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# 1 **Climate change prompts monitoring and systematic utilization of honey** 2 **bee diversity in Turkey**

3 **Mert Kükürer** <sup>\*1,2</sup>, **Cemal Can Bilgin** <sup>1</sup>

4 <sup>1</sup>Biology Department, Middle East Technical University, Ankara, Turkey

5 <sup>2</sup>Molecular Biology and Genetics Department, Kilis 7 Aralik University, Kilis, Turkey

6 **\* Correspondence:**

7 Mert Kükürer

8 mertkukrer@gmail.com

9 <https://orcid.org/0000-0003-1755-1119>

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## 16 **Abstract**

17 Quantitative studies concerning the impact of climate change on pollinators are generally lacking.  
18 Relationship between honey bee diversity, present local adaptations and adaptive capacity of  
19 subspecies and ecotypes in the face of climate change is an urgent but rather poorly studied topic  
20 worldwide. Actually, such an effort lies at the crossroads of various fields of inquiry. Those include  
21 conservation of local honey bee diversity, breeding various local stocks for desirable traits, and  
22 enabling resilient ecosystem services. With the ever-increasing availability of genomic tools, now it  
23 is more probable than ever to simultaneously fill such gaps. Current knowledge and growing  
24 awareness on honey bee diversity in Turkey let us progress into a more systematic utilization of this  
25 resource through development of climate-conscious models. Here we provide a framework that takes

26 genomic diversity into account for assessing and monitoring various aspects of species' response to  
27 climate change which can potentially lead to drastic impacts.

28 **Keywords: global change, adaptive capacity, long-term monitoring, whole genome sequencing,**  
29 **natural selection**

### 30 *1. Introduction*

31 As the global environment alters with an increasing pace, ecosystem resilience becomes more reliant  
32 on the readjustment of species to emerging conditions. For this reason, it is important to evaluate,  
33 monitor and manage genetic diversity and related adaptation capacity based on scientific results.  
34 Given the possible angular effects of climate change in the upcoming decades, it is necessary to  
35 expose how ecosystems can benefit from genetic diversity. In addition, it is essential to develop and  
36 test best practice protocols to monitor genetic diversity that varies in space and time.

37 In terms of honey bee (*Apis mellifera*) biodiversity, the current direction of anthropogenic impact is  
38 in line with the loss of native races and the adaptations they have accumulated over thousands of  
39 years (Jensen, Palmer, Boomsma & Pedersen, 2005; Soland-Reckeweg, Heckel, Neumann, Fluri &  
40 Excoffier, 2009; de la Rúa et al., 2013). The factors that cause colony losses in honey bees are very  
41 diverse. Possible loss or decline of pollinators are thought to be due to a combined result of  
42 destruction and degradation of habitats, pollution and pesticide related toxicity, pathogen and parasite  
43 related diseases, and invasive species many of which also effect honey bees (de la Rúa, Jaffé,  
44 Dall'Olio, Muñoz, & Serrano, 2009; Potts et al., 2010; Goulson, Nicholls, Botías, & Rotheray, 2015;  
45 van der Zee, Gray, Pisa & de Rijk, 2015).

46 Increasing hybridization of honey bee subspecies due to human activities like migratory beekeeping  
47 and queen and colony trade also threaten honey bees by potentially leading to loss of gene  
48 combinations that provide local success (Kükre, Kence & Kence. 2020). The absence of effective  
49 implementation of documentation and monitoring methods for uncovering the genetic basis of  
50 adaptive traits makes it difficult to understand and resist the trend of human induced loss of adaptive  
51 diversity. However, it is not possible to achieve success in long-term monitoring especially, without  
52 developing methods that are inexpensive and feasible but still able to provide meaningful data by  
53 deployment of technology-intensive procedures.

54 New risks and challenges are causing concern as global climate change potentially elevate  
55 temperatures and aridity in many parts of the world. We have very little information - not only in  
56 Turkey but in the world - about the overall impact of climate change on honey bees, even less on  
57 pollinators as a whole. However, most predictions suggest that climate change will worsen the  
58 situation by introducing new stressors (le Conte & Navajas, 2008; González-Varo et al., 2013).

