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**MOLECULAR ECOLOGY****Genomic resources and their influence on the detection of the signal of positive selection in genome scans**

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1 **Genomic resources and their influence on the detection of the signal of positive selection**  
2 **in genome scans**

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25

26 **Running title:** Large genomic resources and genome scans

27 **Abstract**

28 Genome scans represent powerful approaches to investigate the action of natural selection on  
29 the genetic variation of natural populations and to better understand local adaptation. This is  
30 very useful for example in the field of conservation biology and evolutionary biology. Thanks  
31 to Next Generation Sequencing, genomic resources are growing exponentially, improving  
32 genome scan analyses in non-model species. Thousands of SNPs called using Reduced  
33 Representation Sequencing are increasingly used in genome scans. Besides, genomes are also  
34 becoming more available, allowing better processing of short-read data, offering physical  
35 localisation of variants, and improving haplotype reconstruction and data imputation.  
36 Ultimately, genomes are also becoming the raw material for selection inferences. Here, we  
37 discuss how the increasing availability of such genomic resources, notably genomes,  
38 influences the detection of signals of selection. Mainly, increasing data density and having the  
39 information of physical linkage data expand genome scans by i) improving the overall quality  
40 of the data; ii) helping the reconstruction of demographic history for the population studied to  
41 decrease false positive rates; iii) improving the statistical power of methods to detect the  
42 signal of selection. Of particular importance, the availability of a high quality reference  
43 genome can improve the detection of the signal of selection by i) allowing matching the  
44 potential candidate loci to linked coding regions under selection, ii) rapidly moving the  
45 investigation to the gene and function, and iii) ensuring that the highly variable regions in  
46 coding regions of the genomes are also investigated. For all those reasons, using reference  
47 genomes in analyses of genome scans is highly recommended.

48

49

50

51 **Introduction**

52 Species live in a wide variety of heterogeneous and changing environments, where the  
53 environment designs large range of abiotic factors (e.g. temperature, oxygen) and biotic  
54 factors (pathogens, symbionts, sexual partners) potentially causing selection. Understanding  
55 how these environmental factors lead to genetic adaptation is a longstanding question in  
56 evolutionary biology (Kawecki & Ebert 2004). With the rapidly increasing availability of  
57 large genomic resources, this topical question can now be addressed by genome scans, i.e. the  
58 survey of genetic variability across whole genomes or across a large number of loci in a large  
59 number of individuals living in distinct environments (Pritchard 2010). The main objective of  
60 genome scans is to identify signals of selection at the genome level in natural populations and  
61 thus uncover how natural selection affects genetic variation in response to environmental  
62 heterogeneity and changes (Mitchell-Olds *et al.* 2007; Nosil *et al.* 2009; Schluter & Conte  
63 2009).

64 The identification of these signatures of natural selection in genome scans has become an area  
65 of intense research, stimulated by the increasing ease with which a high number of genetic  
66 markers can be discovered and characterized in non-model species thanks to Next Generation  
67 Sequencing (NGS) (Davey *et al.* 2011). Loci identified as targets of natural selection are  
68 likely adaptively and / or functionally important (Vitti *et al.* 2013), and hence candidates for  
69 involvement in **local adaptation**<sup>1</sup>, disease susceptibility, resistance to pathogens, and other  
70 traits of interest to plant and animal breeders. Here, we illustrate our discussion mainly in the  
71 field of conservation and evolutionary biology (Allendorf *et al.* 2010; Segelbacher *et al.*  
72 2010). We focus on studies based on the analysis of the spatial sampling of geo-referenced  
73 individuals or populations in sites characterized by different environmental conditions. In

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<sup>1</sup> Words in bold are defined in the glossary

74 some cases, the measure of the geo-referenced environmental variable is also available. Those  
75 studies aims to better understand local adaptation.

76 One application of genomes scans in conservation biology is the improvement of the  
77 definition of **management units** through integrating adaptive genetic variability (Funk *et al.*  
78 2012). This is particularly important in the case of cryptic genetic lineages which are  
79 identified only when using a sufficient number of markers (e.g. Bourret *et al.* 2013;  
80 Bradbury *et al.* 2013; Hemmer-Hansen *et al.* 2014; Russello *et al.* 2012). For instance,  
81 Bradbury *et al.* (2013) looked for genomic islands of adaptive divergence (ie. genomic regions  
82 associated with adaptation) to refine the delineation of management units in Atlantic cod  
83 *Gadus morhua*. They applied an outlier based detection approach (i.e. BAYESCAN, Foll &  
84 Gaggiotti (2008)) to 1536 SNPs genotyped for 466 individuals. They detected elevated  
85 divergence in 5.2% of SNPs consistent with divergent selection. Those outliers revealed a fine  
86 scale geographic differentiation both in the eastern and the western Atlantic, which enhanced  
87 individual assignment to the region of origin in comparison to neutral markers. More  
88 generally neutral markers **hitchhiking** with selected loci can provide information not only on  
89 **positive selection** but also on restrictions to gene flow, which can be used as a tool to identify  
90 management units (Gagnaire *et al.* 2015). Another important application of genome scans in  
91 conservation biology is the study of species ability to adapt in response to climate change  
92 (Pauls *et al.* 2013). The identification of current adaptive polymorphisms can help to identify  
93 and maintain adaptive genetic potential. For example Dixon *et al.* (2015) have identified  
94 genomic regions potentially involved in the response to selection for thermal tolerance in the  
95 coral *Acropora millepora*. This gives some clues on the possibility of adaptive evolution in  
96 future environments, which is essential for conservation (Allendorf *et al.* 2010). Then,  
97 detecting climatic variables and polymorphisms potentially involved in local adaptation can  
98 improve models of future species dynamics under climate change (Manel *et al.* 2012).

99 Gaining information on the genetic basis of adaptation to different environments could also be  
100 used to improve assisted evolution of natural populations (van Oppen *et al.* 2015).

101

102

103 Here, we focus on genomic data and discuss only the use of NGS-derived markers. **Single**  
104 **Nucleotide Polymorphism** (SNP) data are the marker of choice to conduct genome scans.

