Population Viability Analysis of the Mexican Wolf (*Canis lupus baileyi*):

An Evaluation of Population Demographic Performance in Comparison to Predicted Dynamics

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Introduction

In November 2017, a report was delivered to the U.S. Fish and Wildlife Service (hereafter, Service) that documented a population viability analysis (PVA) of the Mexican wolf, *Canis lupus baileyi* (Miller 2017). This PVA used the best available demographic and genetic data on the two wild (in situ) wolf populations in the United States (occupying the Mexican Wolf Experimental Population Area, or MWEPA) and Mexico (occupying habitat in the northern Sierra Madre Occidental, or SMOCC-N) as well as the captive (ex situ) population (the SSP[1] population, now known as the SAFE[2] population) to assess likely future growth dynamics and to inform the specification of quantitative criteria considered necessary for species recovery. The 2017 PVA document was an important reference for the subsequent recovery plan (USFWS 2017) and its follow-up revision (USFWS 2022).

The Service and its partners are now undertaking an evaluation of recent demographic and genetic characteristics of both in situ and ex situ populations in order to assess "true" population performance in light of the predictions made in the 2017 PVA. In particular, it is instructive to compare recent observed trends of both in situ and ex situ population abundance and genetic diversity with those predicted by the 2017 PVA model and to explore potential causal factors that may explain any differences between them. This report documents the quantitative component of this evaluation.

Methods

The 2017 PVA was conducted using the demographic simulation modeling package Vortex, version 10.2.8 (Lacy and Pollak 2017). New simulations conducted as part of the current evaluation use a newer version of the software (version 10.6.0: Lacy and Pollak 2022) with the same base modeling project used originally. Full details on the structure and function of the PVA model, as well as the data used to create demographic and genetic input values for the model, are not given here but can be found in the original PVA report (Miller 2017). Similarly, details on methods used to generate minimum population abundance counts for in situ populations and to estimate population genetic structure of both in situ and ex situ populations can be found in summary documents published by the appropriate population management authorities (see data source list below).

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[1] Species Survival Plan®

[2] Saving Animals from Extinction

The model scenario used for the predicted values of population performance featured the following characteristics, defined in detail in Miller (2017):

- MWEPA population management target: 379 wolves;
- SMOCC-N population management target: 200 wolves;
- Mean expected annual mortality rate of adults: 0.189;
- Anticipated release schedule:
  - SAFE population to MWEPA: Twice the rate reported in the 2014 Environmental Impact Statement (USFWS 2014), which specified the transfer from the SAFE population of two pairs of adults and associated pups (four adults and six pups) scheduled for calendar years 2017 and 2021 (model years two and six);
  - SAFE population to SMOCC-N: Transfer of two pairs of adults and associated pups (four adults and six pups) each year in calendar years 2017 through 2021 (model years two through six); and
- Anticipated translocation schedule (MWEPA to SMOCC-N): Base rate of two pairs of adults and associated pups (four adults and six pups) moved to Mexico every other year between calendar years 2017 and 2023).

In the scenario labeling scheme described in Miller (2017), this scenario was designated "379_200_200_189_[EISx2]20_20". Additional information contained in this scheme refers to a second wolf population to be established in the southern portion of the Sierra Madre Occidental (SMOCC-S), which is not being considered in this evaluation. See Table 2 of Miller (2017) and associated text for a detailed discussion of the scenario labeling methodology. For the current evaluation, a slight revision was made to this scenario by modifying the studbook file used to initialize both in situ and ex situ populations. All living individuals in the studbook (alive as of 31 December 2015) had their age incremented by one year to properly categorize their age just before the pairing/breeding season in the spring of 2016, which is the beginning of Year 1 of the simulation. Testing of this change to initial conditions did not have an appreciable impact on model outcomes.

Data sources for this evaluation include:

- The original PVA report (Miller 2017);
- USFWS Quarterly and Annual Reports and other documents describing population analysis, made available by Service Mexican wolf biologists and also available on the Mexican Wolf Recovery Program website (https://www.fws.gov/program/conserving-mexican-wolf);
- Annual population estimates for the SMOCC-N population provided by Mexican wildlife management authorities (CONANP);
- Breeding & Transfer Plan (BTP) reports for the SSP®/SAFE population provided by the Association of Zoos and Aquariums (AZA); and
- Personal communications with Service and CONANP personnel.

The period for this analysis covers end-of-year wild population counts from 2015 to 2023 (minimum counts reported as of the end of the reporting period). These counts, then, roughly coincide with the estimated abundance reported in the PVA just before the onset of pairing and breeding in the early spring of the following year. However, the predicted abundance estimates reported from the PVA represent total population size and, therefore, is expected to be higher than the observed minimum wild population counts derived from aerial surveys and ground observations. Observed population genetic parameters are reported by the SAFE program as of 1 July each year, based on detailed analysis of the up-to-date studbook including individuals in both the in situ and ex situ populations. This date is chosen to align with the annual meeting of the SAFE program that creates the breeding and transfer recommendations for the following breeding season. The timing of this analysis is approximately 4-6 months out of phase with the timing of reporting from the PVA, where population genetic structure is reported at the same time as total population abundance, i.e., just before the annual pairing/breeding event in the spring of the year. While the timing of their estimation may not precisely coincide, the two genetic metrics are not expected to differ meaningfully within any given year.

For each of the three populations, the evaluation compares observed ("true") vs. predicted estimates of population size, proportion gene diversity (GD, also known as expected heterozygosity) retained, and population mean inbreeding coefficient (F). In addition to reporting the standard gene diversity values that reflect retention relative to the original wild population that served as a source of the founders to the ex situ population, retention of gene diversity in the wild populations is also calculated relative to the source SAFE population per Miller (2017). Predicted values of these metrics represent the mean values across 1000 iterations of the model scenario described above. In addition to these population output metrics, the evaluation compared the actual schedule of translocations from MWEPA to SMOCC-N and of releases from SAFE to MWEPA and SMOCC-N with the schedules encoded in the PVA scenario. Finally, the evaluation compares observed vs. predicted rates of diversionary/supplemental feeding (i.e., providing food caches near packs caring for pups to either help prevent depredations or assist with the raising of pups associated with foster efforts) in the MWEPA, as this tactic was considered to impact the number of surviving pups per litter (see Miller 2017 for a detailed discussion of this model element).

Results

[Note: tabular results for the figures presented in this section can be found in the Appendix.]

MWEPA Population Performance

The abundance of wolves in the MWEPA population predicted by the PVA model was consistently slightly lower than the observed minimum count estimate across the period of comparison (Figure 1A). As of the end-of-year count in 2023, the observed minimum number of wolves in this population was reported as 257 individuals, with the PVA model predicting a total abundance of 229±85 individuals. The mean rate of growth in the population was observed to be just under 13% per year over the period of analysis, while the predicted growth rate was estimated at slightly greater than 11% per year. The observed estimate of proportional gene diversity (GD) retained (Figure 1B) was greater than predicted by the PVA model, most likely resulting from the slightly larger observed estimate of population abundance and differing release schedule (see below). As of the 1 July 2023 date of calculation, the observed GD retained was 76.09%, while the PVA model predicted a retention of 74.99% as of the preceding spring. In a similar fashion, the observed retention of gene diversity in MWEPA relative to the source SAFE population has been consistently above the predicted value, with both measures exceeding 90% retention in the period 2020 – 2023. In keeping with the higher level of GD retention over time, the observed estimate of mean inbreeding coefficient (F) in the MWEPA population was 0.211 in July 2023, with the PVA model predicting mean F = 0.234 in the spring of that same year (Figure 1C). The different values for GD and F at the onset of the evaluation time series in 2016 may reflect the different time point for calculation of these metrics which leads to slight variation in the dataset of living individuals making up the analyses (Figure 1). This interpretation is also valid for the SMOCC-N and SAFE population analyses (Figures 2 and 3).

SMOCC-N Population Performance

The abundance of wolves in the SMOCC-N population predicted by the PVA model was considerably greater than the observed abundance over the period of comparison (Figure 2A). At the end-of-year count in 2022, the observed minimum number of wolves in the population was reported as 35 individuals, with the PVA model predicting a total abundance of 124±39 individuals. The mean rate of growth in the population was observed to be approximately 11% per year, while the predicted growth rate was estimated to be nearly 33% per year. The observed estimate of proportional gene diversity retained was nearly identical to that predicted by the PVA model. As of the 1 July 2022 date of calculation, the observed GD retained was 79.74%, while the PVA model predicted a retention of 79.80% as of the preceding spring (Figure 2B). Gene diversity retention relative to the source SAFE population has increased substantially in this population since 2016, rising to nearly 97% of the SAFE population value by 2022. Before the ending date of this calculation, the observed GD data analysis found that the observed rate of retention was consistently lower than the PVA model prediction, although the general trend in retention over time was generally quite consistent across the two datasets. The observed estimate of mean inbreeding coefficient in the SMOCC-N population was consistently slightly lower than that predicted by the PVA model. The observed estimate of mean F was 0.166 as of the 1 July date of analysis, with the PVA model predicting mean F = 0.181 in the spring of that same year (Figure 2C).

