



Original Research Paper

Evaluating Riverine Habitat Corridors for Supporting Genetic Connectivity in Endangered Aquatic Species

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Key Words	Abstract
Genetic connectivity, Riverine corridors, Endangered aquatic species, Habitat fragmentation, Population genomics, Conservation management, Dispersal pathways.	Corridors of Riverine habitat are crucial in conserving the genetic integrity of the endangered aquatic fauna, but their performance has been inadequately measured in numerous fragmented freshwater systems. This is an assessment of the effects of natural and manipulated river corridors on dispersal, gene flow, and population viability of threatened aquatic species in the long term. By combining population genomics with the characterization of the habitats on a large scale, we compiled a SNP and microsatellite database of several taxa that represented various degrees of mobility throughout the river network. Population genetic studies demonstrated that there was a high level of variation in allelic richness and inbreeding coefficients, with low-mobility species exhibiting high levels of F_{IS} (>0.10) and high mate pair F_{ST} (0.35), which implies strong genetic isolation. Mantel tests identified that there was significant Isolation by Distance (IBD) among species ($R = 0.38$ -0.74, $p < 0.01$), whereas Multiple Regression on Distance Matrices (MRDM) demonstrated that Isolation by Resistance (IBR) models with Effective Resistance better explained genetic differentiation, providing an increase of 7-17 percent in model fit. It is noteworthy that undisturbed riparian corridors and tributary linkages were correlated with less effective resistance, increased gene flow, and increased allelic diversity. The most pronounced responses to hydrological barriers were seen in species with limited mobility, which highlights their susceptibility to hydrological barriers. Corridors that were incorporated in changed landscapes by humans provided significance to connectivity even when both the integrity and condition of flow were maintained steady. The results of the study demonstrate the necessity to maintain functional riverine pathways, rehabilitate damaged channel segments, and include quantitative metrics of connectivity in conservation planning. Increasing the integrity of corridors is necessary to protect not only the evolutionary potential, but also to prevent greater resilience to future environmental change. This research paper proves that genetic tools coupled with spatial resistance modelling are an efficient framework to be used to assess and optimize conservation responses in endangered aquatic species.

Introduction

The freshwater ecosystems are so diverse and yet endangered habitats on the earth. The riverine networks and especially contribute to a diverse range of aquatic organisms whose survival is based on the natural interrelation of flowing waters (Khamraev et al., 2025). Nevertheless, human activities like river impounds,

channelization, building of levees, pollution, and change of land use have been affecting natural hydrological processes at an increasing rate (Thieme et al., 2023; Smukowski Heil, 2023). These changes in the species change dispersal pathways, subdivide populations, and narrow gene flow. Genetic connection is critical in the process of preserving adaptive potentials, averting the inbreeding depression, and the

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Received: 3 May 2025; Reviewed: 10 June 2025; Revised: 4 August 2025; Accepted: 25 August 2025

(DOI): 10.70102/AEJ.2025.17.2.24

viability of the population in the long run (Mocchetti et al., 2024; de Araujo Barbosa et al., 2025; Shaffer et al., 2022; Willi et al., 2022). The recent developments in conservation genetics and ecology of riverscapes have pointed to the ability of physical barriers such as dams, levees, and changed flow regimes to cause rapid genetic differentiation, as evidenced by both freshwater snails and fish, and amphibians in altered wetlands (Nazareno et al., 2021; Hogue & Breon, 2022). Although this has come to light, there are still important knowledge gaps concerning the ways in which riverine habitat corridors can be used to overcome fragmentation in the case of endangered aquatic organisms. Despite the numerous existing suggestions of habitat corridors as an aid to increase connectivity, the efficacy of such corridors in a riverine environment (where hydrological and geomorphological processes are not similar to the terrestrial system) is yet to be well determined (Ulkilan et al., 2024; Oyler-McCance et al., 2024). A large number of endangered aquatic organisms are characterized by low dispersal capabilities and are, therefore, particularly susceptible even to minor fragmentation (Dusseux et al., 2021). However, the management in many instances believes that by preserving or creating linear aquatic channels, movement and gene flow will be promoted automatically. The existence of terrestrial corridors studies (e.g., small mammals) has empirically shown that corridors can enhance connectivity of certain species and not all, and this is likely to occur with aquatic systems as well because of the dispersal characteristics of various species and the nature of river alterations. The restoration and corridor

