general NCC model for domestication, independently of the specific genes found here, could be, nevertheless, further tested in other early domesticated fish species for which wild counterparts are available and show signs of the domestication syndrome or in the experimentally domesticated foxes.

In summary, our findings show that the farming environment influences the genome of sea bass in the initial stages of domestication by inducing epimutations. These epimutations are established already during early life and involve genes related to developmental processes that are expressed in embryonic structures including the neural crest. The epimutations persist until adulthood in different tissues and some result in measurable changes in gene expression when compared with wild counterparts. Epimutated genes include those found with altered expression in sea bass with phenotypes associated with the domestication syndrome, such as jaw deformities. Epimutations significantly associate with SNPs, suggesting that they can be integrated into the genome as genetic polymorphisms due to the hypermutability of the CpGs and its neighboring sequences. Our results constitute, to the best of our knowledge, the first empirical demonstration incorporating epigenetic mechanisms in support of the NCC-deficit hypothesis to explain the emergence of Darwin's domestication syndrome and suggest a conserved process that could be operating across vertebrates.

Materials and Methods

Animals and Rearing Conditions

Wild adult European sea bass (*Dicentrarchus labrax* L.) were captured around the Medes Islands Natural Reserve (Western Mediterranean, NE of Spain) and farmed sea bass were obtained from a farm located in the same area (St. Pere Pescador, Girona, Catalonia, Spain) (supplementary fig. 3, Supplementary Material online). Farmed sea bass were the offspring of a cross of 3-year-old unselected broodstock that were hatchery raised for no more than one generation. Farmed fish were, thus, at the early stages of domestication and are referred to as early domesticates. Analysis of 93,369 SNPs (see details in the Genetic Analysis section) showed that there were no major genetic differences between the wild and early domesticates used in this study, as confirmed by a mean $F_{ST} = 0.0085$, a value even below the lowest value of the genetic differentiation of natural populations ($F_{ST} = 0.011$) (Loukovitis et al. 2015).

Five days postfertilization (dpf) larvae of early domesticates were transported from the commercial hatchery to the aquarium facilities of the Institute of Marine Sciences. The fish were reared under standard raising conditions for this species as described previously (Díaz et al. 2013) and were maintained under natural conditions of photoperiod and temperature. Fish were fed pelleted food of the appropriate size (YM858, Elico, BioMar). The composition of this diet is considered conservative and is used as the control diet in studies of fish meal substitution (Simó-Mirabet et al. 2018) since among diets it has a composition closest to the diet encountered in the wild.

The aquarium facilities are authorized for experiments with animals by the Ministry of Agriculture and Fisheries (certificate number 08039–46–A) according to Spanish law (R.D. 223 of March 1988). Fish treatments were in accordance with the European Convention for the Protection of Vertebrate Animals used for Experimental and Other Scientific Purposes (ETS Nu 123, 126, January 1, 1991). The experimental protocol was also authorized by the Ethics Committee of the Spanish National Research Council (CSIC) within projects AGL2013–41047–R and AGL2016–78710–R.

Sampling

Tissues from wild fish were dissected immediately upon capture, transported in RNAlater (ThermoFisher Scientific) and stored at -80°C . Early domesticates were sacrificed using an overdose of 2-phenoxyethanol, tissues were immediately frozen in liquid nitrogen following dissection and stored at -80°C . At sampling, both wild fish and early domesticates were more than 3 years old (mean weight 773.88 g; mean length 35.44 cm) to reduce possible effects due to differences in age or size. Both wild fish and early domesticates were sampled in the nonreproductive season (June) to prevent any effect due to differences in the annual reproductive cycle, especially in reproductive tissues. Three replicates per group and tissue were used for DNA methylation analysis and five replicates per group and tissue were used for gene expression analysis.

Fertilized eggs of early domesticates, the product of a natural spawning, were collected at 27–30-h postfertilization (60–90% epiboly). Eggs were briefly rinsed with water and were snap frozen in liquid nitrogen and stored at -80°C until analysis. Three pools of five eggs each were used for DNA methylation analysis.