59 A reduction in adaptive genetic diversity will not only be loss of a historic natural heritage that is  
60 intrinsically valuable but also of various economic and ecological benefits for the society  
61 (Espregueira et al., 2020). Urgently focusing on the genomic analysis of the relationship of honey  
62 bees with their environment in the era of global climate change will be to the benefit of both the  
63 society and the nature. There is now a strong incentive to consider and investigate pronounced  
64 influences of environmental conditions on honey bees through a perspective of ecosystem resilience.  
65 This article aims to emphasize the need for developing a framework that takes genomic diversity into  
66 account for monitoring the adaptive capacities of honey bee subspecies and ecotypes present in  
67 Turkey in response to climate change.

## 68 ***2. It is not known in what way the global climate change will affect honey bee populations***

69 It is predicted that Turkey's climate will in general become hotter and more arid (Bilgin & Türkeş.  
70 2008; Bilgin, 2013). However, the impact of this change on ecosystems and species still needs to be  
71 explored. It is of decisive importance whether the pollinators in general and honey bees in particular  
72 can adapt to a rapidly changing environment due to their role in nature and agricultural activities.  
73 However, our knowledge of the adaptation capacities in those species is limited. In addition to the  
74 identification of genes taking a role in adaption to hot and dry environments, documenting the  
75 existence and distribution of such genes in honey bee populations is important too.

76 Beyond single genes, the distribution of subspecies is determined under the influence of various  
77 climatic, geographical and biological factors. These complex factors can be combined to model the  
78 subspecies' ecological niches whose long-term characteristics will retain themselves under natural  
79 selection (Peterson, 2003). It is not always true that the combination of environmental conditions in  
80 which the species can survive is limited only by the current distribution of the species. Therefore,  
81 when it comes to modeling the distribution of a species, it is also necessary to refer to the basic niche,  
82 realized niche and potential niche concepts (Sillero, 2011).

83 Such models can be used not only to explain the current situation but also to model the distributions  
84 in the past - especially in the ice ages during which subspecies were drawn to refuges (Kozak,  
85 Graham, & Wiens, 2008). If a precise population genetic structure map can be generated based on  
86 genome surveys making use of high-density SNP data it might be possible to clarify how current  
87 distributions of the subspecies are affected by historical processes.

88 Similar models can be used to predict how species and sub-species would react under various climate  
89 change scenarios (Fordham, Akçakaya, Araújo, Keith, & Brook, 2013). Findings to be obtained in  
90 this way are good candidates as contributions to conservation planning, since they provide hints  
91 about how ecologically and economically important gene resources may change in the future.

92 There is no doubt of the various difficulties in terms of distribution modeling in species that interact  
93 with humans. However, these difficulties do not create insurmountable obstacles. For example, in the  
94 case of honey bee subspecies, the fact that these can be transported by people from one region to  
95 another would even be useful, as it will facilitate understanding of the potential niche (Jimenez-  
96 Valverde et al., 2011).

97 Of course, the purpose of creating models related to climate change cannot be to make definitive  
98 judgments about distributions, especially for species that humans utilize. The main purpose should be  
99 to reveal the stress factors and selection pressures that will occur in future ranges. Ecological niche  
100 models assist in determining relative weights of a wide variety of climatic and geographical factors  
101 that will require adaptation or species' adaptive capacities.

102 There is already evidence that the current climate might be playing a role in the distribution of honey  
103 bee subspecies. Separate studies in the Carpathians and on Africanized bees in South America  
104 indicate that borders of the subspecies might be determined by their capacity to adapt to vital factors  
105 such as temperature and precipitation (Coroian et al., 2014; Nelson, Wallberg, Simões, Lawson, &  
106 Webster, 2017). This is in contrast to artificial selection efforts by humans which are not mainly  
107 related to climate and geography, but rather agricultural characteristics such as yield and disease  
108 resistance.

109 Considering that honey bees have an intense interaction with the environment, it is almost impossible  
110 to think that they would not be affected by climate change. Therefore, the detection of genes that may  
111 prove to be useful in adapting climate change and investigating the effects of this change on the  
112 distribution of subspecies and ecotypes would fill an important gap.

### 113 3. *Unique adaptations of honey bees in Turkey are not studied at the genome level*

114 Migratory beekeeping and bee trade are shown to act like a hybrid zone mobile in space and time,  
115 facilitating the partial amalgamation of subspecies in Turkey (Kükrer, 2013; Kükrer et al., 2020;  
116 Oskay, Kükrer, & Kence, 2019). Despite that, high levels of geographically structured genetic  
117 diversity of honey bee subspecies in Turkey and the need to develop policies to maintain it, was also  
118 confirmed.

