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1 Linking Allele-Specific Expression And Natural 2 Selection In Wild Populations

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18 **Abstract**

19 Allele-specific expression (ASE) is now a widely studied mechanism at cell, tissue and organism
20 levels. However, population-level ASE and its evolutive impacts have still never been
21 investigated. Here, we hypothesized a potential link between ASE and natural selection on the
22 cosmopolitan copepod *Oithona similis*. We combined metagenomic and metatranscriptomic data
23 from seven wild populations of the marine copepod *O. similis* sampled during the *Tara* Oceans
24 expedition. We detected 587 single nucleotide variants (SNVs) under ASE and found a
25 significant amount of 152 SNVs under ASE in at least one population and under selection across
26 all the populations. This constitutes a first evidence that selection and ASE target more common
27 loci than expected by chance, raising new questions about the nature of the evolutive links
28 between the two mechanisms.

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36 **Introduction**

37 Allele-specific expression (ASE), or allelic imbalance, refers to difference of expression between
38 two alleles of a locus in a heterozygous genotype due to genetic or epigenetic polymorphism.
39 Through DNA methylation or histone modifications, epigenetics could repress a disadvantageous
40 or a specific parental allele, leading in some cases to monoallelic expression, as demonstrated in a
41 variety of organisms including mouse, maize or bumblebee¹⁻⁴. On the other hand, ASE may have
42 a genetic origin through, for example, mutations in transcription factor binding sites^{5,6}, or post-
43 transcriptional mechanisms like non-sense mediated decay⁷⁻⁹. Recently, several studies led to a
44 better understanding of ASE thanks to the development of advanced tools allowing their
45 detection at the individual, tissue and cell levels^{7,9-15}. ASE has been investigated in the context of
46 *cis*- and *trans*-regulation of gene expression¹⁶, expression evolution¹⁷ and association between
47 gene expression and human diseases¹⁸. First approaches in natural populations of primates and
48 flycatchers have been undertaken with individual-level data¹⁹⁻²¹. Moreover, studies began to
49 question the relative contribution of genetics and environment on gene expression using ASE in
50 human²²⁻²⁵ and fruit flies²⁶.

51 However, population-level ASE in several wild populations of one species and its potential
52 evolutive origins and consequences remain largely uninvestigated. The need for numerous
53 individual RNA-seq and whole-genome genotyping data constitutes the main obstacle for
54 population-scale analyses. Today, the advances of next-generation sequencing technologies allow
55 integrating large metagenomic and metatranscriptomic data from environmental samples, and
56 new approaches can now be considered using whole population information.

57 In natural populations, we expect most loci to be under neutral evolution and balanced expression
58 (Fig. 1a)^{27,28}. When selection occurs on a specific locus, the selected allele tends to homozygosity

59 creating a specific population-level expression pattern of the selected allele (Fig.1b).In the
60 absence of selection, if the same allele is favored by ASE in most of the individuals, the observed
61 population-level expression pattern (Fig. 1c) will be similar to the one observed in the case of
62 selection (Fig.1b).Considering that both mechanisms impact fitness, we hypothesized that ASE
63 and natural selection could preferentially target the same loci, in different populations, showing a
64 possible link between the two mechanisms.

65 In this study, we focus on the widespread epipelagic, temperate and cold water small-sized
66 copepod, *Oithona similis* (Cyclopoida, Claus 1866), notably known to be highly abundant in
67 Arctic³⁰⁻³³. Copepods, and particularly *Oithona*, are small crustaceans forming the most abundant
68 metazoan on Earth, reflecting strong adaptive capacities to environmental fluctuations³⁴⁻³⁶.They
69 play a key ecological role in biogeochemical cycles and in the marine trophic food chain³⁷;
70 therefore copepods constitute an ideal model to study wild population evolution³⁸⁻⁴¹

71 The first goal of our study was to identify loci under selection before demonstrating that
72 population-level ASE can be detected with metagenomic and metatranscriptomic data collected
73 by the *Tara* Oceans expedition⁴² during its Arctic phase. Then we provided evidence of a
74 quantitative link between ASE and natural selection.

75 **Material and Methods**

76 **Material sampling, mRNA extraction and transcriptome sequencing**

77 *Oithona similis* specimens were sampled at the North of the Large Bay of Toulon, France (Lat
78 43°06' 02.3" N and Long 05°56' 53.4"E). Sampling took place in November 2016. The samples
79 were collected from the upper water layers (0-10m) using zooplankton nets with a mesh of 90µm

80 and 200µm (0.5 m diameter and 2.5 m length). Samples were preserved in 70% ethanol and
81 stored at -4°C. From the Large Bay of Toulon samples, *O. similis* individuals were isolated under
82 the stereomicroscope. We selected two different development stages: four copepodites (juveniles)
83 and four adult males. Each individual was transferred separately and crushed, with a tissue
84 grinder (Axygen) into a 1.5 mL tube (Eppendorf). Total mRNAs were extracted using the ‘RNA
85 isolation’ protocol from NucleoSpin RNA XS kit (Macherey-Nagel) and quantified on a Qubit
86 2.0 with a RNA HS Assay kit (Invitrogen) and on a Bioanalyzer 2100 with a RNA 6000 Pico
87 Assay kit (Agilent). cDNA were constructed using the SMARTer-Seq v4 Ultra low Input RNA
88 kit (ClonTech). The libraries were constructed using the NEBNext Ultra II kit, and were
89 sequenced with an Illumina HiSeq2500 (Supplementary Fig. 1).

