

Research Progress on Effects of Environmental Pollution on Animal Genetic Diversity

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Abstract: The negative impacts of environmental pollution on animal genetic diversity are the main topic of the research report. Since the Industrial Revolution, industrial activity has increased, and environmental pollution has become a major worldwide concern. The three primary issues examined in this research are the direct effects of chemical pollutants on genetic integrity, habitat fragmentation that reduces gene flow, and climate change as a pollution-driven danger to genetic diversity. The study uses a mixed-method approach, using data from genetic studies and a literature review on the effects of pollutants on DNA. Information is taken from a number of studies on pesticide resistance, evolutionary toxicity, and how species are affected by climate change. According to the study's findings, environmental contamination is drastically lowering animal populations' genetic diversity. These problems are made worse by climate change, which increases species vulnerability and causes genetic loss.

Keywords: Climate change, biodiversity, environmental pollution, chemical pollution.

1. Introduction

Since the Industrial Revolution, many countries have taken the path of economic development at the expense of the environment. Due to the wanton destruction of human beings, environmental pollution has accelerated its development in an irreversible trend. With the rapid loss of species in recent years, the protection of animal genetic diversity as an important part of maintaining ecosystem balance has become the focus of global society. In this research paper, three main topics are going to be discussed: direct effects of chemical pollutants on genetic integrity; habitat fragmentation and loss reduce gene flow; and climate change as a pollution-driven threat to genetic diversity. For the research methods, the research regarding the effect of pollutants on animal DNA will be discussed, the specifics of reductions in the genetic diversity of animal populations due to habitat fragmentation caused by pollution will be investigated, and certain interviews and lectures on climate science will be discussed. This article contributes to a deeper understanding of how human-induced environmental pollution directly affects the genetic diversity of animal populations. Exploring this relationship emphasizes the biological and ecological consequences of pollution, bridging the gap between environmental science and genetics. Genetic diversity is critical to the adaptation and survival of species. By focusing on the effects of pollution on this diversity, the importance of preserving genetic variation as the basis for ecosystem resilience in the face of environmental change is emphasized.

2. Direct effects of chemical pollutants on genetic integrity

Given the way that chemicals impact evolutionary processes, certain chemicals, or "genotoxins," can alter DNA integrity directly and cause alterations that are inherited. These genotoxic substances raise the frequency of DNA damage and, thus, the risk of mutated DNA sequences being replicated and transcriptionally changed. Factors such as the type of damage incurred, the repair pathway employed, the speed of repair, and the accuracy and integrity of the repair process all influence the probability that DNA damage will result in a permanent and/or heritable sequence change [1].

Mutations in a single gene cause the evolution of resistance to certain substances (monogenic resistance). For instance, a single base pair alteration confers cyclodiene resistance in insects. Monogenic resistance can be very significant, as evidenced by the discovery that cyclodiene resistance in pest insects accounts for more than 60% of documented occurrences of pesticide resistance [2].

A change in morphology may also contribute to an increase in pesticide resistance in addition to physiological adaptation. For instance, the development of a protective footpad cuticle in mosquitoes facilitates DDT resistance by lowering DDT absorption. It is possible that adaptive mutations influencing morphology can occur in both cis-regulatory and protein-coding regions of genes, according to recent work in evolutionary developmental biology [3]. This helps to explain the apparent multi-trait DDT adaptation observed in mosquitoes. These examples illustrate the importance of genetic variation at several loci in the evolution of chemical resistance.

However, it appears uncommon for susceptible, wild-type populations to develop pesticide resistance as a result of de novo mutations [4]. Emigration from pre-existing resistant populations increases the likelihood that resistance may arise [5]. The main processes thought to be responsible for the emergence and dissemination of chemical resistance in wild populations are between-population gene flow and the recombination that results, which boosts genetic variety [6]. The frequency of recombination is higher than that of de novo point mutation. A study conducted by estimated the substitution rate per codon per generation to be between 10^{-8} and 10^{-9} [7], while a study conducted by demonstrated that the crossing-over frequency between two pre-existing mutations in acetylcholine esterase can reach 10^{-5} [8].

The goal of the quickly expanding scientific subject of evolutionary toxicology is to clarify the microevolutionary processes that wild populations experience as a result of environmental contamination [9]. Pollution pressure has the power to significantly alter each of the four primary evolutionary processes—mutation, selection, genetic drift, and gene flow—that shape the genetic patterns of each population. Therefore, a number of effects of pollution impact are hypothesized on the degree of genetic diversity within the population [9]. The most common predicted result is genetic erosion [10], which is a loss of genetic variety throughout the genome brought on by a decrease in the effective size of the exposed population and the ensuing genetic drift. However, genotoxic pollution can lead to an increased mutation burden, which raises the genetic diversity within a population [11]. Due to selection advantages, pollution pressure may potentially change a genotype's ability to survive. While balancing selection works to promote low genetic divergence among populations and an increase in within-population genetic diversity, directional selection is predicted to decrease genetic diversity within populations by favoring resistant genotypes and enhancing genetic differentiation among populations concurrently [12][13]. A barrier to new immigrants or even an "ecological sink" due to increased gene flow into the affected population are two further ways that pollution might alter migration patterns [14] [15].

