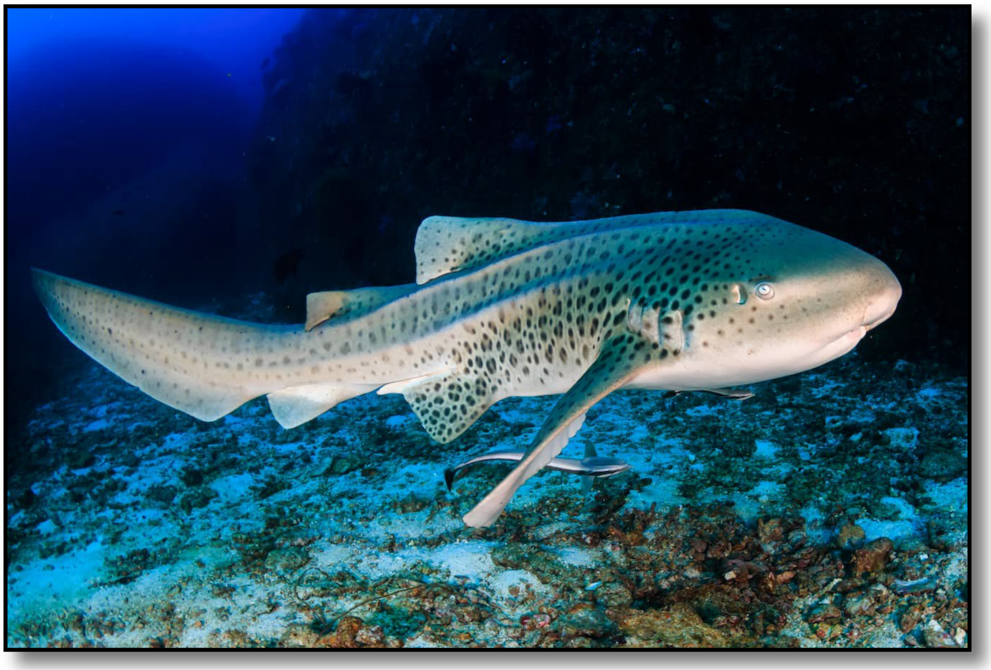
# Population Viability Analysis (PVA) of the Indo-Pacific Leopard Shark (*Stegostoma tigrinum*) in Thailand (Andaman Sea) and Indonesia (Raja Ampat)

## An Addendum to Previous Analyses



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Cover photo: Seattle Aquarium

A contribution of the IUCN/SSC Conservation Planning Specialist Group, in collaboration with the StAR Project.

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## Executive Summary

This report describes the structure of and results from an expanded population viability analysis (PVA) on the Indo-Pacific leopard shark (*Stegostoma tigrinum*). The current work is based on the analysis of Traylor-Holzer (2021) that evaluated potential strategies for augmentation of the leopard shark population in the Raja Ampat Archipelago, Indonesia, as part of the *Stegostoma tirgrinum* Augmentation and Recovery (StAR) Project. Following the successful launch of the StAR Project Indonesia in 2020, the StAR Project Thailand was initiated in 2024. This second project aims to restore the western subpopulation of *S. tigrinum* to waters around Phuket, Thailand in the Andaman Sea. The PVA presented here is designed to provide evidence-based guidance on the translocation efforts that are expected to result in successful outcomes for leopard shark population viability in this portion of the species' range.

In addition, this analysis gives StAR Project Indonesia researchers and managers an opportunity to update the 2021 PVA with new animal tracking data on important release scenario parameters. In particular, given new and more accurate estimates of egg hatch rates and the survival of new hatchlings to the age of release (approximately six months), this extended analysis explores the sensitivity of simulation model outcomes to uncertainty in the survival of pups from the time of release to one year of age. Estimating this survival rate in the wild is a challenging prospect; assessing the importance of this early phase in determining overall success of releases is a necessary first step in allocating resources to accurately measure it in the wild.

The models comprising this analysis, constructed using the simulation modeling package Vortex, were unchanged from the 2021 analysis except for a few key parameters. For the StAR Thailand analysis component, the initial size of the population was adjusted to reflect recent mark-recapture data. In addition, two sets of scenarios were constructed that simulated conditions of comparatively high or low future population growth potential to account for general uncertainty in the true condition present in the wild. Revisions to the StAR Project Indonesia analysis component included new estimates of both hatch rate and hatchling survival to release in the ex situ environment. As estimates of post-release survival to one year of age are unavailable, the PVA featured a sensitivity analysis designed to assess the impact of uncertainty in this parameter on selected measures of simulation model performance.

The new augmentation analyses focused on Thailand suggest that releases of young leopard sharks to suitable habitats in the Andaman Sea can significantly improve average long-term growth of existing wild shark populations, increase the levels of genetic diversity retained in the wild, and promote the establishment and maintenance of a viable leopard shark population that can be buffered from the destabilizing forces that imperil the survival of smaller, more fragile populations. It is important to recognize that careful analysis of current data from the Andaman Sea habitat indicates an existing leopard shark population of somewhere between about 60 to 170 individuals. This abundance is substantially larger than the 2021 estimate for Indonesia's Raja Ampat Archipelago, centered on a likely range of just 15 – 30 individuals. As a result, the Andaman Sea population can be considered inherently more demographically and genetically stable than its Indonesia counterpart, assuming that the Thailand habitat can support conditions favorable for leopard shark population growth. Consequently, it may be feasible to reduce the intensity of a proposed release program in the interest of saving valuable resources to be used across the StAR Project Thailand program through time. However, a conservative approach argues in favor of a dedicated release program intensity that can more quickly stabilize the existing population and facilitate its growth to an abundance that fosters greater levels of demographic and genetic stability. Furthermore, it is worth noting that a shark population of less than 200 individuals can and should still be considered a small population that is susceptible to forces that increase extinction risk. A management program like the StAR Project provides an outstanding opportunity to use the collective expertise and resources and both in situ and ex situ communities in an integrated effort to save endangered species from local extirpation or extinction.

The successful StAR Project Indonesia release efforts in Raja Ampat provide an additional benefit in the form of expanded data collection and analysis as releases are conducted. These new data include estimates of hatch rate (90%) and survival to release (77%) that approach or even exceed the estimates used in the Optimistic scenario used in original analysis (Traylor-Holzer 2021). Incorporating these new estimates into the existing PVA model structure should give leopard shark managers an even greater sense of optimism that their management efforts are likely to pay big future dividends in the form of strong wild population responses to sustained releases. A key survival remains elusive: survival of released individuals to one year of age, approximately six months after their release. The analyses presented here indicate that wild leopard shark population growth is indeed sensitive to this survival parameter, with consistent increases in predicted population growth across the wide range of post-release survival rates tested in this analysis (0.1 to 0.9). The models suggest that post-release survival rates less than 0.3 result in more severe declines in expected population growth. Interestingly, this value was typically used as the minimum across a range of values used in the original Best Guess, Optimistic and Pessimistic release scenarios developed in 2021. It seems clear from the present analysis that additional efforts devoted to better estimating this key parameter would make a valuable contribution to future release program success. Recommending specific methods for improving post-release survival estimates is beyond the scope of this report, and is left to species experts to discuss and develop an efficient and effective long-term research plan.

Finally, it is important to emphasize that despite the additional detail and refined data characterizing this update to the original 2021 PVA, substantial uncertainty remains in our understanding of the true demographic and ecological character of leopard sharks in their wild habitats. Through recognizing this reality, inherent to all detailed demographic analyses of endangered species, we must acknowledge that the results of this updated analysis must be interpreted with caution. In particular, proper interpretation of PVA results should be done in a comparative context and not through adopting the precise numerical results of one or another specific scenario. That said, both the original and updated analyses incorporate the best available knowledge of leopard shark biology and the characteristics of leopard shark release program practice. Responsible use of these data result in robust simulation models that clearly demonstrate the value of concerted population augmentation efforts in suitable wild habitats. Through both responsible scientific analysis and the development of effective, evidence-based management programs for wild populations, the StAR Projects continue to serve as models for responsible integrated management of threatened shark populations worldwide.

## Introduction

This report describes the structure of and results from an expanded population viability analysis (PVA) on the Indo-Pacific leopard shark (*Stegostoma tigrinum*). The current work is based on the analysis of Traylor-Holzer (2021) that evaluated potential strategies for augmentation of the leopard shark population in the Raja Ampat Archipelago, Indonesia, as part of the *Stegostoma tirgrinum* Augmentation and Recovery (StAR) Project. This very successful project is conducted under the guidance of ReShark, a consortium of aquariums, governments, NGOs, academics and local communities dedicated to linking in situ and ex situ shark and ray conservation efforts in the spirit of the One Plan Approach (Byers et al. 2013).

Following the successful launch of the StAR Project Indonesia in 2020, which led to leopard shark translocation efforts into Raja Ampat, the StAR Project Thailand was initiated in 2024. This second project aims to restore the western subpopulation of *S. tigrinum*, as defined through molecular genetic analysis (Dudgeon et al. 2009), to waters around Phuket, Thailand in the Andaman Sea. The PVA presented here is designed to provide evidence-based guidance on the translocation efforts that are expected to result in successful outcomes for leopard shark population viability in this portion of the species' range.

In addition, this analysis gives StAR Project Indonesia researchers and managers an opportunity to update the 2021 PVA with new animal tracking data on important release scenario parameters. In particular, given new and more accurate estimates of egg hatch rates and the survival of new hatchlings to the age of release (approximately six months), this extended analysis explores the sensitivity of simulation model outcomes to uncertainty in the survival of pups from the time of release to one year of age. Estimating this survival rate in the wild is a challenging prospect; assessing the importance of this early phase in determining overall success of releases is a necessary first step in allocating resources to accurately measure it in the wild.

## Summary of Revised Model Input

In this and all subsequent sections, information will be presented in distinct subsections specific to the StAR Project Thailand (Andaman Sea) and StAR Project Indonesia (Raja Ampat) analyses.

All analyses described in this report use the simulation models described in detail in Traylor-Holzer (2021). Except where noted below, all simulation model input parameters for the current analysis are unchanged from their original values. Additionally, the updated analyses use the Vortex PVA software package which is now updated to Version 10.9.0.0 (July 2025). All scenarios are projected for 50 years into the future to align with the results displayed graphically in Traylor-Holzer (2021), with 1000 iterations completed for each unique model scenario.

