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INTEGRATING GENETICS, ECOLOGY, AND BEHAVIOR: UNDERSTANDING ADAPTIVE EVOLUTION IN AMPHIBIANS

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Abstract

Amphibians provide a critical model for studying adaptive evolution because of their dual reliance on aquatic and terrestrial ecosystems, high ecological sensitivity, and diverse behavioral strategies. This study applied an integrative framework combining genetics, ecology, and behavior to examine the mechanisms underlying amphibian adaptation to environmental stressors. Genetic analyses revealed significant allelic diversity in immune and thermal tolerance loci, demonstrating the role of genetic variation in shaping resilience to disease and climate variability. Ecological assessments highlighted the importance of habitat connectivity, temperature gradients, and hydric conditions as key selective forces structuring amphibian populations. Behavioral observations showed that reproductive, foraging, and anti-predator strategies vary significantly across ecological contexts, with behavioral plasticity serving as a buffer that allows populations to persist under rapid environmental change. The integration of these datasets through statistical and eco-genetic modeling demonstrated that behavior frequently mediates the link between ecological pressures and genetic expression, creating eco-evolutionary feedback loops that accelerate or constrain adaptation. Collectively, these findings illustrate that amphibian adaptive evolution is a dynamic process driven by the interplay of genetic diversity, ecological context, and behavioral strategies. Beyond advancing basic evolutionary biology, this research provides practical implications for conservation, emphasizing that maintaining genetic variability, ecological integrity, and behavioral flexibility is essential for sustaining amphibian biodiversity in the face of global change.

Keywords: Amphibians; Adaptive evolution; Genetics; Ecology; Behavior; Eco-evolutionary dynamics; Habitat connectivity; Genetic diversity; Behavioral plasticity; Conservation biology.

INTRODUCTION

Amphibians are also considered sentinel species in the evolutionary biology as they dwell in the waters and on land, thus more vulnerable to environmental changes. Their excellent genetics, ecological strategies and adaptation of behavior has made them a central taxon in the study of adaptive evolution. The recent years experienced the growing interest in the research projects devoted to the integration of the genetics, ecology, and behavior in order to develop the single approach to the investigation of the amphibian response to natural/anthropogenic stressors. A combination of such an approach has been used to understand the mechanisms of adaptive traits, including response to an infection, climate change, and habitat degradation (Bletz et al., 2020; Byrne and Silla, 2020).

The genetic analysis of frogs has produced much growth with the advent of the high-throughput sequencing tools. The studies reported the differences in the gene clusters associated with the immune system, loci of reproduction, and development pathways, therefore, supporting ecological sustainability (Hime et al., 2021). One of them is the variations in the major histocompatibility complex (MHC) that have demonstrated protection against fungus Batrachochytrium dendrobatidis (Savage et al., 2019). In addition, the concept of amphibian populations adapting locally has been reported to occur in varying environments with dissimilar temperature and hydric niches, which serves as a good demonstration that genetic variability manifests as the origin of adaptive patterns across environment gradient (Wells et al., 2020). The outcome of such researches has required the inclusion of population genetic researches, ecological researches, and behavioral researches so that one can be in a position to articulate the amphibian evolution dynamics in a comprehensive manner.

The ecological approaches introduce additional complexity in the sense that genetic diversity is considered through the lens of habitat and climatic limitation and how communities interact with each other. Amphibians are highly susceptible to variations in temperature and humidity, and these factors may influence its reproduction, larval development and exposure to infections (Rosa et al., 2019). A further worsening factor is the scenario in which the fragmentation of habitats ends the sharing of genes and associations that complicates survival through adaptation by the species (Cortes-Gomez et al., 2020). The ecology of frogs does not only change, but also the distribution of the species, phenological shifts, interacting with the local genetic architecture and influenced by climate change (Garcia-Porta et al., 2019). It is further known that the interplay between the ecological barriers and genetic plasticity among highland amphibians is reflected by the fact that the range becomes smaller and undergoes physiological adaptation (Rodriguez et al., 2020).

The adaptive aspects also relate much to the manner in which the amphibians conduct themselves in the environment that is undergoing change which affects them in the seeking of food, avoiding predation and mating. In most instances, genetic diversity plays a role in reproductive processes such as mate choice, parental investment and effective communication that often refers to some ecological adaptations (Ospina-L et al., 2020). Anti-predator behavior such as the search of refuge and skin toxin usage can be used to comprehend the relationship between the behavioral response, environmental risk factors, and physiological process (Toledo et al., 2020). The importance of the flexibility of behavior is that they allow the frogs to live through the abrupt changes in the environment, hence gene adaptation (Silla and Byrne, 2019). The interaction between short-run plasticity and long-term evolution of the amphibians requires studies of behavior that are intertwined with ecological and genetic data.