105 The physical position of these SNPs on the genome can be known or not, with different  
106 degree of precision. SNPs of unknown genomic position are now widely used in non-model

107 species since the recent development of various protocols of **Reduced Representation**  
108 **Sequencing** promoted by the decreasing cost of high throughput sequencing (Davey *et al.*

109 2013; Davey *et al.* 2011). Alternatively, the recent increase of availability of genomes for a  
110 wide variety of species opens the perspective to locate SNPs on the genome using reference

111 genomes (Box 1). The main benefit of moving from thousands of anonymous unpositioned  
112 markers with no reference genome to the case of having a reference genome (or long –read

113 sequences), independently of its quality, is to be able to locate and order markers (SNPs)  
114 along the genome (Bragg *et al.* 2015) (Figure 1). This is important since in most cases,

115 candidate SNPs identified through genome scans are not the direct target of selection but are  
116 rather physically linked to these targets. Then, the knowledge of the **physical linkage** allows

117 the identification of genomic regions, and not only SNPs, with exceptionally high population  
118 differentiation (Tine *et al.* 2014). It also allows to explore the number and physical extent of

119 such regions (Nosil *et al.* 2009; Roesti *et al.* 2012a), to derive robust demographic data  
120 (Huber *et al.* 2014) and to investigate subtle fine spatial structure (Leslie *et al.* 2015) that are

121 necessary for the inference of selection.

122

123 In this review, we discuss the benefits of using additional genomic resources such as reference  
124 genomes on the ability of genome scans to detect selection in conservation and evolutionary

125 biology (Figure 1). We will first discuss which inferences can be made without reference  
126 genomes which is still the rule for most species (Gagnaire *et al.* 2012), and then the  
127 perspectives that are open by the availability of a reference genome or other genomic  
128 resources (Box 1). We then discuss the main challenges remaining even when reference  
129 genome is available. First, when genome scans rely on reference genomes, only high quality  
130 assembly makes it possible to study the highly variable regions of the genomes in coding  
131 regions (Box 2). Second, genome scans only represent a screening tool to reveal potential  
132 differences among environments in the functions and histories of the candidate genes  
133 identified in these analyses. We therefore discuss more extended validations of the adaptive  
134 function of the candidate loci (Pavey *et al.* 2012).

### 135 **Genomic data used in genome scans**

136 We describe here the diversity of genomic data used to conduct a genome scans in function of  
137 the availability of one or several related genomes.

138 On the one hand, Reduced Representation Sequencing (**RRS**) techniques are based on  
139 the use of restriction enzyme digestion to reduce the complexity of the genome and can be  
140 performed without prior genomic resources like a reference genome, a transcriptome, or a  
141 SNP chip. RRS allow the sequencing of a high number of short genomic regions in different  
142 individuals. They notably include Reduced Representation Libraries (RRL), Genotyping By  
143 Sequencing (GBS) and restriction-site-associated DNA sequencing (RADseq) (Box 3) and  
144 other (RAD, ddRAD, EzRAD, 2B-RAD, nextRAD) (Davey *et al.* 2011 ; Peterson *et al.*  
145 2012). Such methods have been increasingly used to produce tremendous amounts of short-  
146 reads data to ultimately genotype a high number of SNPs randomly located in the genome of  
147 fairly large numbers of individuals. Note that the number of individuals can be increased by  
148 multiplexing (at the detriment of individual coverage or the number of sites targeted) or via  
149 sequencing pools of individuals (Combosch & Vollmer 2015). Similarly to RADseq, short-

150 reads sequencing of RNA, RNAseq is also increasingly used to screen polymorphism in DNA  
151 coding regions (Piskol *et al.* 2013). Such methods also have huge potential for searching  
152 signals of local adaptation since they target cDNA and give at once both DNA polymorphism  
153 data and differential expression levels (De Wit & Palumbi 2013). However, the use of  
154 transcriptome data can be limited by allele specific expression. Paralogous loci can also  
155 induce difficulties in the analysis of transcriptome sequences by creating spurious  
156 polymorphic position (Gayral *et al.* 2013). Dedicated approaches are required to limit this  
157 biases such as a search of orthologous genes ( Li *et al.* 2003 ; Pratlong *et al.* 2015) which can  
158 be complemented by the filtering method of SNPs proposed by Gayral *et al.* (2013).

159

160 On the other hand, the availability of reference genomes opens different possibilities  
161 for generating more powerful individual data to be used in genome scans. First, it is possible  
162 to use reference genomes to improve RRS data. The alignment of short-reads produced by  
163 RRS methods on a reference genome can notably improve the overall quality of the SNP  
164 calling since erroneous reads would be pruned out during the alignment. Physically indexing  
165 loci also benefits to data filtering, allowing computing linkage disequilibrium (LD) among  
166 physically close loci. Loci in high LD can then be filtered out to allow the use of the dataset in  
167 software requiring unlinked loci. Instead of pruning linked loci, the LD data obtained can also  
168 be used as a complementary input to limit biases associated with the used of linked loci.  
169 Physically locating loci also increases the strength of the datasets since it allows applying a  
170 wide variety of selection detection tools, taking advantage of both allele frequencies and loci  
171 physical positions (eg  $F_{ST}$  sliding windows). Lastly, the distance and LD among loci can also  
172 be used during the statistical reconstruction of **haplotypes** (Browning & Browning 2011;  
173 Stephens & Scheet 2005).

174 Moreover, as discussed by Buerkle et al. (2011), analyses of multi-allelic DNA  
175 sequences (as haplotypes) rather than bi-allelic markers should help to solve the “n=1  
176 constraint” related to the use of SNP. Besides, haplotypes can be used to improve the  
177 imputation of missing data (Browning & Browning 2007). Indeed, if some alleles are  
178 inherited more frequently together (haplotypes), and that this information is known, it is  
179 crucial to impute data considering these associations rather than only the population  
180 frequencies of the alleles being imputed. However, haplotype phasing will be increasingly  
181 difficult with increasing recombination rate and decreasing SNP density, which would be an  
182 important limitation in studies implementing RRS using relatively rare cutters and single-end  
183 short sequencing since sequenced SNP may often fall too far apart.