Nucleic Acid Isolation

Total RNA was isolated from brain, muscle, testis and liver of adult wild fish and early domesticates using TRIzol Reagent (ThermoFisher Scientific) according to the manufacturer's instructions. Genomic DNA was isolated by phenol/chloroform/isoamyl alcohol extraction from brain, muscle, testis and liver of adult fish and from three pools of five eggs. In brief, cells were lysed by incubation in TENS buffer (0.1 M NaCl, 10 mM Tris-HCl, 1 mM ethylenediaminetetraacetic acid pH 8, 0.5% Sodium dodecyl sulfate, [SDS]) overnight with 1 μg of proteinase K (Sigma-Aldrich) for protein digestion. RNA was digested with 0.5 μg of ribonuclease A

(PureLink RNase A; Life Technologies) and DNA was precipitated with 95% ethanol. Samples from tissues stored in RNeasy later were further cleaned with 2× AMPure XP beads (Beckman Coulter).

RNA-seq

A total of 42 RNA-seq libraries were constructed from the four tissues of wild fish and early domesticates ([supplementary table 2, Supplementary Material](#) online). RNA quality was measured with the Agilent RNA 6000 Nano Kit (Agilent) and only samples with an RNA integrity number higher than 8 were further used for RNA-seq library preparation. The mRNA-seq libraries were constructed according to the manufacturer's instructions using the TruSeqStranded mRNA LT Sample Prep Kit (Illumina Inc., Rev.E, October 2013). A total of 20 libraries for muscle and testis were sequenced using the TruSeq SBS Kit v3-HS and 20 libraries for liver and brain were sequenced using the TruSeq SBS Kit v4 on an Illumina HiSeq 2000 platform in paired-end mode with a read length of 76 bp. Image analysis, base calling and quality scoring of the runs were processed using the manufacturer's software Real Time Analysis and followed by generation of FASTQ sequence files by CASAVA. Decontamination was performed with the BBDuk package (v. 37.61) from the BBTools Suite of the Joint Genome Institute, which employs kmers. The parameters set for adapter trimming were $ktrim = r$, $k = 23$, $mink = 11$, $hdist = 1$, $tpe tbo$, and for quality trimming they were $qtrim = r$, $trimq = 30$, $minlen = 23$. The HISAT2 ([Kim et al. 2015](#)) (v. 2.1.0) program, which uses a graph-based alignment, was employed for the alignment of the reads. The European sea bass genome (dicLab1 v1.0c, July 2012) ([Tine et al. 2014](#)) was indexed using the hisat2-index wrapper function and the trimmed reads were aligned using the core hisat2 function with default parameters. The reads were counted at the gene level with feature Counts ([Liao et al. 2014](#)) (v. 1.6.2) from the Subread ([Liao et al. 2013](#)) package. After performing clustering and principal component analysis, one sample of muscle and one sample of brain from wild fish were excluded from further analysis since they were clear outliers ([supplementary fig. 7, Supplementary Material](#) online). Differential expression was estimated using the default pipeline of the DESeq2 ([Love et al. 2014](#)) package (v. 1.20.0). The \log_2 fold changes were shrunk according to the original DESeq2 shrinkage estimators.

Quantitative Real-Time PCR

RNA extracted from the muscle of eight fish was used for validation of RNA-seq results using quantitative real-time PCR. Five-hundred nanograms of RNA were treated with 0.5 units of amplification grade DNase I (ThermoFisher Scientific, 18068015) and reverse transcribed to cDNA using SuperScript III Reverse Transcriptase (ThermoFisher Scientific, 18080085) with 100 μ M of random hexamers according to the manufacturer's instructions. Primers were designed using Primer3Plus software targeting a short region covering two exons. To calculate the efficiency of the primers, we performed amplification of a pool from all samples and serial dilutions with cDNA concentration of 1, 0.2, 0.1, 0.02, 0.01,

and 0.002. Then, we calculated the slope from the log-linear regression of the calibration curve and the efficiency as $E = 10^{(-1/\text{slope})}$. Two reference genes were used previously validated in sea bass ([Mitter et al. 2009](#)). The reactions were performed in triplicate and negative controls without cDNA were included for each primer. Details of the primers used in qPCR reactions can be found in [supplementary table 5, Supplementary Material](#) online. The EvaGreen Dye (Biotium) was used in the qRT-PCR reactions performed on a QuantStudio 12K Flex (ThermoFisher Scientific). The Cq values were used to calculate the normalized values of each target gene after subtracting the geometric mean of the two reference genes.