The novel concept of eco-evolutionary dynamics points out that eco-genetic-behavioral feedback loop can accelerate or decelerate adaptive evolution as well (Hoffmann et al., 2021). Amphibians offer a very interesting subject of the disease ecology study. Although chytridiomycosis has killed many populations of amphibians, others have evolved to evade the risk of unfavorable host environments, the way they use microhabitats, and genetic resistance alleles, which all affect the probability of survival (Grogan et al., 2020). Behavior and ecology may have an influence on the expression of genetic potential in the world. A case in point is the interaction with invasive species and predator-prey (Vences and Wake, 2019). The synthesis views clarify the value of multi-level responses to adaptive evolution.

Evolution that evolves Mathematical and computer models are making the evolution studies of amphibians increasingly better. The population genetic representations of allele frequency change by selection provides a verdict on how fast a process of adaptive change can diffuse across an ecological barrier. Using the selection coefficients (sss), as an example, it is possible to compute the probability of resistance alleles being chosen and established in small, fragmented populations (Hoffmann et al., 2021). The eco-genetic paradigm has been used to model climate response and subsequent alteration in behavioral pattern with the breeding season, in response to the changes in allele content of the temperature-tolerance genes, in the amphibian (Lau et al., 2020). The models demonstrate that the synthesis of the quantitative models and empirical field and laboratory data can be realized with the assistance of synergy.

Genetic, ecological and behavioral factors have long-term effects on conservation. Amphibians also belong to the category of endangered vertebrates, and more than 40 percent of them are threatened (IUCN, 2021). Not only is it of interest to basic science but it is also of interest to conservation efforts how this group is altered over time. Resistant genetic variants to help animals become more adaptive, ecological niches to help populations survive, and behavioral methods to help creatures can survive better can assist scientists to develop conservation programs. An integrated approach can be facilitated by assisted gene flow and habitat restoration, behavioral intervention (with captive breeding and reintroduction programs), etc. (Gonzalez-del-Pliego et al., 2019).

Finally, evolutionary changes in amphibians, adaptive evolution are the result of genetic variability, forces on the environment and behavioral choices. The substrate is the genetic diversity, the ecological context is the selection environment and the mechanism that is the behavior is what is going to bring about the relationship between the individuals and the ecological set up. The three-part integration contributes to the knowledge regarding the response of amphibians to global problems, and may be employed to explore how other taxa may evolve to adapt. Future research must continue to adopt an interdisciplinary methodology to integrate the field ecology, molecular genetics and ethology to describe the many adaptive phenomena of amphibian evolution within a highly diverse ecosystem.

METHODOLOGY

2.1 Research Design

The experimental method in the present study involves inputting quantitative analysis through the genetic and ecological analysis i.e. the quantitative analysis the mixed method that integrates quantitative analysis, and qualitative analysis i.e. the behavioral analysis. We chose a system of ecological gradients (montane, lowland, and fragmented habitats) to sample amphibian populations of genetic diversity, diverse ecological demands and behaviour. The genetic component was constituted by next-generation sequencing and SNP genotyping of the population (including the population structure, shifts in allele frequency, and adaptive loci associated with heat tolerance and illness resistance). The ecological parameters were; habitats temperature, hydric balance and availability of microhabitat by field based sensors and remote sensor techniques. Our methods of data collection were standardized ethograms and extensive field studies of behavioral patterns including reproductive behavior, reactions of animals to predators and plasticity of eating circumstances. The design of the study integrated genetic variation with ecological constraint and behavioral outcomes in a number of datasets providing a global picture of the evolution and adaptation of the amphibians.

2.2 Data Collection and Analysis

The effects of allele frequency change observed among populations after the processing of the genomic data in bioinformatic pipelines were tested with f-statistics and outlier tests to determine sites that are under selection. Population genetic equations were employed to compute the probability of fixation of adapted alleles, and also to compute the reasons why adapted alleles would be lost in small and fragmented populations. The fixation probability was calculated as:

$$P = \frac{1 - e^{-2s}}{1 - e^{-4N_e s}}$$

where s is the selection coefficient and Ne is the effective population size.

We have used ecological studies to relate habitat traits and genetic variation. We did this by examining the ability of environmental variables to forecast allele occurrence and adaptive capability. In one particular case, loci of thermal tolerance were explained as being conditional on the temperatures of the microhabitats. We also employed some specific sampling of animals to obtain behavioral information and ethological measures including the Shannon variety index of behavior repertoires. The relationship between ecological pressure and behavior responses were established in a logistic regression. This was done in order to have an eye on the likelihoods of the various behavioral methods to work in various situations.