184 Genome sequences are also increasingly considered as raw material for genome scans,  
185 allowing increasing the number of SNPs detected, to construct haplotypes and at larger  
186 divergence scale to perform comparative genomics. Indeed, De novo sequencing can be used  
187 to generate a high number of SNPs for multiple individuals. While sequencing parts of the  
188 genome using RRS (described above) can bring informative results on adaptive diversity, the  
189 number of loci identified through these approaches is also much lower than with genome  
190 sequencing (up to tens of thousands compared to millions of SNPs respectively; Rellstab *et al.*  
191 2015). **De novo assembled genome** by deep-sequencing (Chaisson *et al.* 2015a) is one of the  
192 most informative approaches for selection detection. However, such data cannot be derived  
193 yet for a high number of individuals in conservation projects because it is still too expensive.  
194 Nevertheless, a two-step strategy can be used with first de novo assembly of a reference  
195 genome by deep-sequencing one individual and followed by the resequencing of additional  
196 individuals at lower coverage (Soria-Carrasco *et al.* 2014). In their study of speciation and  
197 adaptation to different host plants in the stick insect *Timema cristinae*, Soria-Carrasco *et al.*  
198 (2014) first sequenced the genome on the basis of libraries of lengths varying from 170 to

199 5000 bp. The total genome size was estimated around 1.3 Gb and the assembled genome was  
200 estimated to cover around 80% of the genome. Then, Soria-Carrasco *et al.* (2014) re-  
201 sequenced at lower coverage the genomes of 160 individuals on eight lanes of Illumina Hi-  
202 Seq 2000. The reads were mapped to the reference genome. They thus obtained more than  
203  $12 \cdot 10^6$  SNPs with a mean coverage of 5 per SNP and per individual. Such sequencing of  
204 several individuals then allowed to produce 4,391,556 SNPs that mapped to one of the 13  
205 linkage group and were used in phylogenetic analysis and to characterize the distribution of  
206 genomic variation across the 160 wild-caught *T. cristinae*. However, this approach is still  
207 relatively expensive for conservation projects needing numerous individuals. As the power of  
208 genome scan approaches can be increased by the number of locations sampled and the  
209 number of individuals sampled per location (Lotterhos & Whitlock 2015), other approaches  
210 can be useful to reduce sequencing costs. Whole genome sequencing of pooled individuals is  
211 a promising and cost effective alternative to individual sequencing (Schloetterer *et al.* 2014).  
212 The cost effectiveness of pooled genome sequencing (Pool-Seq) comes from the cost of the  
213 preparation of libraries and on the sequencing of more individuals which can increase the  
214 estimates of allele frequencies (Schloetterer *et al.* 2014). In their analysis of the pros and cons  
215 of Pool-Seq, Schlöterer *et al.* (2014), indicate their interest to study genetic differentiation,  
216 heterozygosity, or selective sweep (Boitard *et al.* 2012). For instance, Turner *et al.* (2010)  
217 have sequenced *Arabidopsis lyrata* from four populations (two from serpentine soils and two  
218 from granitic soils), with 25 individuals pooled per population, with a 39-fold genome  
219 coverage. On the basis of allele frequency differences and  $F_{ST}$ , they identified candidate SNPs  
220 for the adaptation to soil types. However, Pool-Seq can be limiting for example if one is  
221 interested in linkage disequilibrium (Schloetterer *et al.* 2014).

222

223 Finally, only high quality genomes will allow studying of highly variable regions located in  
224 coding regions (Chaisson *et al.* 2015a) (Box 2). In humans, such plastic regions of the  
225 genome are known to contain important immune gene families such as the *Major*  
226 *Histocompatibility Complex (MHC) class I* and *class II* genes and the *Killer-cell Ig-like*  
227 *Receptor (KIR)* genes that are both critical for the resistance to pathogens and hence for the  
228 adaptation to different environments (Sommer 2005; Vilches & Parham 2002).

229 In summary, the above data can be directly used as raw material in the statistical analysis of  
230 genomes scans: SNPs (from a small to a high number) or haplotypes.

231

### 232 **Detecting the signal of selection without and with a reference genome**

233 Here we discuss how additional genomic resources improve the inferences of the signal of  
234 selection in genome scan analyses. We introduce briefly the main principle of the statistical  
235 methods, but we do not enter into the details of the available methods and software since  
236 multiple reviews have already been published on the subject (Manel *et al.* 2010; Rellstab *et al.*  
237 2015; Schoville *et al.* 2012).

238 Without any reference genome, SNPs sampled in multiple populations are analyzed as  
239 independent variables with methods derived from the test of neutrality of Lewontin and  
240 Krakauer (1973) and looking for outlier loci (i.e. loci with higher or lower levels of  
241 divergence than expected under neutrality). Loci with high values of  $F_{ST}$ , a measure of genetic  
242 differentiation among sampled populations, correspond to loci potentially under divergent  
243 local selection while loci with low  $F_{ST}$  values correspond to loci under balancing selection  
244 (Beaumont & Balding 2004).

245 When environmental variables are available, it is possible to use genetic environment  
246 associations (GEA tests, Hedrick *et al.* 1976; Lotterhos & Whitlock 2015) either in a second

247 round after outlier detection methods or directly for detecting outlier loci. The first application  
248 of GEA in the context of genome scan tests the correlation between allele frequencies and  
249 environmental variables (Joost *et al.* 2007 ; Schoville *et al.* 2012); then other regression based  
250 approaches have been used (Rellstab *et al.* 2015).

