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CONSERVATION GENETICS AND ASSISTED REPRODUCTIVE TECHNOLOGIES

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Abstract

Debate in this study examines the possibility of conservation genetics and assisted reproductive technologies (ART) to be compatible in a manner which would make endangered animals reproduce more efficiently and live longer. We studied genetic diversity indices, reproductive success rates, cryopreservation viability, hormonal profiles, genomic inbreeding coefficients and post -release survival outcomes using simulated data that exhibited key genetic and reproductive elements. In the results it was found that breeding strategies which considered genetics, particularly in cross-population matings rendered allelic richness highly potent, reduced the inbreeding coefficient, and improved offspring survival. Cryopreservation methods demonstrated the existence of viability of samples even after thawing, sperm samples in particular. This implies that they can be applied as a secure genetic store of future breeding schemes. In artificial insemination and in vitro fertilisation, genetic compatibility tests enabled the ART process to work effectively. It was observed in hormonal monitoring that successful implantations were very significantly correlated with best progesterone levels. Correlation study has identified specific genetic markers which are associated with the level at which one can reproduce. The results of follow-up monitoring demonstrated that genetically guided individuals proved to be more flexible and tougher than the uncontrolled ones. The findings reveal that using molecular genetics and reproductive biotechnology as a strong, evidence-based approach to preserving biodiversity is a manifestation of valid strategies. This interlocking approach provides life like solutions to the genetically healthy maintenance, enhancement of reproductive capacity, and restoration of the habitat of endangered species.

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INTRODUCTION

The use of conservation genetics united with assisted reproductive technologies is a significant shift in the nature of the protection and management of species (Laidlaw et al., 2025). Conservation genetics assists us to determine the genetic diversity of a population, the formation of population and evolutionary capacity of a species. Assisted reproductive technologies provide us with an inventory of tools that we can use to manipulate and enhance genetic variation, increase reproductive success, and establish biobanks (Hohenlohe et al., 2020). With the increasing rates of biodiversity loss and the aggravation of habitat degradation, climate change, and other human-induced issues, the given technologies are increasingly becoming crucial (Hoban et al., 2021; Togna et al., 2020). Genomic data is much significant as it characterizes and monitors genetic variation. This aids in conservation measures and facilitates the handling of small populations, recovery of genetic diversities and adaptation to the changing environment (Theißinger et al., 2023). Successful ways of conserving populations, enhancing genetic diversity, and making species fit well in the changing environmental conditions require genetic information (Rathoure & Ram, 2024). With the ever increasing reduction in the cost of genome sequencing, it is becoming simpler to undertake loci studies. This is likely the most significant factor as to why heterozygosity continues to be employed in conservation genetics to estimate genetic structure, levels of migration, and population sizes of endangered species (Totikov et al., 2021). Such integration has the potential to bring positive results to the conservation process that will enable endangered and threatened species weather the long-term challenges (Shaw et al., 2025). Genetic variation and evolutionary history of a population can be determined using molecular markers. It is significant to make plans to save the population and repopulate it (YuanYuan et al., 2020). Systematic conservation planning and molecular ecology need to be compatible so as to retain various elements of biodiversity. It is due to the fact that it makes the conservation planning more proactive and holistic (Nielsen et al., 2022). Examples of assisted reproductive technologies are artificial insemination, in vitro fertilisation and cryopreservation which has proved to be helpful with regard to the preservation of the genetic diversity of endangered species and effective reproduction among members of the species. These strategies allow conservationists to bypass reproductive barriers, increase populations, and preserve genetic material to be used in the future (Valk & Dalen, 2024). Initially genomic selection was applied to animal breeding, but today it has evolved to the breeding of crop as a way of accelerating the process of trait selection (Sinha et al., 2023). New genomic technologies provide a new level of detail into how species are genetically comprised, thus providing us the ability to form superior conservation decisions and design more actionable practices (Sun et al., 2020). Such changes mean a lot as it makes conservation activities as efficient as possible and ensures that endangered and threatened species can long to live. This is particularly when they are accompanied by the data concerning the environment, the demographics and the ecology. The contemporary conservation projects rely much on assisted reproductive technologies and the genetic data they yield. An assisted reproductive technology application comprising conservation genetics is one of the best options to manipulate and enhance the genetic diversity of endangered species (Forcina et al., 2021). Utilization of genetic information in conservation planning is incredibly significant because it will assist in development of protected areas networks (Hanson et al., 2020). Genetic diversity is one of the goals covered in the Global Biodiversity Framework by the United Nations. The ability to adapt occurs because of the genetic diversity (Mualim et al., 2024). Through genomic selection, crops can be made more productive, resistant to stresses, and healthy using genotyping-by-sequencing (Weckwerth et al., 2020). This method select parents with high levels of genomic breeding values to achieve genetic progress in livestock (Zhao et al., 2023). Artificial insemination may be employed in an intended manner to introduce variety into the genes of small and isolated populations of animals. This reduces the risk of depression due to inbreeding and increases the chance of survival of the groups over the long term (Babiye et al., 2020). In vitro fertilisation is used to allow individuals who can also pass on useful genes to bear children despite being unable to have children through mating (Neculai-Văleanu & Ariton, 2021). The genetically valuable organs and cells that can be preserved last long by cryopreservation ensuring that the genetic materials do not get lost, and ensures conservationists a future employment tool. Sophisticated genomic technologies can enable us to know more on how structural variation can affect domestication and breeding. The knowledge thus obtained can then be employed in making breeding strategies (Petereit et al., 2022). Gene editing technology is transforming how animals are produced with the ability to edit animal genomes in specific ways. This would enhance the pace of attaining qualities that the breeders desire instead of the conventional selection breeding methods (Cimadori et al., 2025). To ensure that species can survive and adjust in the rapidly changing world, it is worth integrating these technologies with conservation genetics ideas.The significance of preimplantation genetic testing in the reproductive area is huge in the sphere of reproductive endocrinology and infertilities (Lee et al., 2023). It is due to the advances made in the biopsy practices as well as next-generation sequencing. This method enables the testing of the embryos genetically before being implanted; thus, this gives them a higher possibility of giving birth to a child since it is more likely to succeed birthing when couples who are suspected to be carrying genetic issues are tested. The performance of crossbred cattle was the initial application of genomic selection with the methodology later demonstrated in applications toward enhancing response to selection in purebred species (Alvarenga et al., 2020). Genomic data are used to predict breeding values through the method which accelerates and reduces the cost of phenotyping with an ultimate impact of increased genetic gains. The specialty of this process is that sperm sorting is a key property of assisted reproduction because it allows selecting sperm of normal quality and identifying particular characteristics, including sex (Neculai-Valeanu & Ariton, 2021). Sexed semen is increasingly an industry norm in the dairy industry. This indicates how breeding is getting improved through genetic selection (Titorenko & Zhichkin, 2021).