90 **Transcriptomes assembly and annotation**

91 Each read set was assembled with Trinity v2.5.1⁴³ using default parameters and transcripts were
92 clustered using cd-hit v4.6.1⁴⁴ (Supplementary Table 1). To ensure the classification of the
93 sampled individuals, each ribosomal read set were detected with SortMeRNA⁴⁵ and mapped with
94 bwa v0.7.15 using default parameters⁴⁶ to 82 ribosomal 28S sequences of *Oithona* species used in
95 Cornils et al., 2017 (Supplementary Fig. 2). The transcriptome assemblies were annotated with
96 Transdecoder v5.1.0⁴³ to predict the open reading frames (ORFs) and protein sequences
97 (Supplementary Table 1). In parallel, homology searches were also included as ORF retention
98 criteria; the peptide sequences of the longest ORFs were aligned on *Oithona nana* proteome⁴⁰
99 using DIAMOND v0.9.22⁴⁸. Protein domain annotation was performed on the final ORF
100 predictions with Interproscan v5.17.56.0⁴⁹ and a threshold of e-value <10⁻⁵ was applied for Pfam
101 annotations. Finally, homology searches of the predicted proteins were done against the nr NCBI

102 database, restricted to Arthropoda (taxid: 6656), with DIAMOND v0.9.22 (Supplementary Fig.
103 1).

104 **Variant calling using *Tara* Oceans metagenomic and metatranscriptomic data**

105 We used metagenomic and metatranscriptomic reads generated from samples of the size fraction
106 20–180 μm collected in seven *Tara* Oceans stations TARA_155, 158, 178, 206, 208, 209 and 210
107 (Supplementary Table 2), according to protocols described in Alberti et al. 2017⁵⁰.

108 The reference-free variant caller *DiscoSNP++*^{51,52} was used to extract SNVs simultaneously
109 from raw metagenomic and metatranscriptomic reads, and ran using parameters $-b$ 1. Only SNVs
110 corresponding to biallelic loci with a minimum of 4x of depth of coverage in all stations were
111 initially selected. Then, SNVs were clustered based on their loci co-abundance across samples
112 using density-based clustering algorithm implemented in the R package *dbscan*^{53,54} and ran with
113 parameters $\text{epsilon} = 10$ and $\text{minPts} = 10$. This generated three SNVs clusters, the largest of
114 which contained 102,258 SNVs. To ensure the presence of *O. similis* SNVs without other
115 species, we observed the fitting of the depth of coverage to the expected negative binomial
116 distribution in each population (Supplementary Fig. 3). For each variant in each population, the
117 B-allele frequency (BAF) and the population-level B-allele relative expression (BARE) were
118 computed; $BAF = \frac{G_B}{G_B + G_A}$ and $BARE = \frac{T_B}{T_B + T_A}$, with G_A and G_B the metagenomic read counts of
119 the reference and alternative alleles respectively, T_A and T_B the metatranscriptomic read counts of
120 the reference and alternative alleles respectively.

121 **Variant filtering and annotation**

122 SNVs were filtered based on their metagenomic coverage. Those with a metagenomic coverage
123 lying outside a threshold of $\text{median} \pm 2 \sigma$ in at least one population, with a minimum and

124 maximum of 5x and 150x coverage were discarded. To keep out rare alleles and potential calling
125 errors, only variants characterized by a BAF comprised between 0.9 and 0.1, and a BARE
126 between 0.95 and 0.05 in at least one population were chosen for the final dataset resulting in
127 25,768 SNVs (Supplementary Fig. 4).

128 The variant annotation was conducted in two steps. First, the variant sequences were relocated on
129 the previously annotated *O.similis* transcripts using the “VCF_creator.sh” program of
130 *DiscoSNP++*. Secondly, a variant annotation was carried with SNPeff⁵⁵ to identify the location
131 of variants within transcripts (i.e., exon or UTR) and to estimate their effect on the proteins
132 (missense, synonymous or nonsense). The excess of candidate variant annotations was tested in
133 the following classes: missenses, synonymous, 5' and 3'UTR. A significant excess was
134 considered for a hypergeometric test $p\text{-value} < 0.05$.

135 **Genomic differentiation and detection of selection**

136 The differentiation among the seven populations was investigated through the computation of the
137 F_{ST} metric or Wright's fixation index^{56,57}. For each locus, global F_{ST} including the seven
138 populations and pairwise- F_{ST} between each pair of population was computed, using the
139 corresponding BAF matrix. For the global F_{ST} computation, a Hartigan's dip test for unimodality
140 was performed⁵⁸. We retained the median pairwise- F_{ST} as a measure of the genomic
141 differentiation between each population. The *pcadapt* R package v4.0.2⁵⁹ was used to detect
142 selection among populations from the B-allele frequency matrix. The computation was run on
143 “Pool-seq” mode, with a minimum allele frequency of 0.05 across the populations, and variants
144 with a corrected Benjamini and Hochberg⁶⁰ $p\text{-value} < 0.05$ were considered under selection.