SAFE Population Performance

The observed abundance of wolves in the ex situ SAFE population was considerably larger than that predicted by the PVA model over the full period of comparison (Figure 3A). In 2023, the observed abundance was 356 individuals as of 1 July, while the abundance predicted by the PVA model in the spring of that year (before reproduction) was 251±8 individuals. The mean rate of growth in the population was observed to be approximately 5% per year, while the predicted growth rate was estimated to be just 2% per year. This large discrepancy between observed and predicted abundances is in large part due to a significantly greater number of wolves in the actual SAFE population in recent years (approaching 350 individuals, a value that is currently recognized as exceeding practical management realities) relative to the population carrying capacity used in the 2017 PVA (255 individuals). Despite the differences between observed and expected abundance over time, the proportion of gene diversity retained was nearly identical over the period of observation (Figure 3B). Across both estimates, GD retention remained nearly constant over time with a final estimate in 2023 of 82.44% (observed) or 82.43% (predicted). Mean inbreeding coefficient across the two estimates was also nearly identical across the period of comparison (Figure 3C), with the predicted estimate rising to a very slightly higher value in spring 2023 (F_{Pred} = 0.163) compared to the observed value estimated as of 1 July of that same year (F_{Obs} = 0.151).

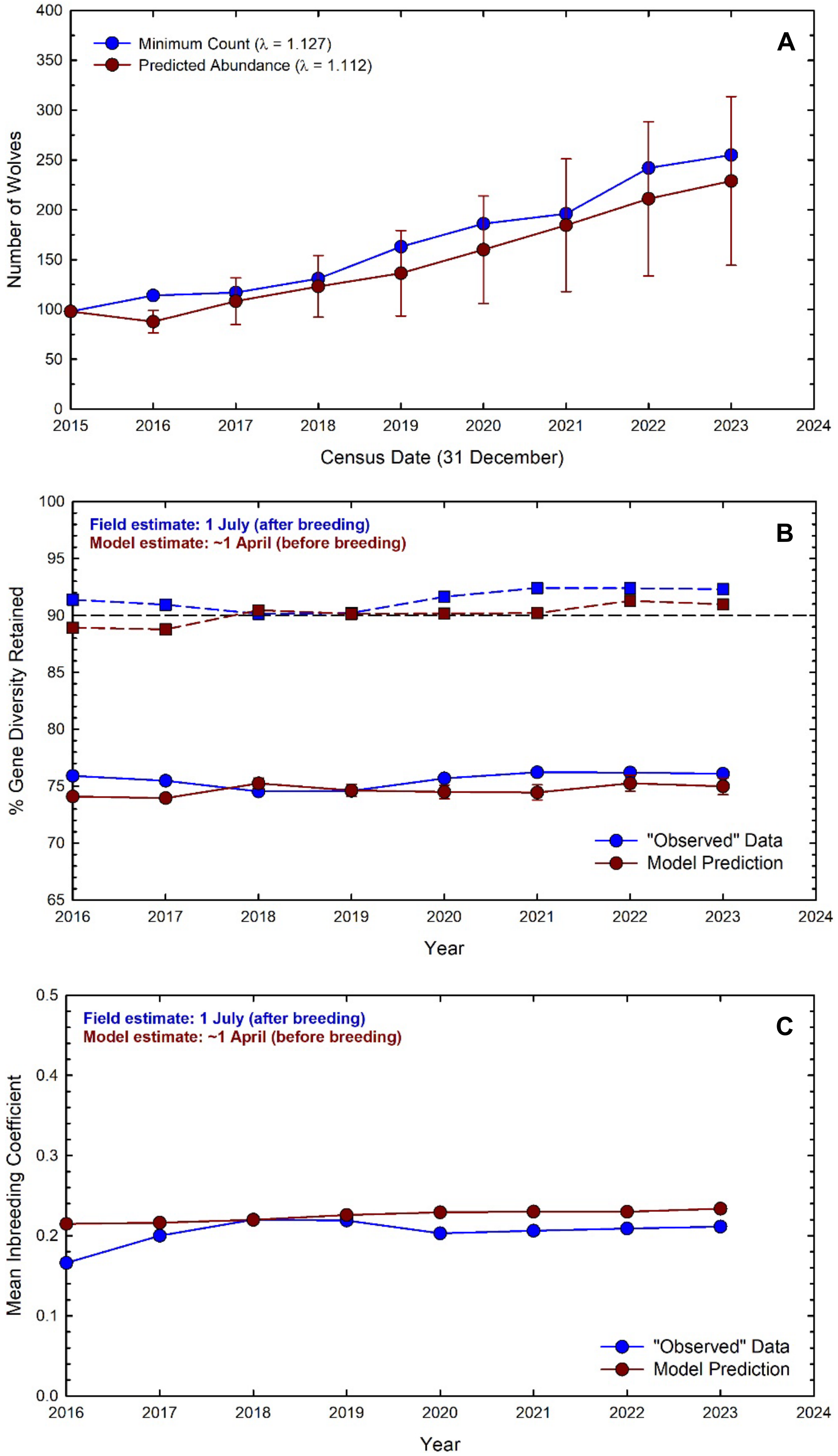

Figure 1. Evaluation of observed vs. predicted performance of the MWEPA population of Mexican wolves. Predicted metrics are reported as (mean±SD) where available. Gene diversity plot (B) includes both base retention values (circles) relative to the original wild population as well as retention relative to the current SAFE population (squares), with the horizontal line denoting a 90% gene diversity retention target. See accompanying text for additional information on definitions of performance metrics and their estimation.

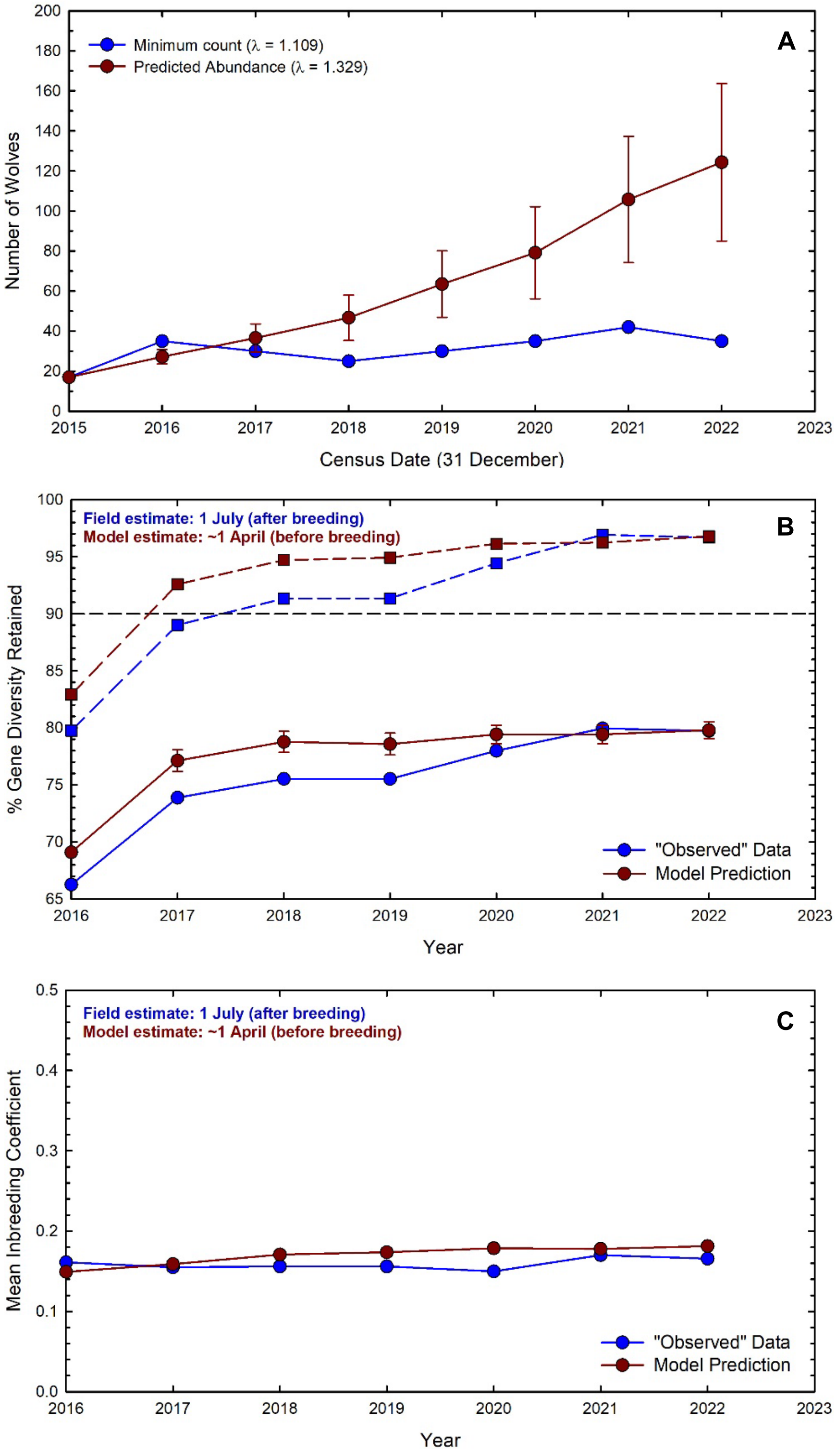

Figure 2. Evaluation of observed vs. predicted performance of the SMOCC-N population of Mexican wolves. Predicted metrics are reported as (mean±SD) where available. Gene diversity plot (B) includes both base retention values (circles) relative to the original wild population as well as retention relative to the current SAFE population (squares), with the horizontal line denoting a 90% gene diversity retention target. See accompanying text for additional information on definitions of performance metrics and their estimation.