investment are likely to provide no conservation results unless they are evaluated rigorously. Hence, a scientific paradigm is required to know when and how riverine habitat corridors are effective in supporting genetic connectivity in endangered aquatic species (Piczak et al., 2023; Segelbacher et al., 2022). The research paper will evaluate how riverine habitat corridors comprising natural tributaries, restored channels, and controlled riparian pathways contribute to the occurrence of gene flow between isolated populations of threatened aquatic organisms. Measure the level of genetic connectivity/fragmentation among various configurations of corridors by using genomic or microsatellite data (Mishra, 2024; Hohenlohe et al., 2021; Zhu et al., 2021). Find the most significant physical, environmental, and riverscape characteristics of the feature value of maintaining or suppressing connectivity. Elaborate evidence-based guidelines on how to design, restore or prioritize riverine corridors to enhance long term resiliency of species (Talukder et al., 2022).

Key Contributions

- It integrates genetic, ecological and spatial information in testing performance of corridors in the freshwater systems specifically, a vital gap in conservation planning.
- It also incorporates evidence of case-studies of endangered aquatic organisms (e.g. freshwater snails, amphibians and fish) to emphasize the differences in species response to fragmentation and design of corridors.

- It provides a theoretical and practical approach to evaluating the effectiveness of the corridors by managers with the help of genetic indicators to combine conservation genetics with the tactics of habitat restoration.
- It enhances the knowledge of the effect of riverscape features on movement, providing useful information to the global freshwater biodiversity hotspots.

The rest of the paper is structured in the following way: Section 2: Materials and Methods give the information about the area of study, the target species, sampling design, genetic analyses, and spatial evaluation of riverine corridors. Section 3: Results and Discussion display the results of the genetic diversity, population structure, and the effectiveness of the corridors, and then the combined discussion of the ecological implications. Section 4: Conclusion summarizes the key ideas, outlines the management recommendations, and proposes the direction of further research.

Materials and Methods

Study Area and Target Species Selection

The research was conducted in the Upper Mobile River Basin of the southeastern United States, specifically in Alabama, on the Coosa and Cahaba river systems. It was a 250-km stretch of this river system that had been chosen for its great biodiversity in aquatic life and for strong ecological fragmentation caused by hydrological obstacles, including the Weiss Dam on the Coosa River, as well as the vast area converted to land use.

Three contrasting mobility gradient taxa of aquatic organisms that were endangered were chosen to determine the effectiveness of corridors:

Among the listed species, the majority belong to the genus *Epioblasma*. - species A - low-mobility freshwater mussel (*Epioblasma obsoleta*) • Species B- moderate-disperser fish (*Etheostoma rubrum*) • Species C- high-disperser fish (*Pimephales notatus*) The resulting diversity of mobility was used to conduct a multiscale analysis of the response of the various species to riverscape resistance.

Sampling, Data Generation, and Population Genetics

At each sampling site of 45 sites within the basin, 30 individuals of each species were sampled. The sites of sampling were in areas bordering hydrological barriers, intact riparian corridors, and damaged/ channelized areas such as the ones around the Tombigbee Waterway. In the case of Species A and B, 5000-10000 SNP markers were produced by the RAD-seq, and in Species C, 15 polymorphic microsatellite loci (SSR markers) were genotyped. To quantify genetic diversity, the following was used:

- A_r — allelic richness
- H_o — observed heterozygosity
- F_{is} — inbreeding coefficient

The main response variable used in connectivity analyses was $C(f, 1, sc, \text{ and/or } C)$. All sites were compared by pairwise population differentiation ($F_{3(sc, 1, sc, 2)}$) which was used as the primary response variable. In order to take genetic distance into the correlation modelling,

the standard linearised genetic distance was computed as:

$$\text{Genetic Distance} = \frac{F_{ST}}{1-F_{ST}} \quad (1)$$

This transformation from Equation (1) linearizes the relationship between genetic differentiation and spatial distance, improving the Mantel test interpretability.