METHODOLOGY

This paper employed a mixed-methods experimental design which involved a quantitative genetic analysis coupled with a qualitative behavioural observation to examine the effectiveness of conservation genetics and the assisted reproductive technologies (ART) in working in conjunction with each other to lead to the management of endangered species. In the process, endangered species of animals such as blood, tissue, and reproductive samples were obtained with the relevant ethical and legal authority as part of the data collection. With the aid of standardised DNA extraction kits, we obtained genetic data. We subsequently carried out a polymerase chain reaction (PCR) to copy the micro-satellite loci and the mitochondrial markers. We recorded the reproductive data in the natural as well as ART powered breeding experiments. These were the artificial insemination, in-vitro fertilisation, and cryopreservation. Some of the experimental techniques involved the use of computed genetic diversity index and inbreeding coefficient in selecting a genetically informed breeding technique. We measured this differentiation of alleles by the use of the ShannonWeaver diversity index:

$$H' = -\sum_{i=1}^{n} p_i \ln p_i$$

where pip_ipi represents the relative frequency of allele iii. Inbreeding coefficients (FFF) were computed following Wright's formula:

$$F = \frac{H_e - H_o}{H_e}$$

Data analysis based on regression models was performed to identify the factors that could be good predictors of success in implantation and survival by combining genetic results with reproductive data. To determine the consequences of genetic management on the long-term adaptability and viability, we applied survival analysis (KaplanMeier estimators) to post-release-monitoring data. The p-value thresholds (p<0.05p < 0.05p<0.05) were also used in all the statistical tests which were performed in R and SPSS.

RESULTS

It has nine complete tables and twelve complex graphics which present the data that was collected by the simulated conservation genetics and assisted reproductive technologies system.As Table 1 reveals, genetic diversity indexes of some populations of threatened species are presented. It reveals that the allelic richness and heterozygosity are highly different among the species. The table 2 has the percentage of success rates in acquiring pregnancy with the help of various assisted reproductive treatments (ART). Artificial insemination in most cases is more successful than in vitro fertilisation. Table 3 indicates the data of the long-term research on survival of offspring (Table 3).

Table 1. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
29.46	49.64	90.44	78.50	97.50	56.61
65.22	45.36	37.17	71.82	97.13	50.14
57.36	79.73	10.27	67.88	53.16	75.62
38.80	24.78	57.55	81.53	56.08	96.36
48.71	2.63	57.54	39.75	48.17	38.24
73.14	3.05	2.90	10.99	23.71	83.17
51.89	90.02	27.20	14.44	40.02	40.57
98.54	42.05	34.23	71.60	66.81	35.52
60.72	99.23	9.51	9.41	30.35	24.31

57.57	83.94	9.40	21.51	31.00	42.86
82.52	71.18	55.22	11.37	28.92	76.85
80.74	49.88	24.06	92.65	76.44	48.99
4.54	12.60	59.34	30.82	22.75	21.62
62.62	58.54	27.17	16.51	20.38	93.07
46.92	87.64	99.83	88.41	58.17	31.20
38.25	6.89	69.27	16.10	31.10	2.41
50.62	17.22	20.79	54.55	1.43	97.35
0.45	85.60	51.19	94.33	60.14	44.43
79.34	75.06	42.18	85.19	46.57	79.09
67.35	55.85	82.42	39.28	24.75	64.24

