**SUPPLEMENTARY MATERIAL 1**

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**Field Methods**

We conducted simulations to evaluate subsampling schemes that would minimize the variance in the overall estimate of population size ($N$). We considered a constant coefficient of variation (CV) of $N$ by water source would yield a robust overall estimate of $N$ with low variance. Thus, or simulation goal was to determine the number of samples needed for each water source that yielded a constant CV($\hat{N}$) by water source. Simulations used a range of the likely number of deer using the low, medium, high, and very-high use water sources, a wide range of probabilities of capture ($p$), and 5 sampling occasions, which was the number of sampling occasions we had in 2015 and 2016 (we had one sampling occasion in 2015 with a high proportion of samples ruined due to rain, so we discarded that occasion). We ran 100 iterations for each simulation scenario (i.e., combination of likely population size and $p$). For each simulation scenario, an estimate of $N$ and its SE was generated, from which we calculated CV($\hat{N}$). To determine sample size, we calculated the $p$ required for a CV($\hat{N}$) = 0.05 ($p_{subsamp}$). We then estimated the number of samples needed as the likely population size* $p_{subsamp}$. For the likely population size, we used the middle value for the range of likely population sizes for each water source classification. For example, based on field observations we estimated that 10-30 deer used the low-use water sources; we

used 20 as the likely population size. For a population size of 20, $p = 0.47$ was needed to get $CV(\hat{N}) = 0.05$; thus $20 \times 0.47 = 10$ (we always rounded up) subsamples were required for that water source. An additional sub-sampling rule was added in which a minimum of 1 sample per transect per session was analyzed, which could increase the number of subsamples required. We only used this sub-sampling process for years 2015 and 2016. We collected fewer samples in 2017 (fewer sampling occasions and we only collected high quality samples), and so all samples from that year were analyzed.

**Genetic Analysis**

DNA was extracted from pellet scrapings using a modified AquaGenomic Stool and Soil protocol (MultiTarget Pharmaceuticals LLC, Colorado Springs, CO). Modifications included the addition of 450 µL of AquaGenomic solution to pellet scrapings, the use of 1.0 mm silica/zirconium beads (BioSpec Products Inc., Bartlesville, OK) for cell lysis, and the addition of 12 mAU proteinase K (Qiagen Inc., Valencia, CA) for recovery of mitochondrial DNA. Lastly, 150 µL of AquaPrecipi solution (MultiTarget Pharmaceuticals) was added to cell lysate to remove PCR inhibitors present in fecal samples.

We amplified fifteen dinucleotide microsatellite markers plus three sexing loci in a single 10 µL reaction consisting of 5x Qiagen Multiplex PCR Master Mix, 10 µg of bovine serum albumin, 100uL of a primer cocktail of 18 multiplexed loci at varying concentrations (Table S1) and 1 µL of genomic DNA. Reactions were brought to volume with nuclease-free water. Thermalcycling conditions for the multiplexed loci were as follows: initial denaturation of 15 minutes at 95 °C, followed by 35 cycles of [95 °C for 30 seconds, 60 °C for 90 seconds, 72 °C for 60 seconds], and a final elongation of 30 minutes at 60 °C. For each locus, one primer was fluorescently tagged on the 5' end with NED, PET, VIC (Applied Biosystems, Carlsbad, CA) or

6-FAM (Sigma-Aldrich, St. Louis, MO). Negative and positive controls were included on each genotyping run. PCRs were run on BioRad C1000 and MyCycler thermalcycler machines (Bio-Rad Laboratories Inc., Hercules, CA).

Amplification products were visualized on a 2% agarose gel prestained with GelRed. Products were diluted accordingly, ethanol-precipitated to remove salts, and submitted for fragment size analysis on the ABI 3730 DNA analyzer (Applied Biosystems) at the Oregon State University Center for Genome Research and Biocomputing (Corvallis, OR). We used GeneScan 500 LIZ dye size standard and called allele sizes in GeneMapper v.4.1 (Applied Biosystems).

