

Supplementary Materials

Livestock indirectly decrease nest abundance of two shrub-nesting species in Patagonian Monte Desert

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Supplementary Materials

Table S1. Table showing the characteristics of the studied rangelands. Grazing history (history) showing the years each rangeland was subjected to livestock grazing. Current livestock density of each rangeland (Livestock density) weighted by the history (cattle ha⁻¹ x years, * these densities remained constant since 2006 while others from 2001 **, data obtained from the rangeland owners) . Area of each rangeland in hectares (Hectares). The number of transects (1 km x 100 m) done in each rangeland to sample nest abundance (transects). Livestock composition with the number of animal units for each type of livestock between parenthesis.

Rangeland	history	Livestock density	Hectares	transects	livestock composition
1	30**	0.06	21000	5	Cattle (25), horses (20)
2	30*	0.075	7500	5	Cattle (28), horses (15)
3	30**	0.11	7500	5	Cattle (9), horses (4), goats (72), sheep (2)
4	10*	0.132	3500	2	Cattle (30), horses (20)
5	10*	0.212	4500	3	Horse (20), goats (150), sheep (150)
6	10*	0.631	550	9	Horses (10), goats (120), sheep (6)
7	10*	0.696	970	5	Cattle (30), horses (30)
8	30**	0.924	7500	3	Cattle (177), horses (3), goats (300)
9	30*	1.632	5000	3	Cattle (250), horses (8), sheep (40)

Table S2. Set of d-separation claims implied by Fig. 2 (the hypothesized causal model) used to calculate de *BU* basis *sensu* Shipley (2009). The *BU* consists on the *N* independence claims with the following properties: (1) all independence claims not in this basis (and all dependence claims) set are logical consequences of some combination of those within it, (2) no independence claim within this basis set can be derived from some combination of the others within it, and (3) if data are generated according to the causal graph then the null probabilities of each independence claim are mutually independent (Shipley 2009). The first two properties mean that a test of the *BU* basis set is also a test of the entire set of patterns of statistical dependence and independence implied by the causal process (Shipley 2009). The third property means that the following statistic (*C*), calculated on the independence claims of *BU*, follows a chi-square distribution with $2k$ degrees of freedom, where k is the number of independence claims in *BU* and p_i is the null probability of the independence test associated with the *i*th independence claim. Model fit was calculated with Eq. 1, comparing *C* to a χ^2 distribution. Equation 1 combines all the null probabilities (p) for each independence claim. The model is rejected if the probability of *C* is below the chosen significance level ($P < 0.05$). Abbreviations are as follow: Livestock density (LD), mean vegetation cover (VC), mean percentage of browsing (B), Nest abundance (NA) and Species (SP). When appropriate, a “weights” function was used to correct residual variance heterogeneity between rangeland or plots ($\text{varIdent}(\text{form} = \sim 1|\text{rangeland or plot})$) and a correlation function to deal with spatial autocorrelation, $\text{corAR1}(\text{form} = \sim 1|\text{rangeland/transect or plot})$ (Zuur et al., 2009). An offset function was used to deal with different number of transect (total sampled area) or plots (number of plots) in each rangeland. All statistical analyses of the path model were conducted using *lme* function of the library *nlme* in R program. The variables percentage of browsing and cover were transformed to the square root.

Eq. 1: $C = -2 \sum_{i=1}^k \ln(p_i)$

D-sep independence claim	Variable whose partial regression slope should be zero	Mixed model	Null probability (distribution)	P value
LD,NA VC,B	LD	NA~LD+VC+B+sp, Offset (log (total area)) random=~1 rangeland/transect, weights=varIdent (form=~1 rangeland) corAR1(form=~1 rangeland/transect)	Normal	0.5981
LD,VC B	LD	sqrootVC~LD+B, offset (log(plots)), random=~1 rangeland/plot	Normal	0.897

		weights=varIdent(form=~1 plot) corAR1(form=~1 rangeland/plot)		
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Models used in R program to estimate the parameters of the path diagram of Fig. 4.