### StAR Project Thailand

#### Habitat designation, initial population abundance and habitat carrying capacity

The target area for leopard shark releases in Thailand's Andaman Sea is shown in Figure 1. This area, including both the Similan Archipelago and the Phang Nga Bay habitats, features connected continental shelf topography. The range of water depths in this area is within the definitions of suitable habitat for the Indo-Pacific leopard shark, with coral reefs, mangroves and sandy bottoms providing connectivity.

Mark-recapture data over the time period 2019-2025, collected by WildAid researchers in consultation with C. Dudgeon, were used to derive a plausible range of contemporary population abundance estimates in the target habitat area. Abundance estimates were calculated using the Lincoln – Petersen method which uses the following formula:

$$\widehat{N} = \frac{MC}{R},$$

where $\widehat{N}$ is the estimate of total population abundance, $M$ is the number of individuals initially marked in the first visit of the sampling effort, $C$ is the number of animals captured in the second visit of the sampling effort, and $R$ is the number of recaptured animals in the second visit that were marked.

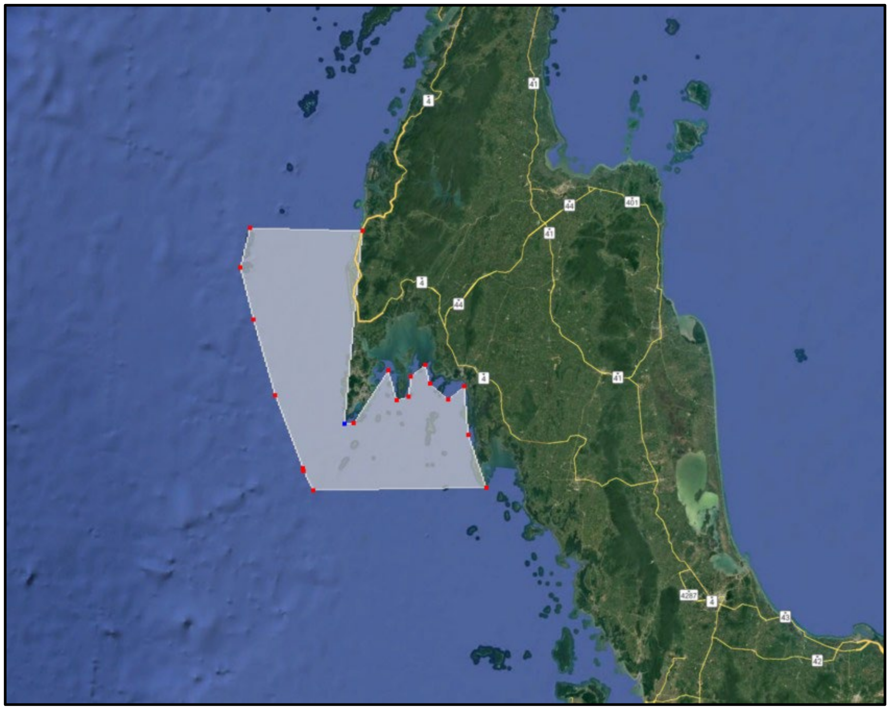

**Figure 1**. Map of the Andaman Sea coastal area of west-central Thailand, with the StAR Project Thailand release site outlined by the light-colored polygon. Map courtesy of M. Chuangcharoendee.

Using this technique, researchers estimate the total population abundance for Indo-Pacific leopard sharks in the target area as 57 – 172 individuals (all age classes included), with a mean of 115 individuals. The current PVA uses this uncertainty by repeating a given set of augmentation scenarios with a specific value of initial population size: 57, 115 or 172 individuals. This approach is different from that used in the Raja Ampat augmentation scenarios of Traylor-Holzer (2021), in which uncertainty in initial abundance was described explicitly as a statistical distribution in the initial population size input for Vortex. That method confounds parametric uncertainty in one parameter (initial abundance) with environmentally driven annual variability in other parameters like survival or reproductive success. As a result, interpreting the range of outcomes for any one scenario (augmentation protocol) and the relative contribution of measurement uncertainty vs. natural demographic variability to that range can be challenging. The decision was made for this updated analysis to explicitly decouple the uncertainty in population abundance by running all augmentation scenarios with a single initial population abundance representing the minimum, maximum or mean across the known range.

The starting population abundance for all simulations was initialized by assuming a stable age distribution calculated from the mean rates of survival and reproduction brought over from the original 2021 analysis. This is also a departure from the original analyses for Raja Ampat, where the starting distribution of age-sex classes was modified to be consistent with the observation of no reproduction occurring in that very small population of less than 20 individuals across an area roughly similar in size to the Thailand target area. As there have been recent observations of leopard shark eggs and juveniles in the Andaman Sea habitat (M. Erdmann, pers. comm.), the decision was made to initialize the starting simulated population across the full age spectrum, i.e., a stable age distribution.

The Andaman Sea target area for leopard shark releases is approximately 12,000 km$^2$ (1.2 million Ha) – roughly the same size as the StAR Project release site in Indonesia's Raja Ampat Archipelago. Consequently, the current models use a similar value for habitat carrying capacity of 1,000 individuals (all age classes), which is approximately 6 – 17 times the size of the initial simulated population of 57 – 172 individuals.

Estimated population growth rates

The original PVA of Traylor-Holzer (2021) uses mean annual rates of reproduction and survival that are consistent with an expected rate of annual population growth of approximately 5% (deterministic multiplicative growth rate $\lambda \approx 1.05$) and a mean generation length of approximately 12 years. This growth rate may be taken as a reasonable estimate under more favorable conditions in which the maximum rate of population increase may be realized more easily. Alternatively, it may be instructive to explore the viability of leopard shark populations living in an environment that may not favor such optimistic rates of population increase. Various threats to population growth, including direct human activities affecting individual sharks or more generalized stresses resulting from reduced habitat quality or global climate changes, may result in more modest rates of population increase.

The current PVA explores two alternative population growth scenarios: a relatively more favorable High Growth scenario (deterministic $\lambda \approx 1.04$) as well as a relatively less favorable Low Growth scenario (deterministic $\lambda \approx 1.02$). Because these expected growth rates are deterministic and not influenced by initial population abundance as a stochastic source of population instability (i.e., smaller populations typically demonstrate intrinsically lower annual growth rates: Gilpin and Soulé 1986), the actual growth rates emerging from the stochastic Vortex population simulation will be lower than the deterministic rates. This approach was used in the recent population viability analysis for the bowmouth guitarfish where future population growth characteristics are highly uncertain (Miller 2025).

To achieve these alternative population growth scenarios, only small changes to age-specific mortality rates were necessary in Vortex. The details are given in Table 1.

**Table 1**. Mean age-specific mortality rates for Indo-Pacific leopard sharks in alternative population growth scenarios used in the StAR-Project Thailand PVA.

| Age Class | High Growth | Low Growth |
|---|---|---|
| Pup (Age-0 – Age-1) | 60.0 | 65.0 |
| Subadult (Age-1 – Age-7) | 20.0 | 21.0 |
| Adult (Age-7+) | 11.0 | 12.0 |

Population immigration mechanism

The original PVA of Traylor-Holzer (2021) included a process in which individuals occasionally immigrated into the Raja Ampat population from outside the release area, and individuals emigrated from that population at an equivalent rate. The immigration rate in this updated PVA was revised slightly to more accurately simulate the desired effect. Instead of Age-7 males and females being introduced into the Andaman Sea population in a regular alternating pattern (e.g., male in year x, female in year x+5) as in the original Raja Ampat simulations, in the Andaman Sea simulation the sex of the immigrating individual is chosen at random every five years. Over multiple model iterations, the net effect is roughly equivalent to the alternating pattern of immigration originally intended in the simulations described in Traylor-Holzer (2021), but now resulting in a more realistic process in which one or the other sex may be more frequently represented in the immigrant pool in any single model projection.

Generic catastrophe frequency

The generic catastrophe included in the original analysis of Traylor-Holzer (2021) featured a frequency of 1%, consistent with the expected frequency of a generic catastrophe as described by Reed et al. (2003) equivalent to approximately 0.14 per generation for a given species (here, 12.55 years for the Indo-Pacific leopard shark). Instead of the simple expression for estimating the annual probability of a generic catastrophe – Prob(catastrophe) = 14/12.55 = 0.011, rounded to 0.01 – as used in Traylor-Holzer (2021), a more precise calculation of annual catastrophe probability was derived according to the following expression:

$$\text{Prob(catastrophe)} = 1 - (0.86^{(1/12.55)}) = 0.012\ ,$$

where 0.86 is the probability of no catastrophe occurring across one leopard shark generation. This revised calculation results in only a small change in the probability of a generic catastrophe in the simulated Andaman Sea population but represents a more defensible estimate of that probability across the duration of the simulation.

Release scenarios

No modifications were made to the three categories of release scenarios developed by Traylor-Holzer (2021). The parameters for Best Guess, Optimistic and Pessimistic release scenarios, defined by the number of eggs shipped per year, the hatch rate, the survival of hatchlings to release at approximately six months, and the post-release survival to one year of age were directly carried over from the Raja Ampat analysis. Finally, these new scenarios (including those for the StAR Project Indonesia scenarios described below) use the allele frequency data from the leopard shark regional studbook managed by the Associated of Zoos and Aquariums (AZA) as implemented in the original PVA (i.e, data compiled through March 2021). These data were consistent with the assumption of an equal probability of breeding among the 22 living potential breeders representing 20 genetic founders. The results presented in Traylor-Holzer (2021) showed little to no difference in model outcome when using alternative hypotheses about predicted founder representation in the wild population. Consequently, a single allele frequency dataset was used in this new analysis for the sake of greater simplicity in model implementation and interpretation.

## StAR Project Indonesia

Release scenario parameters

The primary modifications made to the updated Raja Ampat simulation models target the survival parameters for individuals released to the wild. While there was some uncertainty around these parameter estimates at the time of the original analyses, new tracking data collected during the recent release efforts allows for revised estimates of selected parameters. Specifically, the hatch rate and the survival rate from hatch to release have each been revised to 90% and 77%, respectively. These parameter values are in place at the beginning of the prospective simulations and remain in effect through the full duration of the simulated release program that runs from four to sixteen years in alternative scenarios. The number of eggs available for shipping across the releases program is set at the value defined in the original Best Guess scenarios of Traylor-Holzer (2021), i.e., 10 eggs at the beginning of the program and increasing linearly to 80 eggs by the end of the release program.