119 But how can the natural population genetic structure be preserved, when about 5 million of the 8  
120 million hives in Turkey are taken from one region to another each year, and tens of thousands of  
121 queen bees change hands? Could environmental consequences play a certain role in the maintenance  
122 of distinct subspecies? In order to find answers, it should be examined whether there is a relationship  
123 between the distribution of various geographical and climatic factors such as temperature, humidity,  
124 altitude, precipitation regime, winter severity, insolation, flora, and the current distribution of  
125 subspecies. It can also be tested which particular genetic features obtained from whole genome  
126 sequencing change in a clinal fashion in line with environmental factors (Jones et al., 2013).

127 If honey bee populations are subject to natural selection due to their environment, then this selection  
128 force would emerge as a stabilizing factor for preserving locally adapted subspecies by acting against  
129 hybrids, and eventually restricting gene flow between populations (Feder & Nosil, 2010). In that  
130 case, natural selection would counterweigh the effect of gene flow between populations and random  
131 genetic drift. As a result, it is inevitable to observe different combinations of allele frequencies in  
132 various populations (Savolainen, Lascoux & Merilä, 2013). Sudden changes are to be expected where  
133 selection is relatively strong while a smoother transition would be observed in regions where gene  
134 flow between populations is higher (Beekman, Allsopp, Wossler, & Oldroyd, 2008).

135 Since random genetic drift increases the differentiation between populations isolated from each other,  
136 the effects of geographical barriers also become measurable. In cases where a certain climatic factor  
137 or selection is not causative, it should be considered that the significant genetic distance between  
138 populations depends on geographical isolation (Manel, Schwartz, Luikart, & Taberlet, 2003).

139 The functions of the DNA regions candidates for selection can be easily inferred since honey bee  
140 genome was sequenced at an early stage and is studied relatively well (The Honey Bee Genome  
141 Sequencing Consortium, 2006). Therefore, it is possible to investigate the relationship between  
142 selected genes and environmental factors. At this stage, the goal is to make biologically meaningful

143 inferences about the functions of any candidate genes selected in relation to climatic and  
144 geographical variables.

145 In a recent study on the relationship between environmental conditions and genome-wide selection, it  
146 has been observed that altitude-related adaptations are preserved in two African subspecies where  
147 gene flow between them is so intense that it prevents observation of a genetic structure (Wallberg,  
148 Schöning, Webster, & Hasselmann, 2017). It is normal to expect a similar process in Turkey where  
149 adaptations to environmental factors were preserved despite high levels of gene flow. In another  
150 study from Kenya, genes that could play an important role in adaptation to various climate types and  
151 geographies were investigated by comparing savanna, coastal, mountain and desert populations  
152 (Fuller et al., 2015). In a research conducted on a newly identified subspecies in China, researchers  
153 focused on the genetic effects created by transition from tropics to the temperate zone (Chen et al.,  
154 2016). In the Iberian Peninsula where genome-wide selection signals based on bioclimatic variables  
155 were investigated (Henriques et al., 2018) the findings demonstrate that genes involved in regulation  
156 of the biological clock by biosynthesis of macromolecules are associated with local adaptations.

157 Concerning honey bee subspecies in Turkey, various studies making use of SNP markers in honey  
158 bees have been carried out in the past. Whitfield et al. (2006) included samples from Turkey in their  
159 research, but this work was essentially in the domain of phylogeography. Although 11 genes were  
160 identified as candidates for selection, that comparison was carried out on Italian, Western European  
161 and African bees but bees from Turkey were excluded from that part of the study. Wallberg et al.  
162 (2014) focused on local adaptations but samples obtained from Turkey were only evaluated for  
163 extraction of global population structure. Here, the main comparison was made between A-C, A-M  
164 and C-M lineages leaving aside O-lineage bees which also includes subspecies in Turkey. Cridland et  
165 al. (2017), did not themselves gather samples from Turkey but made use of data generated by  
166 Wallberg et al. (2014). Uncertainties caused by a sequencing method that is no longer available due  
167 to high error rates were revealed and the need for analysis of high-quality genome data belonging to  
168 samples from Turkey and South West Asia was emphasized.