###Path 1: LD-->B

```
P1<- lme (sqrtB ~ LD +offset (log(total area)), random = ~1|rangeland/plot
```

```
  weights= varIdent(form = ~1|rangeland),
```

```
  corAR1(form=~1|rangeland/plot),
```

```
  na.action=na.omit, data=plantpath)
```

####Path 2: B-->VC

```
P2<- lme (sqrtVC ~ sqrtB +offset (log(total area)), random = ~1|rangeland/plot,
```

```
  weights= varIdent(form = ~1|rangeland),
```

```
  corAR1(form=~1|rangeland/plot),
```

```
  na.action=na.omit, data=plantpath)
```

###Path 3: VC-->NA

```
P3<-lme (NA ~ VC+SP + offset (log(total area)), random=~1|rangeland/transect,
```

```
  weights= varIdent(form = ~1|sp),
```

```
  corAR1(form=~1|rangeland/transect),
```

```
  na.action=na.omit, data=nidospath)
```

Table S3. Mean nest width (cm) in rangelands with different livestock density levels for *P. gutturalis*

Level	Livestock density	Mean nest width	SE
Low	0.06-0.07	56.81	3.3
Intermediate low	0.1-0.23	57.1	4.72
Intermediate high	0.6-0.7	59.13	3.85
High	0.9-1.6	73.33	8.62

Figure S1. (a) Photograph of *Pseudoseisura gutturalis* in nest entrance. Nest was placed on *Monttea aphylla*. (b) Photograph of *Leptasthenura aegithaloides* in nest entrance. Nest was placed on *Chuquiraga erinaceae*.



Figure S2. Linear association between weighted livestock density (cattle ha⁻¹ x years) and the mean dung density/plot ($r = 0.7$, $F_{1,7} = 6.5$, $P = 0.038$).