In contrast, the estimate of survival from the time an individual is released to reaching one year of age remains uncertain. Therefore, the current updated analysis for Raja Ampat features a set of simulations that evaluates the relative sensitivity of model output to a wide range of post-release survival values. While all other input parameters were held constant, post-release survival to one year of age was tested between 10% and 90% in increments of 10% for each of the release duration values tested in Traylor-Holzer (2021), i.e., four years to sixteen years. Mean stochastic population growth rate was chosen as the model output parameter for evaluation in this sensitivity analysis.

Population immigration mechanism
Generic catastrophe frequency
These two input parameters were modified as per the methods described for the Thailand scenarios discussed above.

## Results of Simulation Models

The following section uses three metrics to assess simulation model performance:

- Mean stochastic population growth rate – mean annual rate of population growth derived directly from the Vortex simulations. Rate is presented either as the multiplicative rate lambda, $\lambda_s$ or the instantaneous rate of change $r_s = \ln(\lambda_s)$. Increasing populations are those with $\lambda_s > 1.0$ ($r_s < 0.0$), while declining population are those with $\lambda_s < 1.0$ ($r_s < 0.0$).
- Mean extant population size, $N_{ext}$ – mean population size at the end of the 50-year simulation. This metric is calculated for a given scenario using only those simulation iterations that do not decline to extinction (N = 0 or only one sex remaining). In this way, the population size is reported only for those "successful" iterations. A full picture of the performance of any given scenario is possible only when reporting both the mean extant population size as well as the probability of population extinction P(Ext.). When extinction risk is zero, the full complement of simulation iterations are used to calculate mean population size.
- Mean population gene diversity – mean level of gene diversity (expected heterozygosity) retained in the population at the end of the 50-year simulation. The initial value of gene diversity at the beginning of the simulation is a function of the initial population size, with larger populations starting with a higher gene diversity value that represents a larger proportion of the full complement of population-level gene diversity captured in that simulated population subset.

Detailed numerical results of all model scenarios developed in this PVA are given in Appendix II.

### StAR Project Thailand

Population performance under alternative release scenarios
In the absence of leopard shark releases, the simulated Andaman Sea leopard shark population is predicted to increase in abundance under conditions of high or low expected population growth (Figure 2, No Releases scenario). The probability of population extinction under these conditions is less than 0.02 after 50 years, indicating comparatively strong resilience over time. Under conditions of high expected long-term population growth, the final mean population size is 631 individuals across all age classes (Age-1 and older), representing a simulated observed population growth rate of $\lambda_s = 1.035$. Note that this growth rate of lower than the expected rate of $\lambda = 1.044$, which is the result of stochastic forces leading to some population instability through time. Despite this instability, the population maintains the capacity for growth and is largely protected from risk of extinction. Under the assumption of low expected long-term population growth, the final population abundance is just 216 individuals, representing a simulated observed population growth rate of $\lambda_s = 1.013$. Similarly, this observed growth rate is less than the long-

term expectation of λ = 1.021, again the result of population instability from annual stochastic variation in demographic rates through time.

Gene diversity in the absence of releases follows a generally predictable pattern, with a consistent erosion of diversity through time in accordance with theoretical expectations (Figure 3, No Release scenario). Despite the observed erosion over time, the absolute value of gene diversity after 50 years exceeds $GD_{50} = 0.935$ under both High and Low growth rate scenarios, which is higher than the typical threshold of 0.90 associated with long-term population genetic resilience to both inbreeding depression and loss of population adaptive potential.

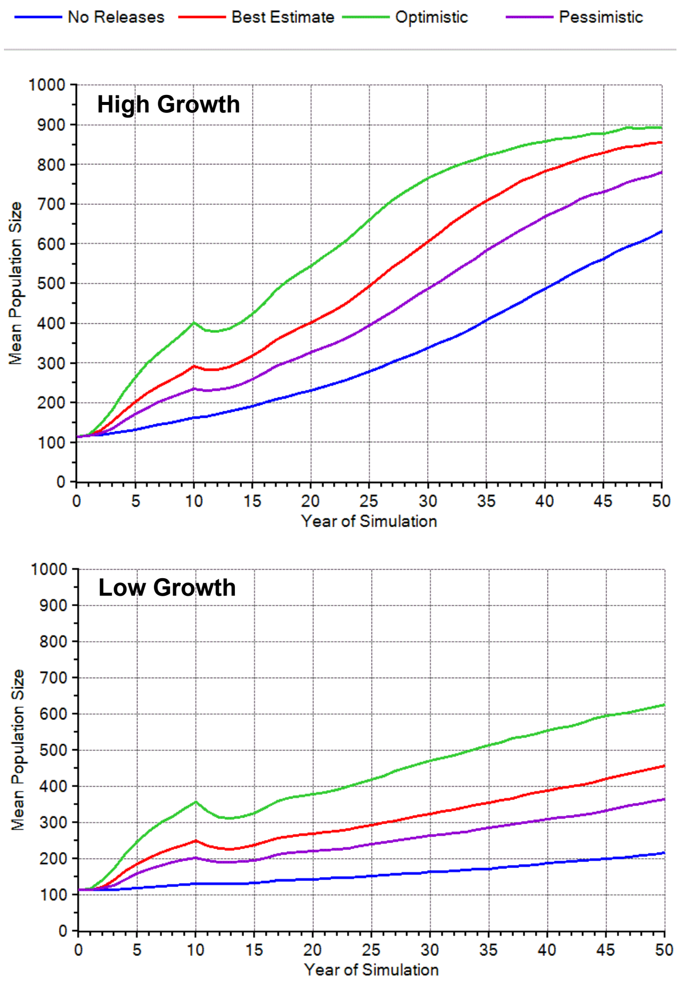

**Figure 2**. Projected mean size (extant iterations) of simulated Andaman Sea leopard shark populations, assuming an intermediate initial abundance of 115 individuals and under alternative 10-year release strategies. Top panel assumes a capacity for relatively high long-term expected population growth (λ = 1.044), while the bottom panel assumes relatively low expected population growth (λ = 1.021).

Simulated augmentation of the Andaman Sea leopard shark population through releases leads to a substantial increase in final population abundance (Figure 2) and gene diversity retention (Figure 3) across both scenarios of expected long-term population growth. Under an expected High growth scenario, final population abundance increases by 24% to 42% over the No Release scenario, depending on the underlying parameters defining the alternative release strategies (Pessimistic, Best Estimate, or Optimistic). When long-term expected population growth is lower, augmentation improves final population abundance by 69% to 189% across Pessimistic to Optimistic release strategies. In a similar fashion, final gene diversity retention is substantially enhanced across all release strategies and in particular under conditions of lower expected population growth. Note that while the gains in final population performance are proportionally greater in the Low growth scenario the absolute values of mean population size and gene diversity retained are higher in the High growth scenario compared to the Low growth scenario. This difference is a direct consequence of the larger mean population sizes realized in the High growth scenario, which leads to a corresponding increase in the rate of gene diversity retention.

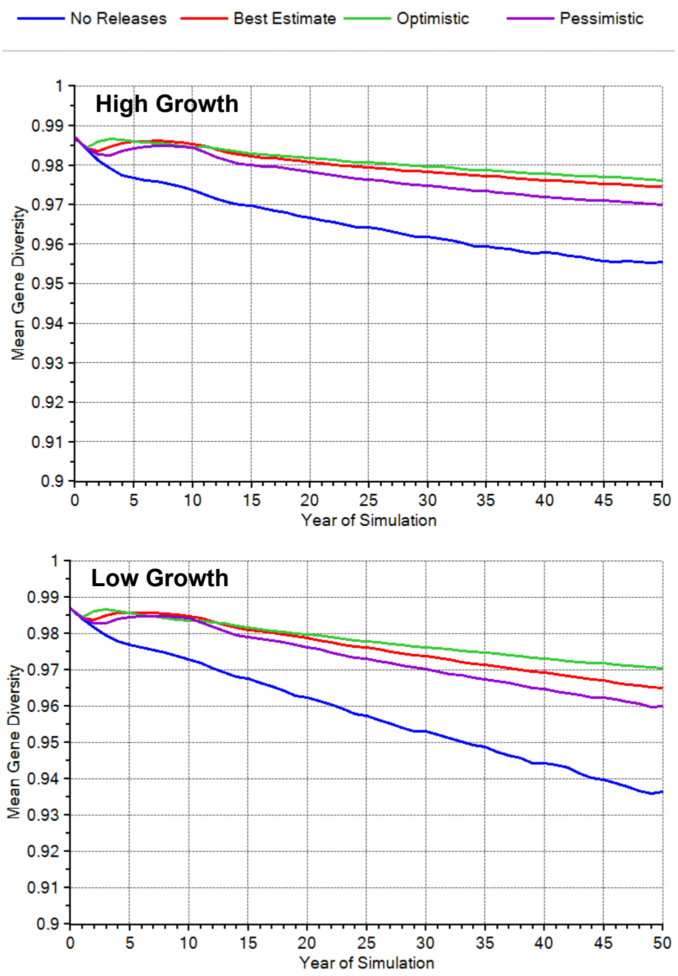

**Figure 3**. Projected gene diversity of simulated Andaman Sea leopard shark populations, assuming an intermediate initial abundance of 115 individuals and under alternative 10-year release strategies. Top panel assumes a capacity for relatively high long-term expected population growth (λ = 1.044), while the bottom panel assumes relatively low expected population growth (λ = 1.021).

<u>Population performance under alternative scenarios of release program duration</u>

As expected, increasing the duration of leopard shark releases to the Andaman Sea population leads to a correspondingly more rapid increase in population abundance and a larger final abundance after 50 years (Figure 4A). If releases (assuming a Best Estimate of release strategy parameters) are conducted over a four-year period, after 25 years the Andaman Sea leopard shark population is predicted to increase to a mean of 338 individuals compared to 278 individuals in a No Release scenario (22% increase). Under a ten-year release program, the population increases to 493 individuals at 25 years (77% increase) and a 16-year release program yields a population of 598 individuals at 25 years (115% increase). As shown most clearly in the Optimistic release scenario shown in Figure 2, the release programs lasting at least ten years result in a mean population abundance that begins to approach the assumed Andaman Sea habitat carrying capacity of approximately 1000 individuals, i.e., the population trajectory begins to reach an asymptote defined by the availability of suitable habitat.