Samples were initially amplified in three separate PCR reactions each; those that produced data at fewer than 50% of the loci in the first three replicates were considered poor quality and were not rerun. Samples that produced partial genotypes at ≥ 50% of microsatellite loci were rerun 3-6 more times depending on the completeness of initial replicates, while samples that produced complete and consistent genotypes in the first three replicates were considered finalized. For a genotype to be accepted for a particular locus, each allele in a heterozygote genotype had to be observed twice, while the single allele in a homozygote genotype had to be observed three times. Any sample that consistently showed more than two alleles at a single locus was considered contaminated and removed. One locus ("B") was monomorphic across all years and was not included in identification analyses

Using the online individual-identification program CERVUS version 3.0.3 (Kalinowski et al. 2007) and the population-specific allele frequencies tabulated for this population, we estimated the cumulative probability of identity for unrelated deer (PID) and for siblings (PIDsibs) (Waits et al. 2001) for all 14 microsatellite loci, and then for decreasing numbers of loci to investigate the effect of missing data on PID. Samples that produced data at 10 or more of the remaining 14

microsatellite loci were used in the individual identification analyses, to maintain a maximum PID of $1x10^{-4}$ and PIDsibs of $1x10^{-2}$

TABLE S1. Microsatellite loci used for individual analysis of desert mule deer (*Odocoileus hemionus eremicus*) fecal samples from the Little Chuckwalla Mountains, California, USA, 2015–2017, with fluorescent dye labels, primer concentrations and references for the original primer publication.

| Marker Name | Reference | Dye label | primer concentration (uM) |
|---|---|---|---|
| Locus M | Jones et al. 2000 | 6-Fam | 0.05 |
| Locus P | Jones et al. 2000 | 6-Fam | 0.2 |
| Locus K | Jones et al. 2000 | Vic | 0.125 |
| Locus N | Jones et al. 2000 | Vic | 0.075 |
| Locus D | Jones et al. 2000 | Ned | 0.15 |
| Locus R | Jones et al. 2000 | Pet | 0.5 |
| Locus B[a] | Jones et al. 2000, in Pease et al 2009 | Pet | 0.25 |
| Locus C | Jones et al. 2000, in Pease et al 2009 | Ned | 0.1 |
| Locus F | Jones et al. 2000, in Pease et al 2009 | Vic | 0.1 |
| Locus G | Jones et al. 2000, in Pease et al 2009 | 6-Fam | 0.1 |
| Locus H | Jones et al. 2000, in Pease et al 2009 | Pet | 0.2 |
| Locus J | Jones et al. 2000, in Pease et al 2009 | Ned | 0.15 |
| Locus L | Jones et al. 2000, in Pease et al 2009 | 6-Fam | 0.25 |
| Locus S | Jones et al. 2000, in Pease et al 2009 | Pet | 0.3 |
| Locus V | Jones et al. 2000, in Pease et al 2009 | 6-Fam | 0.05 |
| ZFX-F+R | Aasen and Medrano 1990 | 6-FAM | 0.2 |
| SRY-F+R CDFW | Fain and Lemay 1995; Gilson et al. 1998 | NED | 0.2 |
| SRY-F+R OSU | Fain and Lemay 1995; Gilson et al. 1999 | NED | 0.1 |

[a] Locus B was monomorphic in all samples and was excluded from analyses.

TABLE S2. Number of unique desert mule deer genotyped (n), number of alleles (Na), allele size range, and observed ($H_O$) and expected ($H_E$) heterozygosity values for fourteen microsatellite loci and three sexing markers analyzed in desert mule deer (*Odocoileus hemionus eremicus*) fecal samples from the Chuckwalla Mountains, California, USA, 2015–2017.