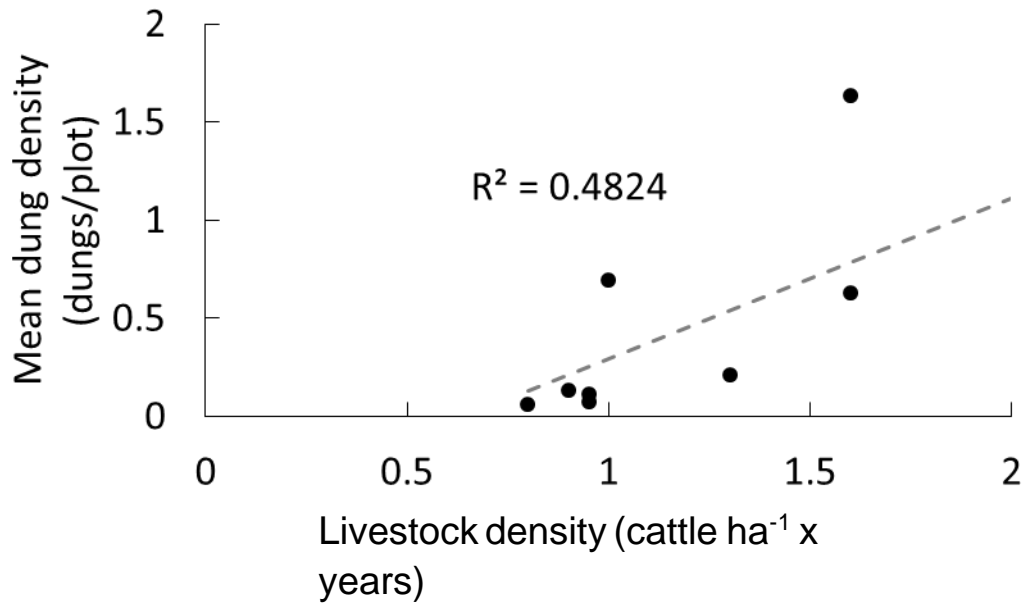
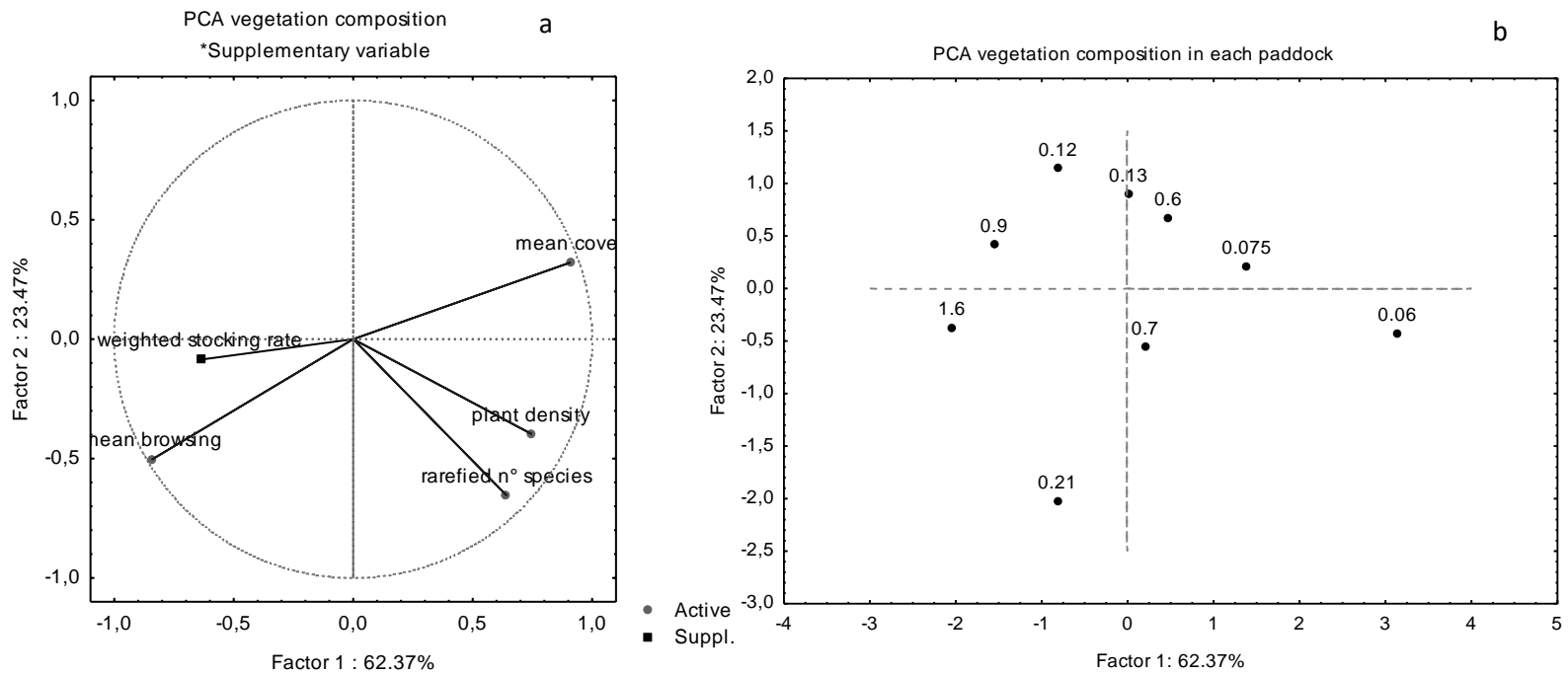


Figure S3. PCA analysis of vegetation composition based on plant cover, density and richness of each rangeand (from the data obtained with the 135 plots, see details in section *Plant sampling*). (a) projection of supplementary variables. (b) Projection of the cases, number near the dots are the corresponding weighted livestock density (cattle ha⁻¹ x years). The first two axes of the PCA explained 85.8 % of the variance.