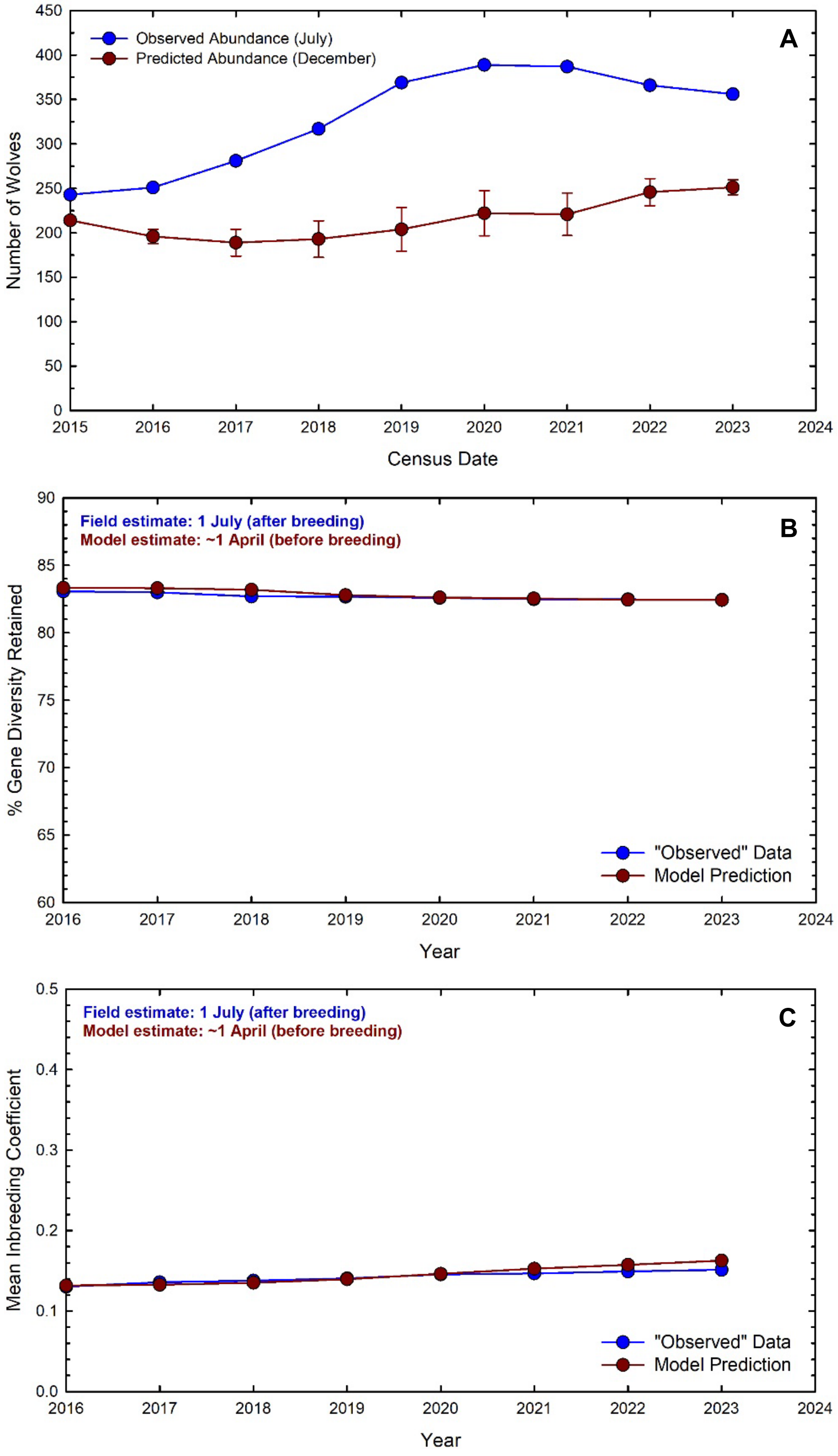

Figure 3. Evaluation of observed vs. predicted performance of the SAFE population of Mexican wolves. Predicted metrics are reported as (mean±SD) where available. See accompanying text for additional information on definitions of performance metrics and their estimation.

Wolf Translocation Dynamics: MWEPA to SMOCC-N

The PVA model featured removal from the MWEPA population of four adults and six pups every other year from 2017 to 2023 for the purpose of translocation to Mexico (i.e., not inclusive of removals for all purposes), leading to a total predicted removal of 16 adults and 24 pups over the period of evaluation. Wolf removals from MWEPA to SMOCC-N occurred less frequently than predicted, with removal events taking place in 2020, 2021 and 2023. During those three years, a total of nine adults, two yearlings (Age-1) and five pups were removed from MWEPA for a total of 16 individuals or 40% of the predicted number (Figure 4).

Thus, the number of wolves translocated to SMOCC-N from the MWEPA population was 40% of the originally predicted number, with the first wild wolves moved to Mexico (2020) three years after the original predicted date (2017). Slightly more than 50% of the intended adult cohort was translocated, but only 21% of the originally predicted pups were translocated during the period of evaluation.

Wolf Release Dynamics: SAFE to MWEPA, SMOCC-N

As predicted in the 2017 PVA simulations, eight adults and twelve pups were to be released from the ex situ SAFE population and released to MWEPA in each of two years covering the evaluation period (2017 and 2021). The total number of individuals predicted to be released during this period, therefore, was 16 adults and 24 pups. Only pups, however, are recorded to have been released to MWEPA from the SAFE population, and in substantially larger numbers than what was predicted in the 2017 PVA (Figure 5). Over the evaluation period 2016-2023, a total of 99 pups (412% of the predicted number of pups, 247% of the total predicted number of wolves) were released to MWEPA from the ex situ population, with a gradual increase in the annual release rate up to a maximum of 22 pups released in 2021.

The 2017 PVA also predicted a total of 20 adults and 39 pups to be released from the SAFE population to the SMOCC-N population between 2016 and 2021, with four adults and six pups released each year between 2017 and 2021. In reality, a total of eight adults, four yearlings, and seven pups were released between 2018 and 2021 (19 wolves in total, 32% of the predicted value: Figure 6). More recent releases in 2020 and 2021 included only half of the scheduled adults and just 16.7% of the scheduled pups.

Overall, the original prediction in the 2017 PVA included a total of 36 adults and 63 pups to be released into the wild during the period of evaluation (Figure 7). The MWEPA population was to receive 16 adults and 24 pups (40.4% of the total), while SMOCC-N was to receive 20 adults and 39 pups (59.6% of the total). In total, the actual release schedule amounted to 119% of the predicted number but was heavily biased towards pups (106 actual vs. 63 predicted) and to releases into MWEPA (99 actual vs. 40 predicted) with only 19 wolves released to Mexico.

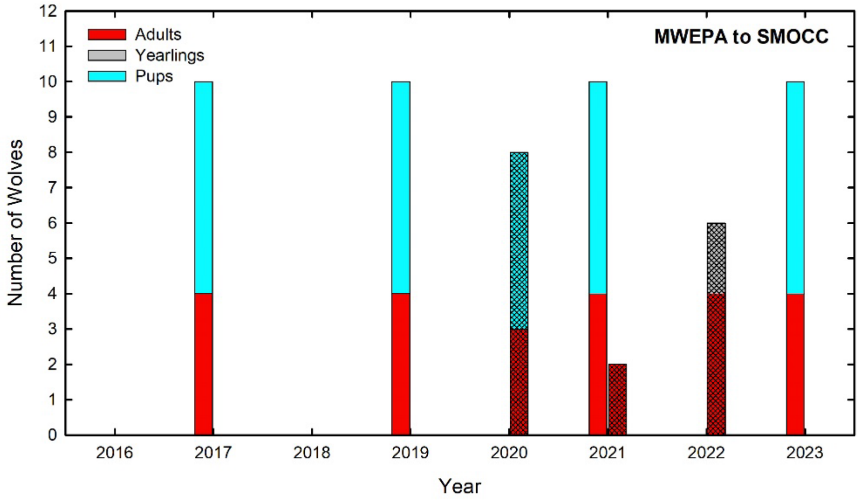

Figure 4. Evaluation of observed vs. predicted events in which wolves were to be removed from the US MWEPA population and translocated to the Mexico SMOCC_N population. In each year of the plot, light-color stacked bars to the left of the year on the x-axis indicate the predicted translocation schedule included in the PVA simulation, while the cross-hatched stacked bars to the right of the year indicate the actual translocation schedule reported by wolf management authorities. See accompanying text and Miller (2017) for additional information on PVA model structure and function.