145 **Population-level ASE detection using metagenomic and metatranscriptomic data**

146 In each population, we first selected variants for $BAF \neq \{0,1\}$. Then, we computed $D = BAF -$
147 $BARE$, as the deviation between the BAF and the BARE. In the absence of ASE, D is close to 0,
148 as most of the biallelic loci are expected to have a balanced expression^{7,28,61} we expect the D
149 distribution to follow a Gaussian distribution centered on 0. We estimated the Gaussian
150 distribution parameters and tested the probability of a variant to belong to this distribution (“ D -
151 test” or “deviation test”). Given the large number of tests, we applied the Benjamini and
152 Hochberg approach to control the False Discovery Rate (FDR).

153 We also computed a “low expression bias” test by comparing the read counts T_A and T_B to the
154 observed metagenomic proportion $1-BAF$ and BAF respectively with a chi-square test and
155 applied the Benjamini and Hochberg correction for multiple testing. These two tests were applied
156 to BAFs, BAREs and read counts of the seven populations separately and the seven sets of
157 candidate loci targeted by ASE (deviation test q-value < 0.1 and low expression bias test q-
158 value < 0.1) were crossed to identify loci under ASE in different populations, or shared ASEs.

159 To identify alleles targeted by both ASE and selection, the set of variants under ASE in each
160 population was crossed with the set of loci detected under selection. The size of the intersection
161 was tested by a hypergeometric test, Hypergeometric(q,m,n,k), with q being number of alleles
162 under ASE in the population and under selection (size of intersection), m being the total number
163 of alleles under selection, n being the total number of variants under neutral evolution, and k
164 being the total number of alleles under ASE in the tested population. We considered that, in a
165 given population, the number of alleles under both ASE and selection was significantly higher
166 than expected by chance for p-value < 0.05 .

167 **Gene enrichment analysis**

168 To identify specific biological function or processes associated to the variants, a domain-based
169 analysis was conducted. The Pfam annotation of the transcripts carrying variants targeted by ASE
170 and selection was used as entry for dcGO Enrichment⁶². A maximum of the best 300 GO-terms
171 were chosen based on their z-score and FDR p-value ($<10^{-3}$) in each ontology category. To
172 reduce redundancy, these selected GO-terms were processed using REVIGO⁶³, with a similarity
173 parameter of 0.5 against the whole Uniprot catalogue under the SimRel algorithm. To complete
174 the domain-based analysis, the functional annotations obtained from the homology searches
175 against the nr were manually curated.

176 **Results**

177 ***Oithona similis* genomic differentiation and selection in Arctic Seas**

178 From metagenomic and metatranscriptomic raw data of seven sampling stations (Fig. 2a), we
179 identified 25,768 expressed variants. Among them, 97% were relocated on *O. similis*
180 transcriptomes.

181 The global distribution of F_{ST} of the seven populations was unimodal (Hartigans' dip test,
182 $D=0.0012$, p-value=0.99) with a median- F_{ST} at 0.1, confirmed by the pairwise- F_{ST} distributions
183 (Supplementary Fig. 5). The seven populations were globally characterized by a weak to moderate
184 differentiation, with a maximum median pairwise- F_{ST} of 0.12 between populations from
185 TARA_210 and 155/178 (Fig. 2c,d). Populations from stations TARA_158 (Norway Current),
186 206 and 208 (Baffin Bay) were genetically closely-related, with the lowest median pairwise F_{ST}
187 (0.02), despite TARA_158 did not co-geolocalize with the two other stations. The four other
188 populations (TARA_155, 178, 209, and 210) were equally distant from each other (0.1-0.12).

189 Finally, TARA_158, 206 and 208 on one side, and TARA_155, 178, 210 and 209 on the other
190 side showed the same pattern of differentiation (0.05-0.07).

191 The PCA decomposed the genomic variability in six components; the first two components
192 discriminated TARA_155 and 178 from the others (32% and 28.1% variance explained
193 respectively, Fig. 2b), and the third component differentiated TARA_210 and 209 (19.5%). The
194 fourth principal component separated TARA_209 and 210 from 158/206/208 (11.3 %), with the
195 last two concerning TARA_158/206/208 (Supplementary Fig. 5). Globally, these results
196 dovetailed with the F_{ST} analysis, with details discussed later. Finally, we detected 674 variants
197 under selection, representing 2.6% of the dataset (corrected p-value < 0.05).

198 **Loci targeted by population-level ASE and selection in Arctic populations**

199 The number of SNVs tested for ASE varied between 13,454 and 22,578 for TARA_210 and 206
200 respectively. As expected, the D deviation, representing the deviation between B-allele frequency
201 and B-allele relative expression, followed a Gaussian distribution in each population (Fig. 3a and
202 Supplementary Fig. 6). Variants under ASE (i.e. having a D significantly higher or lower than
203 expected) were found in every population, ranging from 26 to 162 variants for TARA_178 and
204 206 respectively (Table 1). Overall, we found 587 variants under ASE, including 535 population-
205 specific ASEs, and 52 ASEs shared by several populations (Fig.3b). Remarkably, 30 ASEs out of
206 the 52 were present in the populations from TARA_158, 206 and 208 that correspond to the
207 genetically closest populations. The seven sets of variants under ASE were crossed with the set of
208 variants under selection, as illustrated for TARA_209 (Fig. 3c). The size of the intersection
209 ranged from 5 to 42 variants (TARA_155 and 210/206) and was significantly higher than
210 expected by chance for all the populations (hypergeometric test p-value < 0.05). It represented a
211 total of 152 unique variants under selection and ASE in at least one population (Table 1,