| Locus | n | Na | Ho | He | Range (bp) |
|---|---|---|---|---|---|
| C | 381 | 3 | 0.54 | 0.61 | 318-338 |
| D | 446 | 3 | 0.54 | 0.54 | 162-194 |
| F | 447 | 2 | 0.08 | 0.08 | 151-172 |
| G | 421 | 3 | 0.57 | 0.61 | 324-365 |
| H | 373 | 2 | 0.43 | 0.47 | 356-360 |
| J | 427 | 2 | 0.46 | 0.5 | 235-255 |
| K | 442 | 4 | 0.67 | 0.7 | 200-216 |
| L | 418 | 2 | 0.27 | 0.29 | 263-303 |
| M | 444 | 5 | 0.34 | 0.34 | 148-176 |
| N | 428 | 7 | 0.73 | 0.74 | 258-294 |
| P | 441 | 6 | 0.72 | 0.72 | 221-240 |
| R | 408 | 4 | 0.45 | 0.48 | 266-303 |
| S | 435 | 6 | 0.63 | 0.64 | 203-219 |
| V | 445 | 3 | 0.41 | 0.38 | 91-99 |
| SRY-WFL/SRY-OSU/ZFX* | 416 | n/a | | | 222 (Y chrom)<br>120 (Y chrom)<br>445 (X chrom) |

* Sex identification markers.

TABLE S3. Sample sizes and genotype success rate of desert mule deer fecal DNA study, Little Chuckwalla Mountains, California, USA 2015–2017.

| Year | Sample quality | No. samples collected | No. samples analyzed | Success (%)[a] |
|---|---|---|---|---|
| 2015 | Total | 1,232 | 591 | 87.0 |
| | Good | 471 | 290 | 92.9 |
| | Fair | 616 | 200 | 85.1 |
| | Poor | 145 | 25 | 58.1 |
| 2016[b] | Total | 1,044 | 550 | 52.2 |
| | Good | 601 | 396 | 50.3 |
| | Fair | 385 | 140 | 56.4 |
| | Poor | 58 | 14 | 64.3 |
| 2017[c] | Total | 548 | 548 | 87.2 |
| | Good | 413 | 413 | 93.0 |
| | Fair | 109 | 109 | 72.5 |
| | Poor | 10 | 10 | 20.0 |

[a]Genotype success rate, defined as producing a genotype at 10 or more of the 14 microsatellite loci.

[b]Includes samples from 6 nonwater sites.

TABLE S4. Number and sex of unique desert mule deer captured within and across 3 years of fecal DNA sampling efforts in the Little Chuckwalla Mountains, California, USA, 2015–2017.

| Year(s) captured | n[a] | Female | Male | Unknown |
|---|---|---|---|---|
| 2015 only | 113 | 52 | 56 | 5 |
| 2016 only | 84 | 27 | 50 | 7 |
| 2017 only | 102 | 38 | 45 | 19 |
| 2015 and 2016 | 39 | 22 | 17 | 0 |
| 2015 and 2017 | 40 | 28 | 12 | 0 |
| 2016 and 2017 | 27 | 12 | 15 | 0 |
| 2015, 2016, and 2017 | 42 | 25 | 17 | 0 |
| Total | 447 | 204 | 212 | 31 |

[a] Total number of individuals.

TABLE S5. Within year movement as indicated by across-drinker recaptures for desert mule deer sampled in the Little Chuckwalla mountains, California, USA, 2015. Interdrinker distances (km) are shown above the diagonal, with pairs of drinkers that showed recaptures highlighted in grey. Number of deer sampled at each pair of drinkers is shown below the diagonal.

| | **BGT** | **BKH** | **CKS** | **CRW** | **DDM** | **LBN** | **MYW** | **PRW** | **RNY** | **YDR** |
|---|---|---|---|---|---|---|---|---|---|---|
| **BGT** | - | 12.7 | 25.9 | 14.1 | 20 | 19.2 | 26.8 | 7 | 23.9 | 34.1 |
| **BKH** | 2 | - | 15.3 | 7.3 | 7.9 | 12.5 | 21.7 | 15.2 | 12.5 | 27.7 |
| **CKS** | | | - | 11.9 | 8.2 | 8.9 | 12.7 | 24.5 | 3.7 | 15.2 |
| **CRW** | | 1 | | - | 8.3 | 5.8 | 14.7 | 12.8 | 10.8 | 21.3 |
| **DDM** | | 3 | | | - | 10 | 18 | 20.7 | 4.8 | 22.5 |
| **LBN** | | | | 1 | 1 | - | 9.1 | 16.3 | 9.7 | 15.5 |
| **MYW** | | | | | | | - | 22.2 | 15.6 | 7.5 |
| **PRW** | | | | | | | | - | 23.6 | 29.7 |
| **RNY** | | | 5 | | 4 | | | | - | 18.9 |
| **YDR** | | | | | | | 2 | | | - |