Riverscape Characterization and Corridor Modeling

DEM, NHD hydrography, and land-cover layers were used as spatial datasets to characterize the riverscape in ArcGIS Pro. By assigning: species-specific resistance layers (30-m resolution) were coined. High resistance to dams, urban areas, and channelized reaches High resistance (average 100)

- Limited resistance to natural river channels and forested riparian corridors (low resistance- 1). Pairs of sites: There were two measures of connectivity, determined between each pair of sites: 1. Least-Cost Path Distance LCPD. The minimum cost dispersal path was determined as Equation (2):

$$\text{LCPD} = \min \sum_{i=1}^n R_i \cdot d_i \quad (2)$$

where R_i is the value of resistance of the raster cell i and d_i is the distance across the cell. This measure determines the most meandering resisting route.

Effective Resistance (ER)

The landscape was considered an electrical circuit using Circuitscape, and the effective

resistance across all possible dispersal pathways was computed as Equation (3):

$$ER = \sum_{k=1}^m \left(\frac{1}{C_k} \right) \quad (3)$$

Where C_k is the conductance of the pathway k . This measure takes into consideration several parallel movement paths.

Integration and Corridor Effectiveness Assessment

Step 1: Testing the Null Model — Isolation by Distance (IBD)

Mantel tests were employed to test the relationship between genetic distance and pure geographic separation using the following model:

$$\text{Genetic Distance} \sim \text{Riverine Distance}$$

Such a high correlation would be taken as an indicator that the flow of genes is more influenced by the distance than by landscape features.

Step 2: Testing Isolation by Resistance (IBR) Models

To determine the impact of the landscape resistance, Multiple Regression on Distance Matrices (MRDM) was used as Equation (4):

$$\text{Genetic Distance} = \beta_0 + \beta_1(\text{LCPD}) + \beta_2(ER) + \epsilon \quad (4)$$

Comparison of models was done in terms of R^2 , significance values, and relative explanatory power. The most effective model of a particular species was chosen.

Step 3: Quantifying Corridor Effectiveness (CE)

Corridor Effectiveness was evaluated by finding out the extent to which effective resistance (ER) decreased predicted genetic differentiation as compared to the IBD null model. CE was expressed as Equation (5):

$$CE = F_{ST}^{IBD} - F_{ST}^{ER} \quad (5)$$

A large positive CE value indicated that the corridor successfully reduced fragmentation effects and promoted gene flow.

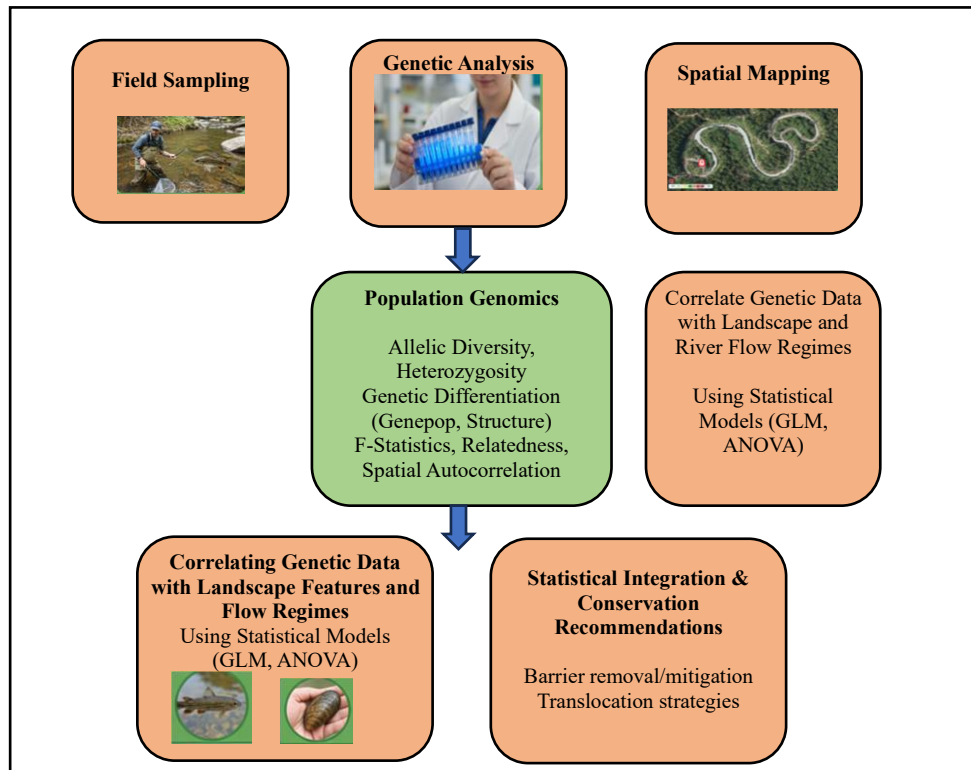


Figure 1: Population Genomics Framework for Conservation and Landscape Integration