251

252 However the signature of adaptive processes are not always distinguishable from the neutral  
253 genomic background as assumed to have uniform effects across the entire genome, generating  
254 a high number of false positive outliers (Schoville *et al.* 2012). Population structure causes  
255 correlated allele frequencies and increases the number of false positives generated by genome  
256 scans for **selective sweeps** (Excoffier *et al.* 2009). Demographic history can create patterns  
257 resembling selection, as in cases of severe bottlenecks, allele surfing during population  
258 expansion, secondary contact, and isolation by distance (Novembre & Di Rienzo 2009).  
259 Genetic incompatibilities or background selection on gene-coding regions can also confound  
260 the signal of selection (Bierne *et al.* 2013). Although, refinements have been introduced to  
261 account for those confounding effects (Lotterhos & Whitlock 2015), false positives remain.

262

263 Without additional genomic resources, those analyses produce a list of loci that are potentially  
264 under selection or linked to alleles under selection, and when available the relevant  
265 environmental variables acting as pressures of selection. They generally detect single loci  
266 with important effects on adaptation. However some questions may remain, the most evident  
267 caveats being that the loci identified as potential targets of selection are usually only  
268 statistically linked with close targets of adaptive significance.

269

270 We describe below how the reference genome may improve the power of genome scans and  
271 help to decrease the number of false positives either through the use of reference genomes to  
272 improve previous analysis, or in a direct analysis of raw data.

273

274 Mapping SNPs (e.g. identified through RRS loci) to reference genomes can give insights into  
275 the potential genes involved in adaptation (see next section) and on the distribution of  
276 population genetic statistics along the genome since additional inferences as genetic  
277 differentiation and genetic diversity on chromosomal regions become possible with a dense,  
278 ordered set of genome-wide markers (Figure 1). In practice, a sliding window sweeps across  
279 the genome, to look for regions showing significant deviation of the statistics inferred. Sliding  
280 windows are implemented to average locally those statistics and to compare them toward a  
281 random set of windows that can be taken from a larger genomic region (eg. the considered  
282 chromosome or the whole genome). This sliding-based windows method reinforces the  
283 statistical power of the detection of selection since it can highlight regions that may  
284 potentially not be spotted using non genomic outlier SNP approaches. It also allows inferring  
285 the physical extent of the signal of selection. The size of the window on which the average is  
286 calculated and the size of the step are usually defined around 150kb and 50kb, respectively,  
287 the step-size being equal or smaller than the windows-size. These windows and step sizes are  
288 crucial parameters that can largely influence the detection power of such analyses and should  
289 be defined according to the SNP density and sampling variance (Hohenlohe *et al.* 2010). It  
290 should be noted that SNP densities obtained in RRS using rare cutters would probably be too  
291 small to allow applying with robustness sliding windows along the entire genome.

292 Comparing the classical local averaged  $F_{ST}$  among populations to windows-based  $F_{ST}$  would  
293 reveal the presence of putative targets of positive selection. For example, this strategy has  
294 been used to study the variation of  $F_{ST}$  in different lineages of the European sea bass

295 *Dicentrarchus labrax* using a window size of 150 kb (Tine *et al.* 2014) (Box 4). This  
296 technique can also be used on whole genome resequencing data, as illustrated in Kardos *et al.*  
297 (2015) in which they implemented windows of 100 kb, with step size of 50 kb, and found  
298 elevated  $F_{ST}$  in regions spanning growth hormone receptor gene. To go even further, Roesti *et*  
299 *al.* (Roesti *et al.* 2012b) suggested correcting SNP  $F_{ST}$  by local recombination rates. In fact,  
300 they showed patterns of within-chromosome large-scale variations in recombination and  
301 hitchhiking and thus in  $F_{ST}$  that were probably largely influenced by chromosomes structure.  
302 They propose to correct for this potential bias by applying sliding window tests on corrected  
303  $F_{ST}$  rather than raw  $F_{ST}$ , to avoid potential false positive and false negative outliers. Another  
304 way of considering this potential bias is to estimate locally averaged recombination rate,  
305 nucleotide diversity, and genetic differentiation and to interpret these indices in an integrated  
306 manner as illustrated in the European sea bass *Dicentrarchus labrax* (Tine *et al.* 2014).

307 The information of physical linkage among SNPs also opens the possibility to detect reduced  
308 genetic diversity in the neighborhood of a selected (directional selection) site along a  
309 chromosome, which can be the consequence of **selective sweep** (Nielsen 2005). The extent of  
310 the area displaying reduced diversity will depend on the intensity of selection, on  
311 recombination rate, on the breeding system and on the age of the selective event. The  
312 elimination of slightly deleterious mutations (background selection) can be difficult to  
313 separate from selective sweeps (Nielsen, 2005). Specific statistical methods have been  
314 developed to detect selective sweeps at the population level (Nielsen 2005; Sabeti *et al.*  
315 2006). They differ in the type of the genomic signature of selection detected (Oleksyk *et al.*  
316 2010): local reduction in genetic variation at the proximity of the loci under selection  
317 (Oleksyk *et al.* 2008), changes in the shape of the frequency distribution of genetic variation,  
318 i.e. **site frequency spectrum** (Tajima 1989), extended linkage disequilibrium segments  
319 (Sabeti *et al.* 2002; Vatsiou *et al.* 2015), or elevated admixture contribution from one

320 population (Tang *et al.* 2007). Such methods rely on the analysis of haplotype. They open  
321 perspectives to capture the signal of selection left by both hard and soft sweep. If adaptation  
322 has been shaped by new mutations rapidly driven to high frequency in a new environment,  
323 those alleles will be detected on haplotypes with low genetic diversity and not observed in  
324 ancestral populations or environment (Stapley *et al.* 2010). In this current issue, Vatsiou *et al.*  
325 (2015) compared seven methods that either focus on patterns of long range haplotype  
326 homozygosity (Sabeti *et al.* 2002) or on the effect of linkage on multilocus genetic  
327 differentiation (Chen & Slatkin 2013). Those methods open perspectives to capture the signal  
328 of selection left by both hard and soft sweep.

329

330 As previously mentioned above, neutral processes can confound the signal of selection.  
331 Sophisticated methods using physically indexed SNPs, haplotype or sequence data have been  
332 recently developed to improve the inference of demographic processes by helping to  
333 reconstruct an accurate demographic history, potentially implicating heterogeneous gene flow  
334 along the genome, for the population studied and hence decrease confounding effects  
335 (Excoffier *et al.* 2013; Gutenkunst *et al.* 2009; Liu & Fu 2015).