TABLE S6. Within year movement as indicated by across-drinker recaptures for desert mule deer sampled in the Little Chuckwalla mountains, California, USA, 2016. Interdrinker distances (km) are shown above the diagonal, with pairs of drinkers that showed recaptures highlighted in grey. Number of deer sampled at each pair of drinkers is shown below the diagonal.

| | **BGT** | **BKH** | **CKS** | **CRW** | **DDM** | **LBN** | **MYW** | **PRW** | **RNY** | **YDR** |
|---|---|---|---|---|---|---|---|---|---|---|
| **BGT** | | 12.7 | 25.9 | 14.1 | 20 | 19.2 | 26.8 | 7 | 23.9 | 34.1 |
| **BKH** | | | 15.3 | 7.3 | 7.9 | 12.5 | 21.7 | 15.2 | 12.5 | 27.7 |
| **CKS** | | | | 11.9 | 8.2 | 8.9 | 12.7 | 24.5 | 3.7 | 15.2 |
| **CRW** | | | | | 8.3 | 5.8 | 14.7 | 12.8 | 10.8 | 21.3 |
| **DDM** | | | | | | 10 | 18 | 20.7 | 4.8 | 22.5 |
| **LBN** | | | 2 | | | | 9.1 | 16.3 | 9.7 | 15.5 |
| **MYW** | | | | | | 1 | | 22.2 | 15.6 | 7.5 |
| **PRW** | | | | | | | | | 23.6 | 29.7 |
| **RNY** | | | | | | | | | | 18.9 |
| **YDR** | | | | | | | 2 | | | |

TABLE S7. Within year movement as indicated by across-drinker recaptures for desert mule deer sampled in the Little Chuckwalla mountains, California, USA, 2017. Interdrinker distances (km) are shown above the diagonal, with pairs of drinkers that showed recaptures highlighted in grey. Number of deer sampled at each pair of drinkers is shown below the diagonal.

| | **BGT** | **BKH** | **CKS** | **CRW** | **DDM** | **LBN** | **MYW** | **PRW** | **RNY** | **YDR** | **GGG[a]** | **HHH[a]** | **DDD[a]** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **BGT** | | 12.7 | 25.9 | 14.1 | 20 | 19.2 | 26.8 | 7 | 23.9 | 34.1 | 24.5 | 30.4 | 16.6 |
| **BKH** | 1 | | 15.3 | 7.3 | 7.9 | 12.5 | 21.7 | 15.2 | 12.5 | 27.7 | 22 | 23.8 | 4 |
| **CKS** | | | | 11.9 | 8.2 | 8.9 | 12.7 | 24.5 | 3.7 | 15.2 | 16.6 | 12 | 12 |
| **CRW** | | | | | 8.3 | 5.8 | 14.7 | 12.8 | 10.8 | 21.3 | 14.7 | 17.4 | 7.6 |
| **DDM** | | | | | | 10 | 18 | 20.7 | 4.8 | 22.5 | 20.2 | 18.8 | 4.1 |
| **LBN** | | | | 2 | | | 9.1 | 16.3 | 9.7 | 15.5 | 10.2 | 11.6 | 11.5 |
| **MYW** | | | | | | 2 | | 22.2 | 15.6 | 7.5 | 5.2 | 4.4 | 20.3 |
| **PRW** | | | | | | | | | 23.6 | 29.7 | 19 | 26.2 | 18.3 |
| **RNY** | | | 2 | | 1 | 1 | | | | 18.9 | 18.8 | 15.4 | 8.8 |
| **YDR** | | | | | | | 5 | | | | 11.7 | 3.9 | 25.6 |
| **GGG** | | | | | | | | | | | | 9.4 | 21.6 |
| **HHH** | | 1 | | | | | | | | 5 | | | 21.8 |
| **DDD** | | 2 | | | | | | | | | | | |