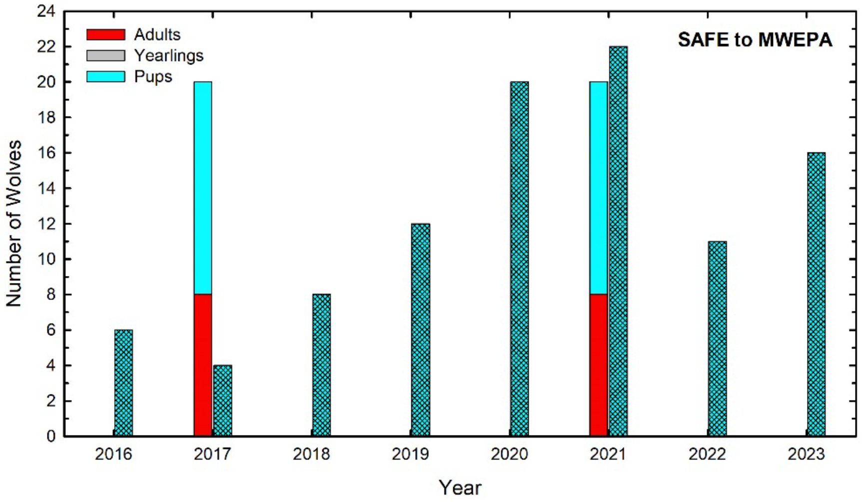

Figure 5. Evaluation of observed vs. predicted events in which wolves were to be released from the ex situ SAFE population to the MWEPA population. In each year of the plot, light-color stacked bars to the left of the year on the x-axis indicate the predicted release schedule included in the PVA simulation, while the cross-hatched stacked bars to the right of the year indicate the actual release schedule reported by wolf management authorities. See accompanying text and Miller (2017) for additional information on PVA model structure and function.

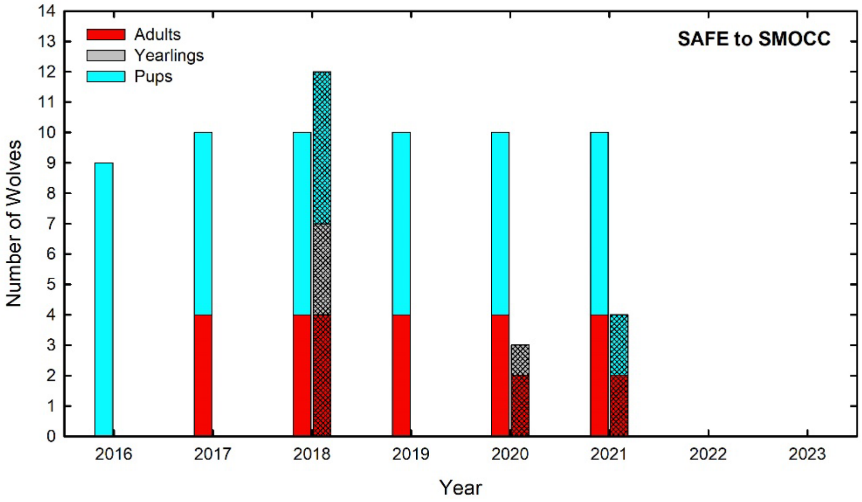

Figure 6. Evaluation of observed vs. predicted events in which wolves were to be released from the ex situ SAFE population to the SMOCC-N population. In each year of the plot, light-color stacked bars to the left of the year on the x-axis indicate the predicted release schedule included in the PVA simulation, while the cross-hatched stacked bars to the right of the year indicate the actual release schedule reported by wolf management authorities. See accompanying text and Miller (2017) for additional information on PVA model structure and function.

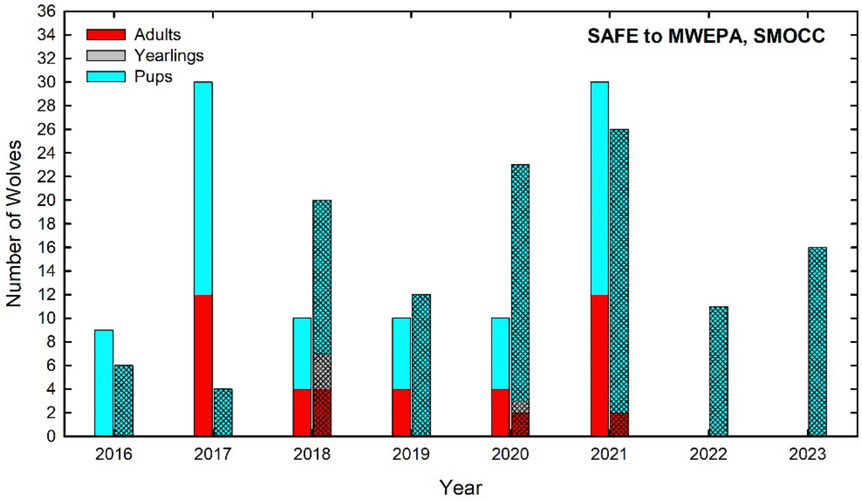

Figure 7. Evaluation of observed vs. predicted levels of removal of wolves from the SAFE population to be released to wild populations in the US (MWEPA) and to Mexico (SMOCC-N). In each year of the plot, light-color stacked bars to the left of the year on the x-axis indicate the predicted removal schedule included in the PVA simulation, while the cross-hatched stacked bars to the right of the year indicate the actual removal schedule reported by wolf management authorities. See accompanying text and Miller (2017) for additional information on PVA model structure and function.

MWEPA Feeding Dynamics

With the exception of 2018, the observed proportion of wolf pairs documented with live pup(s) in the MWEPA population that were provisioned with food caches in the pup-rearing season generally declined over the period of evaluation (Figure 8). In contrast, Figure 8 shows that this proportion was predicted to remain constant over the time period 2016 – 2021, after which time the proportion of pairs documented with live pup(s) with food caches was to begin steadily declining to a much smaller value. The total number of pairs documented with live pup(s) provisioned with caches remained relatively constant over time (Table 1), while the total number of pairs documented with live pup(s) increased 2.5-fold as the MWEPA population grew rapidly during the period of evaluation (see Figure 1).

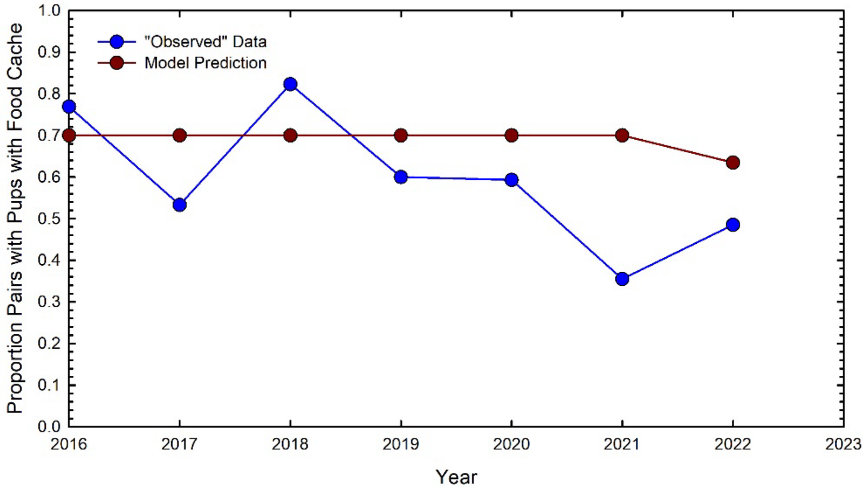

Figure 8. Evaluation of observed vs. predicted levels of supplemental/diversionary feeding among wolf pairs documented with live pup(s) in the MWEPA population. See accompanying text and Miller (2017) for additional information on PVA model structure and function.

Table 1. Total number of wolf pairs documented with live pup(s) in the MWEPA population over the time period 2016-2022, and the subset of those pairs on nearby food caches during the pup-rearing season. Data from USFWS.

Year	Pairs with live pups on food cache (>2 weeks, April – Sept.)	Total pairs
2016	10	13
2017	8	15
2018	14	17
2019	12	20
2020	16	27
2021	11	31
2022	16	33

Conclusion

Overall, the analyses described in this report indicate that the true estimated minimum abundance of the MWEPA population is larger than that predicted by the 2017 PVA model. Additionally, genetic measures of viability – proportional gene diversity retention and mean inbreeding level – are more favorable compared to what was predicted in the PVA. Factors that likely contribute to this observation include:

- Lower adult mortality in the population (15.8%) compared to 18.9% which marked the low end of the range of simulated mortality rates (but also note that the new annual pup mortality rate estimate of 32.4% (based on collared pup mortality rate after six months of 18.5% (new estimate based on the average from 2017 to 2023 of the 183-day pup mortality (phase 2 in Miller 2017), and previous mortality estimate in Miller 2017 prior to collaring pups of 17.0%) since 2015 is slightly higher than the simulated rate of 28.2%);
- A smaller number of wolves removed from the MWEPA for translocation to Mexico; and
- A substantially larger number of wolves (all pups) released into MWEPA from the SAFE population.

It is worth noting that the analysis showed that fewer wolf pairs with documented live pup(s) were provisioned with food caches compared to model predictions. Based on the assumed benefits to pup survival that are to be derived from the presence of these nearby caches, we would expect the reduction in the proportion of packs enjoying this benefit would lead to slightly lower rates of pup survival. Given the high growth rates observed in the MWEPA population – sustained growth since 2009 – this observed increase in pup mortality may be at least partially masked by other management activities that promote observed increases in population abundance.