Retention of population gene diversity is likewise improved when the release program duration is extended (Figure 4B). Even the shortest release program duration leads to a substantial improvement in the amount of gene diversity retained, with relatively smaller gains realized as the release program is extended. When evaluating both metrics of population performance, relatively little additional benefit is observed when the simulated release program is extended to 14 – 16 years. This is the direct result of setting the habitat carrying capacity *K* at the lower level of 1000 individuals, where population growth begins to attenuate as the simulated population approaches the hard reflective boundary defined in the Vortex model by *K*. If the carrying capacity were to be increased to 1500 – 2000 individuals, the simulated populations would be expected to continue increasing in size and showing great levels of separation in final abundance and gene diversity.

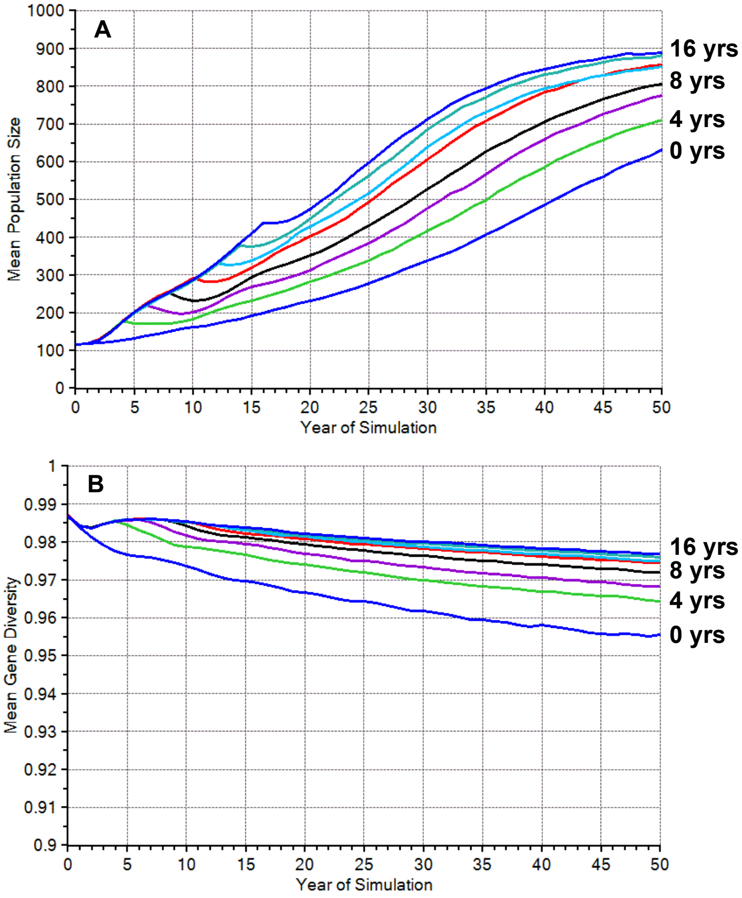

**Figure 4**. Projected extant population size (A) and gene diversity (B) of simulated Andaman Sea leopard shark populations, assuming an intermediate initial abundance of 115 individuals and under alternative scenarios of release duration. All scenarios assume a Best Estimate set of release strategy parameters, and a capacity for relatively high long-term expected population growth (λ = 1.044).

Summary of population performance across key PVA model parameters

Figure 5 presents a summary of simulation results (mean final population size) for a total of 48 scenarios defined by unique combinations of initial population size ($N_0$), expected long-term population growth rate (High or Low), and release program duration (zero to 16 years). [All scenarios use the Best Estimate dataset of release program characteristics.] It is clear from the figure that the final population abundance is negatively impacted by smaller initial population abundance, lower expected long-term population growth potential in the wild Andaman Sea habitat, and shorter release program duration. Across all scenarios examined here, the risk of population extinction over the 50 years of the simulation exceeded 0.005 only twice and was otherwise 0.000 – 0.003.

The results displayed in Figure 5 suggest that, on a comparative basis, the estimate of initial size of the leopard shark population in the Andaman Sea habitat has a considerable influence on the predicted final population size across the range of models analyzed here and, in particular, those scenarios with relatively short release duration. The assumption regarding the underlying population growth potential can also strongly influence model outcome, particularly when the size of the starting leopard shark population is small. Similarly, the duration of releases has the strongest relative impact when initial population size is small, and the impact is attenuated under the assumption of larger standing population abundance. Overall, the results indicate that the outcome of the simulations is governed by a substantial interaction between the initial size of the existing leopard shark population and the anticipated growth potential of that population, which is itself a function of the underlying age-specific reproductive and survival rates among wild individuals.

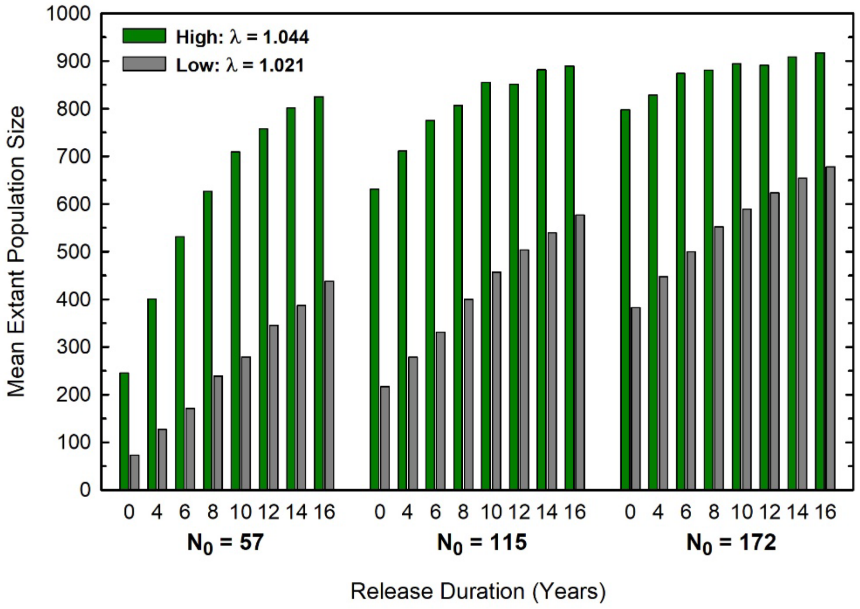

**Figure 5**. Projected extant population size of simulated Andaman Sea leopard shark populations across the full range of scenario conditions examined in this analysis. All scenarios use the Best Estimate dataset of release program characteristics.

Gene diversity outcomes show a narrower range of values; for ease of presentation, a subset of results is shown in Figure 6 that represent the ends of the range in scenario characteristics. As with the population size outcomes reported in Figure 5 above, gene diversity results are strongly influenced by an interaction between initial population size and expected wild population growth potential. In the absence of releases and assuming only a low level of expected population growth potential, a wild leopard shark population of just 57 individuals loses gene diversity at a rate that can maintain a minimum of 90% gene diversity retention in the population for no more than 35 years. Even minimal release efforts under these conditions can increase gene diversity retention to almost 92% over the timeframe of the simulation. When releases continue for 16 years in a population starting with 172 individuals under an expected potential for relatively high population growth, population gene diversity retention approaches 98% after 50 years.

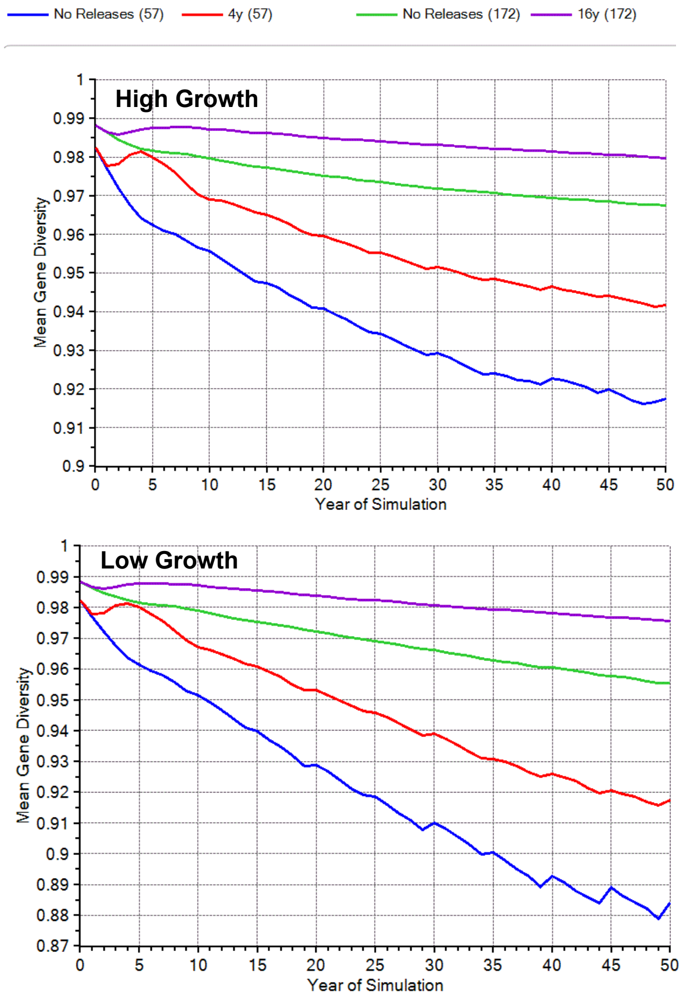

**Figure 6**. Projected gene diversity of simulated Andaman Sea leopard shark populations spanning the full range of model parameter values assessed in this analysis.

## StAR Project Indonesia

Population performance of revised models under alternative release scenarios

The revised models presented here, based on the models presented in Traylor-Holzer (2021) but featuring updated estimates of leopard shark release characteristics (hatching rate and survival to release), show population growth dynamics that are very similar to the original analysis (see Figures 11 and 12 in Traylor-Holzer (2021)). The updated trajectories are presented in Figure 7. It is worth noting that the final population abundance for the No Release scenario shown here in Figure 7A is slightly larger ($N_{50}$ = 90.8) than the abundance reported in the previous analysis ($\mathrm{N}_{50}$ = 70). This is because the present analysis presents the mean abundance of extant replicate populations, thereby removing from the calculations those iterations from the scenario that decline to extinction. The risk of Raja Ampat population extinction in the present analysis is estimated at 0.284 – substantially greater than that reported in the original analysis (0.080: Table 4 in Traylor-Holzer (2021)). The higher extinction risk reported here is likely the result of the small adjustments made to the current model as discussed in the preceding Model Input section. Additional examination of model details and resulting output would be required to fully investigate this discrepancy. The mean abundance across all scenario iterations in the present analysis, including those that become extinct is 65.3 which agrees statistically with the final abundance reported by Traylor-Holzer (2021).