Reduced Representation Bisulfite Sequencing

A total of 27 RRBS libraries were constructed as previously described ([Anastasiadi, Esteve-Codina, et al. 2018](#)). Briefly, 20 units of *MspI* (NEB) were used to digest 100 ng of genomic DNA at 37 °C overnight. In the same reaction, five units of Klenow fragment (3' → 5'-exo-; NEB) were added along with dNTPs at a final concentration of 300 μ M dATP, 30 μ M dCTP, and 30 μ M dGTP. Incubation at 30 °C for 20 min was performed for end repair, followed by a 37 °C incubation for 20 min to account for A-tailing and 20 min incubation at 75 °C to inactivate the enzyme. Illumina TruSeq Adapters v2 were added to the fragments using the Quick Ligase (NEB) and incubating at 25 °C for 20 min. Size selection was performed using a ratio of 0.75× AMPure XP beads (1:5 diluted). The libraries were then quantified by qPCR and pooled according to the qPCR values. The pooled samples were further cleaned up using 2.5× AMPure XP beads (1:5 diluted). Bisulfite conversion was performed using the EZ DNA Methylation-Direct kit (Zymo Research) with 0.9× CT Conversion Reagent and 30 min of desulphonation. qPCRs were used to determine the optimal number of cycles per sample in the enrichment reaction. Enrichment of the libraries was performed using the PfuTurbo Cx HotStart Polymerase (Agilent Technologies) with the following cycling program: 95 °C for 2 min, determined number of cycles of 95 °C for 30 s, 65 °C for 30 s, and 72 °C for 45 s, and a last step at 72 °C for 7 min. AMPure XP beads at 1× were used to clean up the final product. The RRBS libraries of liver, brain, and eggs were constructed using the Premium RRBS kit (Diagenode, Cat. No. C02030032) which compiles the exact manual protocol and which was followed according to the instructions of the manufacturer. Qubit High Sensitivity assays (ThermoFisher Scientific) were used to quantify the final RRBS libraries. Their quality was checked using the Experion DNA 1 k assays (BioRad) in the case of muscle and testis and with the DNA High Sensitivity assay (Agilent) for liver, brain and eggs. RRBS libraries were sequenced on an Illumina HiSeq 2000 instrument in single-end mode with a length of 50 bp.

Data analysis was performed in parallel exactly as described in [Anastasiadi, Esteve-Codina, et al. \(2018\)](#). The Trimmomatic software ([Bolger et al. 2014](#)) (v.0.32) was used for quality trimming with the following parameters: sliding window of 4, Phred score > 15, adaptive quality trimming with largest

length of 20, and strictness of 0.50 and 18 as minimum read length. Reads were then aligned with the European sea bass genome using BSMAP (Xi and Li 2009; Xi et al. 2012) (v. 2.90) and restricting the parameters to RRBS mode and at least 5 reads coverage. The *methratio.py* script of the BSMAP package was used for methylation extraction. The *bsrate* script from the MethPipe pipeline (Song et al. 2013) (v. 3.4.3) was used to calculate the efficiency of bisulfite conversion.