3. Habitat fragmentation and loss reduces gene flow

The amount of habitat accessible for natural communities declines as human use of the environment increases, and the habitat that remains gets more and more fragmented. In other words, habitats split up into "habitat islands" that are encircled by other environments—mostly ones that have been altered by humans.

There has already been significant fragmentation of many tropical and temperate environments, and this fragmentation will only get worse soon. Because habitat fragmentation has the potential to accelerate extinction rates, as predicted by island biogeographic theory, conservation biologists are concerned about it [16].

Zangger's field investigation, which found that no species of forest ground beetle was collected in pitfall traps set up for four weeks along the grass strip dividing a highway's two lanes, provides evidence of the highway's significant impact.

The main routes, and the highway in particular, seem to have isolated ground beetle populations to a substantial extent. The genetic variability in the small peripheral portion south of the highway was much lower than that of the remainder of the study area, according to a comparison of allelic richness [17].

4. Climate change as a pollution-driven threat to genetic diversity

The analysis's findings demonstrated that climate change has a significant impact on genetic diversity. It has been established that intraspecific differences result in genetic variants and raise intraspecies homogeneity, particularly in research done at the species and population level. This decreases tolerance to climate change and results in losses in the gene pool and diversity of genes. The studies that are the focus of this investigation have provided ample evidence of this.

A species's genetic adaptability, physiological sensitivity to changes, and dispersion ability—the latter of which is influenced by extrinsic variables like geographic barriers—all play a role in its capacity to adjust to future climate change [18].

Hence, given the increased fragmentation and isolation of remaining suitable areas—factors already implicated in the recent climate-induced genetic erosion of an alpine mammal [19] — population extinctions and loss of approximately half of the species' genetic diversity may be a likely outcome. The significance of stable refugial populations as long-term repositories of genetic variety for the survival and evolution of species makes these losses especially worrisome [20]. For instance, bats have a relatively high capacity for dispersal. Therefore, the genetic effects of climate change may be considerably more severe for non-volant species.

Gene flows can potentially alter as a result of climate change. *Garrulus glandarius*, or chestnut crows, for instance, have the ability to spread genes from oak populations to other tree populations. The introduction of new members into a population through migration can alter the group's gene frequency. Long-term gene flows that produce diversity may lessen population differences and lead neighboring populations to unite into a single group with the same genetic makeup [21]. This is not how things should be. because populations' heroziot gene richness decreases as a result of this event. The population becomes more fragile and vulnerable as a result, and its capacity for adaptation declines. It causes greater species and population losses as well as a decline in biological richness [22].

5. Conclusion

In conclusion, this study examined three main aspects of how environmental pollution affects animal genetic diversity: the direct effects of chemical pollutants on genetic integrity, the decrease in gene flow brought on by habitat fragmentation, and the threat that climate change poses to genetic diversity.

To gain a better understanding of how pollution-induced environmental changes are jeopardizing species resilience, these subjects were investigated.

Several conclusions can be drawn from the research. First, by damaging DNA and speeding up mutations, chemical pollutants like genotoxins have a direct impact on the genetic integrity of animal populations, resulting in heritable changes. Second, pollution-induced habitat fragmentation severely restricts gene flow between populations, which raises the danger of extinction and reduces genetic variability. Last but not least, pollution-induced climate change further diminishes genetic variety by making it harder for species to adapt and endure in more unstable and fragmented settings.

Notwithstanding the insights offered, this study has a number of drawbacks. Data on the long-term consequences of pollution on certain species are still scarce, and some factors may not have been properly taken into consideration due to the intricacy of genetic and environmental interactions. More species-specific case studies, longitudinal studies to track genetic changes over time, and the creation of more sophisticated instruments for assessing genetic diversity should be the main goals of future study. Furthermore, in order to fully address these issues, interdisciplinary strategies that integrate genetics, climate science, and conservation biology will be essential.