336 Lastly, the fact that adaptation may rely on polygenic traits with small changes in allele  
337 frequencies has been discussed (de Villemereuil *et al.* 2014). One interesting development  
338 here is to test outliers not on a single marker basis but on set of genes linked in biological  
339 pathways (Daub *et al.* 2013). This is possible only for species with good genomic knowledge,  
340 as it requires to assign SNPs to genes on the basis of their physical location and to use  
341 functional relationships between genes.

342

343 **From prioritization of candidate loci to validation**

344 Genome scans characterize loci potentially involved in the adaptation to particular  
345 environments but because these methods can generate false positives, a prioritization of  
346 candidate loci help to focus on the most reliable candidates. Mapping loci on a reference  
347 genome can allow the identification of coding candidates or to loci in physically proximity to  
348 coding regions (in this case, a transcriptome can be enough to identify expressed loci). If these  
349 genes are annotated in the studied species or a closely related one, it can highlight candidate  
350 genes functionally consistent with the studied selective context. For example, using exome  
351 sequencing, Yi *et al* (2010) studied the adaptation of human to high altitudes and found that  
352 the candidate gene with the strongest signal of selection was a transcription factor involved in  
353 response to hypoxia. In this case, the consistence between the function and the environmental  
354 context of the study provided a strong support for this candidate. For the non-model  
355 organisms for which the reference genome sequence lacks functional annotations, Gene  
356 Ontology (GO) could be a useful tool to find pertinent functions in the studied context among  
357 the candidate genes (Gu *et al.* 2009). The identification of loci repeatedly involved in the  
358 same biological or ecological function in different taxonomic groups exposed to comparable  
359 pressures can also be a good argument for the choice of candidate loci (Pratlong *et al.* 2015).  
360 For example, Fischer *et al.* (2013) studied the local adaptation of *Arabidopsis halleri* to local  
361 climatic conditions by the use of SNPs obtained from Pool Seq. First they detected outlier  
362 SNPs on the basis of  $F_{ST}$  and differentiation tests. Then they tested the association between  
363 these outliers and environmental conditions while controlling for population structure. A GO  
364 enrichment was applied to the outlier loci as well and led to the discovery of the implication  
365 of functions linked with the response to biotic factors (such as “defence response to  
366 bacterium”). Conversely they considered genes with GO potentially involved in the  
367 adaptation to climate conditions: among these candidate genes, four were indeed associated  
368 with the corresponding environmental factor. This study then underlines how multiple

369 approaches can help identify the factors involved in local adaptation.

370

371 Finally, to improve our understanding of the genomic architecture of adaptation (and  
372 speciation) and the nature of the genes involved in these processes, genome scans can be  
373 combined with QTL mapping, genome wide association studies (GWAS) and/or sequence and  
374 functional analysis (Gagnaire *et al.* 2013; Strasburg *et al.* 2012). In cases of divergent  
375 selection, the challenge is to document how functional polymorphisms at individual genes  
376 translate into different phenotypes, including quantitative traits values, which in turn translate  
377 into fitness differences (Storz & Wheat 2010). In such investigations, the statistical tests used  
378 to detect the signatures of natural selection, as well as all the steps before the functional  
379 validation, provide the basis for functional inferences: association studies for example link  
380 polymorphism at one locus to a phenotypic difference, as was done for the shell color  
381 polymorphism in the snail *Cepaea nemoralis* (Richards *et al.* 2013). An important argument  
382 to confirm the adaptive function of a particular allele is the design of appropriate experiments  
383 to study the resulting effects on protein function or protein expression (Storz & Wheat 2010).  
384 This can be done through functional genetic approaches: in the Darwin finches for example, a  
385 genomic region with high differentiation levels corresponded to genes previously identified as  
386 involved in beak morphology (Lamichhaney *et al.* 2015). For polygenic traits, QTL  
387 approaches or GWAS are useful. RAD sequencing was also used to identify QTL associated  
388 with ecologically important traits and to gene expression differences in the lake whitefish  
389 (*Coregonus clupeaformis*) (Gagnaire *et al.* 2013). The opportunity of whole genome  
390 sequencing allows nowadays to move toward GWAS, mostly in the identification of sequence  
391 variants associated with risks of complex traits in human genetics, where genomes are  
392 available at population scales (Hawley *et al.* 2014). In this field, GWAS was used in the  
393 identification of loci linked with the specialized diet of greenlandic Inuit, and associated with

394 metabolic and anthropometric phenotypes (Fumagalli *et al.* 2015). Nevertheless, the last and  
395 probably the most difficult step will be to link phenotypic or genetic differences with fitness  
396 differences. Here the analysis of the fitness of all possible point mutants in different  
397 controlled environmental conditions open perspectives to make such link. For example,  
398 Heiptas *et al.* (2011) analyzed the effect on fitness (growth rate during binary competition in  
399 this case) of all possible point mutations for a nine-amino acid region of Hsp90 in yeast. They  
400 observed a large proportion of mutation with strong deleterious effect eliminated via purifying  
401 selection and few mutation with neutral effect which is consistent with the neutral model of  
402 molecular evolution. Linking genotype to fitness open new perspectives such as the  
403 possibility to study the population of origin (central population vs margin population) of the  
404 mutation in the species range (Rolland *et al. in press*).

405 Finally as adaptation points to differences in fitness, an experimental validation by comparing  
406 different genotypes seems to be the most informative validation step. Experimental tests of  
407 local adaptation can be done for example with common garden or reciprocal transplant  
408 experiments with different genotypes for candidate loci (Kawecki & Ebert 2004). This should  
409 be easier for traits that not relying on too many loci.