212 Supplementary Table 3), corresponding to 23% and 26% of variants under ASE and under
213 selection respectively.

214 **Functional analysis of genes targeted by ASE and selection**

215 Among the 152 loci targeted by ASE and selection, 145 were relocated on *O. similis* transcripts
216 (Supplementary Table 4). Amid these transcripts, 137 (90%) had a predicted ORF, 97 (64%)
217 were linked to at least one Pfam domain and 90 (59%) to a functional annotation. Fifteen SNVs
218 were missense variations, 59 synonymous, 31 and 29 were located in 5' and 3' UTR, without any
219 significant excess (Supplementary Table 4 and 5). Based on homology searches (Supplementary
220 Table 4), eight genes were linked to nervous system (Table2). Among them, two genes were
221 involved in glutamate metabolism (omega-amidase NIT2 and 5-oxoprolinase), three were
222 predicted to be glycine, γ -amino-butyric acid (GABA) and histamine neuroreceptors. Finally,
223 four were also implicated in arthropods photoreceptors. The domain-based analysis confirmed
224 these results, with an enrichment in GO-terms biological process also linked to nervous system
225 (Supplementary Fig. 7).

226 **Discussion**

227 ***O. similis* populations are weakly structured within the Arctic Seas**

228 Global populations of *O. similis* are known to be composed of cryptic lineages⁴⁷. Thus the
229 assessment that the seven populations used in our study belong to the same *O. similis* cryptic
230 lineage was a prerequisite for further analyses. The high proportion of variants mapped on the
231 Mediterranean transcriptomes (97%) showed that the variant clustering method was efficient to
232 regroup loci of an *O. similis* cryptic species. Plus, the unimodal distribution of F_{ST} showed that
233 these populations of *O. similis* belong to the same polar cryptic species.

234 Secondly, we see that the seven populations examined are well connected with low median
235 pairwise- F_{ST} , despite the large distances separating them. Weak genetic structure in the polar
236 region was already highlighted for other major Arctic copepods like *Calanus glacialis*⁶⁴, and
237 *Pseudocalanus* species⁶⁵. The absence of structure was explained by ancient diminutions of
238 effective population size due to past glaciations⁶⁵⁻⁶⁷, or high dispersal and connectivity between
239 the present-day populations due to marine currents⁶⁴.

240 Going into details, three different cases can be described. First, the differentiation of populations
241 from TARA_155 and 178 compared to the others could be explained by isolation-by-distance.
242 Secondly, the geographically close populations from TARA_210 and 209 present higher
243 differentiation (median pairwise- F_{ST} of 0.11). This could be explained by the West Greenland
244 current acting as a physical barrier between the populations, which could lead to reduced gene
245 flow⁶⁸. At last, the strong link between TARA_158 from Northern Atlantic current and
246 TARA_206/208 from the Baffin Bay is the most intriguing. Despite the large distances that
247 separate the first one from the others, these three populations are well connected.

248 Metagenomic data enable to draw the silhouette of the population genetics but lacks resolution
249 when dealing with intra-population structure. However, our findings are concordant with
250 previous studies underpinning the large-scale dispersal, interconnectivity of marine zooplankton
251 populations in other oceans, at diverse degrees^{38,69-71}.

252 **Toward the link between ASE and natural selection**

253 Usually, at the individual level, the ASE analyses are achieved by measuring the difference in
254 RNA-seq read counts of a heterozygous site. But at the population level, obtaining a large
255 number of individuals remains a technical barrier especially for uncultured animals, or when the

256 amount of DNA retrieved from a single individual is not sufficient for high-throughput
257 sequencing. Here, the detection of ASE at population level was possible by comparing the
258 observed frequencies of the alleles based on metagenomic and metatranscriptomic data, which by
259 passes the obstacles previously described.

260 In our study, the amount of detected ASE in each population was always lower than 1% of tested
261 heterozygous variants, which altogether correspond to 2% of the total set of variants. In humans
262 ⁷², baboons ²¹ and flycatchers ¹⁹, 17%, 23% of genes and 7.5% of transcripts were affected by
263 ASE respectively. The difference with our results can be explained by one main reason. The
264 detection of population-level ASE identifies only the ASE present in a large majority of
265 individuals, which can be considered as “core ASEs”.

266 These core ASEs constitute the majority of detected ASEs and are population-specific, meaning
267 the main drivers of this expression pattern are local conditions like different environmental
268 pressures or population dynamics including, for example, the proportion of each developmental
269 stage and sex, known to vary between populations and across seasons ^{30,73}. Another result is the
270 presence of a small amount of variants affected by ASE in different populations. Most of these
271 variants are under ASE in at least two of the three closest populations from TARA_158, 206 and
272 208. First, the genetic closeness and large geographic distances between these three populations
273 suggest that their shared ASEs are under an environmental independent genetic control.
274 Secondly, the number of variants tested for ASE is higher in these three populations than the
275 others, leading to a greater proportion of ASEs detected which also elevates the chances for a
276 variant to be declared under ASE in several populations.