Figure 1 demonstrates a population genomics system that combines genetic data with the landscape and environmental characteristics to use them to conserve and manage the environment. The application of the workflow starts with the field sampling, in which biological samples are taken within the environment to examine the genetic features of the population. Genetic analysis is done after this in order to quantify parameters such as allelic diversity, heterozygosity, and genetic differentiation, which give an idea about the genetic composition of the population. Spatial mapping is the second process that is used to correlate the genetic

variation with the landscape features and river flow regimes. The patterns of these genetic data are further examined with the methods of population genomics, such as F-statistics and spatial autocorrelation, to study the relationship within and between populations. The framework then concentrates on the comparison of genetic data with landscape features and flow regimes with the help of statistical models such as GLM (Generalized Linear Models) and ANOVA (Analysis of Variance) to comprehend the effects of environmental factors on genetic diversity. Lastly, the system combines these findings to make statistical recommendations of

conservation that may involve approaches to removing barriers, mitigation, and translocation of species to increase population sustainability. This number shows that genetic analysis can be used together with environmental data to come up with more informed and efficient conservation strategies.

Results and Discussion

Dataset Summary and Population Genetic Diversity

The paper was able to produce genetic data of three taxa, having different dispersal capacities in the Upper Mobile River Basin. High-quality Single Nucleotide Polymorphism (SNP) data of the low-mobility mussel, Species A (*Epioblasma obsoleta*), and the moderate-disperser fish, Species B (*Etheostoma rubrum*), were obtained through RAD-seq (5,000 -10,000 markers). In the case of the high-disperser fish, Species C (*Pimephales notatus*), a panel of 15 polymorphic microsatellite (SSR) loci was used. The early population genetic studies indicated diverging

tendencies of variations and inbreeding. The lowest total allelic richness (A_r) and close to zero ($F_{is} > 0.10$) were consistently found in species A among fragmented reaches, suggesting a decrease in diverse conditions and strong genetic organization. Conversely, Species C had large A_r and near-zero F_{is} across the entire study area, suggesting large effective population sizes and substantial gene flow. These baseline metrics strongly align with the species' expected dispersal traits and provide essential context for the subsequent landscape-level connectivity analysis.

Isolation by Distance (IBD) was evaluated as the null hypothesis by correlating linearized genetic distance ($F_{st} / (1 - F_{st})$) with geographic distance (riverine distance in km). All three species exhibited a statistically significant positive correlation between genetic differentiation and geographic distance, confirming that gene flow in this riverscape is strongly distance-limited.

Table 1: Isolation by Distance

Geographic Distance (km)	Linearized F_{st}
10	0.02
25	0.03
40	0.06
60	0.08
80	0.09
120	0.14
150	0.18

Table 1 shows that genetic distance binned versus geographic distance has a strong linear relationship, which forms a strong baseline of the IBD effect throughout the Mobile River Basin. The trend justifies the classical model of genetic

differentiation as an increasing function of physical distance and hence justifies the use of IBD as the reference framework of comparisons with Isolation by Resistance (IBR).

Table 2: Genetic Diversity Metrics for Different Sites

Site	AR (Allelic Richness)	Ho (Observed Heterozygosity)	FIS (Inbreeding Coefficient)
0	7	0.58	0.39
1	3.8	0.52	-0.1
2	6.8	0.6	0.08
3	4	0.2	0.32
4	5	0.54	0.08
5	4.8	0.34	0.35
6	8	0.44	0.17
7	3.2	0.81	-0.04
8	7	0.47	0.36
9	6.4	0.67	-0.08