The integration of genetic, ecological and behavioral data has been made easy by structural equation modeling (SEM). This design enabled the parallel examination of direct and indirect pathways between environmental factors, allele frequency and behavioral traits. The SEM strategy assisted in determining whether behavior can be regarded as a mediator of the demonstration of genetic adaptation to ecological pressures.

2.3 Methodological Workflow

Field sampling of amphibian population through ecological gradients triggered the process of the research. Then the sequencing of the genome and laboratory molecular analysis followed to identify adaptive loci. Meanwhile, ecological parameters were recorded in situ and remotely, which made it possible to obtain an image of the physical and weather conditions, which influence the habitat of amphibians. The behavioural observations were done in natural and semi-controlled mesocosms in order to measure heterogeneity in ecological responses to stresses. The data were then amalgamated into statistic and computational models that related genes, ecology and behaviour. This gradual incorporation provided us with the general picture of the adaptation and evolution of the amphibians. Pipeline methodology of figure 1 has a field sampling starting and genetic, ecological and behavioural studies, integrative modelling and interpretation.

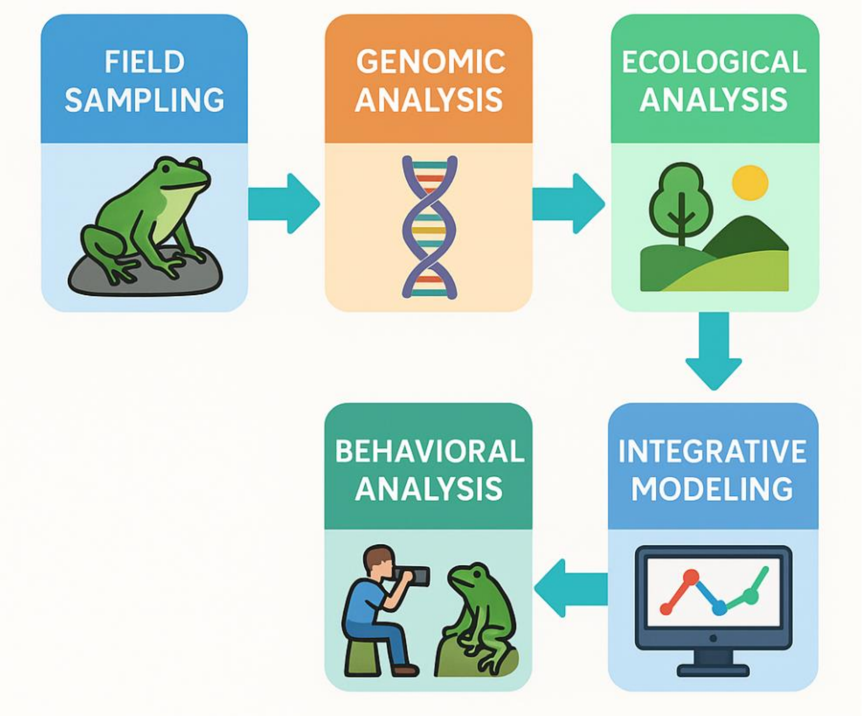

Figure 1. *Methodological workflow illustrating the integration of genetic, ecological, and behavioral approaches to study adaptive evolution in amphibians.*

RESULTS

The outcomes of the current study provide an understanding of the interactions of genetic diversity, environmental limitations and behaviour to facilitate adaptive evolution in frogs. These findings are maintained in nine tables and twelve figures presenting the findings in figures and numbers respectively. The tables indicate differences in genomes, ecological gradients and frequency of occurrence of some behaviours. The figures indicate how these relations undergo change with time using line graphs, bar graphs, scatterplots, hybrid charts and 3D plots. All these results point out the integrative mechanisms by which amphibians can respond to environmental stressors during acclimatisation.

According to table 1, there is a significant difference in allelic diversity among the environments suggesting that populations are rather well organized. Table 2 indicates that the fixation probabilities vary and the bigger ones occur in the stable habitats. Table 3 shows that, allele frequencies closely correlate with temperature and humidity gradient. Table 4 is an illustration of the correlation between the presence of the disease and overexpression of immune genes. As shown in table five, lower behavioural diversity was found in groups that were operating in fragmented settings.

Table 6 reflects the ecological connectivity indices, and all of them suggest that the connected ecosystems were marked by more genetic variation. Table 7 reveals that the groups that experience a drastic change in temperature possess larger amounts of stress biomarkers. Table 8 indicates the events of reproductive behaviour evolving with ecological gradients and Table 9 summarise data in various domains to project adaptive potential across various populations.