277 A significant amount of SNVs (152) were subject to selection among the seven populations and
278 to ASE in at least one population. We confirmed our first hypothesis (Fig. 1), as exemplified with
279 the variant 841109 (Fig. 3d), characterized by an ASE in favor of the B-allele in TARA_209 and
280 fixation of this allele in TARA_210. Three main features of ASE can be under selection. First,
281 the observed variant can be in linkage with another variation in upstream *cis*-regulatory elements
282 like transcription factors fixation sites, or epialleles⁷. Secondly, the annotation of candidate
283 variants with SNPeff revealed a majority of variants located in 5' and 3'UTRs, which are
284 variations known to both affect transcription efficiency through mRNA secondary structures,
285 stability and location⁷⁴⁻⁷⁶. For variants located in exons, a majority were identified as
286 synonymous mutations, growingly described as potential target of selection by codon usage bias,
287 codon context, mRNA secondary structure or transcription and translation dynamics^{77,78}. Finally,
288 fifteen missense mutations were spotted, but with moderate predicted impact on protein amino
289 acid composition. However, we did not find premature nonsense mutation, even if variants under
290 ASE has been described to trigger or escape potential nonsense-mediated decay^{28,61,79}, but the
291 possibility that the causal variation is located in introns cannot be ruled out.

292 The process of adaptation through gene expression was suspected in human populations and
293 investigated thanks to the large and accessible amount of data. In a first study, a link has been
294 established between gene expression and selection, affecting particular genes and phenotypes,
295 looking at *cis*-acting SNPs⁸⁰. In a second study, the team was able to detect ASE in different
296 populations and to quantify genetic differentiation and selection⁶¹. They found particularly one
297 gene that shows strong differentiation between European and African populations and under ASE
298 in Europeans and not in Africans. However, they did not quantify this phenomenon. Both
299 emphasized the impact of selection on gene expression. In the same way, another approach

300 showed that ASE or expression variations with high effect size were rare in the populations,
301 based on intra-population analyses in *Capsella grandiflora* and human^{28,81}. This situation is
302 presumably encountered in our analysis, as exemplified with the B-allele of variant 20760212,
303 under ASE and with a low genomic frequency in TARA_210, but fixed in the others (Fig. 3d).
304 Our results complete previous analyses, as they quantify the link between ASE and selection in
305 populations and reveal the evolutive potency of ASE, for the first time at the population-level. It
306 remains to understand the nature of the association between ASE and selection. To address this
307 question, we formulate the hypothesis that they impact chronologically the same loci, following
308 constant or increasing selective pressure as well as environmental changes (Fig. 4).

309 **Nervous system and visual perception are important targets of the natural selection and**
310 **ASE in *O. similis***

311 This evolutive link between ASE and selection is supported by the biological functions associated
312 to the targeted genes, which are involved notably in the copepods nervous system in two ways.
313 The first result is the presence of genes implicated in glutamate metabolism and glycine and/or
314 GABA receptors. Glutamate and GABA are respectively excitatory and inhibitory
315 neurotransmitters in arthropods motor neurons⁸². Plus, glycine and GABA receptors have
316 already been described as a target of selection in *O. nana* in Mediterranean Sea^{40,41}. Secondly, the
317 functional analysis revealed also the importance of the eye and visual perception in the *O. similis*
318 evolution.

319 Copepod nervous system constitutes a key trait for its reproduction and survival, and based on
320 our data, a prime target for evolution, allowing higher capacity of perceiving and fast reacting
321 leading to more efficient predator escape, prey catching and mating. This can explain the great
322 evolutive success of these animals^{35,83,84}.

323 **Conclusion**

324 Gene expression variation is thought to play a crucial role in evolutive and adaptive history of
325 natural populations. Herein, we developed proper methods integrating metagenomic and
326 metatranscriptomic data to detect ASE at the population-level for the first time. Then, we
327 demonstrated the link between ASE and natural selection by providing a quantitative observation
328 of this phenomenon and its impact on specific biological features of copepods. In the future, we
329 will try to generalize these observations to other organisms. Then, we will understand the nature
330 of the link between ASE and natural selection by questioning the chronology between the two
331 mechanisms.

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342 number XX from *Tara* Oceans.

343 **Author's contributions**

344 Individuals for transcriptome production were sampled by J-LJ and KS. KS extracted RNA, EP
345 and KL prepared the libraries and sequencing, MAM assembled the reads and RLJ annotated
346 transcriptomes. PP and CA gave expertise support on *DiscoSNP++* and statistical framework
347 respectively. RLJ and MAM performed the analyses and wrote the manuscript. MAM designed
348 and supervised the study. J-LJ and PW offered scientific support.

349 **Competing interests**

350 The authors declare no competing interests.

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572 **Tables**

573 **Table 1:** Allele-specific expression detection and link with selection by population

574 **Table 2:** Functional annotations of variants targeted by ASE and selection implicated in nervous
575 system

576 **Supplementary Table 1:** *Oithona similis* Mediterranean transcriptomes summary

577 **Supplementary Table 2:** *Tara* Oceans and *Oithona similis* Mediterranean transcriptomes
578 samples accession numbers

579 **Supplementary Table 3:** Variants targeted by ASE and selection statistics

580 **Supplementary Table 4:** Variants targeted by ASE and selection functional annotations

581 **Supplementary Table 5:** Variant annotation by SNPeff

582 **Figures**

583 **Figure 1:** Population genomic and transcriptomic profiles of a biallelic locus in a case of **a**,
584 Neutral evolution and balanced expression; **b**, Selection in favor of the B-allele; **c**, ASE in favor
585 of the B-allele.