In contrast to the results for the MWEPA population, the estimated abundance of the SMOCC-N population in Mexico as measured in the field is substantially smaller than that predicted by the 2017 PVA model. Despite the declining rate of growth observed for this population, observed estimates of genetic measures of viability – proportional gene diversity retention and mean inbreeding level – do not diverge to the same extent, suggesting lower levels of sensitivity in these population-wide metrics. Factors that likely contribute to the observed divergence between observed and predicted results include:

- Higher overall mortality of adult wolves (wild born wolves or individuals predicted to survive greater than one year following release or translocation) in the wild (39.0%) compared to what was included in the simulation (note: adult mortality is considered one of the parameters that most impact population performance. Simulations in the 2017 PVA suggested that wolf populations with adult mortality rates above 24.9% have a high probability of extinction). We modeled all future scenarios in Mexico with a 24.9% adult mortality rate (see 5-year evaluation for further discussion);
- A smaller number of wolves with similar survival rates to previous simulations were translocated from MWEPA; and
- A substantially smaller number of wolves with similar survival rates to simulations were released from the SAFE population.

The genetic signature of the initial founding event for this population, along with selection of individuals for translocation and release based on genetic measures of relatedness, are likely to at least partially explain the relatively favorable genetic metrics in the population, even as that population has remained at a small abundance since the beginning of this evaluation period.

Finally, the analyses described here indicate that the true abundance of the SAFE population is now about 40% larger than that simulated in the 2017 PVA. This difference is a result of the expansion in the number of institutions participating in the SAFE program and the number of available spaces within those institutions, which results in a functional increase in the overall size of the ex situ population. SAFE program managers recognize the difficulties that can result from this expansion and are working to avoid overcrowding, etc. where appropriate. Interestingly, even with this expansion of the ex situ population, the genetic metrics of interest to the program show high levels of concordance with 2017 PVA prediction that emerge from simulating a much smaller population through time. This observation is likely a consequence of both the restricted genetic base present at the time of the PVA, as well as the positive benefits of careful genetic management of the ex situ population leading to minimal losses of gene diversity through time.

Taken together, the results of this analysis further reinforce the idea that significant differences between intended and actual schedules of translocation and release efforts play a major role in explaining deviations in predicted vs. actual abundance trajectories for Mexican wolf populations in both the United States and, in particular, Mexico. These results confirm the value of the 2017 PVA model as an effective tool determining the utility of management actions guided by the 2022 Mexican Wolf Recovery Plan, Second Revision and the associated Recovery Implementation Strategy.

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Appendix

Table I. Data used for Figure 1, characterizing the MWEPA population of Mexican wolves as evaluated in the field (Observed) and in the PVA model described in this report (Predicted).

	Number of Wolves		% Gene Diversity Retained		% Gene Diversity Retained (SAFE)		Mean Inbreeding Coefficient	
Year	Observed	Predicted	Observed	Predicted	Observed	Predicted	Observed	Predicted
2015	98	98	NA	NA	NA	NA	NA	NA
2016	114	87.8 (11.2)	75.91	74.10	91.38	88.92	0.166	0.215
2017	117	108.3 (23.4)	75.48	73.96	90.94	88.78	0.200	0.216
2018	131	123.1 (31.0)	74.54	75.25	90.13	90.46	0.220	0.220
2019	163	136.3 (42.8)	74.59	74.63	90.22	90.14	0.219	0.226
2020	186	160.0 (53.8)	75.69	74.50	91.65	90.17	0.203	0.229
2021	196	184.6 (66.6)	76.23	74.45	92.41	90.20	0.206	0.230
2022	242	211.1 (77.4)	76.20	75.26	92.39	91.28	0.209	0.230
2023	257	229.0 (84.8)	76.09	74.99	92.30	90.97	0.211	0.234

Table II. Data used for Figure 2, characterizing the SMOCC population of Mexican wolves as evaluated in the field (Observed) and in the PVA model described in this report (Predicted).

	Number of Wolves		% Gene Diversity Retained		% Gene Diversity Retained (SAFE)		Mean Inbreeding Coefficient	
Year	Observed	Predicted	Observed	Predicted	Observed	Predicted	Observed	Predicted
2015	17	17	NA	NA	NA	NA	NA	NA
2016	35	27.2 (3.6)	66.26	69.10	79.76	82.92	0.161	0.149
2017	30	36.6 (7.0)	73.88	77.13	89.01	92.58	0.155	0.159
2018	25	46.7 (11.4)	75.53	78.78	91.33	94.70	0.156	0.171
2019	30	63.5 (16.6)	75.53	78.58	91.35	94.91	0.156	0.174
2020	35	79.2 (23.1)	77.99	79.43	94.43	96.14	0.150	0.179
2021	42	105.7 (31.6)	79.95	79.43	96.92	96.23	0.170	0.178
2022	35	124.4 (39.3)	79.74	79.80	96.68	96.79	0.166	0.181
2023	NA	NA	NA	NA	NA	NA	NA	NA

Table III. Data used for Figure 3, characterizing the SAFE population of Mexican wolves as evaluated in the field (Observed) and in the PVA model described in this report (Predicted).

	Number of Wolves		% Gene Diversity Retained		% Gene Diversity Retained (SAFE)		Mean Inbreeding Coefficient	
Year	Observed	Predicted	Observed	Predicted	Observed	Predicted	Observed	Predicted
2015	243	214	NA	NA	NA	NA	NA	NA
2016	251	195.9 (7.9)	83.07	83.33	NA	NA	0.130	0.132
2017	281	188.9 (15.0)	83.00	83.31	NA	NA	0.136	0.133
2018	317	193.0 (20.6)	82.70	83.19	NA	NA	0.138	0.135
2019	369	203.9 (24.5)	82.68	82.79	NA	NA	0.141	0.140
2020	389	222.0 (25.3)	82.59	82.62	NA	NA	0.146	0.146
2021	387	220.9 (24.0)	82.49	82.54	NA	NA	0.147	0.153
2022	366	245.8 (15.2)	82.48	82.45	NA	NA	0.149	0.158
2023	356	251.2 (8.4)	82.44	82.43	NA	NA	0.151	0.163

Table IV. Data used for Figure 4, characterizing the release schedule of Mexican wolves from the MWEPA population to the SMOCC population in Mexico as implemented in the field (Observed) and in the PVA model described in this report (Predicted).

	Observed			Predicted		
Year	Adults	Yearlings	Pups	Adults	Yearlings	Pups
2016	0	0	0	0	0	0
2017	0	0	0	4	0	6
2018	0	0	0	0	0	0
2019	0	0	0	4	0	6
2020	3	0	5	0	0	0
2021	2	0	0	4	0	6
2022	4	2	0	0	0	0
2023	0	0	0	4	0	6

Table V. Data used for Figure 5, characterizing the release schedule of Mexican wolves from the SAFE population to the MWEPA population in the United States as implemented in the field (Observed) and in the PVA model described in this report (Predicted).

	Observed			Predicted		
Year	Adults	Yearlings	Pups	Adults	Yearlings	Pups
2016	0	0	6	0	0	0
2017	0	0	4	8	0	12
2018	0	0	8	0	0	0
2019	0	0	12	0	0	0
2020	0	0	20	0	0	0
2021	0	0	22	8	0	12
2022	0	0	11	0	0	0
2023	0	0	16	0	0	0

Table VI. Data used for Figure 6, characterizing the release schedule of Mexican wolves from the SAFE population to the SMOCC population in Mexico.

	Observed			Predicted		
Year	Adults	Yearlings	Pups	Adults	Yearlings	Pups
2016	0	0	0	0	0	9
2017	0	0	0	4	0	6
2018	4	3	5	4	0	6
2019	0	0	0	4	0	6
2020	2	1	0	4	0	6
2021	2	0	2	4	0	6
2022	0	0	0	0	0	0
2023	0	0	0	0	0	0

Table VII. Data used for Figure 7, characterizing the release schedule of Mexican wolves from the SAFE population to the MWEPA population in the United States and to the SMOCC population in Mexico.

	Observed			Predicted		
Year	Adults	Yearlings	Pups	Adults	Yearlings	Pups
2016	0	0	6	0	0	9
2017	0	0	4	12	0	18
2018	4	3	13	4	0	6
2019	0	0	12	4	0	6
2020	2	1	20	4	0	6
2021	2	0	24	12	0	18
2022	0	0	11	0	0	0
2023	0	0	16	0	0	0

Table VIII. Data used for Figure 8, specifying the observed and predicted proportion of Mexican wolf pairs in the MWEPA population with pups with a nearby food cache.

	Proportion of Pairs	
Year	Observed	Predicted
2016	0.769	0.700
2017	0.533	0.700
2018	0.823	0.700
2019	0.600	0.700
2020	0.593	0.700
2021	0.355	0.700
2022	0.485	0.635
2023		

ADDENDUM:
Exploring Recommended Conditions for Successful Establishment of Mexican Wolves in northern Mexico

Introduction

In response to the comparatively poor demographic performance of the wolf population in Mexico over the period of this evaluation, the Service and its partners are interested in evaluating alternative methods of transferring wolves from other sources that can help to establish a viable wolf population within historic range in Mexico. In particular, the number of individuals to introduce annually into suitable habitat, the demographic composition of each group, and the survival of those individuals after their release are key parameters that collectively influence the likelihood of successfully establishing a viable population. A set of scenarios was developed using the current simulation model to shed light on these important questions.