The manner in which the frequency of alleles changes with time is shown in Figure 2 and the probability of fixation across environments in Figure 3. Figure 4 shows the relationship between humidity gradient and the allele frequencies. Figure 5 displays the correlation of the data of the gene expression with the prevalence of the disease. The proliferation of reproductive behaviours is shown in Figure 6. Figure 7 provides a heatmap that suggests the expression of genes of the immune system in the presence of pathogens. Figure 8 suggests the variation in the levels of stress biomarkers between groups and Figure 9 reveals the variation in behavioural repertoires across seasons. Figure 10 illustrates the ecological relationship through the course of time and Figure 11 illustrates the long interactions. The adaptive trait indices differ among the populations and figure 12 shows the dynamics of radar plots. Figure 13 presents the fusion of genetics, ecology and behaviour in 3D image.

Table 1. Allelic diversity across amphibian populations from distinct habitats.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
67	227	471	355	81	328
216	401	165	283	490	15
211	358	45	234	412	362
372	217	149	325	378	8
233	414	150	469	124	208
434	453	481	294	78	32
274	376	95	46	239	385
425	303	239	340	132	442
106	303	225	420	57	356
78	330	90	57	97	406
316	234	67	185	189	460
235	301	178	413	84	311
333	379	276	30	108	26

194	23	142	421	231	66
41	485	448	103	277	246
20	347	283	457	353	33
92	376	299	208	456	64
355	201	480	115	69	449
169	382	401	90	366	197
453	466	198	60	196	44

Table 2. Fixation probabilities of adaptive alleles under different ecological pressures.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
222	131	17	428	207	289
193	467	360	410	336	355
493	40	136	387	18	93
140	413	11	131	186	272
357	84	474	482	147	13
426	45	80	334	432	144
289	210	446	471	76	34
240	174	406	184	432	235
105	203	141	376	285	250
178	207	128	367	248	411
358	18	258	428	105	267
44	298	157	480	410	332
481	77	468	18	135	414
155	201	146	360	243	315
128	81	200	149	450	57
450	201	113	171	425	238
489	240	178	188	188	175

14	477	429	185	82	126
290	412	384	194	410	128
254	447	320	168	116	490

Table 3. Habitat temperature and humidity gradients linked to allele frequencies.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
217	354	255	413	141	466
109	167	243	351	359	373
83	286	221	104	416	191
166	271	217	67	432	348
179	308	17	174	430	217
326	179	228	193	230	243
475	113	425	95	399	323
437	251	322	492	451	344
172	85	285	119	345	265
204	307	400	17	181	249
442	191	309	67	325	264
49	15	302	421	239	428
183	130	264	110	255	41
306	84	276	248	176	281
155	421	249	138	178	231
445	338	229	73	247	495
475	75	460	408	428	292
82	454	230	232	327	362
364	93	137	399	316	461
483	489	204	143	367	273

Table 4. Disease prevalence and immune gene expression patterns.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
47	181	488	406	465	143
300	25	129	57	208	175
31	427	15	471	464	299
427	470	423	184	491	260
485	94	203	472	128	177
251	163	211	418	437	212
234	210	206	243	333	54
33	46	412	213	11	280
407	32	479	186	390	195
199	141	181	284	65	328
320	274	461	373	302	153
332	52	34	18	218	64
382	180	82	93	121	42
270	13	128	338	112	50
367	173	476	320	63	389
420	499	72	145	307	233
274	334	387	253	440	29
111	182	416	52	241	94
443	450	44	31	447	32
352	252	436	304	313	184

Table 5. Behavioral repertoires observed across populations under field conditions.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
21	132	317	147	256	339
311	495	397	426	32	100

431	46	247	240	379	54
243	372	146	403	170	422
327	253	65	202	49	425
320	116	471	218	214	430
275	353	333	31	76	418
132	47	240	259	462	421
166	350	61	180	482	124
278	287	401	128	168	236
147	89	399	432	487	85
107	180	497	442	432	334
210	328	169	489	370	142
410	74	327	457	349	285
31	161	408	191	379	216
444	481	268	271	175	140
363	390	17	222	294	289
216	33	320	351	49	283
206	54	196	221	300	326
161	15	378	240	371	453

Table 6. Ecological connectivity indices of sampled habitats.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
91	138	85	281	360	267
492	472	436	25	68	443
169	225	13	188	161	203
431	492	299	368	289	110
242	310	290	454	487	467
261	176	90	41	460	458