586 **Figure 2:** Genomic differentiation of *O. similis* populations from Arctic Seas. **a**, Geographic
587 locations of the seven *Tara* Oceans sampling sites: Northern Atlantic (blue), Kara Sea (green),
588 Baffin Bay (orange) and Labrador Sea (grey). **b**, Principal Component Analysis (PCA) computed
589 by *pcadapt* based on allele frequencies. **c**, Pairwise- F_{ST} matrix. The median (mean) of each
590 pairwise- F_{ST} distribution computed on allele frequencies is indicated. **d**, Graph representing the
591 genomic differentiation of the seven populations of *O. similis*. The nodes represent the
592 populations; their width reflects their centrality in the graph. The edges correspond to the genetic
593 relatedness based on the median pairwise- F_{ST} between each pair of population; 0.02 (large solid
594 line), 0.05 to 0.07 (thin solid line) and 0.11 to 0.12 (dashed line).

595 **Figure 3:** Population Allele-specific expression detection and link with natural selection. **a**, The
596 deviation D distribution in TARA_209. The red line corresponds to the Gaussian distribution
597 estimated from the data. **b**, Upset plot of the ASE detection in the seven populations. Each bar of
598 the upper plot corresponds to the number of variants under ASE in the population(s) indicated by
599 black dots in the lower plot. **c**, Crossing ASE and selection. The yellow circle represents the total
600 set of variants. In green, the number of heterozygous variants tested for ASE in TARA_209. In
601 blue and red, the amount of detected variants under ASE in TARA_209 and under selection
602 among the populations respectively. In purple, the intersection comprising variants under ASE in
603 TARA_209 and under selection, with its hypergeometric test p-value. **d**, Metagenomic and
604 metatranscriptomic profiles of variants 841109 and 20760212. Each population is indicated on
605 the x-axis, with the associated B-allele frequency (red) and B-allele relative expression (blue).
606 The frequency is shown on the y-axis. The asterisks mean ASE was detected in the corresponding
607 population.

608 **Figure 4:** From Allele-specific expression to natural selection. **a**, Evolution of allele frequency
609 and allele relative expression over time. **b**, Evolution of selective pressure over time

610 **Supplementary Fig 1:** Method pipeline overview

611 **Supplementary Fig 2:** Validation of taxonomic assignment

612 **Supplementary Fig 3:** *Oithona similis* depth of coverage of biallelic loci in seven *Tara* Oceans
613 samples

- 614 **Supplementary Fig 4:** Metagenomic coverage distribution of the seven *Tara* Oceans samples
- 615 **Supplementary Fig 5:** Genomic differentiation of Arctic Seas *Oithona similis* populations
- 616 **Supplementary Fig 6:** Allele-specific expression detection
- 617 **Supplementary Fig 7:** Functional analysis of *O. similis* transcripts targeted by ASE and
618 selection
- 619
- 620

621 **Table 1:** Allele-specific expression detection and link with selection by population

Population	Genomic median depth of coverage	Number of tested variants	Number of variants under ASE	Number of variants under ASE and selection	Hypergeometric test p-value
TARA_155	25	18,812	91	6	9.89E-3*
TARA_158	35	21,476	131	29	5.06E-20*
TARA_178	24	18,145	26	9	5E-11*
TARA_206	55	22,578	162	42	4.82E-31*
TARA_208	48	21,469	133	14	2.2E-6*
TARA_209	12	13,956	62	24	1.05E-23*
TARA_210	14	13,454	69	42	8.89E-51*
Overall	-	25,768	587 (2.3%)	152 (0.59%)	-

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625 **Table 2:** Functional annotations of variants targeted by ASE and selection implicated in nervous system

VarID	Ref	Alt	Homology search	Pfam	SnpEff Localization	SnpEff Impact	References
722267	A	G	histamine H1 receptor	PF00001	3' UTR	MODIFIER	85-87
9665345	T	G	chaoptin	PF13306 PF13855	synonymous variant	LOW	88,89
15623788	G	A	eye-specific diacylglycerol kinase	PF13637	synonymous variant	LOW	90,91
23795359	A	T	vang-like protein 2-B	PF06638	synonymous variant	LOW	92,93
1276227	C	T	glycine receptor subunit alpha-2 / gamma-aminobutyric acid receptor subunit alpha-6	PF02932 PF2931	3' UTR	MODIFIER	-
1404415	G	C	omega-amidase NIT2	PF00795	3' UTR	MODIFIER	-
11174785	A	G	5-oxoprolinase	PF02538 PF05378 PF01968	5' UTR	MODIFIER	-
11690229	A	T	glycine receptor subunit alpha-2	PF02931	synonymous variant	LOW	-