410

## 411 **Conclusion**

412 In summary, the availability of a reference genome can incontestably improve the detection  
413 of the signal of selection at all steps of the genome scans: production of genomic data,  
414 statistical detection of the signal of selection, and prioritization of candidate genes. Main  
415 improvements can be summarized as follows: i) improving the overall quality of the data; ii)  
416 helping to reconstruct an accurate demographic history for the population studied and hence  
417 decrease confounding effects (Huber *et al.* 2014) ; with deep coverage, genome sequence data

418 from a single individual are also sufficient to make demographic inference (Miller *et al.* 2012;  
419 Oleksyk *et al.* 2012); iii) improving the statistical power of methods to detect the signal of  
420 selection. Finally, if the available genome is of high quality, i) it allows matching the  
421 potential candidate loci to linked coding regions under selection , ii) it rapidly moves the  
422 investigation to the gene and function (Lamichhaney *et al.* 2015), iii) it ensures that the  
423 highly variable regions of the genomes in coding regions are also investigated. This last point  
424 is important when region under selection are located in such variable regions (Box 2).

425

426 We state that having reference genomes represent a critical step to fully address the question  
427 of local adaptation. The community of researchers working in ecology on non-model species  
428 will thus gain to collaborate with the community of researchers working on species for which  
429 large genomic resources have long been available (human and other model species), as the  
430 latter have a long tradition of sequence analysis to detect signatures of natural selection.  
431 Combining evolution, ecology, genomics and comparative genomics will help to better  
432 address the question of local adaptation, which is topical in a context of global change. Finally  
433 we should keep in mind that adaptation *sensu lato* does not only rely on genetic diversity.  
434 Indeed the question of non-genetic effects, including epigenetic mechanisms, is of great  
435 interest in evolutionary biology (Danchin 2013); yet, here again the use of genomic  
436 information should be useful to study the diversity in epigenetic modifications.

437

438

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448

449

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739

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740 **Glossary**

741

742 **De novo assembled genome:** sequence of a genome from overlapping DNA sequences  
743 without having a reference genome.

744

745 **Haplotype** : set of genetic variants or alleles physically linked on a chromosome and  
746 statistically associated. They are inherited together until disrupted by recombination.

747

748 **Hitchhiking** (to fixation): when a genetic variant that is physically linked to a selectively  
749 advantageous mutation goes to fixation because of the selection on that advantageous  
750 mutation.

751

752 **Linkage disequilibrium (LD):** the non-random association of alleles at different loci. LD can  
753 strongly increase around selected sites when selection is strong.

754

755 **Local adaptation:** the result of fitness differences between alleles (Wollstein & Stephan  
756 2015). A fitness value can be assigned to each possible genotype.

757

758 **Management unit:** Genetically differentiated population to be managed separately because of  
759 its demographic independence

760

761 **Negative selection** (or purifying selection): any type of selection where new mutations are  
762 selected against (Nielsen 2005). In this case, the derived allele is detrimental to the organisms.

763

764 **Physical linkage** describes the tendency of alleles near each other on a chromosome to be  
765 inherited together

766

767 **Positive selection** as introduced by Darwin and Wallace (1858) ), “is the principle that  
768 beneficial traits – those that make it more likely that their carriers will survive and reproduce-  
769 tend to become more frequent in populations over time” (Sabeti *et al.* 2006). Then, it is any  
770 type of selection where coefficient of selection has a positive value. It occurs when the  
771 derived allele has a higher fitness than the ancestral allele. It comprises both directional  
772 selection and balancing selection as overdominance. Positive selection is the mechanism that  
773 can lead to local adaptation (Nosil *et al.* 2009; Pritchard 2010).

774

775

776 **Reduced Representation Sequencing (RRS):** a technique based on the use of restriction  
777 enzyme digestion to reduce the complexity of the genome.

778

779 **Selective sweeps:** reduction or elimination of genetic variation in a genomic region as the  
780 result of natural selection having favored one particular variant in this region.

781

782 **Site frequency spectrum.** The genomic signatures of recent adaptations can be measured by  
783 the site frequency spectrum (SFS), which summarizes the counts of derived variants in a  
784 region.

785

786 **Soft sweep:** Selection can occur either on standing genetic variation, i.e. existing genetic  
787 variation, creating a **soft sweep** or on a *de novo* mutation, creating a **hard sweep**.

788

789

## 790 **Legend of figures**

791 **Figure 1.** Schematic representation of the benefits of using additional genomic resources  
792 (mainly reference genomes) in the different steps of genome scans. GBS: Genotyping by  
793 sequencing.

794

## 795 **Boxes**

796

### 797 **Box 1- A reference genome**

798 A reference genome is an assembly of a genome that is representative of a species and can be  
799 used to align sequence reads for population-genomic studies. In genome scan analyses, a  
800 reference genome can either be the genome of the targeted species or that of a closely related  
801 species. Similarly, this reference can be based on a single individual or on a collection of  
802 individuals; in the former situation however, the reference genomes do not capture the full  
803 extent of nucleotide or structural variation segregating within a species. With the dramatic  
804 decrease in the cost of DNA sequencing of the past few years, an ever increasing number of  
805 genome are characterized, yet the quality of these genomes can be highly dependent upon the  
806 quality of the assembly (Simpson 2014). As further developed below, reference genomes can  
807 thus be of two types: they can be represented by a single sequence ('golden path' reference  
808 genomes) or they can be representative of the genetic diversity of the species ('high quality'  
809 reference genomes). For these 'high quality' reference genomes, genetic variation does not just  
810 refer to single nucleotide polymorphisms (SNPs) but also to structural variation that  
811 represents a large source of genomic diversity (Church *et al.* 2011).

### 812 **High quality genome (like human, mouse or *A. thaliana*).**

813 A 'high quality' reference genome is defined here as a reference sequence that is both  
814 complete in terms of coverage and representative of the genetic diversity of the species  
815 investigated. Because current sequencing technologies can only target the euchromatic portion

816 of the genome (hence excluding the heterochromatin that includes the centromere and  
817 telomere regions), 'complete' refers here to the euchromatic genome. 'Finished' quality  
818 genome projects typically cover >95% of the euchromatin sequence, a target that can however  
819 be difficult to achieve depending on the genome size and complexity of the targeted species.  
820 Here genetic variation does not just refer to single nucleotide polymorphisms (SNPs) but also  
821 to structural variation that represents a large source of genomic diversity (Church *et al.* 2011).