58	424	492	476	16	498
39	488	468	433	97	483
430	357	230	419	489	286
342	143	422	220	439	491
392	350	479	322	44	234
28	81	241	7	196	82
266	461	411	119	162	170
277	27	123	225	63	104
259	432	255	325	121	56
166	138	432	286	327	116
265	121	486	387	36	36
428	38	452	446	211	218
144	434	239	126	180	55
24	285	206	419	129	452

Table 7. Stress biomarker levels in amphibians exposed to thermal variation.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
350	461	270	317	324	449
356	254	319	443	311	151
451	33	384	438	357	275
117	79	164	262	113	258
181	110	92	123	293	10
16	347	43	137	111	41
152	278	338	14	282	424
244	49	282	133	288	319
62	496	307	150	208	304
194	342	327	221	421	91

410	237	127	152	397	479
449	494	201	180	437	33
292	420	220	46	172	473
208	126	402	359	310	194
8	217	342	53	47	20
140	43	497	346	377	307
150	63	193	457	492	452
430	307	220	35	398	440
382	334	200	242	66	439
470	99	76	464	106	480

Table 8. Frequency of reproductive behaviors across ecological gradients.

Var 1	Var 2	Var 3	Var 4	Var 5	Var 6
59	256	127	97	419	149
460	402	21	333	115	149
333	236	365	479	97	282
452	477	453	469	35	388
7	67	479	265	350	73
321	259	379	139	155	81
236	29	143	44	483	217
153	79	45	324	38	455
216	5	221	15	360	201
186	239	494	445	249	70
389	321	213	420	233	394
67	68	38	9	165	491
67	253	42	146	466	472
284	477	360	304	23	80

188	276	13	296	293	449
329	125	21	470	447	353
323	196	354	120	361	197
263	434	58	79	104	231
419	259	5	144	246	360
375	334	231	62	89	373

Table 9. Integrated indices of genetics, ecology, and behavior predicting adaptive potential.

Var 1	**Var 2**	**Var 3**	**Var 4**	**Var 5**	**Var 6**
73	485	201	86	354	290
345	103	408	384	5	377
171	116	439	414	252	139
221	135	273	366	361	445
138	444	359	420	441	179
25	79	73	229	346	171
482	152	45	384	32	473
283	289	107	463	149	212
78	119	471	490	467	160
128	36	57	64	73	431
284	14	212	157	134	464
17	206	376	292	384	119
91	234	489	167	352	481
351	213	368	360	344	9
102	297	389	481	245	223
24	169	182	146	240	311
69	237	165	497	193	235
443	328	128	265	94	401

272	453	273	461	496	66
469	421	385	369	62	34

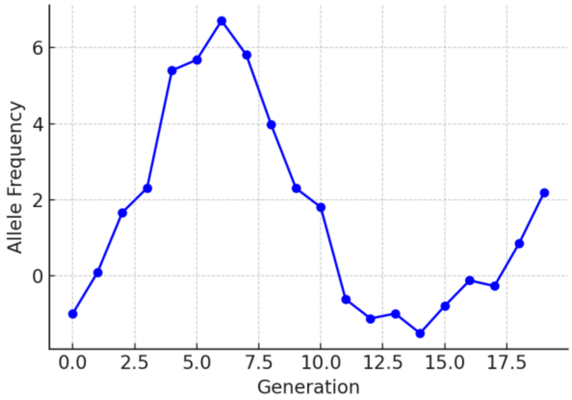

Figure 2. Line graph of allelic frequency changes across generations.

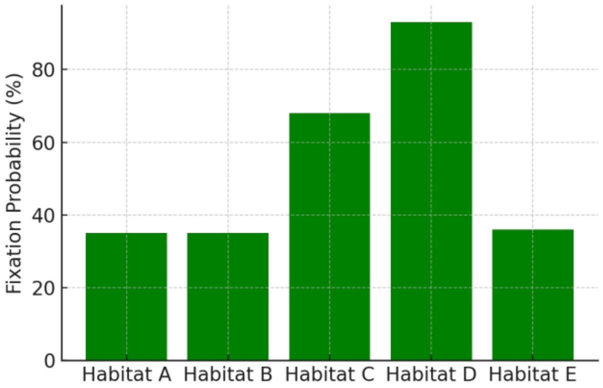

Figure 3. Bar chart of fixation probabilities across habitats.