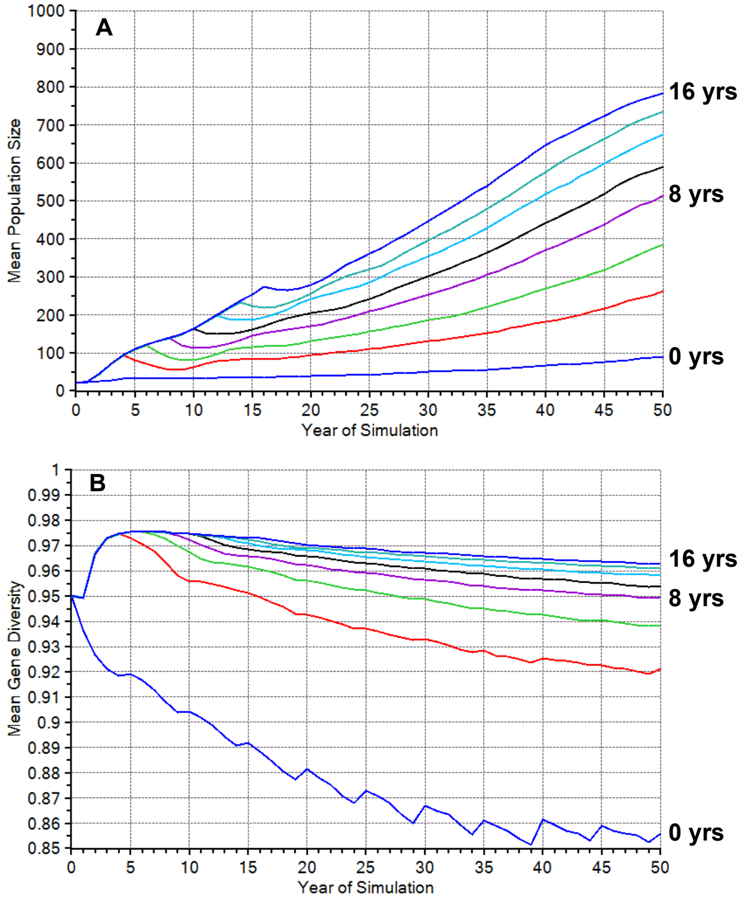

**Figure 7**. Projected extant population size (A) and gene diversity (B) of simulated Raja Ampat leopard shark populations under alternative scenarios of release duration. All scenarios feature the revised set of release strategy parameters as described in the accompanying text: egg production as per the Best Estimate scenario of Traylor-Holzer (2021); hatch rate of 90%; survival rate hatch to release of 77%; post-release survival rate of 50%.

As observed in the Thailand scenarios, the observed gain in gene diversity resulting from the release program is substantial, even when implementing releases over a short time period of four years (Figure 7B). As the program duration increases, the gains to gene diversity are relatively more modest owing to the finite set of new genes from the ex situ population that can be introduced into the wild population. Nevertheless, it is important to note that the final gene diversity in the simulated populations featuring releases is greater than the starting value, demonstrating the benefits of introducing new genetic variants into a small population that, by definition, represents a comparatively small sample of the total complement of genetic material present in the species across its current distribution.

As stated earlier, the results shown in Figure 7 are quite similar numerically to those presented in Figures 11 and 12 of Traylor-Holzer (2021). The original analysis featured a release mechanic in which the early years of a given release program included relatively low rates of egg production and survival, but with improvements to those rates across the arc of the program. The updated analysis here features single estimates of hatching rate and hatchling survival to release that are roughly intermediate values in the range of values included in the original analysis. As a result, the dynamics of the updated analysis are generally expected to show similar dynamics when compared to the original models. It is indeed satisfying that the base modifications made to this new set of scenarios are in accordance with the original analyses – an observation that sets the foundation for a more detailed exploration of model sensitivity to uncertainty in post-release survival. This sensitivity analysis forms the basis for the updated Raja Ampat simulation models included in this report, as discussed below.

Impact of uncertainty in post-release survival on simulated population performance

The specification of alternative estimates of post-release survival of leopard sharks released to Raja Ampat significantly impacts the resulting wild population abundance (Figure 8A) and retention of gene diversity (Figure 8B) in the updated Indonesia simulations. When employing a 10-year release program, an incremental increase of 10% in post-release survival to one year of age results in a corresponding increase in mean population abundance at the end of the release program (model year 10) of 26.5 individuals, from 57 individuals at 10% post-release survival to 269 individuals at 90% post-release survival. [Note that no extinctions at 10 years were recorded in any of the simulations presented in Figure 8.] By the end of the 50-year simulation, that incremental increase in mean population abundance grows to 80 additional individuals in the wild population per 10% increase in post-release survival to one year of age.

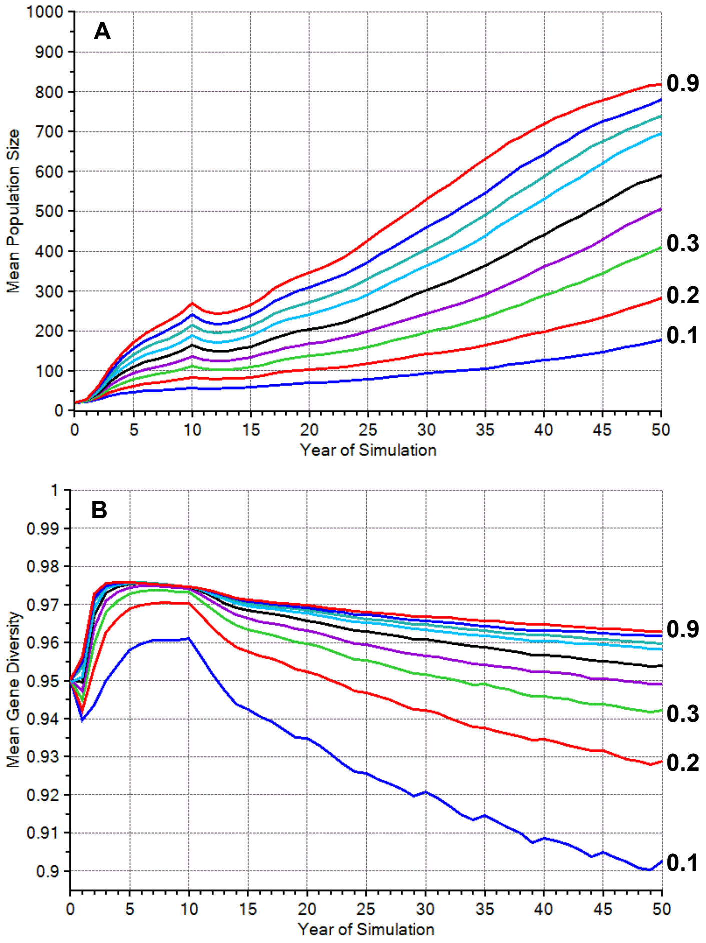

**Figure 8**. Projected extant population size (A) and gene diversity (B) of simulated Raja Ampat leopard shark populations in scenarios featuring alternative estimates of survival to one year of age of individuals after their release to the wild. All scenarios feature releases for 10 years and include the revised set of release strategy parameters as described in the accompanying text: egg production as per the Best Estimate scenario of Traylor-Holzer (2021); hatch rate of 90%; survival rate hatch to release of 77%.

Gene diversity retention follows a generally similar pattern, and once again shows a proportionally larger benefit at the lower end of the spectrum of post-release survival rates, i.e., between 0.1 and 0.4. Even when using the minimum estimate of post-release survival equal to 0.1, final gene diversity retention remains just above the desired threshold of 90% after 50 years.

A broader examination of the impact on simulated population performance of post-release survival to one year of age ($S_{\text{Rel-1yr}}$) is presented in Figure 9. In this plot, the output metric of interest is the mean stochastic multiplicative population growth rate, $\lambda_{\text{stoch}}$, across the range of years during which the simulated release program is implemented. It is particularly noteworthy to observe the increasing negative impact on population growth at mean post-release survival values less than 0.3. If post-release survival rates are at least 0.3, an incremental increase in $S_{\text{Rel-1yr}}$ of 0.1 roughly translates to an increase in $\lambda_{\text{stoch}}$ of approximately 0.0044 or an absolute increase of about 0.44%. The resulting benefit gained from increasing $S_{\text{Rel-1yr}}$ is roughly unchanged as the release program duration is extended, as judged by the trajectories in Figure 9 showing roughly equivalent slopes across the range of survival rates from 0.3 to 0.9.

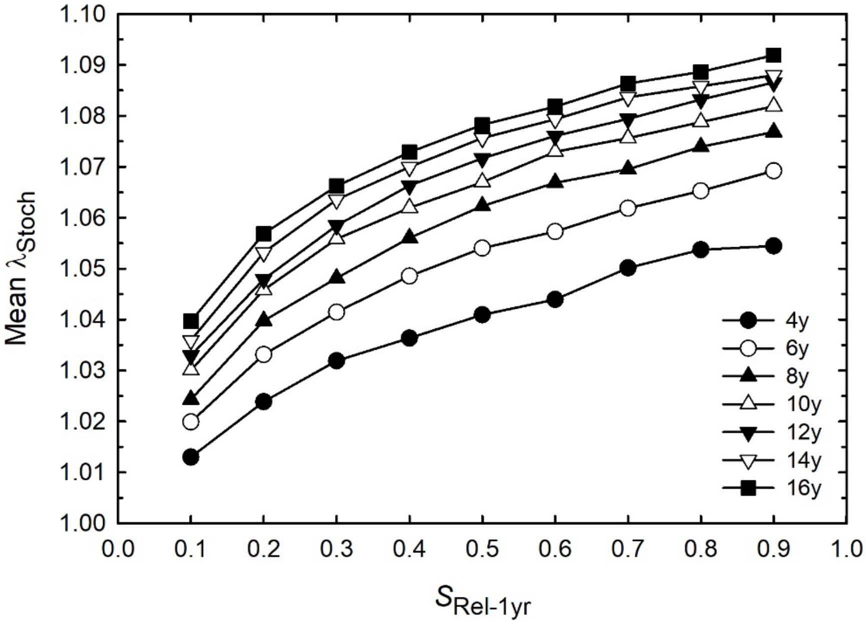

**Figure 9**. Mean stochastic multiplicative population growth rates from simulations of the Raja Ampat leopard shark population across the full range of release program duration (four to 16 years) and as a function of post-release survival rate to one year of age, $S_{\text{Rel-1yr}}$.