PVA Model Characteristics

For this additional analysis, the base model structure was largely unchanged from that described in this report and discussed in detail in Miller (2017), with the following modifications:

- The second population in Mexico, labeled SMOCC-S representing the southern Sierra Madre Occidental habitat area, was removed from the simulation. All simulated wolf transfer efforts target the northern Sierra Madre Occidental habitat, designated SMOCC-N in all models comprising this broad analysis.
- The model featured a start date of early spring 2023, with initial population abundances tallied as of 31 December 2022. This more contemporary start date (the initial PVA published in 2017 featured census data as of 31 December 2015) made it necessary to update the studbook data file with the latest data on living individuals in both in situ and ex situ populations, their ancestry and, where suitable, the identity of their mate. This new information was painstakingly compiled and analyzed by L. Faust (Lincoln Park Zoo, Chicago IL) and C. Gardner (USFWS, Albuquerque NM) to create the updated studbook file. Because of some uncertainty in the exact identity and relationships of some young wolves in the wild MWEPA population, it was necessary to “create” these individuals in the studbook based on the best information on their parentage, etc. More information on this studbook preparation is available from the Service on request.
- Based on the updated studbook, the MWEPA population size as of 31 December 2022 was initialized at 240 individuals, and the SAFE (previously SSP) population at 355 individuals (aged one year and older). Additionally, since no wolves currently in Mexico are wearing radio collars, there is considerable uncertainty in the number of animals alive there as of the start date of this analysis. Therefore, the model development group elected to adopt a conservative approach and set initial population abundance in the SMOCC-N habitat area to zero.
- From analysis of recent wild population mortality data discussed elsewhere in this report, the mean annual adult mortality rate for the MWEPA population was set at 18.9%. This value represents the low end of the range of adult mortality rates previously tested in the 2017 PVA. Adult mortality for the SMOCC-N population was set at 24.9%, representing the high end of acceptable mortality that emerged from analysis of results from the 2017 PVA. A wolf population in the SMOCC-N habitat would be expected to exhibit at least a moderate rate of population growth with this mortality rate, and by extension possess at least a reasonable opportunity for successful establishment following sufficient releases of wolves to that habitat.

- As described elsewhere in this report, the number of wolves recently comprising the SAFE population was and is well above the stated carrying capacity (K = 255: 2017 PVA) of the member institutions making up the ex situ management program. A reduction in the number of individuals managed within that program is generally considered an essential goal of future population management. Consequently, the added analysis included an initial carrying capacity of 370 individuals – roughly equal to the current abundance – but with a gradual linear reduction in K to 300 individuals over a five-year timespan. This would correspond in reality to calendar year 2027.
- All scenarios were simulated for 15 years, i.e., spring 2023 – spring 2037.

With this general model structure as a guide, the following parameters were systematically varied to create the full set of wolf transfer scenarios:

1. All wolf transfers were conducted annually for ten years, beginning in model year three (calendar year 2025) and ending in model year twelve (calendar year 2034).
2. Four distinct wolf cohorts were included in the analysis:
    a. Adults only;
    b. Yearlings (Age-1 wolves) only;
    c. Adults and yearlings; and
    d. Adults with pups (Age-0 wolves).

   Each distinct model scenario featured the same type of cohort being transferred throughout the ten-year duration of the transfer process.
3. A total of 6, 12 or 18 wolves were transferred each year. When yearlings or pups were transferred with adults, the number of younger wolves was always twice the number of adults; for example, a total of 12 mixed-age wolves would be made up of four adults and eight yearlings or pups.
4. All scenarios featured an equal sex ratio among transferred wolves. When the total number of wolves dictated an odd number of wolves of a given age class to be transferred, the majority of individuals was made to be female (e.g., five females and four males).
5. Transfers were conducted assuming three separate mechanics:
    a. All wolves released to SMOCC-N from the SAFE population;
    b. All wolves translocated to SMOCC-N from the MWEPA population;
    c. A combination of transfer methods, i.e., 50:50 distribution of released wolves from SAFE and translocated wolves from MWEPA.
6. Each unique scenario defined by cohort type and transfer strategy was tested across a range of plausible post-release survival rates. These rates described the probability of a transferred wolf surviving from its introduction to the SMOCC-N population to the time of the next model census just before breeding the following spring. This duration aligns with field data collected by the Service and partners on survival rates of released and translocated wolves in the MWEPA population. It is acknowledged here that ultimate success of a transfer program is measured by the number of transferred wolves that survive to breeding age and successfully reproduce. This process is captured in the PVA model through simulation of continued survival of individuals through time and their successfully pairing and reproduction. The shorter-term six-month survival window is a focus here both because of the explicit data provided by the Service and the explicit methods by which this survival can be best implemented in the model

   Six-month post-release survival rates chosen for a given scenario ranged from a minimum of 0.1 to a maximum of 0.7 in increments of 0.1. The approximate midpoint of these ranges – 0.5 for pups, 0.4 for yearlings, and 0.3 for adults – generally correspond to the mean post-release survival rates observed in earlier transfer efforts and used in the 2017 PVA (see Table 3 in Miller 2017 for more details).

Data used in the 2017 PVA showed no meaningful difference in post-release survival of pups (and, by extension, yearlings) when either released from the ex situ SAFE population or translocated from the in situ MWEPA population. In contrast, the post-release survival among adults released from the SAFE population was markedly lower compared to those that were translocated from the MWEPA population. This feature was carried over to the present analysis, allowing for an examination of the relative efficacy of each transfer strategy. In all scenario sets that included transfers of wolves from the SAFE population, adult wolves transferred to Mexico were given a reduced rate of post-release survival compared to wolves transferred from the MWEPA population. For example, if a given scenario featured a post-release survival of adults transferred from MWEPA equal to 0.5, the corresponding survival rate for wolves transferred to Mexico from the SAFE population was set at 0.3. This difference was maintained across the sliding scale of post-release survival rates defining the scenarios in this analysis; in this way, a given transfer scenario would be characterized by broadly poor, mid-range or favorable survival rates among the wolves making up that transfer cohort.

Using the above rules, the various combinations of parameters resulted in a grand total of 250 unique scenarios making up the analysis. Each scenario was run across 1000 iterations. The output from each scenario chosen for analysis included (a) the probability that the SMOCC-N population would exceed 100 individuals (Age-1 and older) at the end of the 15-year simulation; (b) the average size of the SMOCC-N population among those iterations where the population was extant at the end of the simulation; and (c) average population gene diversity (expected heterozygosity) among surviving populations at the end of the 15-year simulation.

Results and Conclusions

The likelihood of successfully establishing a Mexican wolf population in the Sierra Madre Occidental (designated SMOCC-N in the 2017 PVA) within 15 years is highly variable and depends strongly on the type of individuals chosen for transfer, the number of wolves transferred each year of the program, and the survival rate of those individuals following their transfer (Figure A-1; Tables A-1 to A-3). These results illustrate the following observations from the analysis:

- Under the conditions simulated here, a total of six wolves transferred each year for ten years – regardless of the transfer method used or the extent of post-transfer survival – is inadequate to successfully establish a demographically healthy wolf population in northern Mexico. The low rate of introducing wolves to an empty habitat as simulated here is insufficient to overcome the stochastic forces that act to destabilize small populations.
- Compared to transfer cohorts composed of mixed-age groups, strategies focusing on transferring only adults or yearlings were slightly more successful in establishing populations of at least 100 wolves in northern Mexico within 15 years. Replacing some of the adults in a transfer cohort with younger individuals reduces the total number of wolves that survive to breeding age, thereby lowering the aggregate longer-term reproductive output of that cohort.
- Under the conditions and assumptions used to construct this analysis, a transfer program composed of translocating wild wolves from the MWEPA population generally exhibits a greater likelihood of successful Mexiso population establishment compared to a transfer program composed only of releasing wolves from the SAFE population (i.e., compare plots A and B of Figure A-1 and Tables A-1 and A-2). This is best explained as a consequence of the simulated lower rates of post-release survival among adults transferred to Mexico from the SAFE population. However, the comparatively more robust genetic structure of the source SAFE population means that gene

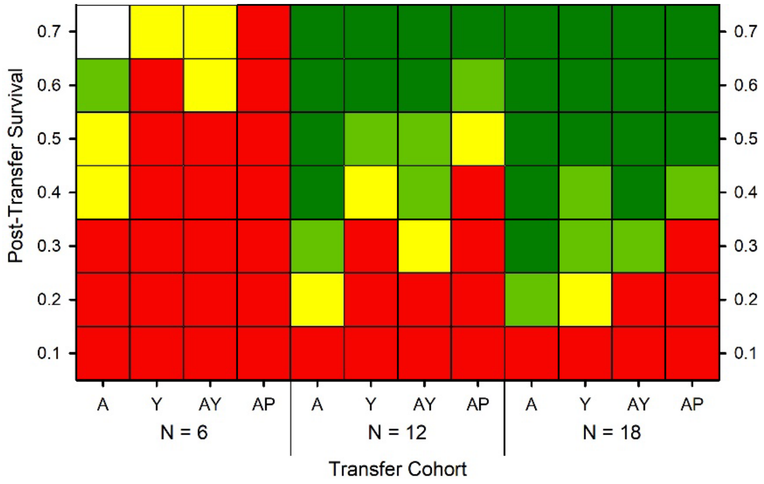
diversity retention in the Mexico population can be greater under a Release-Only transfer strategy. For example, at the highest levels of predicted success of a release program – namely 18 wolves released each year with a mean post-release survival rate of 0.5 (adults) to 0.7 (pups), mean gene diversity in the Mexico population is about 6.7% higher (GD = 0.800: Table A-1, bottom right) than in the same population established solely through translocation from MWEPA (GD = 0.750: Table A-2, bottom right). This is to be expected given the simulation mechanic in which the SAFE source population is more intensively managed than the wild MWEPA population to reduce gene diversity loss resulting from inbreeding and genetic drift.