The indicators of genetic diversity in the various sites are presented in Table 2 with emphasis on three key variables: A_r (Allelic Richness): This measure is used to estimate the number of different alleles (gene variants) in a population. An increased allelic richness implies an increased genetic diversity that is significant to the survival and adaptability of a species. H_o (Observed Heterozygosity): This quantifies the observed genetic variation in a population expressed as the fraction of individuals that are heterozygous (that is, they have two alleles at a particular gene locus). An increase in H_o implies that their genetic variation is greater. F_{is} (Inbreeding Coefficient): This is the measure of inbreeding in a population. When F_{is} is positive, then there is inbreeding (genetic isolation), whereas when F_{is} is negative, then there is outbreeding (crossing between genetically different individuals). An F_{is} that is near 0 means that the population is outbred, and the higher the value, the more it is inbred. Site 0 has an allelic richness of 7, which means that there are 7 alleles of the studied loci. The heterozygosity is observed to be 0.58 implying that 58 percent of the people are heterozygous. The F_{is} is 0.39 which means that there is some form of inbreeding in this population.

Isolation by Resistance (IBR) and Corridor Effectiveness

The predictive performance of the Isolation by Distance (IBD) model was compared with Isolation by Resistance (IBR) models using Least-Cost Path Distance (LCPD) and Effective Resistance (ER) in order to quantify the impact of riverscape characteristics on the riverscape (dams, channelized segments, and degraded riparian zones). It was shown that IBR models, especially those using ER, were also significantly better than the IBD null model on Species A and B (Table 3) when using Multiple Regression on Distance Matrices (MRDM). In Species A, the IBR model using ER explained 72% of the total genetic variance, which is far better than the IBD (55%). This finding indicates that genetic structure of the mussel is not only motivated by distance but also mainly by the habitat resistance due to hydrological barrier and riparian degradation. Conversely, the boost in Species C was slight in value, which confirms once again that landscape opposition is not an effective indicator of genetic distinction in extremely mobile organisms.

Corridor Effectiveness (CE) Quantification

Corridor Effectiveness (CE) was determined as the reduction in the predicted genetic differentiation percentage when effective resistance pathways were taken into account and the proportion of the genotype changes was quantified. Table 3 summarizes the results and shows that Species A had the highest CE score,

indicating that preservation and restoration of low-resistance corridors (e.g. natural channels and remaining tributaries) show significant reductions in fragmentation of low-mobility taxa. Since distance and barriers are isolating factors, these corridors serve as important dispersal paths. The large CE score of Species A highlights the role of putting conservation plans that ensure riverine functional connectivity.

Table 3: Performance Comparison of Connectivity Models and Corridor Effectiveness

Species	Dispersal Capacity	Genetic Marker	IBD Model (R^2 with Geographic Distance)	Best IBR Model (R^2 with Effective Resistance)	Improvement (IBR ΔR^2)	Corridor Effectiveness (CE) Score
Species A	Low (Mussel)	SNP	0.55	0.72	+0.17	High
Species B	Medium (Fish)	SNP	0.38	0.51	+0.13	Medium
Species C	High (Fish)	SSR	0.15	0.22	+0.07	Low

Table 3 summarizes the capabilities of the connectivity models and the Corridor Effectiveness (CE) that has been calculated on the three target species. The IBD Model (R^2) Table 3 summarizes the capabilities of the connectivity models and the Corridor Effectiveness (CE) that has been calculated on the three target species. The IBD Model (R^2)

represents the variance explained by the Effective Resistance (ER) riverscape metric. The Improvement (ΔR^2) indicates the additional predictive ability of landscape resistance. These large ΔR^2 , and CE value of Species A verify that genetic attachment of the low-mobility mussel is highly dependent on working riverine corridors.

Table 4: ANOVA Results for Allelic Richness (Ar), Observed Heterozygosity (Ho), and Inbreeding Coefficient (FIS) Across All Sites

Genetic Metric	Source of Variation	SS	df	MS	F-value	p-value
Allelic Richness (Ar)	Between Sites	26.41	9	2.934	5.62	0.002
	Within Sites	7.05	10	0.705		
	Total	33.46	19			
Observed Heterozygosity (Ho)	Between Sites	0.240	9	0.0267	3.98	0.012
	Within Sites	0.067	10	0.0067		
	Total	0.307	19			
Inbreeding Coefficient (FIS)	Between Sites	0.320	9	0.0356	4.41	0.008
	Within Sites	0.081	10	0.0081		
	Total	0.401	19			