## Conclusions

The simulations presented in this report are an extension of the valuable analysis conducted in 2021 for the leopard shark population inhabiting the Raja Ampat Archipelago, Indonesia. As an extension of those important efforts, which shaped the design and implementation of the StAR Project in Indonesia, ReShark's StAR Project Thailand commissioned an extension of the original analysis to inform a similar effort to augment the leopard shark population inhabiting the waters of the Andaman Sea off the western coast of Thailand. By adapting those original analyses to the specific ecological conditions defining the Andaman Sea population, StAR Project Thailand personnel can acquire a base of evidence to guide the design of an effective release program to improve the long-term viability of leopard sharks in that part of the species' distribution.

In addition, new tracking data from the newly-implemented StAR Project Indonesia leopard shark release program allows for an update to the existing PVA modeling tool to further revise and improve the collective understanding of key drivers of success for releases designed to improve viability of the small leopard shark population inhabiting the Raja Ampat Archipelago. Even with these revised estimates of important survival data defining the release program, additional key estimates of post-release survival of individuals remain uncertain. The revised StAR Project Indonesia models presented in this report examine the impact of both updated estimates of early-stage release program parameters as well as the uncertainty in post-release survival to one year of age. This examination can help justify the additional fieldwork that may be required to more accurately estimate this vital element of a successful release program.

The new augmentation analyses focused on Thailand suggest that releases of young leopard sharks to suitable habitats in the Andaman Sea can significantly improve average long-term growth of existing wild shark populations, increase the levels of genetic diversity retained in the wild, and promote the establishment and maintenance of a viable leopard shark population that can be buffered from the destabilizing forces that imperil the survival of smaller, more fragile populations. For this optimal outcome to be realized, the following conditions should be achieved:

- Ecological and demographic factors that govern population stability should be managed to promote sustained rates of leopard shark population growth, targeting a minimum annual growth rate of at least 3-4%;
- Releases of juvenile leopard sharks should continue on an annual basis for at least 10 years; and
- The health of individuals identified for release – from the time that eggs hatch to the date that individuals are released to the wild – should be maintained at the highest standards possible to facilitate high survival of released individuals and their successful integration into the existing wild population.

As a valuable side note in this analysis, the expected mean population growth rate in wild leopard shark populations appears to be quite sensitive to the underlying age-specific mortality rates, as demonstrated in Table 1 (page 3). Population growth more than doubles on an annual basis from approximately 2% to 4% when pup mortality decreases from 65% to just 60% and when both subadult and adult mortality rates decrease by rather small amounts. It may be quite difficult to generate accurate estimates of age-specific mortality rates, making more general statements about measured population growth over time challenging at best. The relatively small size of the Andaman Sea leopard shark population makes this estimation procedure even more difficult. Nevertheless, population managers fully appreciate the value of thorough and consistent monitoring programs designed to characterize the underlying demographics of small populations and the added benefits that are predicted to come from sustained release efforts like those defining the StAR Project (e.g., Nichols and Armstrong 2012).

It is important to recognize that careful analysis of current data from the Andaman Sea habitat indicates an existing leopard shark population of somewhere between about 60 to 170 individuals. This abundance is substantially larger than the 2021 estimate for Indonesia’s Raja Ampat Archipelago, centered on a likely range of just 15 – 30 individuals. As a result, the Andaman Sea population can be considered inherently more demographically and genetically stable than its Indonesia counterpart, assuming that the Thailand habitat can support conditions favorable for leopard shark population growth. Consequently, it may be feasible to reduce the intensity of a proposed release program in the interest of saving valuable resources to be used across the StAR Project Thailand program through time. However, a conservative approach argues in favor of a dedicated release program intensity that can more quickly stabilize the existing population and facilitate its growth to an abundance that fosters greater levels of demographic and genetic stability. Furthermore, it is worth noting that a shark population of less than 200 individuals can and should still be considered a small population that is susceptible to forces that increase extinction risk. A management program like the StAR Project provides an outstanding opportunity to use the collective expertise and resources of both in situ and ex situ communities in an integrated effort to save endangered species from local extirpation or extinction.

The successful StAR Project Indonesia release efforts in Raja Ampat provide an additional benefit in the form of expanded data collection and analysis as releases are conducted. These new data include estimates of hatch rate (90%) and survival to release (77%) that approach or even exceed the estimates used in the Optimistic scenario used in the original analysis (Traylor-Holzer 2021). Incorporating these new estimates into the existing PVA model structure should give leopard shark managers an even greater sense of optimism that their management efforts are likely to pay big future dividends in the form of strong wild population responses to sustained releases. A key survival estimate remains elusive: survival of released individuals to one year of age, approximately six months after their release. The analyses presented here indicate that wild leopard shark population growth is indeed sensitive to this survival parameter, with consistent increases in predicted population growth across the wide range of post-release survival rates tested in this analysis (0.1 to 0.9). The models suggest that post-release survival rates less than 0.3 result in more severe declines in expected population growth. Interestingly, this value was typically used as the minimum across a range of values used in the original Best Guess, Optimistic and Pessimistic release scenarios developed in 2021. It seems clear from the present analysis that additional efforts devoted to better estimating this key parameter would make a valuable contribution to future release program success. Recommending specific methods for improving post-release survival estimates is beyond the scope of this report and is left to species experts to discuss and develop an efficient and effective long-term research plan.

Finally, it is important to emphasize that despite the additional detail and refined data characterizing this update to the original 2021 PVA, substantial uncertainty remains in our understanding of the true demographic and ecological character of leopard sharks in their wild habitats. Through recognizing this reality, inherent to all detailed demographic analyses of endangered species, we must acknowledge that the results of this updated analysis must be interpreted with caution. In particular, proper interpretation of PVA results should be done in a comparative context and not through adopting the precise numerical results of one or another specific scenario. That said, both the original and updated analyses incorporate the best available knowledge of leopard shark biology and the characteristics of leopard shark release program practice. Responsible use of these data result in robust simulation models that clearly demonstrate the value of concerted population augmentation efforts in suitable wild habitats. Through both responsible scientific analysis and the development of effective, evidence-based management programs for wild populations, the StAR Projects continue to serve as models for responsible integrated management of threatened shark populations worldwide.

## Acknowledgements

Special thanks to M. Chuangcharoendee (WildAid / StAR Project Thailand) for PVA project coordination, M. Erdmann (ReShark / StAR Project) and C. Dudgeon (Biopixel Oceans Foundation and StAR Project) for valuable discussions around revised data and model structure, and K. Traylor-Holzer (CPSG) for sharing the original 2021 PVA modeling files.

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## Appendices

Appendix I. Summary of basic PVA model input values

| Model Parameter | Parameter Value | |
|---|---|---|
| Reproduction | | |
| Mating system | Short-term polygyny (maximum female mates = 10) | |
| Age of first reproduction (years) | 7 (females and males) | |
| Proportion adult females breeding annually | Density dependent: 0.51 (low density) to 0.785 (high density) | |
| Hatchlings produced per successful female (mean, SD) | 5.43 (6.67); maximum = 20 | |
| Sex ratio of hatchlings | 50:50 | |
| Mortality, % (mean (SD)) | | |
| | High Growth scenario | Low Growth scenario |
| Pups (hatch to Age-1) | 60.0 (6.0) | 65.0 (6.5) |
| Immature (Age-1 to Age-7) | 20.0 (2.0) | 21.0 (2.1) |
| Adult (Age-7+) | 11.0 (1.1) | 12.0 (1.2) |
| Additional Parameters | | |
| Initial Population Size | Thailand (Andaman Sea) | Indonesia (Raja Ampat) |
| | 57 – 172<br>(stable age distribution) | 20, range 15-28 (beta distributed)<br>(specified distribution) |
| Maximum age (years) | 28 | |
| Inbreeding depression | 3.0 lethal equivalents; 50% recessive lethals | |
| Catastrophe | 1.2% annual probability of occurrence; 50% reduction in survival | |