Active nests results

Twenty two active nests of LA (*L. aegithaloides*) and six from PG (*P. gutturalis*) were found mainly in rangelands from low to moderate grazing levels showing significant differences in their sizes (PG > LA, $F_{\text{length}(1,17)} = 71.4$, $P < 0.00001$, $F_{\text{width}(1,17)} = 119$, $P < 0.00001$, Figure A4 a-b). Nest size (i.e. width and length) was different among rangelands ($F_{\text{width}(3,17)} = 28.5$, $P < 0.00001$, $F_{\text{length}(3,17)} = 7.05$, $P = 0.003$, Figure A4 a-b). Nest height tended to be higher for LA than PG (97.3 ± 3.9 cm and 77.5 ± 6.3 cm, respectively; $F_{\text{species}(1,16)} = 2.8$, $P = 0.11$) but was similar between rangelands ($F_{\text{rangelands}(3,16)} = 0.38$, $P = 0.77$). The mean nest entrance height was similar between species ($F_{\text{species}(1,16)} = 0.0003$, $P = 0.98$; 119.9 ± 3.6 cm and 113.7 ± 7.5 cm, respectively) and rangelands ($F_{\text{rangelands}(3,16)} = 0.42$, $P = 0.74$).

Figure S4. Anova results showing differences among rangelands and species (factors) for: a) nest length (Mean (\pm SE)) and b) nest width of active nests for each bird species (*P. gutturalis* and *L. aegithaloides*). Rangelands were expressed as weighted livestock density (cattle Ha^{-1} x years). Different capital letters denote statistical difference (Tukey post-hoc test, $P < 0.10$).