- When transferring the larger number of 18 wolves each year during a program of this type, a post-transfer survival rate of at least 0.4 appears to provide the greatest chance of establishing a population of at least 100 wolves in northern Mexico within 15 years, with a transfer scheme focused on translocation offering the best oppoortunity for demographic success. This level of survival is similar to survival rates used in the original 2017 PVA, albeit with some improvement necessary for adults released from the SAFE population (post-transfer survival of 0.284: Table 3 of Miller 2017).
- As simulated here, the Combination transfer scheme – featuring a 50:50 mix of both release from the SAFE population and translocation from the MWEPA population – does not appear to offer measurable benefits over either base transfer strategy. For a given total transfer effort (i.e., total number of wolves transferred), the lower post-relase survival rate of adults transferred from the SAFE population and the 50% reduction in the number of wolves transferred from the MWEPA population act in synergy to dampen the overall likelihood of successful Mexico population establishment.

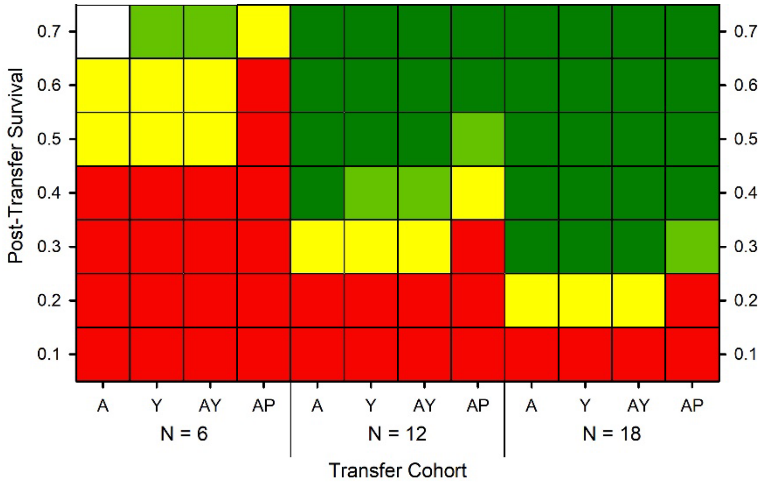
Finally, Table A-4 shows final population size and gene diversity in the source SAFE and MWEPA populations to facilitate an examination of the cost of the tested transfer strategies on source population viability. The SAFE population, constrained by a lower carrying capacity, demonstrates a marked reduction in population abundance in the latter years of a relatively aggressive Release-Only transfer strategy, as shown in the top-right row of results data in Table A-4. However, since individuals selected for release generally represent at least slightly genetically over-represented founders, the cost to population gene diversity of this reduced abundance is very slight. Overall, impacts on source population gene diversity are negligible for all transfer strategies.

Lastly, it is important to remember that this report is not designed to include specific recommendations for implementing a particular wolf transfer strategy in Mexico. Instead, the results of the many complex simulations are presented in an attempt to provide population managers with valuable information on predicted outcomes of alternative management strategies, with the intention that managers will use the quantitative results to inform thoughtful decision-making designed to improve opportunities for Mexican wolf recovery.

C. Release Only



A. Translocate Only



B. Combination

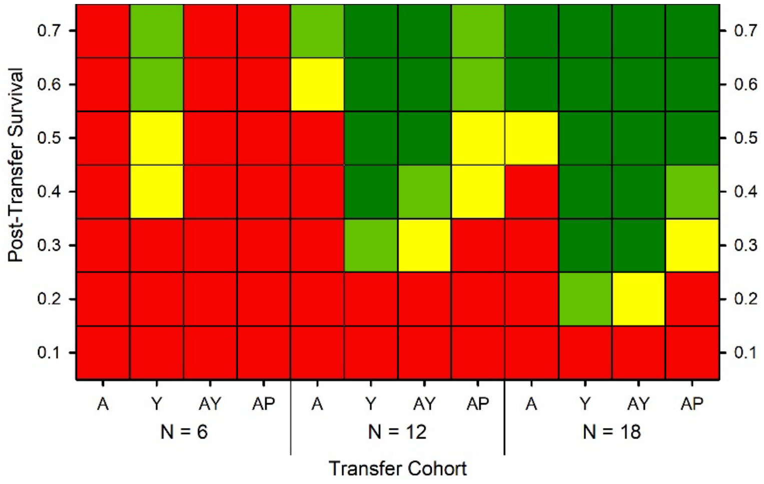


Figure A-1. Probability of the SMOCC-N wolf population in Mexico growing to at least 100 individuals (Prob[N>100]) after 15 years under a range of simulated transfer strategies and post-transfer (six-month) survival rate estimates. Transfer cohort definitions: A, adults; Y, yearlings; AY, adults with yearlings; AP, adults with pups.
Color codes for each cell define Prob[N>100]:
Red = Probability < 0.25;
Yellow = 0.25 < Probability < 0.5;
Light green = 0.5 < Probability < 0.75;
Dark green = Probability > 0.75.
See text for additional information on model structure and function.

Table A-1. Results of simulation models evaluating the efficacy of the Release-Only transfer strategy on establishing a population of Mexican wolves in the northern Sierra Madre Occidental (SMOCC-N). Column headings define the details of transfer strategies, according to the number of wolves transferred each year during the simulated program (N = 6, 12 or 18) and the cohort type used in the transfer (A, adults; Y, yearlings; AY, adults and yearlings; AP, adults and pups). Row headings at the far left of the table give the range of post-transfer survival rates. Each cell represents a unique model scenario, with numerical output listed as the probability of the SMOCC-N wolf population abundance exceeding 100 individuals after 15 years (top), the mean number of wolves across iterations in which the population was extant after 15 years (middle), and the mean population gene diversity at the end of the simulation (bottom). See accompanying text for more information on model structure and function.

Release Only

	N = 6				N = 12				N = 18			
	A	Y	AY	AP	A	Y	AY	AP	A	Y	AY	AP
0.1	0.000 17.0 0.558	0.001 13.5 0.514	0.000 14.2 0.516	NA	0.022 34.2 0.705	0.003 22.0 0.670	0.002 26.5 0.678	NA	0.111 58.2 0.745	0.023 38.0 0.729	0.058 43.4 0.730	NA
0.2	0.022 34.0 0.700	0.003 22.3 0.674	0.004 20.4 0.643	0.002 15.4 0.581	0.289 81.7 0.761	0.071 50.2 0.747	0.045 44.7 0.739	0.017 32.9 0.721	0.61 120.3 0.779	0.255 79.5 0.769	0.218 74.4 0.765	0.081 52.7 0.752
0.3	0.133 60.4 0.745	0.011 35.4 0.726	0.025 34.8 0.714	0.001 19.8 0.653	0.616 120.1 0.778	0.229 76.3 0.769	0.262 81.3 0.768	0.047 44.1 0.745	0.871 157.3 0.791	0.542 112.3 0.783	0.599 118.2 0.784	0.205 71.9 0.768
0.4	0.277 80.6 0.761	0.075 50.0 0.744	0.077 52.3 0.745	0.015 31.0 0.716	0.826 147.3 0.787	0.457 101.4 0.779	0.536 110.9 0.781	0.193 71.1 0.767	0.961 175.3 0.796	0.748 135.7 0.791	0.852 153.4 0.793	0.529 110.1 0.784
0.5	0.443 102.2 0.771	0.136 61.7 0.757	0.186 69.7 0.759	0.04 44.0 0.740	0.909 164.5 0.792	0.633 123.7 0.786	0.746 137.3 0.788	0.431 99.0 0.779	0.981 183.3 0.799	0.865 156.0 0.795	0.960 174.8 0.797	0.821 144.5 0.791
0.6	0.636 122.3 0.778	0.209 74.7 0.766	0.315 85.0 0.769	0.121 59.3 0.756	0.961 175.8 0.795	0.729 135.6 0.790	0.869 155.7 0.793	0.637 123.5 0.786	0.996 186.5 0.800	0.923 166.3 0.797	0.980 180.6 0.799	0.992 160.9 0.796
0.7	NA	0.354 89.2 0.774	0.441 101.0 0.775	0.190 71.3 0.765	NA	0.831 149.7 0.793	0.932 168.9 0.796	0.814 143.2 0.791	NA	0.965 174.9 0.800	0.991 184.7 0.801	0.948 172.5 0.799

Table A-2. Results of simulation models evaluating the efficacy of the Translocate-Only transfer strategy on establishing a population of Mexican wolves in the northern Sierra Madre Occidental (SMOCC-N). Column headings define the details of transfer strategies, according to the number of wolves transferred each year during the simulated program (N = 6, 12 or 18) and the cohort type used in the transfer (A, adults; Y, yearlings; AY, adults and yearlings; AP, adults and pups). Row headings at the far left of the table give the range of post-transfer survival rates. Each cell represents a unique model scenario, with numerical output listed as the probability of the SMOCC-N wolf population abundance exceeding 100 individuals after 15 years (top), the mean number of wolves across iterations in which the population was extant after 15 years (middle), and the mean population gene diversity at the end of the simulation (bottom). See accompanying text for more information on model structure and function.