169 Although different aspects of genetic diversity of honey bee subspecies in Turkey were examined, the  
170 way they are adapted to the local conditions were not studied at the genome level. In addition, despite  
171 extensive research, the exact distributional ranges of the subspecies and the core areas where they are  
172 found in “pure” forms are still not clear. This also holds for regions where subspecies’ ranges overlap

173 and they exchange genes with each other, as well as for critical regions where sudden changes in the  
174 subspecies composition occur.

175 It is possible that these deficiencies would be eliminated with a well-planned countrywide study  
176 which, in this way, would lead to a better understanding of genetic resources of native honey bee  
177 races and provide the most basic information that could be utilized in breeding efforts. Bearing in  
178 mind the global climate change, uncovering how climate and geography affect honey bees will be  
179 vital for the success of future breeding and conservation projects.

#### 180 ***4. There is no model yet to monitor honey bee genetic diversity in Turkey***

181 In Turkey, within the last decade, awareness about the potential value of the honey bee diversity has  
182 radically improved due to intensive efforts of scientists, beekeepers' associations and civil society  
183 organizations. In parallel, there has been an increase in conservation implementations and  
184 rehabilitation in the field of honey bee ecotypes (Gül, 2020). Currently, breeding herds are either  
185 being created or have already been established in Ankara, Ardahan, Artvin, Çanakkale, Çorum,  
186 Düzce, Hatay, İzmir, Kırklareli, Kırşehir and Muğla provinces. Since these activities are aimed at  
187 local ecotypes, important genetic material is thus put under protection. In concordance with these  
188 efforts, a number of subspecies and ecotypes are in the process of being registered by The Ministry of  
189 Agriculture and Forestry as native genetic resources of Turkey. This action, too, can be expected to  
190 contribute to conservation and breeding efforts in Turkey.

191 Monitoring programs are implemented in order to detect changes in genetic variability or in the  
192 frequencies and the distribution of adaptive variants (Flanagan, Forester, Latch, Aitken & Hoban,  
193 2018). It is possible now, to further enhance the valuable steps taken till the moment and start  
194 monitoring of honey bee genetic diversity in Turkey and to consider making use of emerging  
195 technological tools in the field of genome sequencing as well as the decreasing costs.

196 However, till now, methods used for discrimination of subspecies in such efforts are mainly based on  
197 morphology, geometric morphometry and on mitochondrial as well as nuclear DNA markers like  
198 microsatellites. Resolution provided by such methods are far from precise discrimination of ecotypes,  
199 let alone allowing accurate reflection of diversity present in Turkey. Furthermore and more  
200 importantly, they do not let us to take into account a conscious incorporation of genomic elements  
201 that play role in adaptation of ecotypes to their natural environment. Today conservation and  
202 breeding efforts should focus more on genetic variation specifically improving the subspecies'

203 capacity to adapt climate change. Constraints related to the adequate documentation of genetic  
204 diversity in Turkey do not enable yet, the development of functional and at the same time low-cost  
205 monitoring models.

206 An adaptive management context with an integrated monitoring step will enjoy the chances of both  
207 learning more about the local ecotypes and evaluating the effectiveness of management actions once  
208 they are initiated. After an initial genomic assessment by sequence capture methods or SNP arrays, it  
209 is possible to consistently genotype many individuals over time. This would certainly help to reach  
210 diverse objectives like diagnosing introgression and conservation efficacy, characterization of neutral  
211 and adaptive genetic variation especially related to climate change, as well as retrieving information  
212 about desirable traits (Aykanat, Lindqvist, Pritchard, & Primmer, 2016).

### 213 *5. A potent long-term ecological research perspective and scope*

214 Basically, any research addressing the adaptive capacities of subspecies in Turkey against climate  
215 change should cover the following scope:

216 (i) Core regions in which 5 honey bee subspecies stay unmixed should be identified by an intense  
217 sampling effort across the country from stationary apiaries whose beekeepers reject to replace queens  
218 and colonies with non-native races. In order to achieve this, genome-wide data obtained with next  
219 generation sequencing techniques should be utilized.

220 (ii) Despite the anthropogenic impact in the form of migratory beekeeping and trade, subspecies are  
221 known to preserve their identities at certain places. Selection at the genomic level naturally relies on  
222 environmental conditions. Investigation of this phenomenon necessarily means comparing relative  
223 weights of natural selection, gene flow and genetic drift within populations.