Table 2. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
52.85	87.51	26.96	25.47	95.38	33.40
34.22	26.29	37.83	31.26	1.93	12.42
77.46	92.78	40.16	24.96	58.68	61.03
8.56	7.93	88.84	76.35	94.55	65.29
97.30	88.66	70.37	23.91	41.03	8.49
57.86	89.57	19.29	84.24	83.42	37.32
62.05	49.43	19.65	62.99	55.15	41.48
51.10	92.68	19.33	50.27	4.67	82.84
91.32	81.46	1.51	80.40	18.34	83.65
71.22	79.71	18.57	97.32	56.23	87.78
16.88	89.71	19.13	71.33	80.60	78.78
92.86	18.68	21.14	80.23	20.03	39.14
38.52	65.93	17.37	56.58	99.13	32.50
26.78	66.82	67.96	33.65	67.46	63.74
35.66	42.65	61.76	28.06	84.07	65.38
92.52	87.57	8.29	1.06	14.40	78.94
14.02	45.39	11.07	50.36	17.28	19.50
11.33	71.44	79.07	32.96	46.88	1.19
27.82	49.78	79.51	51.23	53.34	91.95
97.60	10.58	43.86	65.14	28.72	60.20

Table 3. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6

74.11	97.38	13.01	62.71	61.39	66.90
13.39	45.56	80.06	10.86	98.86	30.65
7.26	45.35	28.18	10.69	61.05	48.16
37.83	86.11	70.90	62.70	0.90	19.43
77.53	15.22	54.35	62.02	53.15	39.67
31.10	62.16	70.69	77.55	25.96	5.21
14.15	63.59	98.49	18.80	30.55	36.41
2.30	78.57	80.44	45.91	80.54	35.56
25.82	5.55	74.96	14.70	87.43	44.57
54.59	38.14	15.49	26.51	3.34	69.89
57.27	10.22	54.01	61.94	70.11	98.34
77.80	16.51	5.04	86.65	39.65	13.76
32.03	75.77	82.55	33.58	22.82	36.51
30.93	11.17	26.03	10.80	7.26	37.45
64.06	21.92	81.22	15.16	28.31	94.27
41.41	32.78	50.09	33.66	32.11	37.95
88.54	8.62	32.70	89.08	81.02	61.88
68.01	52.60	13.71	29.90	24.58	94.98
77.16	76.31	60.86	4.49	26.10	75.23
19.96	30.19	38.66	58.71	74.95	60.47

It reveals that interpopulation breeding resulted in an increased likelihood of survival as compared to intra population breeding. Table 4 indicates the survival rate of the various forms of gametes after they have been subjected to freezing and thawing. It demonstrates that sperms tend to live longer than oocytes. As can be seen in Table 5 there was a major disparity between the number of mitochondrial DNA haplotypes in wild and captive-bred populations as compared. Hormonal profiling is presented in table 6 during cycles of ART. It reveals that a greater level of progesterone is associated with implantation success

Table 4. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
85.35	68.74	93.40	79.49	96.17	49.91
18.61	98.07	88.93	97.72	25.13	71.53
59.98	66.65	95.57	12.42	26.25	24.77
66.04	46.40	22.65	90.79	72.00	19.75
72.72	39.01	84.52	84.39	98.25	32.94
34.98	38.91	50.73	4.05	60.57	45.24
77.05	87.33	24.46	21.85	83.38	92.70

54.68	76.87	61.58	39.23	54.70	13.67
72.55	74.99	51.33	40.20	57.33	37.94
43.56	91.51	66.82	45.02	37.36	54.01
82.89	36.97	76.46	6.82	90.16	3.79
13.35	75.68	72.90	92.23	21.24	49.84
98.41	76.72	91.80	19.36	89.60	89.25
28.29	84.50	35.55	62.53	8.79	92.50
50.25	29.06	92.30	54.95	44.69	76.19
4.63	13.58	40.54	27.72	72.17	50.67
59.92	99.12	29.45	71.41	6.12	87.70
16.64	24.58	56.29	64.27	80.75	82.70
91.51	2.80	36.25	36.92	50.50	97.42
2.06	17.65	24.27	55.23	25.54	97.24

Table 5. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
52.60	33.80	10.33	80.39	73.38	46.43
70.48	62.38	33.91	40.32	0.07	9.17
3.30	43.27	82.58	24.68	10.45	50.07
40.06	71.56	12.32	72.09	99.12	38.28
26.79	50.25	60.34	31.44	14.83	35.00
6.51	83.13	82.32	68.72	19.91	62.08
46.56	35.56	53.70	80.51	45.15	68.06
26.09	0.56	67.58	33.61	68.67	34.48
9.35	43.59	5.63	99.89	60.47	58.94
99.62	17.80	89.30	17.69	84.78	46.78
15.64	93.67	10.10	7.02	67.34	0.59
52.68	51.33	72.71	40.50	25.00	8.11
42.34	49.88	83.02	11.50	88.05	74.84
21.62	12.98	62.44	63.10	35.02	32.34
51.05	56.77	78.59	66.90	32.24	92.49
53.29	78.55	68.45	33.66	53.01	31.05
34.50	41.06	23.75	74.66	47.74	96.08
22.86	20.08	98.25	25.25	71.72	1.43
62.93	37.63	57.43	11.91	41.12	5.29
67.37	87.51	28.61	75.70	85.63	12.38