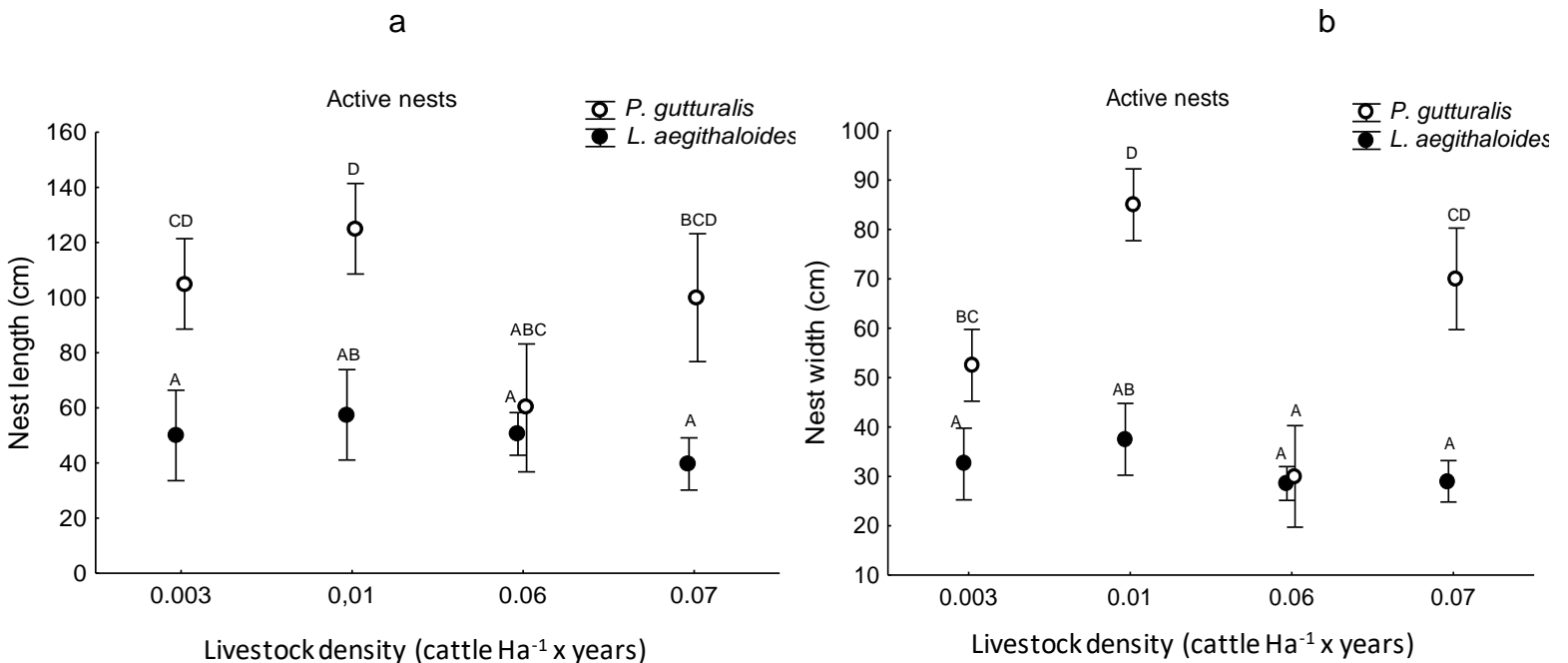
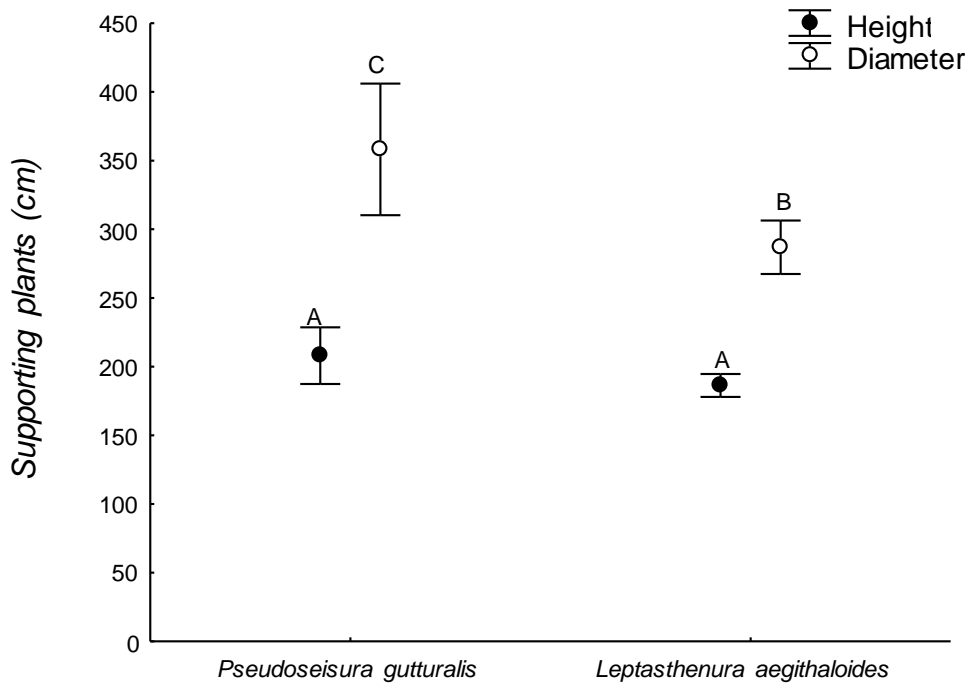


Figure S5. Nest supporting plant characteristics for each bird species. Mean (\pm SE) supporting plant height and diameter.



References

Shiple, B. 2009. Confirmatory path analysis in a generalized multilevel context. *Ecology* **90**: 363–368

Zuur, A.F., Ieno, E.N., Walker, N.J., Saveliev, A.A., and Smith, G.M. 2009. *Mixed Effects Models and Extensions in Ecology with R, Statistics for Biology and Health*. (M. Gail, K. Krickeberg, J.M. Samet, A. Tsiatis, and W. Wong, eds.) Springer Science+Business Media, LLC