822 With the notable exception of the human genome however, most genome sequences only  
823 satisfy the first criterion ('complete' sequence) and thus represent what was defined as a  
824 'golden path' during the course of the sequencing of the human genome: a non-redundant  
825 haploid representation of the genome (Kent & Haussler 2001).

### 826 **A 'golden path' reference genome**

827 A 'golden path' reference genome thus represents the first level of reference sequence that  
828 could be used for genome scans. It is now possible to rapidly generate such a reference  
829 sequence thanks to modern sequencing technologies that have led to a rapid decrease in the  
830 cost of sequencing: for example in 2014-15, typical cost for re-sequencing of a human-size  
831 genome (3,000Mb) with paired-ends reads at 30X coverage on an Illumina HiSeq platform is  
832 \$4,211. This cost includes labor, administration, management, utilities, reagents, and  
833 consumables; sequencing instruments and other large equipment (amortized over three years);  
834 informatics activities directly related to sequence production; submission of data to a public  
835 database and indirect costs (source: National Human Genome Research Institute (NHGRI);  
836 <http://www.genome.gov/sequencingcosts/>).

837 With sufficient coverage (>30X), this approach should lead to a reference genome covering  
838 >95% of the euchromatin sequences. Those values are however highly dependent on the size  
839 of the genome and on factors such as the frequency of repeated regions in the genome. Such  
840 complete sequences are rarely obtained in conservation biology at the moment however, as  
841 illustrated by the de novo sequencing of the genome of *Arabis alpina*, which resolved less  
842 than 50% of the genome (172 Mb out of 370 Mb) (Lobreaux *et al.* 2014). Similarly, complex  
843 regions with recently duplicated segments for example or plastic regions in diploid genomes  
844 may not be well resolved by this approach (Alkan *et al.* 2011).

### 845 **Improving quality of assembly**

846 Over the past couple of years, ways to improve initial genome assemblies have emerged. In  
847 particular, technology from Pacific Biosciences (PacBio) for long-read single molecule, real-  
848 time (SMRT) sequencing can upgrade genomes to a higher quality finished state (Huddleston  
849 *et al.* 2014). SMRT sequencing is however still costly and can thus only be applied to small  
850 genomes or to targeted resequencing of specific regions. To avoid the problems associated  
851 with sequencing plastic regions in diploid genomes, an interesting alternative is also to work  
852 with haploid cell lines generated from the same organism such as specific tissues Chaisson *et*  
853 *al.* 2015b) or specific life stages (Rensing *et al.* 2008). Although such cell lines will likely  
854 not be available for most organisms, single cell genomics are rapidly progressing so that  
855 single gametes could become an adequate resource to establish reference genome (Macaulay  
856 & Voet 2014). The sequencing of the genome of the European Sea Bass was based on the use  
857 of a meiogynogenetic individual (Tine *et al.* 2014). Finally, in addition to the experimental  
858 improvements, the quality of the reference genomes also increases with the development of  
859 better assemblers, i.e. the software used to assemble genomes. Indeed, software now exists to  
860 help *de novo* assembly from whole – genome shotgun short reads (Kajitani *et al.* 2014) and  
861 efforts are being made to evaluate the performance of these methods (Bradnam *et al.* 2013).

#### 862 **Status on genome sequencing**

863 Progress on genome information can be found here:  
864 <http://www.ncbi.nlm.nih.gov/genome/browse/#>

865

**866 Box 2- Challenges of highly variable regions**

867 While progress is being made to generate 'golden path' reference genomes, this will at best  
868 lead to the complete sequencing of one haploid genome in a given species. Such a sequence  
869 will be sufficient for the analysis of genome scans for the vast majority of genes and genomic  
870 regions but will be problematic to investigate the more plastic regions of the genome. Indeed,  
871 even for the highest quality mammalian genome, the human genome, it was found that some  
872 genomic regions were missing in the reference sequence (Kidd *et al.* 2010). These specific  
873 regions display structural differences between the genomes of the individuals investigated and  
874 the reference genome, either because of specific deletions or because of underrepresented  
875 multi-copy genes in the reference genome (Sudmant *et al.* 2010).

876 In human such plastic regions of the genome are known to contain important immune gene  
877 families such as the *Major Histocompatibility Complex (MHC) class I* and *class II* genes and  
878 the *Killer-cell Ig-like Receptor (KIR)* genes that are critical for the resistance to pathogens and  
879 hence for the adaptation to different environments (Sommer 2005; Vilches & Parham 2002).  
880 Indeed recent genome scans approaches on human populations underlined the critical roles of  
881 pathogens in local adaptation (Fumagalli *et al.* 2011). Both gene families display a high  
882 level of polymorphism but also gene-content variation (see Figure for the *KIR* locus) so that a  
883 single reference sequence will not represent correctly the gene content in all individuals and  
884 could lead to problematic analyses for genome scans. Indeed, not including multiple  
885 references for such regions produces misalignments of the reads and spurious variant calls.  
886 The human reference genome was thus organized to include multiple sequences for these  
887 regions (Church *et al.* 2011). Thus 'high quality' reference genomes that include multiple  
888 sequences for the plastic regions are necessary to produce unbiased results in genome scans.  
889 Such a reference sequence requires two additional steps once a first complete sequence of the  
890 genome is known: the identification of these regions and the characterization of the variation  
891 at these regions. Finally, data from these regions might need to be adapted to run some of the  
892 usual tests of local adaptation such as  $F_{ST}$  outliers: for example by encoding presence/absence  
893 of genes (*KIR* locus) as SNPs or by considering complete alleles rather than individual SNP  
894 (*MHC* genes). Because these highly variable gene families have a strong impact on immune  
895 adaptation, they are often investigated by targeted analyses, outside of genome scans  
896 (candidate gene approaches)