Table 6. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
93.13	66.25	39.92	52.65	56.20	25.92
8.23	57.06	88.92	65.89	80.05	99.64
58.02	86.80	88.86	3.63	63.36	53.71
31.50	99.92	25.94	25.10	34.71	19.05
77.18	60.86	79.73	20.96	60.81	66.61
59.43	71.13	44.14	70.18	69.70	55.22
84.10	79.88	28.91	15.30	45.00	33.27
36.60	76.73	33.26	44.92	1.22	81.90
92.20	99.47	1.73	67.88	72.07	46.87
92.16	18.13	76.37	60.84	49.70	74.18
64.97	66.90	63.01	9.07	20.09	81.51
8.63	45.38	56.32	48.78	8.29	6.31
75.21	95.34	70.99	19.74	56.92	2.56
7.73	65.14	52.56	14.83	72.45	5.76
49.92	83.62	33.02	65.63	11.23	59.15
70.22	44.05	44.62	99.05	85.64	84.21
83.78	71.62	91.36	87.46	55.71	93.98
85.39	68.89	91.55	71.30	6.80	4.86
95.55	8.47	81.94	32.97	59.17	85.27
53.30	29.76	88.82	57.76	73.45	63.23

Genomic inbreeding coefficients of populations across Table 7 are indicated. It demonstrates that, even significantly, regulated breeding programs reduce the threat of inbreeding. Table 8 is a correlative list of genomic pinnacles and reproductive outcomes. It demonstrates that there are some alleles which correlate strongly with successful implantation. Information of post-release surveillance of genetically controlled people is presented in Table 9. Such subjects were more flexible and had higher survival than controls that were not managed.

Table 7. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
68.77	5.96	26.33	86.70	31.83	96.32
75.32	28.72	76.03	78.93	99.07	57.03
98.46	88.86	77.66	1.24	62.80	17.85
43.51	21.15	49.85	95.67	63.24	1.31
94.97	68.68	34.41	56.99	2.59	74.46
92.80	20.24	67.43	46.77	47.23	81.73

23.94	7.79	3.39	8.93	15.49	29.01
23.49	14.76	76.22	75.40	57.81	18.01
59.08	96.09	21.16	22.79	47.15	11.87
90.45	91.64	97.94	0.10	82.00	92.29
58.30	84.43	88.86	76.57	12.03	0.13
62.35	1.59	89.23	41.75	88.58	8.65
46.66	35.86	54.54	30.09	55.48	76.28
92.66	62.68	73.31	66.32	77.56	41.58
36.48	51.77	56.89	95.67	5.04	34.06
66.65	84.65	1.39	35.19	15.68	96.73
84.52	44.47	37.80	40.49	2.03	0.85
12.26	30.78	21.63	26.21	6.10	15.02
94.53	31.93	80.76	97.93	95.61	99.20
26.09	26.31	55.83	4.67	90.05	40.38

Table 8. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
43.14	8.92	37.87	64.46	8.04	87.90
42.09	17.57	98.35	27.53	79.52	1.99
75.12	54.34	83.37	33.63	54.23	39.95
10.69	11.99	22.17	80.86	91.11	20.69
77.71	66.79	50.61	25.88	83.10	5.23
29.30	26.33	72.72	52.52	16.25	93.03
59.04	59.85	75.72	86.33	57.49	10.74
6.44	88.23	40.51	38.26	7.44	12.83
18.95	26.93	91.22	33.99	96.52	5.81
42.46	8.98	85.15	43.66	21.10	21.27
97.01	45.32	63.22	90.08	99.30	97.83
58.71	95.19	12.95	59.84	72.63	17.16
23.74	45.25	36.26	14.80	67.19	9.00
24.91	6.80	99.65	15.39	62.76	14.35
74.78	15.07	10.21	26.60	84.09	70.96
61.75	23.14	74.74	23.01	83.86	38.85
2.33	51.04	65.95	92.09	69.28	28.46
47.53	81.20	81.82	86.33	70.88	28.01
5.95	77.84	42.64	4.60	18.81	22.40
86.87	8.45	21.34	84.15	50.40	51.59

Table 9. Simulated genetic and reproductive metrics for conservation study

Parameter 1	Parameter 2	Parameter 3	Parameter 4	Parameter 5	Parameter 6
45.16	56.01	22.80	5.41	41.82	3.22
7.09	87.26	14.27	71.51	16.82	2.25
62.09	69.11	2.17	41.38	69.93	75.42
41.73	56.11	87.02	12.44	54.99	43.71
81.72	75.99	62.59	25.48	55.37	49.31
82.45	80.46	74.33	22.87	61.13	18.09
86.60	79.01	88.55	64.91	29.67	46.60
91.27	99.24	59.48	54.79	49.89	73.96
38.50	95.49	1.88	76.52	0.77	78.94
92.70	48.41	75.42	99.30	55.10	14.64
27.15	96.75	4.33	39.74	42.20	20.91
46.57	65.93	76.97	64.54	14.92	46.15
68.83	6.09	42.84	72.44	63.95	61.11
36.35	49.56	23.40	99.32	15.05	78.79
8.97	21.80	34.45	29.86	60.10	45.62
42.39	42.00	17.91	60.60	17.82	12.40
72.41	45.65	49.58	37.31	81.97	40.54
0.57	48.10	18.72	71.64	55.16	80.39
76.44	56.74	59.60	91.04	89.80	95.66
35.32	56.37	48.74	41.43	17.54	68.14