Further analyses were performed with the R (R Core Team 2015) and Bioconductor (Gentleman et al. 2004) packages using Rstudio (RStudio Team 2015), unless stated otherwise. The methylKit package (Akalin et al. 2012) (v. 1.6.3) was used for estimation of methylation values and for differential analysis for each tissue. CpGs with <10 reads coverage or with coverage higher than 99.9% of the distribution of read counts were filtered out. Coverage was then normalized across samples for each tissue and only CpGs covered in all samples of one tissue were maintained for further analysis. Eggs were analyzed in batches with all tissues from farmed fish and the methylation percentage for each CpG was extracted. To detect DMCs between wild and farmed fish, a logistic regression model was applied with correction for overdispersion as proposed by Feng et al. (2014) and McCullagh and Nelder (1989), and the χ^2 test was used to determine methylation differences. We chose this method after testing the logistic regression with and without correction for overdispersion using the χ^2 and the *F*-test to determine methylation differences, the beta-binomial model with parameter shrinkage as implemented by the DSS package (Feng et al. 2014), and the binomial mixed model integrating genetic relatedness data derived from the sequencing as implemented in MACAU (Lea et al. 2015). This method is characterized by high specificity without compromising its sensitivity (Wreczycka et al. 2017). The SLIM method was used to correct *P* values after multiple testing. The DMCs detected by methylKit were used in the edmr package (Li et al. 2013) (v. 0.6.2) to identify empirical DMRs based on bimodal normal distribution model and a weighted cost function to optimize regional methylation. The implementation of the algorithm followed the default settings and DMRs were further defined as regions containing a minimum of 4 CpGs, 2 DMCs with methylation difference >15% and *q*-value < 0.1 (as used previously [Lea et al. 2016; Ingerslev et al. 2018]), total methylation difference >15% and *q*-value < 0.05. The combination of this threshold, sample size, and depth coverage ensures detection of biologically meaningful differences. The COMBINED ANNOTATION track of the European sea bass genome (dicLab v1.0c, July 2012) was used for annotation procedures. Regions 5,000-bp upstream of the transcription start site and 5,000-bp downstream the 3' UTR were included together with the full gene bodies to determine whether a DMR was present in a gene. The genomic association of DMRs with gene bodies and regulatory regions was tested using the Bioconductor package regioneR (Gel et al. 2016) (v. 1.12.0), which offers a permutation framework to evaluate statistically the association of genomic regions. We evaluated whether the number of overlaps of DMRs and gene bodies ± 5 kb could be attributed to chance alone using a randomization

strategy of creating a new set of the same number of regions with the same width, randomly placing all regions along the genome and performing 10,000 permutations.

Genetic Analysis

SNP data were extracted in parallel with DNA methylation data using BisSNP (Liu et al. 2012) (v. 0.82.2) from the four tissues of each individual per group separately and using the SNVs ILLUMINA track of the European sea bass as SNP reference. The VCFtool (Danecek et al. 2011) (v. 0.1.15) was used to prepare the files and calculate the Weir and Cockerham (Weir and Cockerham 1984) F_{ST} population estimates using only diploid sites per tissue, and then the F_{ST} population estimates were averaged.

SNPs were also extracted from the sequenced genomes of sea bass populations from two commercial hatcheries after 25 years of selective breeding for production traits from a previous study (Bertolini et al. 2016). Only SNPs that had a quality between 20 and 40, a minimum depth of 4 and were biallelic were retained for further analysis using samtools and bcftools (Li et al. 2009) (v. 1.9).

The genomic association of SNPs in selected populations of sea bass with the DMCs was tested using regioneR (Gel et al. 2016). Only SNPs from C to T, or from G to A, to take into account the reverse strand, were used to test whether their overlap with the DMCs was significantly higher than expected by chance. We evaluated the number of overlaps of SNPs and DMCs using the same strategy as before and performing 10,000 permutations.

Multiplex Bisulfite Sequencing

MBS (Anastasiadi, Vandeputte, et al. 2018) libraries were constructed to validate the RRBS results. Six genes were selected as candidates for validation and eight fish samples were used for each tissue. The genes selected had to follow three criteria: 1) contain DMRs between wild versus early domesticated fish, 2) the DMRs had to be already established in the eggs, and 3) genes of the same family had to under positive selection in at least one mammalian or avian domesticated. We targeted the identified DMRs of *gria4a* and *phldb1* in the brain, *adamts9* and *mapk8a* in the muscle, *foxc1* in the testis, and protocadherin γ -*a11-like* in the liver (supplementary table 6, Supplementary Material online). Primers were designed using MethPrimer (Li and Dahiya 2002) and in silico validated using Primer3Plus (Untergasser et al. 2012, p. 3) against the bisulfite-converted amplicon sequence. The overhang adapter sequences (Illumina 18S Metagenomic protocol) were added to the 5' of the locus-specific primers.

Five-hundred ng of genomic DNA were converted using the EZ DNA Methylation-Direct Kit (Zymo Research) extending the desulphonation time to 30 min and eluting in 40 μ l of elution buffer. Two microliters of the bisulfite-converted DNA were used to amplify the targeted regions with 2.5 units of GoTaq G2 Hot Start polymerase (Promega) in a reaction that contained a final concentration of 4 mM of $MgCl_2$, 0.8 mM dNTPs, and 0.8 μ M of primers. The amplification was performed under the following conditions: 7 min at 95 °C, 40 cycles of 95 °C for 1 min, T_m specific for each primer pair

(supplementary table 6, Supplementary Material online) for 2 min, 65 °C for 2 min, and finally 10 min at 65 °C. T_m was determined after gradient PCR, amplification was visually confirmed by gel electrophoresis and its specificity by Sanger sequencing using both the forward and the reverse adapter.