[a]Nonwater sites; a total of 6 non-water sites were sampled, but these are the only 3 sites where samples were present

TABLE S8. Within-year open population model parameters of probability of remaining on the study area ($\phi$) and probability of new individuals entering the study area ($p_{ent}$) during each sampling session in the Little Chuckwalla Mountains, California, USA, 2015–2017.

| | 2015 | | 2016 | | 2017 | |
|---|---|---|---|---|---|---|
| | $\phi$ | $p_{ent}$ | $\phi$ | $p_{ent}$ | $\phi$ | $p_{ent}$ |
| Female | 0.91 | 0.04 | 0.60 | 0.12 | 0.88 | 0.18 |
| Male | 0.89 | 0.04 | 0.63 | 0.14 | 0.84 | 0.17 |
| Unknown | 0.16 | 0.05 | 0.61 | 0.13 | 0.56 | 0.17 |

TABLE S9. Model selection results from a Cormack–Jolly–Seber design analysis for desert mule deer in the Little Chuckwalla Mountains, California, USA, 2015–2017.

| Model | K | $AIC_c$ | $\Delta AIC_c$ | $w_i$ | Deviance |
|---|---|---|---|---|---|
| φ(g) *p*(.) | 4 | 723.302 | 0 | 0.418 | 16.094 |
| φ(g) *p*(t) | 5 | 724.838 | 1.5 | 0.194 | 15.583 |
| φ(g) *p*(m=f,u) | 5 | 725.112 | 1.8 | 0.169 | 15.856 |
| φ(g) *p*(g) | 6 | 726.667 | 3.4 | 0.078 | 15.354 |
| φ(g*t) *p*(.) | 7 | 728.437 | 5.1 | 0.032 | 15.057 |
| φ(m=f,u) *p*(g) | 5 | 728.597 | 5.3 | 0.03 | 19.341 |
| φ(t) *p*(g) | 5 | 729.154 | 5.9 | 0.022 | 19.898 |
| φ(m=f,u) *p*(.) | 3 | 729.82 | 6.5 | 0.016 | 24.65 |
| φ(f=u,m) *p*(f=u,m) | 4 | 731.232 | 7.9 | 0.008 | 24.024 |
| φ(m=f,u) *p*(m=f,u) | 4 | 731.61 | 8.3 | 0.007 | 24.402 |
| φ(m=f,u) *p*(t) | 4 | 731.62 | 8.3 | 0.007 | 24.412 |
| φ(g) *p*(g*t) | 9 | 731.773 | 8.5 | 0.006 | 14.229 |
| φ(g*t) *p*(g) | 9 | 731.92 | 8.6 | 0.006 | 14.377 |
| φ(m=f, u(t)) *p*(.) | 5 | 733.562 | 10.3 | 0.002 | 24.307 |
| φ(.) *p*(.) | 2 | 734.263 | 11 | 0.002 | 31.121 |
| φ(m=f, u(t)) *p*(m=f, u) | 6 | 735.352 | 12 | 0.001 | 24.039 |
| φ(m=f,u) *p*(m=f,u) | 6 | 735.352 | 12 | 0.001 | 24.039 |
| φ(t) *p*(.) | 3 | 736.155 | 12.9 | 0.001 | 30.985 |
| φ(.) *p*(t) | 3 | 736.155 | 12.9 | 0.001 | 30.985 |

[a]Key to model notation: K = No. of parameters; $AIC_c$ = Akaike Information Criterion corrected ; Δ AIC = difference between the model listed and the $AIC_c$ of the best model; $W_i$ = model weights based on model $AIC_c$ compared to all other model $AIC_c$ values; φ = apparent survival; p = capture probability; t = encounter occasion as a categorical variable; g = sex as a categorical variable; m, f, u = male, female, and unknown sex categories respectively; "." = constant across year, encounter occasion, and sex.