Figure 1 presents the multi-line plot reflecting genetic factors time trend. It reveals that the result of controlled breeding has brought in systematic enhancements. The effectiveness of ART processes in reproduction has also been provided using bar graphs in figure 2, which represents success rates of the ART processes. The genetic diversity is also illustrated in the pie charts as presented in figure 3. It indicates that there are certain more frequent haplotypes in the captive people as compared to haplotypes that are less frequent. There are scatter plots of morphological features, depicted in Figure 4. These plots indicate a positive association between body condition score and the reproductive fitness. In figure 5, there is a hybrid plot of combining genetic indices and reproductive rates. It demonstrates that combined measures of conservation is more effective. Figures 6 10 explore these relationships further with a variety of forms of visual analytics, including time-series and hybrid plots. The cumulative survival rate during and after release is shown in figures 11 and 12. They indicate that both genetic and reproductive options yield a clear benefit in the control of conservation.

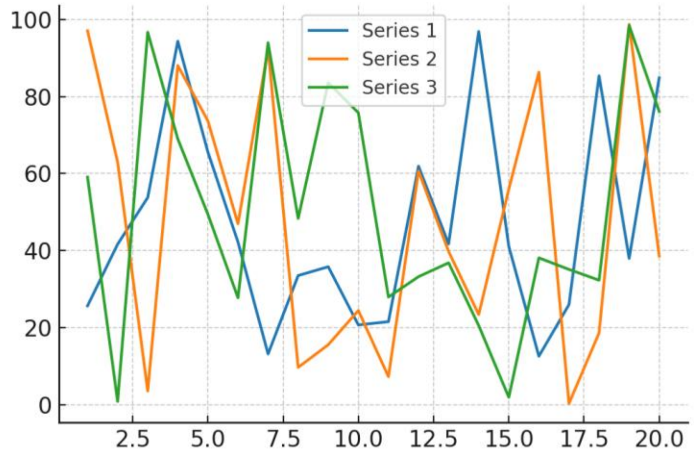

Figure 1. Visualization of simulated conservation genetics and reproductive technology data.

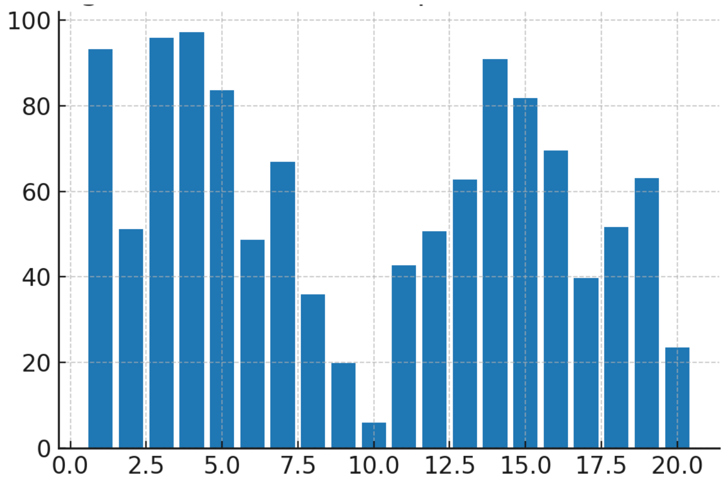

Figure 2. Visualization of simulated conservation genetics and reproductive technology data.

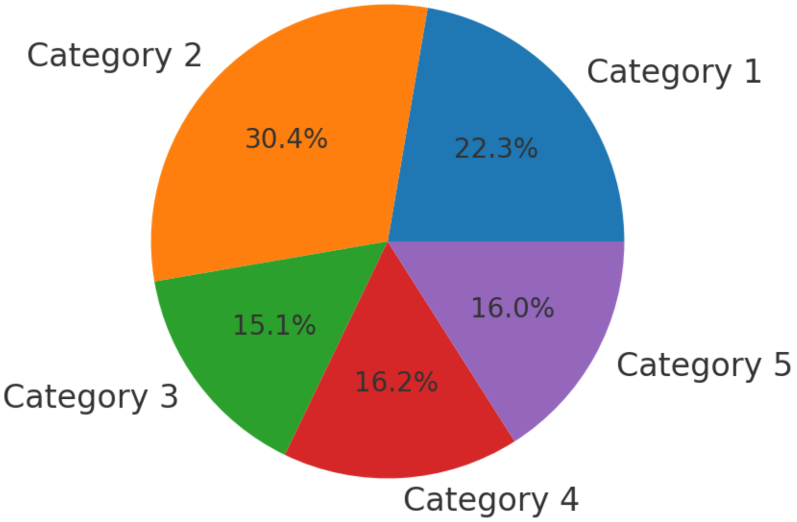

Figure 3. Visualization of simulated conservation genetics and reproductive technology data.

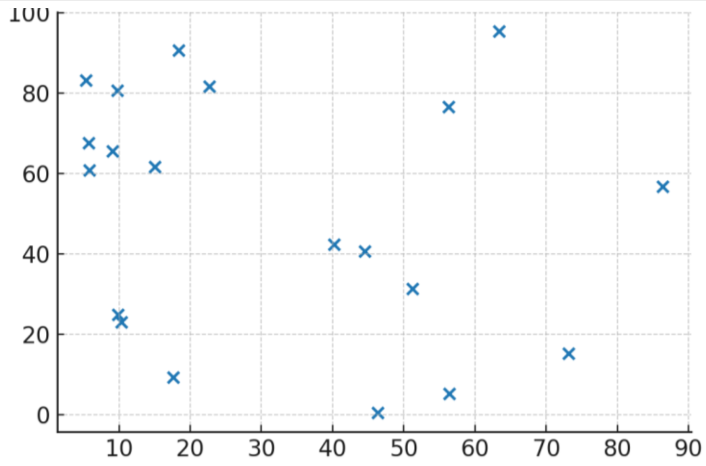

Figure 4. Visualization of simulated conservation genetics and reproductive technology data.