References

- [1] Klaassen, C. D., & Amdur, M. O. (Eds.). (2013). *Casarett and Doull's toxicology: The basic science of poisons* (Vol. 1236, pp. 189-190). New York: McGraw-Hill.
- [2] Georghiou, G. P., & Taylor, C. E. (1986). *Pesticide resistance: Strategies and tactics for management*. By Committee on Strategies for the Management of Pesticide Resistant Pest Population. Nat. Acad. Press, Washington, DC, 157-168.
- [3] Hoekstra, H. E., & Coyne, J. A. (2007). *The locus of evolution: Evo devo and the genetics of adaptation*. *Evolution*, 61(5), 995-1016.
- [4] Pasteur, N., & Raymond, M. (1996). *Insecticide resistance genes in mosquitoes: Their mutations, migration, and selection in field populations*. *Journal of Heredity*, 87(6), 444-449.
- [5] Futuyma, D. J. (2017). *Evolutionary biology today and the call for an extended synthesis*. *Interface Focus*, 7(5), 20160145.
- [6] Leslie, J. F., & Watt, W. B. (1986). *Some evolutionary consequences of the molecular recombination process*. *Trends in Genetics*, 2, 288-291.
- [7] King, J. L., & Jukes, T. H. (1969). *Non-Darwinian evolution: Most evolutionary change in proteins may be due to neutral mutations and genetic drift*. *Science*, 164(3881), 788-798.
- [8] Nagoshi, R. N., & Gelbart, W. M. (1987). *Molecular and recombinational mapping of mutations in the Ace locus of Drosophila melanogaster*. *Genetics*, 117(3), 487-502.
- [9] Bickham, J. W. (2011). *The four cornerstones of evolutionary toxicology*. *Ecotoxicology*, 20, 497-502.
- [10] Van Straalen, N. M., & Timmermans, M. J. (2002). *Genetic variation in toxicant-stressed populations: An evaluation of the "genetic erosion" hypothesis*. *Human and Ecological Risk Assessment*, 8(5), 983-1002.
- [11] Rinner, B. P., Matson, C. W., Islamzadeh, A., McDonald, T. J., Donnelly, K. C., & Bickham, J. W. (2011). *Evolutionary toxicology: Contaminant-induced genetic mutations in mosquitofish from Sumgayit, Azerbaijan*. *Ecotoxicology*, 20, 365-376.
- [12] Wirgin, I., Roy, N. K., Loftus, M., Chambers, R. C., Franks, D. G., & Hahn, M. E. (2011). *Mechanistic basis of resistance to PCBs in Atlantic tomcod from the Hudson River*. *Science*, 331(6022), 1322-1325.
- [13] Mäkinen, H. S., Cano, J. M., & Merilä, J. (2008). *Identifying footprints of directional and balancing selection in marine and freshwater three-spined stickleback (Gasterosteus aculeatus) populations*. *Molecular Ecology*, 17(15), 3565-3582.
- [14] Puritz, J. B., & Toonen, R. J. (2011). *Coastal pollution limits pelagic larval dispersal*. *Nature Communications*, 2(1), 226.
- [15] Matson, C. W., Lambert, M. M., McDonald, T. J., Autenrieth, R. L., Donnelly, K. C., Islamzadeh, A., ... & Bickham, J. W. (2006). *Evolutionary toxicology: Population-level effects of chronic contaminant exposure on the marsh frogs (Rana ridibunda) of Azerbaijan*. *Environmental Health Perspectives*, 114(4), 547-552.
- [16] Dogan, S., Özgelik, S., Dolu, Ö., & Erman, O. (2010). *Global warming and biodiversity*. *İklim Degisikligi ve Cevre*, 3.

- [17] Keller, I., & Largiadèr, C. R. (2003). Recent habitat fragmentation caused by major roads leads to reduction of gene flow and loss of genetic variability in ground beetles. *Proceedings. Biological Sciences*, 270(1513), 417–423. <https://doi.org/10.1098/rspb.2002.2247>
- [18] Dawson, T. P., Jackson, S. T., House, J. I., Prentice, I. C., & Mace, G. M. (2011). Beyond predictions: biodiversity conservation in a changing climate. *Science*, 332(6025), 53-58.
- [19] Rubidge, E. M., Patton, J. L., Lim, M., Burton, A. C., Brashares, J. S., & Moritz, C. (2012). Climate-induced range contraction drives genetic erosion in an alpine mammal. *Nature Climate Change*, 2(4), 285-288.
- [20] Hampe, A., & Petit, R. J. (2005). Conserving biodiversity under climate change: The rear edge matters. *Ecology Letters*, 8(5), 461-467.
- [21] Scheffers, R. B., De Meester, L., Bridge, L. C. T., Hoffmann, A. A., Pandolfi, M. J., Corlett, T. R., ... & Watso, M. E. J. (2016). The broad footprint of climate change from genes to biomes to people. *Science*, 354, 767. <https://doi.org/10.1126/science.aaf7671>
- [22] Pauls, S. U., Nowak, C., Bálint, M., & Pfenninger, M. (2013). The impact of global climate change on genetic diversity within populations and species. *Molecular Ecology*, 22(4), 925–946. <https://doi.org/10.1111/mec.12152>