Bead-based size selection and normalization (Hosomichi et al. 2014) was performed according to Anastasiadi, Vandeputte, et al. (2018) using a home-made solution of Sera-mag SpeedBeads (Fisher 099981123) (Rohland and Reich 2012). The size selection followed a double incubation with beads, starting with 0.4× beads (2×) and followed by a second incubation of the supernatant with 0.6× beads (2×). The normalization was performed by incubating a 3:1 volume of 20-fold 2× diluted beads with the size-selected DNA. Two microliters of each of the six amplicons were pooled per sample. Indices from the Nextera XT index Kit SetA (Illumina FC-131-2001) were added using 1 unit of PCRBio HiFi Polymerase and 10 µl of the pooled amplicons under the following conditions: 3 min at 95 °C, 8 cycles of 95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s, and finally 5 min at 72 °C. Clean up of the reactions was performed using 0.4× beads (2×). The DNA was then quantified with a Qubit High Sensitivity assay (ThermoFisher Scientific) and these values were used to calculate the volumes used for the final pooling in a single tube which was cleaned up using 1× beads (2×). DNA High Sensitivity assays (Agilent) were performed separately for the 16 samples and for the final MBS library. The MBS library was quantified using the Kapa system and sequenced on a MiSeq (Illumina) instrument using the paired-end 300-bp protocol.

Demultiplexed raw reads were trimmed for adapter contamination and quality using the Trimmomatic (Bolger et al. 2014) (v. 0.32) and the same parameters used for RRBS data. FastQC software (Andrews 2010) (v. 0.11.4) was used for quality controls before and after trimming. The Bismark aligner (Krueger and Andrews 2011) (v. 0.14.4) was used for aligning the paired reads against the in silico converted genome using the following parameter: score_min L, 0-0.6. Methylation was extracted using the bismark_methylation_extractor. The detailed statistics of the MBS libraries are found in supplementary table 7, Supplementary Material online.

Gene List Enrichment Analysis

The coding sequences of the European sea bass genome were used for annotation of transcripts and GO term (Ashburner et al. 2000) annotation using the go_enrichment (https://github.com/enormandeau/go_enrichment; last accessed July 05, 2019) suite. The nr and the Swissprot databases were downloaded from the blast databases of NCBI in August 2018. The sequences were blasted against the Swissprot database and annotated from Uniprot. The GOATOOLS python library (Klopfenstein et al. 2018) (v. 0.8.4) was used to test over- and under-representation of GO terms in gene lists using the GO database (August 3, 2018). The background set consisted of all annotated genes of the European sea bass genome (26,719 genes), which constitutes the most conservative approach for enrichment testing. Adjustment of P

values was avoided since an FDR procedure can result in very conservative P values and interesting terms may be lost. Furthermore, an enrichment analysis includes many previous steps, so the sole number of GO terms may not be appropriate for multiple corrections, whereas the algorithms that take into account the terms' topology perform dependent tests (Alexa and Rahnenfuhrer 2009). GO term enrichment was, nevertheless, performed by other means: using the GOATOOLS against a background set consisting only of feasible genes with RRBS (genes that within their gene body, 5-kb upstream the transcription start site or 5-kb downstream the 3' UTR contained at least one CpG in the sample with the highest number of CpGs covered more than five times), with and without multiple correction and using the PANTHER tool (Mi et al. 2016) with human or zebrafish genes as reference with multiple testing correction. The chosen method was found to show overall consistency of the most important GO terms between pipelines without losing interesting information on gene set functions. For visualizations, REVIGO software (Supek et al. 2011) was used to summarize the GO term lists by removing redundant GO terms. For further gene set enrichment analysis, the Enrichr tool (Chen et al. 2013; Kuleshov et al. 2016) was used, and results from the Reactome pathway database 2016 (Fabregat et al. 2018) and the Tissue expression database (Santos et al. 2015; Palasca et al. 2018) were presented.

Supplementary Material

Supplementary data are available at *Molecular Biology and Evolution* online.

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