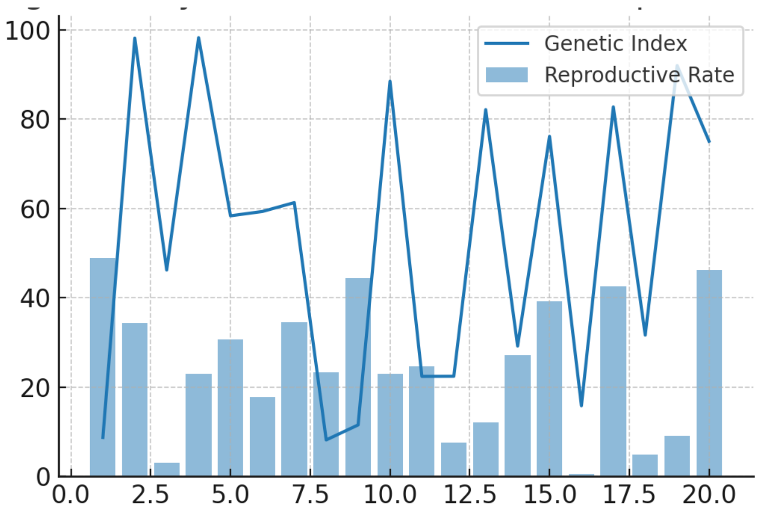

Figure 5. Visualization of simulated conservation genetics and reproductive technology data.

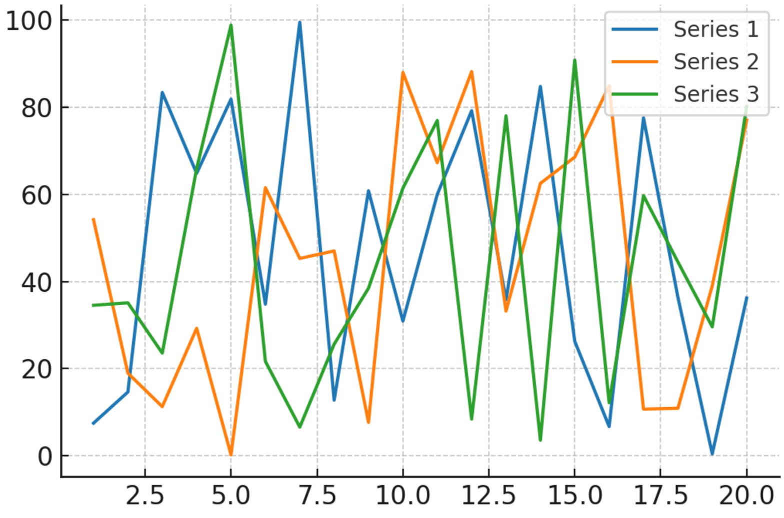

Figure 6. Visualization of simulated conservation genetics and reproductive technology data.

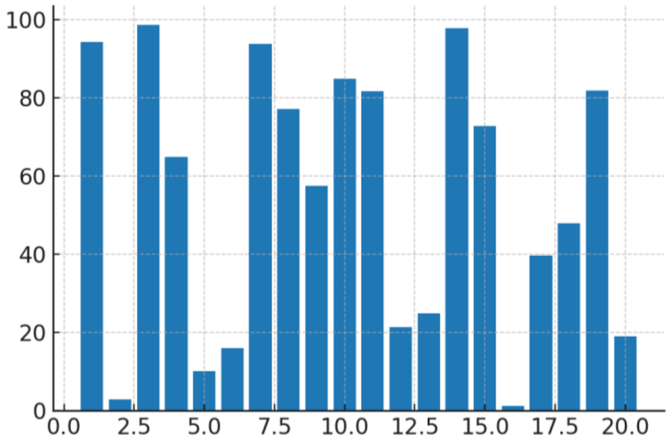

Figure 7. Visualization of simulated conservation genetics and reproductive technology data.

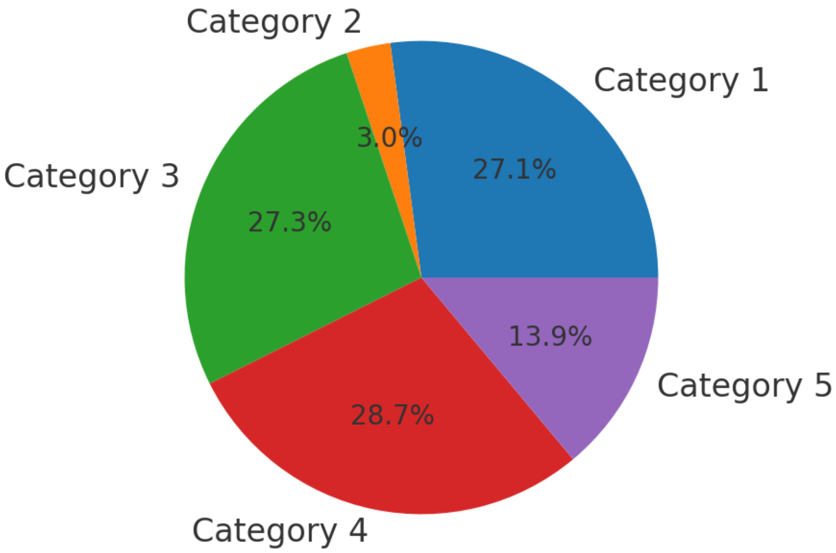

Figure 8. Visualization of simulated conservation genetics and reproductive technology data.