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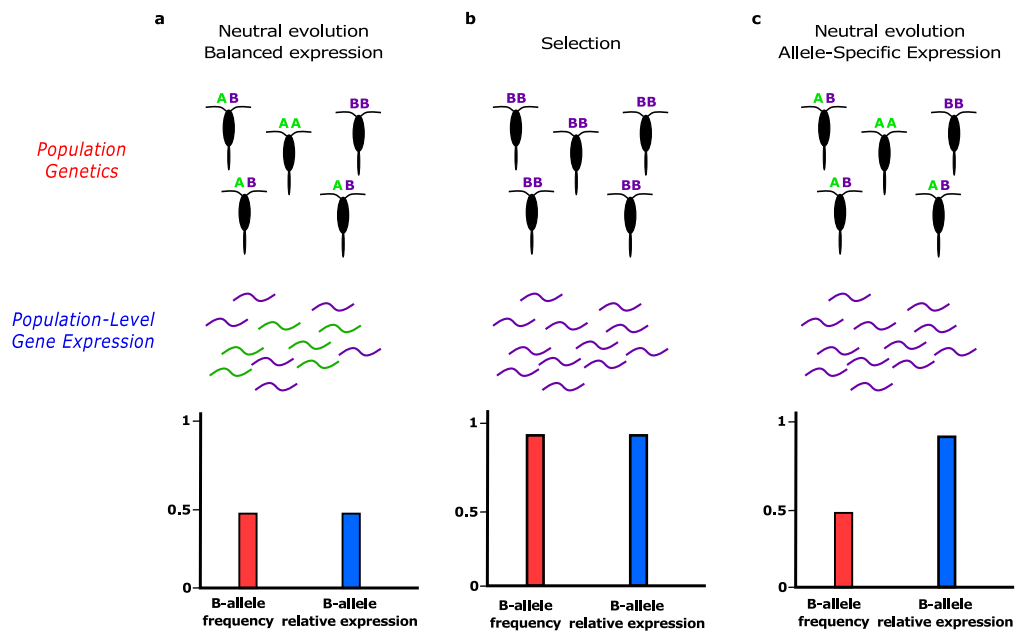


Figure 1: Population genomic and transcriptomic profiles of a biallelic locus in a case of **a**, Neutral evolution and balanced expression; **b**, Selection in favor of the B-allele; **c**, ASE in favor of the B-allele.

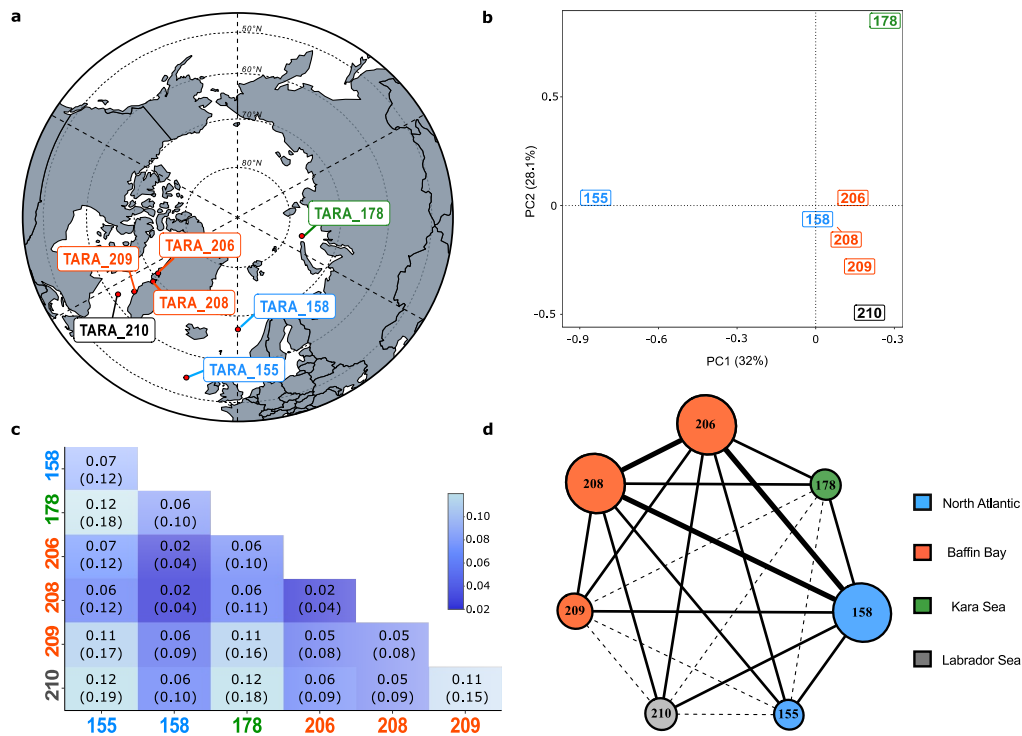


Figure 2: Genomic differentiation of *O. similis* populations from Arctic Seas. **a**, Geographic locations of the seven *Tara* Oceans sampling sites: Northern Atlantic (blue), Kara Sea (green), Baffin Bay (orange) and Labrador Sea (grey). **b**, Principal Component Analysis (PCA) computed by *pcadapt* based on allele frequencies. **c**, Pairwise- F_{ST} matrix. The median (mean) of each pairwise- F_{ST} distribution computed on allele frequencies is indicated. **d**, Graph representing the genomic differentiation of the seven populations of *O. similis*. The nodes represent the populations; their width reflects their centrality in the graph. The edges correspond to the genetic relatedness based on the median pairwise- F_{ST} between each pair of population; 0.02 (large solid line), 0.05 to 0.07 (thin solid line) and 0.11 to 0.12 (dashed line).