SD: standard deviation

## Appendix II. Numerical results of simulation models

### IIA. StAR Project Thailand

| **Scenario Description** | | | | **stoch-r** | **SD(r)** | **PE** | **N-extant** | **SD(N-ext)** | **N-all** | **SD(N-all)** | **GeneDiv** |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $N_0$ | Population Growth Condition | Release Scenario | Release Duration (Years) | | | | | | | | |
| 57 | High Growth | NoReleases | 10 | 0.0166 | 0.1493 | 0.051 | 245.36 | 202.99 | 232.91 | 204.91 | 0.9174 |
| | | Best Estimate | 10 | 0.0503 | 0.1215 | 0.001 | 709.34 | 284.17 | 708.64 | 284.91 | 0.9646 |
| | | Optimistic | 10 | 0.0617 | 0.1281 | 0 | 869.26 | 215.13 | 869.26 | 215.13 | 0.9692 |
| | | Pessimistic | 10 | 0.0429 | 0.1224 | 0.001 | 570.07 | 299.32 | 569.51 | 299.71 | 0.9581 |
| | | Best Estimate | 4 | 0.0314 | 0.1417 | 0.013 | 400.63 | 276.47 | 395.44 | 278.36 | 0.9418 |
| | | Best Estimate | 6 | 0.0398 | 0.1339 | 0.002 | 531.14 | 305.53 | 530.08 | 306.14 | 0.9533 |
| | | Best Estimate | 8 | 0.0456 | 0.1276 | 0.003 | 626.63 | 301.77 | 624.75 | 303.25 | 0.9605 |
| | | Best Estimate | 12 | 0.053 | 0.1191 | 0 | 757.96 | 281.92 | 757.96 | 281.92 | 0.9663 |
| | | Best Estimate | 14 | 0.056 | 0.116 | 0 | 801.57 | 258.44 | 801.57 | 258.44 | 0.9683 |
| | | Best Estimate | 16 | 0.0578 | 0.1158 | 0 | 825.09 | 238.47 | 825.09 | 238.47 | 0.9694 |
| | Low Growth | NoReleases | 10 | -0.0146 | 0.1727 | 0.182 | 73.12 | 71.17 | 60.04 | 70.08 | 0.8843 |
| | | Best Estimate | 10 | 0.0256 | 0.1354 | 0.01 | 278.92 | 185.67 | 276.14 | 186.8 | 0.9502 |
| | | Optimistic | 10 | 0.039 | 0.1387 | 0.001 | 497.94 | 279.99 | 497.44 | 280.29 | 0.9611 |
| | | Pessimistic | 10 | 0.0167 | 0.1384 | 0.014 | 198.96 | 153.06 | 196.19 | 153.75 | 0.9372 |
| | | Best Estimate | 4 | 0.0035 | 0.1586 | 0.067 | 127.07 | 105.78 | 118.65 | 106.89 | 0.9174 |
| | | Best Estimate | 6 | 0.0132 | 0.1492 | 0.022 | 171.11 | 131.17 | 167.37 | 132.09 | 0.9325 |
| | | Best Estimate | 8 | 0.0215 | 0.1389 | 0.011 | 238.87 | 172.08 | 236.26 | 172.9 | 0.9438 |
| | | Best Estimate | 12 | 0.0315 | 0.1274 | 0.001 | 345.48 | 208.32 | 345.14 | 208.5 | 0.956 |
| | | Best Estimate | 14 | 0.0333 | 0.1277 | 0.003 | 387.37 | 231.33 | 386.22 | 231.94 | 0.958 |
| | | Best Estimate | 16 | 0.0367 | 0.1236 | 0 | 437.97 | 241.97 | 437.97 | 241.97 | 0.9613 |

Key to column headings

$N_0$: Initial population size
Stoch-r: Stochastic instantaneous population growth rate
SD(r): Standard deviation in stochastic instantaneous population growth rate
PE: Probability of population extinction during the 50-year simulation
N-extant: Mean population size, including only extant simulation iterations
SD(N-ext): Standard deviation in mean extant population size
N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIA. StAR Project Thailand (Continued)

| Scenario Description | | | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $N_0$ | Population Growth Condition | Release Scenario | Release Duration (Years) | | | | | | | | |
| 115 | High Growth | NoReleases | 10 | 0.0313 | 0.119 | 0.007 | 630.91 | 310.16 | 626.51 | 313.5 | 0.9555 |
| | | Best Estimate | 10 | 0.0471 | 0.1074 | 0 | 855.36 | 221.6 | 855.36 | 221.6 | 0.9745 |
| | | Optimistic | 10 | 0.0532 | 0.114 | 0 | 892.55 | 191.1 | 892.55 | 191.1 | 0.9762 |
| | | Pessimistic | 10 | 0.0411 | 0.1116 | 0 | 780.85 | 272.63 | 780.85 | 272.63 | 0.97 |
| | | Best Estimate | 4 | 0.0365 | 0.1172 | 0.001 | 711.05 | 303.09 | 710.34 | 303.77 | 0.9644 |
| | | Best Estimate | 6 | 0.0406 | 0.115 | 0 | 775.3 | 283 | 775.3 | 283 | 0.9682 |
| | | Best Estimate | 8 | 0.0432 | 0.1123 | 0 | 806.53 | 264.48 | 806.53 | 264.48 | 0.972 |
| | | Best Estimate | 12 | 0.0478 | 0.1086 | 0 | 851.28 | 223.75 | 851.28 | 223.75 | 0.9751 |
| | | Best Estimate | 14 | 0.0501 | 0.1058 | 0 | 881.52 | 201.73 | 881.52 | 201.73 | 0.976 |
| | | Best Estimate | 16 | 0.0515 | 0.1052 | 0 | 889.61 | 191.64 | 889.61 | 191.64 | 0.9768 |
| | Low Growth | NoReleases | 10 | 0.0038 | 0.1318 | 0.019 | 216.38 | 165.35 | 212.29 | 166.39 | 0.9364 |
| | | Best Estimate | 10 | 0.0233 | 0.1183 | 0 | 457.17 | 262.7 | 457.17 | 262.7 | 0.965 |
| | | Optimistic | 10 | 0.032 | 0.1197 | 0.001 | 625.02 | 282.99 | 624.4 | 283.53 | 0.9705 |
| | | Pessimistic | 10 | 0.0181 | 0.1195 | 0.003 | 364.83 | 227.51 | 363.74 | 228.04 | 0.9599 |
| | | Best Estimate | 4 | 0.01 | 0.1292 | 0.012 | 278.65 | 202.06 | 275.33 | 203.1 | 0.9488 |
| | | Best Estimate | 6 | 0.0149 | 0.1265 | 0.005 | 331.12 | 217.09 | 329.47 | 217.79 | 0.9551 |
| | | Best Estimate | 8 | 0.0198 | 0.122 | 0.002 | 399.89 | 244.18 | 399.09 | 244.59 | 0.961 |
| | | Best Estimate | 12 | 0.0258 | 0.1162 | 0 | 503.92 | 270.06 | 503.92 | 270.06 | 0.9676 |
| | | Best Estimate | 14 | 0.0277 | 0.1139 | 0.001 | 539.41 | 269.02 | 538.88 | 269.42 | 0.9693 |
| | | Best Estimate | 16 | 0.03 | 0.1114 | 0 | 576.28 | 266.53 | 576.28 | 266.53 | 0.9709 |

Key to column headings

$N_0$: Initial population size
Stoch-r: Stochastic instantaneous population growth rate
SD(r): Standard deviation in stochastic instantaneous population growth rate
PE: Probability of population extinction during the 50-year simulation
N-extant: Mean population size, including only extant simulation iterations
SD(N-ext): Standard deviation in mean extant population size
N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIA. StAR Project Thailand (Continued)

| Scenario Description | | | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|---|---|
| $N_0$ | Population Growth Condition | Release Scenario | Release Duration (Years) | | | | | | | | |
| 172 | High Growth | NoReleases | 10 | 0.0351 | 0.1103 | 0 | 798.04 | 271.74 | 798.04 | 271.74 | 0.9675 |
| | | Best Estimate | 10 | 0.0448 | 0.1043 | 0 | 893.76 | 191.8 | 893.76 | 191.8 | 0.9782 |
| | | Optimistic | 10 | 0.0501 | 0.1083 | 0 | 903.37 | 177.4 | 903.37 | 177.4 | 0.9795 |
| | | Pessimistic | 10 | 0.0411 | 0.1061 | 0 | 859.3 | 226.3 | 859.3 | 226.3 | 0.9757 |
| | | Best Estimate | 4 | 0.0379 | 0.111 | 0.001 | 828.06 | 250.01 | 827.23 | 251.25 | 0.972 |
| | | Best Estimate | 6 | 0.042 | 0.105 | 0 | 873.87 | 208.3 | 873.87 | 208.3 | 0.9755 |
| | | Best Estimate | 8 | 0.0435 | 0.1061 | 0 | 880.48 | 203.67 | 880.48 | 203.67 | 0.9772 |
| | | Best Estimate | 12 | 0.0463 | 0.1053 | 0 | 891.32 | 193.9 | 891.32 | 193.9 | 0.979 |
| | | Best Estimate | 14 | 0.0476 | 0.102 | 0 | 908.34 | 171.72 | 908.34 | 171.72 | 0.9796 |
| | | Best Estimate | 16 | 0.0487 | 0.1029 | 0 | 917.39 | 163.24 | 917.39 | 163.24 | 0.9798 |
| | Low Growth | NoReleases | 10 | 0.0095 | 0.1208 | 0.006 | 382.43 | 254.21 | 380.15 | 255.15 | 0.9555 |
| | | Best Estimate | 10 | 0.0219 | 0.1117 | 0.002 | 589.15 | 285.68 | 587.98 | 286.6 | 0.9722 |
| | | Optimistic | 10 | 0.0286 | 0.1136 | 0 | 707.12 | 274.77 | 707.12 | 274.77 | 0.9755 |
| | | Pessimistic | 10 | 0.0184 | 0.1127 | 0.003 | 527.31 | 284.4 | 525.74 | 285.43 | 0.9686 |
| | | Best Estimate | 4 | 0.0144 | 0.1166 | 0.002 | 447.38 | 267.09 | 446.49 | 267.56 | 0.9625 |
| | | Best Estimate | 6 | 0.0171 | 0.1168 | 0.002 | 500.07 | 284.7 | 499.07 | 285.29 | 0.9667 |
| | | Best Estimate | 8 | 0.02 | 0.1138 | 0.002 | 552.12 | 283.43 | 551.02 | 284.21 | 0.9699 |
| | | Best Estimate | 12 | 0.0239 | 0.1113 | 0 | 623.2 | 290.49 | 623.2 | 290.49 | 0.9736 |
| | | Best Estimate | 14 | 0.0256 | 0.1105 | 0 | 653.77 | 282.98 | 653.77 | 282.98 | 0.9747 |
| | | Best Estimate | 16 | 0.0267 | 0.1092 | 0.001 | 678.08 | 277.79 | 677.41 | 278.46 | 0.9756 |