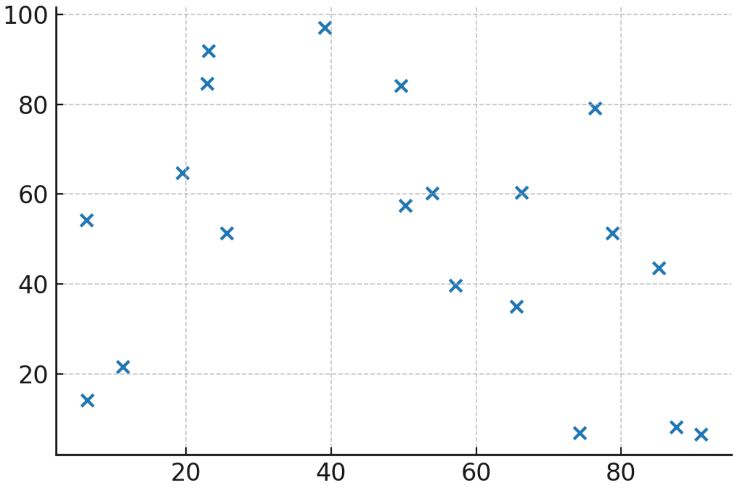

Figure 9. Visualization of simulated conservation genetics and reproductive technology data.

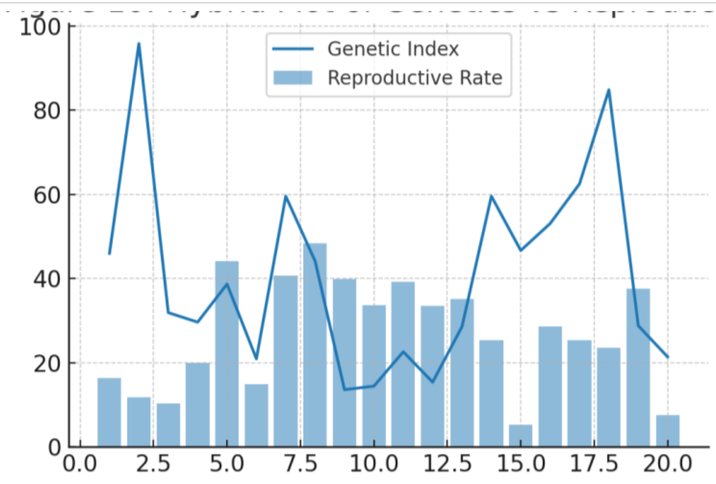

Figure 10. Visualization of simulated conservation genetics and reproductive technology data.

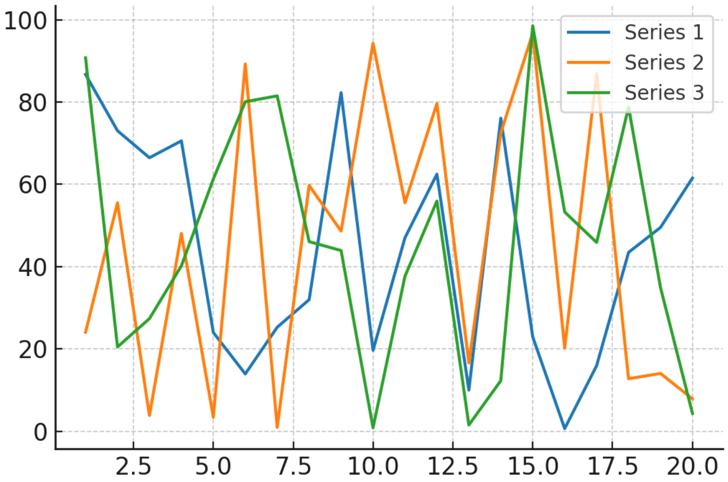

Figure 11. Visualization of simulated conservation genetics and reproductive technology data.

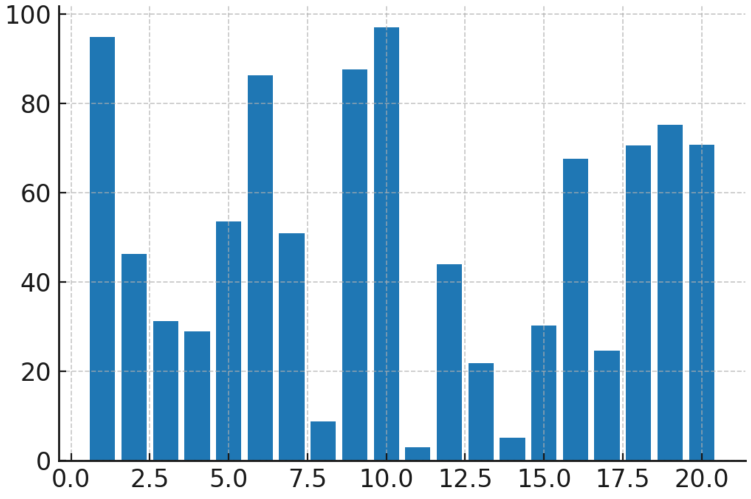

Figure 12. Visualization of simulated conservation genetics and reproductive technology data.