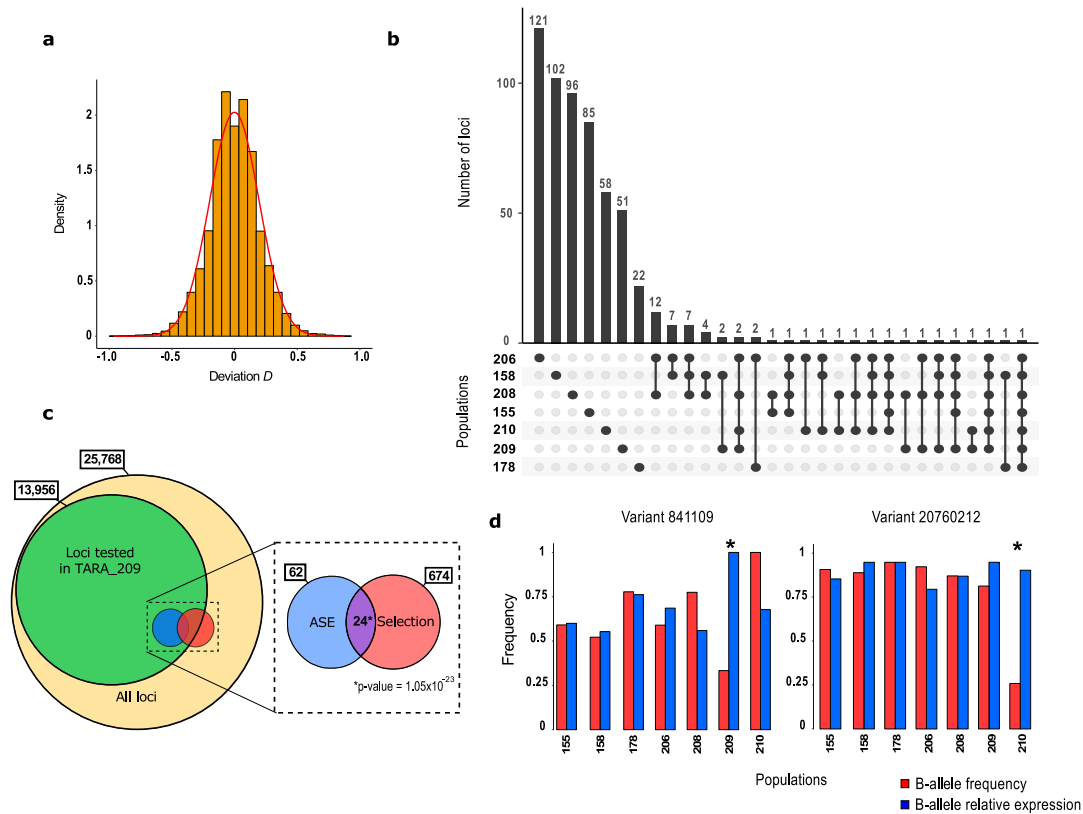


Figure 3: Population allele-specific expression detection and link with natural selection. **a**, The deviation D distribution in TARA_209. The red line corresponds to the Gaussian distribution estimated from the data. **b**, Upset plot of the ASE detection in the seven populations. Each bar of the upper plot corresponds to the number of variants under ASE in the population(s) indicated by black dots in the lower plot. **c**, Crossing ASE and Selection. The yellow circle represents the total set of variants. In green, the number of heterozygous variants tested for ASE in TARA_209. In blue and red, the amount of detected variants under ASE in TARA_209 and under selection among the populations respectively. In purple, the intersection comprising variants under ASE in TARA_209 and under selection, with its hypergeometric test p-value. **d**, Metagenomic and metatranscriptomic profiles of variants 841109 and 20760212. Each population is indicated on the x-axis, with the associated B-allele frequency (red) and B-allele relative expression (blue). The frequency is shown on the y-axis. The asterisks mean ASE was detected in the corresponding population.

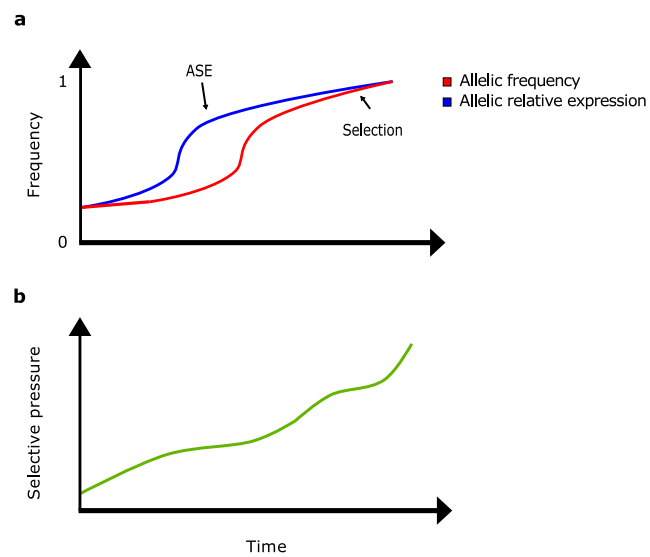


Figure 4: From allele-specific expression to natural selection. **a**, Evolution of allele frequency and allele relative expression over time. **b**, Evolution of selective pressure over time