224 (iii) Candidate genes located in genome regions under selection and playing a role in adaptation to  
225 local conditions should be identified. The functions of these genes and their relation with the  
226 environmental conditions should be examined. Genetic features that play a role in adaptation to  
227 elevated temperatures and aridity should be revealed through various comparisons between  
228 populations residing in such milieu. Existing conservation and breeding efforts like those supported  
229 and carried out by The Ministry of Agriculture and Forestry and Turkish Beekeepers' Association  
230 should better be reinforced by evolutionary knowledge. This will be achieved through purposeful



231 introduction of locally adaptive genetic variants in addition to genetic variants that provide adaptive  
232 potential under climate change within such stocks.

233 (iv) In order to preserve the genetic diversity and adaptation capacities documented in this way, a  
234 low-cost, feasible, but technology-intensive monitoring method should be developed. After an initial  
235 assessment, intensive sampling coupled with monitoring of conservation areas for these alleles by at  
236 least 5-year intervals should be guaranteed.

237 (v) Population structure obtained from genetic data should be used in models that will shed light on  
238 the evolutionary histories of subspecies and how their natural distribution would be affected under  
239 various global climate change scenarios.

## 240 6. *Discussion*

241 The most important needs of the actual period include the establishment of quantitative and regular  
242 implementations to appraise, monitor and manage the genetic resilience and adaptive capacity for  
243 species under human use or those not. This points to relevance for incorporation of genetic and  
244 evolutionary knowledge in policies concerning conservation planning and sustainability of ecosystem  
245 services, particularly under the severe impact of global climate change (COST Committee of Senior  
246 Officials, 2018).

247 The challenges faced in this area can be more easily overcome via piecing together of the following  
248 pursuit, akin but not limited to providing integration platforms in order to link together stakeholders  
249 and developing collaborations that combine experience in various areas of expertise to form the basis  
250 of a sustainable impact as well as integrating emerging technological tools into existing activities;  
251 explaining decision-makers how genetic diversity can benefit ecosystems; developing and testing  
252 best practice protocols for monitoring genetic diversity in space and time. As a key pollinator, honey  
253 bees (*Apis mellifera*) draw much attention among species aimed for determination and monitoring of  
254 the genetic adaptation capacities in response to climate change.

255 Although honey bees are intensively managed by humans, they cannot be regarded as fully  
256 domesticated. Apart from wild populations in the natural distribution range of the species or feral  
257 colonies that escaped from human hands, even colonies under human control act as part of wildlife  
258 due to nectar and pollen foraging activities. Their unique role in pollination makes bees a critical  
259 species for ecosystem resilience in addition to agricultural production and ecosystem services.

260 We need to put forward a monitoring model that can process honey bee diversity throughout the  
261 country. This also provides an opportunity to go beyond a general characterization of biodiversity. It  
262 can be aimed to monitor, in terms of presence and distribution, both specific alleles involved until  
263 now in local adaptation to native conditions and also genetic features that may contribute to adaptive  
264 potential under conditions of global climate change.

265 Long-term monitoring is a costly and labor-intensive process. This is also the most important reason  
266 for the fact that monitoring studies with a large spatial scale are not always possible. A technology-  
267 intensive monitoring model that combines the most cost-effective, feasible, state-of-the-art scientific  
268 methods developed and tested till now is likely to contribute to the goal of creating standard and  
269 routine tools.

270 Developing a model for monitoring and utilization of honey bee genomic diversity is not only useful  
271 for revealing the adaptive potential to climate change, but also with simple customizations, would  
272 provide new opportunities for implementation of marker assisted selection in breeding for disease  
273 resistance (varroosis, Nosema, foulbrood, etc.), obtaining desirable phenotypic characters  
274 (gentleness, wintering success, low swarming tendency, etc.) and increased yield (honey, royal jelly,  
275 pollen, propolis, bee venom and other bee products).

276 Genomic diversity and adaptive potentials are rapidly lost or undergoing serious changes under  
277 human influence. With such a model, decision-makers and field operators might have a chance to  
278 benefit from genomic and evolutionary information in the face of adverse human-induced effects.

279 This piece focuses on the limits of our knowledge on honey bee diversity in Turkey, its interaction  
280 with the environment, the consequences of this interaction for natural selection, and its implications  
281 for the future under global climate change. We recommend that further research in honey bee  
282 genetics would better seek previously unexplored phenomenon, structures and relationships. Such  
283 investigation would have the potential to innovatively apply to the situation the knowledge and  
284 techniques in the field of genomics and to contribute in the formation of an understanding that will be  
285 utilized in a way which may concern many stakeholders.

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