897

898

899 **Figure.** Example of a highly-variable region of the genomes of primates: the Killer-cell Ig-  
900 like Receptor (KIR) locus. This drawing compares the organization and gene-content  
901 variability of the human and chimpanzee *KIR* loci. The branching pathways illustrate how  
902 different gene-content motifs can combine to produce different *KIR* haplotypes. Genes that  
903 are typically found on all haplotypes of both species (framework genes) are colored grey;  
904 chimpanzee-specific KIR are colored green. Humans have two broad groups of haplotypes  
905 called A and B haplotypes that differ in gene content and level of allelic variability (Parham *et*  
906 *al.* 2012): genes characteristic of human A haplotypes are colored red while genes  
907 characteristic of human B haplotypes are colored blue (2DP1 and 2DL1 in humans are  
908 colored grey to indicate their presence both on A and B haplotypes). Adapted from Abi-  
909 Rached *et al.* (Abi-Rached *et al.* 2010).

910

911

912

913

914 **Box 3:** Methods based on the use of restriction enzyme digestion of target genomes to reduce  
915 the complexity of the target: example of RAD-seq

916

917 RAD-Seq is based on the sequencing of short sequences flanking restriction sites (Baird *et al.*  
918 2008). It requires choosing the restriction enzyme(s) in combination with the sequencing  
919 depth and the number of individuals multiplexed in order to modulate the number of expected  
920 markers. This choice is done on the basis of genome knowledge (size and GC-content) for the  
921 target species or on phylogenetically related species as proposed by Herrera *et al.* (2014). The  
922 analysis of RAD-Seq data can be done thanks to different software packages such for example  
923 as Stacks (Catchen *et al.* 2013), PyRAD (Eaton 2014), RADtools (Baxter *et al.* 2011), GATK  
924 (DePristo *et al.* 2010), or dDozent (Puritz *et al.* 2014).

925

926 As an illustration, (Pavey *et al.* 2015) used RAD-Seq to study the genetic basis of the  
927 differentiation between ecotypes of the American eel (*Anguilla rostrata*). They used the  
928 EcoRI restriction enzyme and analyzed 379 individuals with around 24 individuals per lane of  
929 an Illumina HiSeq 2000. After cleaning and filtering the data they retained 42 424 SNPs  
930 which corresponded to 1 SNP every 40 kb. This density allowed them to identify 331 SNPs  
931 associated with the ecotypes, with 99 SNPs corresponding to annotated protein-coding genes.

932

933

934 **Box 4- Genome scan and genomic resources: a case study on the European sea bass**  
935 **(*Dicentrarchus labrax*)**

936 Population genomic studies can be useful both for the management of wild and domestic  
937 hatchery populations and for a better understanding of the evolution of species, which is  
938 useful for conservation purposes. The study on the European sea bass (*Dicentrarchus labrax*)  
939 provides a good illustration of the multiple interests and applications of genomic data. This  
940 species is heavily harvested. Its distribution range, from the Atlantic Ocean to the Black Sea,  
941 encompasses an important barrier to gene flow at the Almeria-Oran front which separate two  
942 genetic lineages (Lemaire *et al.* 2005). The European sea bass can be present in different  
943 levels of salinity which raises the question of its adaptation to different environments (e.g  
944 (Lemaire *et al.* 2000)). Getting genomic information on this species would be useful to better  
945 understand its evolutionary history and would be useful for aquaculture purposes. Tine *et al.*  
946 (2014) published the first draft genome of *D. labrax*. The sequencing of the genome was  
947 based on a meiogynogenetic male, with an average coverage depth of 30X and used a  
948 combination of whole-genome shotgun, mate pair and BAC end sequencing. The length of the  
949 assembled genome reached 650 Mbp and 86% of the contigs were assigned to the 24  
950 chromosomes of this species. The genome annotation led to the identification of 26,719 genes  
951 and an important collinearity was observed with other teleosts genomes. This genome  
952 corresponds to the 'golden path' genome as described in Box 1. RAD-sequencing was then  
953 used to study the polymorphism at the genome scale for 100 individuals (and three from  
954 an outgroup, *D. punctatus*). The authors obtained around 178,000 RAD loci which, after  
955 mapping on the genome, allowed them to analyze one locus every 7.5 kb and to reach a 2.5%  
956 genome coverage. The combination of the reference genome and RAD loci allowed for a  
957 better understanding of the evolutionary and adaptive history of the species. For example, the  
958 identification of signatures of positive selection in duplicates of genes involved in  
959 osmoregulation (e.g. *PRL-L2*) opened the way to a better understanding of euryhalinity in this  
960 species and in other teleosts as well. Here important information comes from the combination  
961 of a good annotation, the discovery of multiple gene copies of the same family and from  
962 statistical test of molecular evolution. The genomic analysis of differentiation between  
963 Atlantic and Mediterranean lineages led to a mean  $F_{ST}$  of 0.28 but with highly heterogeneous  
964 repartition: genomic islands of differentiation were observed with lengths varying from  
965 several hundred kb to more than one Mb. These islands were negatively correlated with local  
966 recombination rate and diversity levels (with a few exceptions). Mapping SNPs obtained

967 through RAD sequencing to a reference genome is here useful to understand the evolution of  
968 genomic differentiation and ultimately of speciation. Similar approaches could be applied to  
969 the study of adaptation to different environments. Having such genomic information,  
970 including gene annotation and knowledge on the evolution of gene contents (i.e. duplications)  
971 is a highly valuable complement to the analysis of isolated SNPs.

972

973

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### Steps in genome scans

### Benefits

### Genome sequences / Genomic resources

(1) Genomic data

- Hypervariable regions
- Physical linkage
- Haplotypes



High quality genome



SNPs obtained from reduced representation sequencing; High density of SNPs obtained from genome resequencing ;



(2) Detection of the signal of selection

- Sliding windows statistics
- Haplotype analysis: demographic inference ; signal of selection

(3) Prioritization

- Detection of the physical closest coding gene
- Detection of the functions of the gene



High quality genome

Figure 1