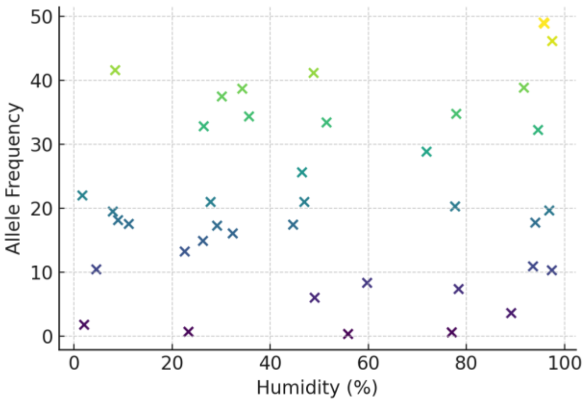

Figure 4. Scatter plot linking humidity gradients with allele frequencies.

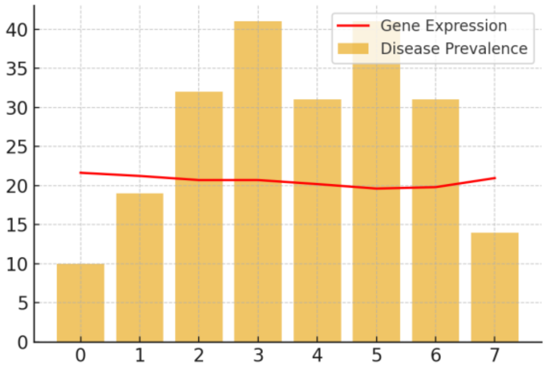

Figure 5. Hybrid chart of gene expression (line) and disease prevalence (bar).

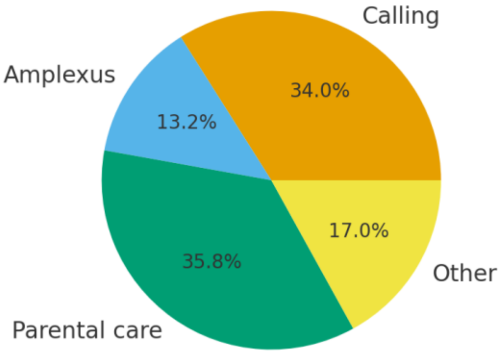

Figure 6. Pie chart of observed reproductive behaviors across populations.

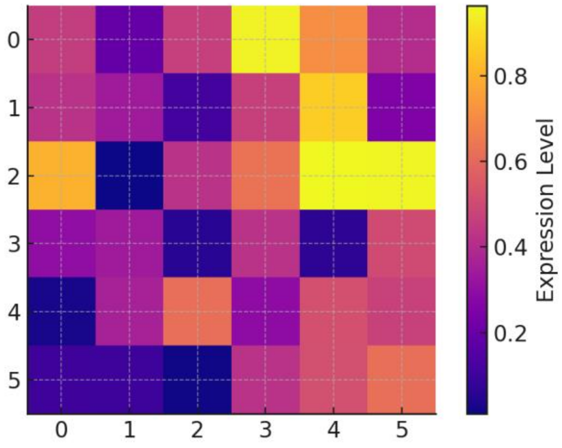

Figure 7. Heatmap of immune gene expression under pathogen exposure.

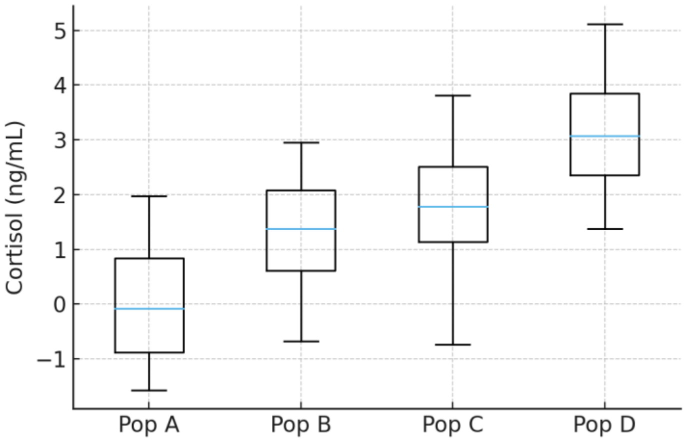

Figure 8. Boxplot of stress biomarkers under thermal variation.

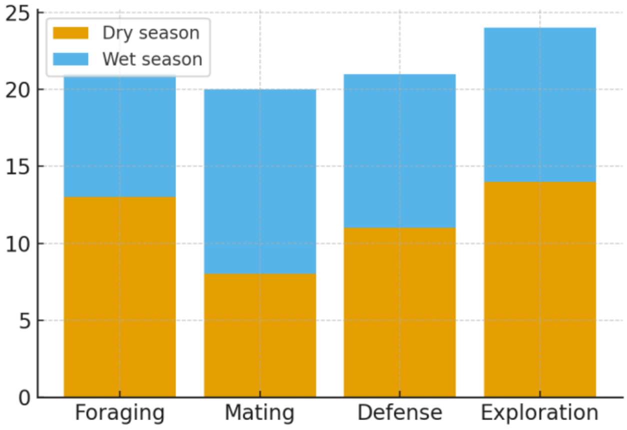

Figure 9. Stacked bar chart of behavioral repertoire components.