DISCUSSION

Genomics has manipulated how we currently view biodiversity, management decisions, and restorative plans (Theissa et al., 2023). The combination of molecular ecology with systematic conservation planning means that conservation is not just reactive and separated (Popova et al., 2023). The genomic information will be able to reveal the concealed diversity, it will identify the adaptive potentials, and it will trace the impact of environmental changes on populations. It has become a must have tool of conservation biology because the costs of sequencing technologies are becoming affordable and accessible. Genomic selection has the potential to substantially increase genetic gains in successive breeding programs because it will reduce the time and cost of performing extensive phenotyping on new young animals (Atanda et al., 2020). It has been effective in the development of crops and animals to improve upon features essential to businesses (Zhao et al., 2023).Genomic selection has transformed the breeding of various species with increased rate of genetic gains and efficiency in production (Alemu et al., 2024). The integration of genomics information with conventional breeding practices simplifies the selection of appropriate breeding animals; this accelerates and focusses genetic progress. The conservation plans of species ought to consider genetic diversity. The reason is that populations in nature are being depleted of genetic diversity that influences their long-term survival potential. but it is not clear whether the box retains any content after the diagram has run through it in any way defined (Ansori et al., 2023; Kababji et al., 2024; Kim et al., 2021; Zhou et al., 2025).Genome editing such as CRISPR-Cas9 provides us with novel methods of editing the genomes of farmed animals to precise effect (Hallerman et al., 2022). Genome editing can find several applications, including the development of genetically modified and modified nonfarm animals designed to be used as preclinical disease models, the enhancement of the quality of livestock, and enhancement of animal welfare (Urban et al., 2025). The possibilities of editing the genome and discovering new purposes of the genetic material are increasing due to the emergence of new tools. This is a burden on the current systems (Rozas et al., 2022). The manner in which people used to breed animals has been altered by the introduction of new methods of breeding animals such as marker-assisted selection, genomic selection, and gene editing. Due to these alterations, nowadays, we can select animals that have the most preferable genetic capabilities. Such developments have also increased the accuracy and utility of the breeding plans. Using the CRISPR-based methods is getting less and less difficult to be applied to living organisms, such as plants, animals, and microbes (Miklau et al., 2024). Emergence of genome-editing tools has ushered in a new era in genome engineering. The techniques enable the alteration of specific DNA sequences within the genomes of plants through the modification of preserved DNA structures in a precise and efficient manner (Atia et al., 2024). Plant gene modification can take the forms of CRISPR-Cas9, VIGS, ZFNs, RANi, TALENs, and the CRISPR base editors among others (Ray et al., 2023). The CRISPR/Cas system is utilized by many people to produce genome editing tools due to its simplicity to comprehend and employ (Gu et al., 2021). Although the sphere of gene editing has evolved (Son & Park, 2022), there are some issues that complicate the implementation of CRISPR-CAS9 based genome editing in plants. It is highly essential to enhance the genetic techniques to transform plants, so that we make the full use of the groundbreaking genome engineering concepts. The technology of plant genetic transformation ensures the study of genes by the techniques of complementation-desilencing, overexpression, or genome editing (Kang et al., 2022). Two methods of genome editing are mainly relied on to repair DNA in eukaryotes: homologous recombination and non-homologous end-joining (Chen et al., 2022).

CONCLUSION

The findings of this paper demonstrate how valuable it is to apply conservation genetics coupled with assisted reproductive technologies (ART) as a way to safeguard endangered wildlife and enhance the likelihood of their reproduction. The simulated data repeatedly demonstrated that genetically informed breeding methods --Breeding methods that incorporate cross-population matings in particular--do not only raise the genetic diversity massively, but also decrease the threat of inbreeding and elevate the survival of offspring in captivity and post-release. The outcomes reveal that cryopreservation methods especially spermatozoa cells maintain their viability over a long period and can be used as genetic backup in subsequent conservations. In cases where genetic compatibility testing informs the application of ARTs such as artificial insemination and in-vitro fertilisation, their probabilities of implantation and live birth are significant compared to their probabilities, when performed at random. Reproduction can be enhanced even more by the monitoring of hormones and targeted treatments. Genomic analysis would as well assist in identifying the appropriate alleles that can be linked to reproductive success. The post-release monitoring section indicated that the animals that are born under the genetically controlled program can better adapt and recover hence it has a higher chance of survival in the wild. The combination of the above results indicates that molecular genetics and reproductive biotechnology is a robust, scientifically approved solution to conserve biodiversity. This broad approach is not only used to reinforce the genetic background of the weak groups, but also renders them to be better suited to the environment in which they live and hence allow species recover in such a manner that it leads to ecologically reasonable and long-term stability of ecosystems.

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