Translocate Only

	N = 6				N = 12				N = 18			
	A	Y	AY	AP	A	Y	AY	AP	A	Y	AY	AP
0.1	0.000 13.8 0.497	0.000 14.0 0.515	0.000 15.0 0.499	0.000 12.0 0.452	0.010 28.7 0.651	0.014 31.1 0.653	0.010 27.9 0.641	0.001 20.1 0.605	0.075 51.1 0.692	0.069 49.2 0.690	0.065 47.1 0.686	0.013 31.4 0.666
0.2	0.017 30.2 0.650	0.009 28.9 0.649	0.012 29.2 0.641	0.001 20.5 0.610	0.169 68.3 0.708	0.17 68.5 0.707	0.172 65.8 0.706	0.053 45.8 0.692	0.474 103.4 0.725	0.490 103.9 0.725	0.414 98.9 0.723	0.198 71.8 0.713
0.3	0.066 50.7 0.692	0.058 48.9 0.691	0.055 45.2 0.686	0.011 30.0 0.666	0.468 102.6 0.726	0.471 104.0 0.725	0.464 102.8 0.724	0.216 73.8 0.715	0.800 145.0 0.737	0.797 143.9 0.737	0.792 143.6 0.736	0.535 109.8 0.729
0.4	0.170 66.6 0.707	0.161 68.2 0.708	0.173 66.5 0.706	0.053 44.5 0.691	0.723 132.5 0.734	0.719 132.4 0.734	0.716 130.4 0.733	0.423 99.0 0.726	0.930 166.7 0.743	0.934 169.0 0.743	0.928 165.0 0.742	0.803 142.7 0.738
0.5	0.304 84.7 0.178	0.327 87.2 0.717	0.324 87.0 0.717	0.104 57.5 0.705	0.875 153.7 0.739	0.894 156.8 0.739	0.864 154.2 0.739	0.641 122.7 0.733	0.980 178.3 0.745	0.978 180.8 0.746	0.98 177.6 0.745	0.910 161.3 0.742
0.6	0.457 102.1 0.725	0.469 103.8 0.724	0.482 93.1 0.724	0.219 73.2 0.714	0.938 167.4 0.743	0.935 168.4 0.743	0.935 167.5 0.742	0.806 142.5 0.738	0.990 182.3 0.747	0.994 183.9 0.747	0.991 183.8 0.747	0.951 172.6 0.745
0.7	NA	0.617 120.1 0.730	0.613 118.7 0.730	0.312 83.7 0.721	NA	0.980 176.8 0.745	0.957 176.3 0.744	0.873 155.4 0.741	NA	0.997 185.9 0.748	0.996 184.6 0.748	0.975 178.9 0.747

Table A-3. Results of simulation models evaluating the efficacy of the Combination transfer strategy (50:50 distribution of Release and Translocation strategies) on establishing a population of Mexican wolves in the northern Sierra Madre Occidental (SMOCC-N). Column headings define the details of transfer strategies, according to the number of wolves transferred each year during the simulated program (N = 6, 12 or 18) and the cohort type used in the transfer (A, adults; Y, yearlings; AY, adults and yearlings; AP, adults and pups). Row headings at the far left of the table give the range of post-transfer survival rates. Each cell represents a unique model scenario, with numerical output listed as the probability of the SMOCC-N wolf population abundance exceeding 100 individuals after 15 years (top), the mean number of wolves across iterations in which the population was extant after 15 years (middle), and the mean population gene diversity at the end of the simulation (bottom). See accompanying text for more information on model structure and function.

Combination

	N = 6				N = 12				N = 18			
	A	Y	AY	AP	A	Y	AY	AP	A	Y	AY	AP
0.1	0.000 8.5 0.288	0.001 16.2 0.525	0.000 9.6 0.389	0.000 8.6 0.363	0.001 16.1 0.547	0.014 31.8 0.684	0.004 25.8 0.644	0.001 17.1 0.584	0.002 20.8 0.616	0.079 53.3 0.723	0.031 39.9 0.702	0.009 25.7 0.657
0.2	0.000 8.6 0.290	0.018 31.6 0.676	0.001 15.2 0.587	0.000 11.2 0.518	0.001 16.6 0.565	0.208 72.3 0.741	0.115 57.2 0.726	0.014 34.1 0.692	0.01 25.4 0.643	0.592 115.2 0.758	0.377 94.2 0.751	0.128 61.2 0.730
0.3	0.001 9.5 0.325	0.085 54.0 0.721	0.014 32.7 0.708	0.001 15.2 0.610	0.001 19.9 0.573	0.532 110.8 0.759	0.352 90.2 0.750	0.026 39.2 0.736	0.019 30.8 0.650	0.871 156.6 0.771	0.724 134.5 0.765	0.379 93.8 0.748
0.4	0.002 14.9 0.490	0.261 79.0 0.739	0.016 31.0 0.713	0.002 20.7 0.674	0.031 42.2 0.698	0.804 144.7 0.768	0.618 120.8 0.762	0.255 79.1 0.741	0.214 72.2 0.733	0.964 177.7 0.775	0.915 163.8 0.772	0.673 126.6 0.759
0.5	0.002 21.3 0.595	0.46 102.0 0.751	0.029 39.8 0.735	0.008 27.0 0.709	0.201 70.1 0.733	0.899 164.2 0.773	0.790 144.4 0.770	0.443 100.9 0.751	0.537 111.4 0.752	0.988 184.1 0.778	0.976 178.2 0.777	0.831 148.2 0.765
0.6	0.016 28.1 0.645	0.558 112.4 0.758	0.054 49.1 0.745	0.015 33.4 0.763	0.39 94.4 0.747	0.944 171.0 0.777	0.889 158.9 0.774	0.610 119.8 0.758	0.752 135.0 0.761	0.997 187.9 0.780	0.995 183.1 0.779	0.919 162.9 0.768
0.7	0.036 37.5 0.678	0.655 125.4 0.763	0.112 58.8 0.754	0.031 38.7 0.739	0.604 116.8 0.755	0.962 177.2 0.780	0.940 167.3 0.778	0.722 134.1 0.762	0.853 153.9 0.766	0.997 186.9 0.782	0.994 185.5 0.782	0.953 172.9 0.771

Table A-4. Demographic and genetic characteristics of the SAFE and MWEPA source populations from simulation models evaluating the efficacy of the each transfer strategy on establishing a population of Mexican wolves in the northern Sierra Madre Occidental (SMOCC-N). Column headings are defined as in Tables 2 through 4. Transfer strategies abbreviated as “Release” (Release-Only); “Transloc” (Translocate Only): and “Combo” (Combination). Data for final (year 15) population abundance (N) and gene diversity (GD) are reported as proportional values calculated relative to a “control” scenario in which transfers were not implemented. For example, “N: 0.752” indicates a transfer scenario category in which the final abundance of the source population is 75.2% of that population when transfers are not implemented in the “control” scenario. Note that the values reported here are averaged across all post-transfer survival rates for a given transfer strategy (e.g., value of N = 0.912 for the “Release / N = 12 / AY” scenario set represents an average across the range of post-transfer survival rates tested with that strategy). See accompanying text for more information on model structure and function.

	N = 6				N = 12				N = 18			
	A	Y	AY	AP	A	Y	AY	AP	A	Y	AY	AP
Release (SAFE)	N: 0.991 GD: 1.000	N: 0.986 GD: 0.999	N: 0.990 GD: 1.000	N: 0.988 GD: 0.999	N: 0.917 GD: 0.998	N: 0.923 GD: 0.998	N: 0.912 GD: 0.998	N: 0.919 GD: 0.999	N: 0.759 GD: 0.993	N: 0.802 GD: 0.995	N: 0.756 GD: 0.993	N: 0.752 GD: 0.995
Transloc (MWEPA)	N:0.994 GD: 1.000	N: 0.978 GD: 1.000	N: 0.991 GD: 1.000	N: 0.993 GD: 1.000	N: 0.977 GD: 0.999	N: 0.967 GD: 0.999	N: 0.970 GD: 0.999	N: 0.983 GD: 1.000	N: 0.940 GD: 0.996	N: 0.922 GD: 0.999	N: 0.931 GD: 0.996	N: 0.966 GD:0.999
Combo (SAFE)	N: 0.998 GD: 1.000	N: 0.998 GD: 1.000	N: 0.992 GD: 1.000	N: 0.993 GD: 1.000	N: 0.993 GD: 1.000	N: 0.987 GD: 0.999	N: 0.989 GD: 1.000	N: 0.988 GD: 1.000	N: 0.981 GD: 1.000	N: 0.960 GD: 0.999	N: 0.976 GD: 0.999	N: 0.978 GD: 0.999
Combo (MWEPA)	N: 0.997 GD: 1.000	N: 0.992 GD: 1.000	N: 0.995 GD: 1.000	N: 0.994 GD: 1.000	N: 0.993 GD: 1.000	N: 0.993 GD: 0.999	N: 0.988 GD: 1.000	N:0.993 GD: 1.000	N: 0.981 GD: 0.999	N: 0.982 GD: 0.999	N: 0.979 GD: 1.000	N: 0.986 GD: 1.000