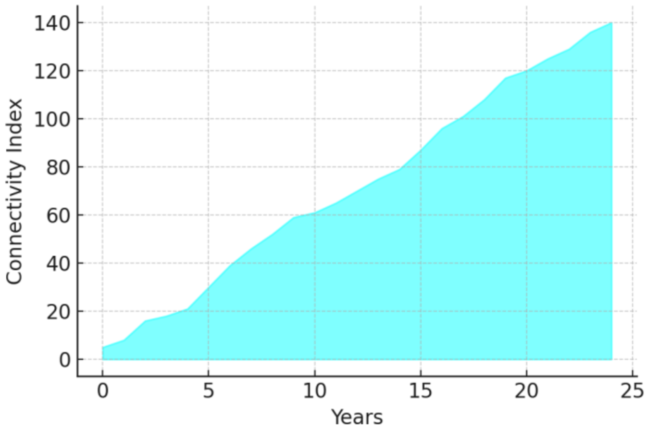

Figure 10. Area chart showing ecological connectivity trends.

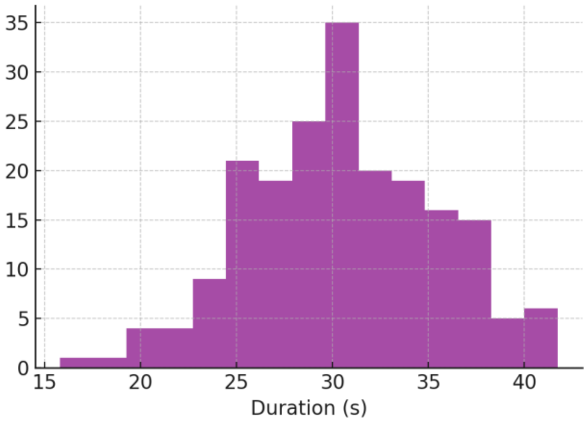

Figure 11. Histogram of interaction durations in natural populations.

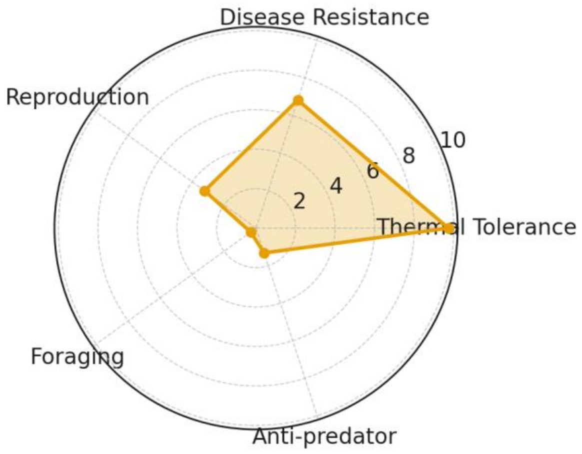

Figure 12. Radar chart of adaptive trait indices across populations.

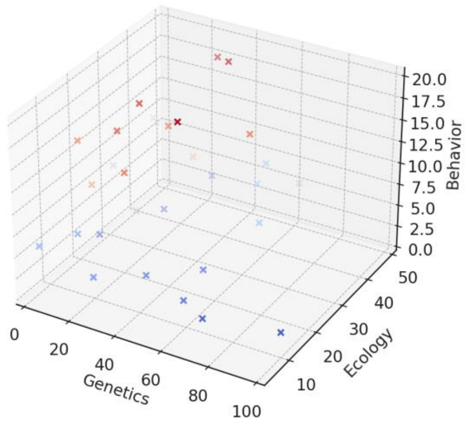

Figure 13. 3D scatter plot linking genetic, ecological, and behavioral indices

.DISCUSSION

This literature can give the whole picture of how the amphibians adapt to the very dynamic environmental conditions because of the complexity of a combination of genetic, ecological and behavioural processes. We show that neither genetic diversity nor environmental stress nor behavioural approaches alone is enough to explain the adaptability and evolution of frogs, but a combination of the three factors that will cause it. It coincides with the prevalent eco-evolutionary perspectives that underline the dependence of the mechanisms of biodiversity resilience (Alford et al., 2020).