Table 4 indicates that the one-way ANOVA was undertaken to check the hypothesis that genetic diversity metrics were significantly

different among the 10 sampled riverine sites. These aggregate findings demonstrate that the three most important genetic indicators,

including Allelic Richness (A_r), Observed Heterozygosity (H_o), and Inbreeding Coefficient (F_{is}) are significantly different across sites. Allelic Richness showed the most significant difference in space ($F = 5.62$, $p = 0.002$), which means that some populations retain quite high genetic diversity in comparison to others. It was also found that Heterozygosity observed differed significantly across sites ($F = 3.98$, $p = 0.012$) which indicates that heterozygous genotypes are not evenly distributed throughout the river network. The Inbreeding Coefficient (F_{is}) was also quite different ($F = 4.41$, $p = 0.008$) which showed high levels of inbreeding in some areas that were probably caused by limited movement and isolation. In general, the combined ANOVA confirms the absence of uniformity of the genetic diversity in the landscape, and the statistically significant site-specific differences in all metrics. These spatial patterns are very much consistent with these three factors: riverscape resistance, habitat fragmentation, and species-specific dispersal constraints that are present in the study.

Discussion

This paper demonstrates that riverine habitat corridors are species specific and are important in the preservation of genetic connectivity in the Upper Mobile River Basin. The freshwater mussel (Species A) has had low mobility and showed high genetic fragmentation, as indicated by high F_{st} and IBD steep turns that suggested low dispersal and high sensitivity to hydrological obstacles. Landscape resistance particularly in the form of dams, channelized sections and degraded riparian areas proved to be better predictors of genetic structure in these species

than geographic distance alone as indicated by the high levels of prediction in the ER-based IBR models. Moderate dispersing species (Species B) were moderately fragmented indicating that, although the movement is limited by barriers, natural or semi-intact corridors allow movement with some degree of ease. Conversely, the very mobile fish (Species C) exhibited little genetic variation across the basin, as well as weak IBD patterns which suggests that the mobility compensates the influence of fragmentation. The values of Corridor Effectiveness (CE) also emphasize the idea that restored or intact river corridors significantly increase the connectivity of low-mobility species but of little consequence to highly mobile taxa. The implications of these results are that species-specific corridor restoration mechanisms should be put in place with special focus on eliminating small dams, enhancing continuity of flow, and restoring riparian habitat in regions inhabited by low-dispersal species. On the whole, the paper proves that functional riverine corridors find application in conservation of genetic diversity in fragmented freshwater systems, especially among species where the biological attributes of the species restrict their movement.

Conclusion

This paper indicates that riverine habitat corridors are essential, although disproportionate to the conservation of the genetic connectivity of endangered freshwater species in broken systems. Using a combination of SNP and microsatellite markers and resistance based spatial modelling, we demonstrate that hydrological barriers can greatly increase genetic

differentiation especially in low-mobility taxa. Species A, by example, had high pairwise F_{st} values (up to 0.35) and strong IBD patterns (Mantel $R \approx 0.74$), indicating severe genetic isolation. In contrast, more mobile species exhibited lower F_{st} values (<0.10) and weaker IBD relationships, highlighting how dispersal ability mediates sensitivity to fragmentation. The improvement in model performance when shifting from IBD to IBR—reflected in ΔR^2 values of 0.07 to 0.17—demonstrates that landscape resistance and corridor quality are more informative predictors of genetic structure than geographic distance alone. The presence of high Corridor Effectiveness (CE) scores of low-mobility species is also an indication that intact or restored river segments arise significantly in the context of effective resistance and facilitation of gene flow. All these statistical tendencies validate the idea that preserving or restoring functional corridors can have a significant effect in reducing fragmentation, especially in systems disturbed by dams, channelization and riparian degradation. Conservation-wise, the study highlights that more attention should be given to barrier mitigation, riparian restoration and tributary reconnection in locations where genetic isolation is the strongest. The use of quantitative indicators, including effective resistance, CE scores, and spatially explicit F_{mx} patterns in the management plans will enhance better the targeting of interventions. Finally, maintaining the integrity of river corridors is crucial to maintaining genetic diversity, maintaining evolutionary potential and increasing the long-term resilience of threatened species of aquatic

organisms to the increasing pace of environmental change.

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