Key to column headings

$N_0$: Initial population size
Stoch-r: Stochastic instantaneous population growth rate
SD(r): Standard deviation in stochastic instantaneous population growth rate
PE: Probability of population extinction during the 50-year simulation
N-extant: Mean population size, including only extant simulation iterations
SD(N-ext): Standard deviation in mean extant population size
N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIB. StAR Project Indonesia

| Scenario Description | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|
| Release Program Duration (Years) | Post-Release Survival Rate | | | | | | | | |
| No Releases | | 0.0041 | 0.203 | 0.284 | 90.81 | 99.28 | 65.34 | 93.23 | 0.856 |
| 4 | 0.1 | 0.0129 | 0.1942 | 0.202 | 110.98 | 113.86 | 88.79 | 110.86 | 0.8759 |
| | 0.2 | 0.0236 | 0.1865 | 0.117 | 156.33 | 155.8 | 138.19 | 154.64 | 0.8899 |
| | 0.3 | 0.0314 | 0.184 | 0.075 | 193.74 | 175.59 | 179.3 | 176.33 | 0.9043 |
| | 0.4 | 0.0357 | 0.1846 | 0.051 | 222.84 | 195.99 | 211.55 | 197.04 | 0.9121 |
| | 0.5 | 0.0401 | 0.1881 | 0.052 | 262.54 | 208.34 | 248.96 | 210.98 | 0.9212 |
| | 0.6 | 0.043 | 0.1922 | 0.026 | 286.7 | 228.57 | 279.28 | 230.11 | 0.925 |
| | 0.7 | 0.0489 | 0.19 | 0.019 | 350.85 | 250.42 | 344.21 | 252.58 | 0.9324 |
| | 0.8 | 0.0523 | 0.1933 | 0.014 | 381.07 | 258.15 | 375.77 | 260.18 | 0.9383 |
| | 0.9 | 0.053 | 0.199 | 0.009 | 396.97 | 275.42 | 393.42 | 276.7 | 0.9393 |
| 6 | 0.1 | 0.0197 | 0.1839 | 0.131 | 133.28 | 141.36 | 115.96 | 139.13 | 0.8848 |
| | 0.2 | 0.0326 | 0.1748 | 0.055 | 193.49 | 172.32 | 182.91 | 173.16 | 0.9084 |
| | 0.3 | 0.0406 | 0.1719 | 0.036 | 256.72 | 214.25 | 247.52 | 215.68 | 0.9198 |
| | 0.4 | 0.0474 | 0.1718 | 0.016 | 317.63 | 237.93 | 312.57 | 239.33 | 0.9309 |
| | 0.5 | 0.0526 | 0.175 | 0.006 | 384.8 | 261.28 | 382.5 | 262.17 | 0.9382 |
| | 0.6 | 0.0557 | 0.1784 | 0.005 | 440.03 | 284.93 | 437.84 | 285.9 | 0.9424 |
| | 0.7 | 0.06 | 0.181 | 0.004 | 510.96 | 299.81 | 508.93 | 300.92 | 0.9472 |
| | 0.8 | 0.0632 | 0.1846 | 0.003 | 563.55 | 306.76 | 561.86 | 307.83 | 0.9508 |
| | 0.9 | 0.0669 | 0.1857 | 0 | 640.38 | 306.73 | 640.38 | 306.73 | 0.9537 |

Key to column headings

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SD(N-ext): Standard deviation in mean extant population size
N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIB. StAR Project Indonesia (Continued)

| Scenario Description | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|
| Release Program Duration (Years) | Post-Release Survival Rate | | | | | | | | |
| No Releases | | 0.0041 | 0.203 | 0.284 | 90.81 | 99.28 | 65.34 | 93.23 | 0.856 |
| 8 | 0.1 | 0.024 | 0.1776 | 0.111 | 151.91 | 147.39 | 135.2 | 146.79 | 0.8936 |
| | 0.2 | 0.039 | 0.1647 | 0.038 | 242.81 | 204.09 | 233.64 | 205.43 | 0.9188 |
| | 0.3 | 0.047 | 0.1602 | 0.014 | 310.74 | 229.18 | 306.41 | 230.45 | 0.9305 |
| | 0.4 | 0.0545 | 0.1605 | 0.013 | 423.15 | 274.12 | 417.67 | 276.49 | 0.9428 |
| | 0.5 | 0.0604 | 0.1621 | 0.004 | 513.32 | 292.61 | 511.27 | 293.81 | 0.9493 |
| | 0.6 | 0.0647 | 0.1646 | 0.003 | 595.3 | 304.35 | 593.52 | 305.63 | 0.9526 |
| | 0.7 | 0.0672 | 0.1712 | 0.001 | 634.93 | 306.85 | 634.3 | 307.35 | 0.9549 |
| | 0.8 | 0.0713 | 0.1735 | 0.001 | 710.89 | 288.22 | 710.18 | 288.95 | 0.958 |
| | 0.9 | 0.074 | 0.177 | 0 | 751.08 | 277.1 | 751.08 | 277.1 | 0.9603 |
| 10 | 0.1 | 0.0296 | 0.1667 | 0.067 | 178.13 | 170.1 | 166.29 | 170.14 | 0.9027 |
| | 0.2 | 0.0448 | 0.1526 | 0.018 | 282.58 | 209.84 | 277.52 | 211.28 | 0.9289 |
| | 0.3 | 0.0543 | 0.1507 | 0.008 | 411.15 | 266.85 | 407.88 | 268.27 | 0.9422 |
| | 0.4 | 0.0601 | 0.152 | 0.004 | 506.96 | 292.53 | 504.94 | 293.68 | 0.9492 |
| | 0.5 | 0.0648 | 0.1584 | 0 | 590.63 | 306.64 | 590.63 | 306.64 | 0.954 |
| | 0.6 | 0.0704 | 0.1603 | 0.001 | 694.64 | 296.65 | 693.95 | 297.31 | 0.9583 |
| | 0.7 | 0.0729 | 0.165 | 0 | 738.01 | 285.12 | 738.01 | 285.12 | 0.9598 |
| | 0.8 | 0.0758 | 0.1699 | 0.001 | 780.26 | 270.12 | 779.48 | 271.1 | 0.9617 |
| | 0.9 | 0.0787 | 0.1723 | 0 | 817.95 | 253.29 | 817.95 | 253.29 | 0.963 |

Key to column headings

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N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIB. StAR Project Indonesia (Continued)

| Scenario Description | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|
| Release Program Duration (Years) | Post-Release Survival Rate | | | | | | | | |
| No Releases | | 0.0041 | 0.203 | 0.284 | 90.81 | 99.28 | 65.34 | 93.23 | 0.856 |
| 12 | 0.1 | 0.0324 | 0.1624 | 0.056 | 183.88 | 163.71 | 173.66 | 164.51 | 0.9108 |
| | 0.2 | 0.0468 | 0.1515 | 0.015 | 314.86 | 241.39 | 310.17 | 242.58 | 0.9334 |
| | 0.3 | 0.0568 | 0.1492 | 0.004 | 454.75 | 282.37 | 452.94 | 283.25 | 0.9472 |
| | 0.4 | 0.0642 | 0.1499 | 0.002 | 575.17 | 292.16 | 574.02 | 292.99 | 0.9544 |
| | 0.5 | 0.0692 | 0.1539 | 0.002 | 674.88 | 298.82 | 673.54 | 300.03 | 0.9583 |
| | 0.6 | 0.0733 | 0.1578 | 0 | 738.43 | 271.15 | 738.43 | 271.15 | 0.9609 |
| | 0.7 | 0.0764 | 0.1627 | 0 | 781.63 | 265.95 | 781.63 | 265.95 | 0.9623 |
| | 0.8 | 0.0799 | 0.1659 | 0 | 838.79 | 232.25 | 838.79 | 232.25 | 0.964 |
| | 0.9 | 0.083 | 0.1698 | 0 | 867.28 | 211.64 | 867.28 | 211.64 | 0.9647 |
| 14 | 0.1 | 0.0353 | 0.1587 | 0.045 | 206.09 | 171.04 | 196.87 | 172.46 | 0.9159 |
| | 0.2 | 0.0518 | 0.1448 | 0.009 | 361.29 | 242.83 | 358.05 | 244.11 | 0.9409 |
| | 0.3 | 0.0616 | 0.1424 | 0.001 | 530.62 | 296.58 | 530.09 | 296.9 | 0.9516 |
| | 0.4 | 0.0676 | 0.1464 | 0 | 645.6 | 299.25 | 645.6 | 299.25 | 0.9571 |
| | 0.5 | 0.0729 | 0.1503 | 0 | 736.05 | 277.94 | 736.05 | 277.94 | 0.961 |
| | 0.6 | 0.0763 | 0.1559 | 0 | 784.87 | 265.02 | 784.87 | 265.02 | 0.9629 |
| | 0.7 | 0.0803 | 0.1603 | 0 | 841.02 | 228.59 | 841.02 | 228.59 | 0.9643 |
| | 0.8 | 0.0823 | 0.1653 | 0 | 857.73 | 219.85 | 857.73 | 219.85 | 0.9651 |
| | 0.9 | 0.0843 | 0.1711 | 0 | 871.64 | 207.64 | 871.64 | 207.64 | 0.9658 |

Key to column headings

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N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation

## Appendix II. Numerical results of simulation models (Continued)

### IIB. StAR Project Indonesia (Continued)

| Scenario Description | | stoch-r | SD(r) | PE | N-extant | SD(N-ext) | N-all | SD(N-all) | GeneDiv |
|---|---|---|---|---|---|---|---|---|---|
| Release Program Duration (Years) | Post-Release Survival Rate | | | | | | | | |
| No Releases | | 0.0041 | 0.203 | 0.284 | 90.81 | 99.28 | 65.34 | 93.23 | 0.856 |
| 16 | 0.1 | 0.0389 | 0.1544 | 0.027 | 229.82 | 195.14 | 223.64 | 196.03 | 0.9218 |
| | 0.2 | 0.0553 | 0.1405 | 0.002 | 403.71 | 252.31 | 402.9 | 252.69 | 0.9466 |
| | 0.3 | 0.0641 | 0.1396 | 0 | 569.46 | 293.19 | 569.46 | 293.19 | 0.9555 |
| | 0.4 | 0.0703 | 0.1442 | 0.001 | 691.61 | 287.85 | 690.92 | 288.53 | 0.96 |
| | 0.5 | 0.0753 | 0.1478 | 0 | 783.54 | 264.31 | 783.54 | 264.31 | 0.9627 |
| | 0.6 | 0.0786 | 0.1539 | 0 | 818.63 | 244.67 | 818.63 | 244.67 | 0.9645 |
| | 0.7 | 0.0828 | 0.1564 | 0 | 871.38 | 210.97 | 871.38 | 210.97 | 0.9658 |
| | 0.8 | 0.0849 | 0.164 | 0 | 878.83 | 193.25 | 878.83 | 193.25 | 0.9661 |
| | 0.9 | 0.0879 | 0.1664 | 0 | 905.83 | 176.76 | 905.83 | 176.76 | 0.9669 |

Key to column headings

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SD(N-ext): Standard deviation in mean extant population size
N-all: Mean population size, including all simulation iterations
SD(N-all) Standard deviation in mean population size
GeneDiv: Gene diversity retained during the 50-year simulation