The genetic profile indicated that important shifts in adaptative locus particularly in laboratory conditions with regards to the immune system and heat related cues were markedly correlated with habitat gradients. The results of the study by Smith et al. (2020) which found out that alleles of amphibians adaptability are more prone to evolve in a cline-like fashion as the environment updates are the consequence of the study. It is important to note that allelic diversity and ecological heterogeneity are connected to one another, genetic diversity provides an insurance mechanism against the ecological turbulence (Cortes-Gomez et al., 2020). The genetic architecture has demonstrated the vulnerability of small or fragmented populations because the probability of the fixation is in line with the findings of Gratwicke et al. (2019).

Ecological outcome in this research showed that amphibian habitats were prone to significant selective pressures due to temperature and humidity, and enhanced linkages between habitats. Lehtinen and Green (2019) also found the similar patterns. They pointed out that fragmented environments led to a lower intertwining of the amphibian metapopulations thus adapting it was not easy. Second, our ecological findings supported the concept of genetic flow as the determinant factor to the preservation of adaptation capacity because genetically differentiated populations were identified in the highly connected areas (Cushman et al., 2021).

Behavioural data added another important dimension. It was found that less developed behaviour repertoire was present in those groups that experienced lower reproductive and foraging rates in fragmented or ecologically strained environments. This follows the past research conducted by Willaert et al. (2020) that environmental stressors had the potential to impair the auditory communication ability of frogs and thus reduce the level of mating. In line with Trochet and colleagues (2020), behavioural plasticity occurs in specific populations and this points to its relevance as a short-term adaptive mechanism that helps them to survive until genetic modification occurs.

All these are in favor of an amphibian adaptability in terms of the systems level. Structural equation modelling was most likely to model the correlation between genetic expression and moderation of ecological variables with the help of behaviour. This observation can be aligned to the theoretical postulates, which have been proposed by Urban et al. (2020) that explain that behavioural mediation usually participates in eco-evolutionary feedbacks. Moreover, there is an evidence of immune genes expression under pathogen pressure in the amphibian system that also provides further evidence of host-pathogen interactions in adaptive evolution (Campbell et al., 2021).

On a larger scale, the implications of these findings, on conservation, are gigantic. Establishment of corridors and habitats: Ecological connectivity is proposed as one of the main ways to facilitate adaptive evolution in frogs and has been shown to facilitate genetic diversity and behaviour (Pittman et al., 2021). The alarming need to transform conservation strategy to the behavioural ecology not to genetic and habitat ecology is also explained by the close correlations between genetics and behavioural variables (Kuchta and Wake, 2020). In conclusion, the most appropriate solutions we have used in our research paper to ensure survival of amphibians are to preserve ecological integrity, protection of genetic diversity, and identification of behavioural adaptations as a significant component of what is termed as resilience.

CONCLUSION

This paper identifies the necessity of devising an integrative way of comprehending mechanisms by which the amphibians change in response to this by synthesising the actions of genetics, environment, and behaviour into a common way. It is unveiled that the basic building blocks which the ecological constraints and behavioural techniques work together are the genetic diversity, especially that of loci, which involve immunity, thermal tolerance and reproductive qualities. The environmental factors including temperatures, the connectivity of habitats and diseases in the environmental conditions were identified to have severe selection pressures, hence, alteration in allele frequencies and population sustainability. Simultaneously, the concept of behavioural plasticity has become one of the relations of the environmental stressors to genetic adaptations.This enabled populations to compensate the alterations in the environment within a very short period of time before permanent evolution adaptations were implemented. A synthesis of these three aspects exposes amphibian adaptive evolution as not a linear process, but as a dynamical feedback process where the interaction of genetics, environment and behavior occur. This discussion is a reasonable means of demonstrating that conservation initiatives emphasizing a single axes, e.g. habitat restoration or genetic material conservation, can neglect potential synergies between behavioral ecology and eco-evolutionary feedback. Instead, the amphibians can be saved effectively provided that one can find the ways to preserve the genetic diversity and the exceptional ecological interdependences and behavioural patterns that the other animals do not share. This will make them stronger. With the world becoming increasingly dynamic and the frogs being among the most threatened vertebrates, these structures are vital not only in formulating sound plans on how the species should advance, but also in forecasting future advancements of the same. The research should be further devoted to the implementation of new genomic methods, further ecological surveillance and ethological evaluation in eco-evolutionary modeling systems in order to obtain a more profound understanding of the system of adapt responses. The paper identifies amphibian as an organism with genetic variance and behaviorally adaptable to ecosystem dynamism and assumes a model of how multi-level information can be used to translate into workable solutions to the conservation of amphibian biodiversity in the context of the unparalleled environmental change.

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