Intra-specific multi-trait approach reveals scarce ability in the variation of resource exploitation strategies for a dominant tall-grass under intense disturbance

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Table S1. List of plant traits collected, with their respective variable type, sampling time, observation unit on which the measurement was taken, error distribution family, fixed and random effects included in the mixed-effects models, R-package, and R-function used. B – Block; B/T – Tussock nested inside block; B/T/S – Shoot nested inside tussock, nested inside block.

Plant traits	Variable type	Sampling time	Observation unit	Error distribution family	Fixed effects	Random effect	*R-package* and R-function
Number of shoots	Integer	early summer	Tussock	Poisson (link = log)	Treatment * Phenological status	1|B	*lme4* glmer
Plant height (mm)	Numeric	early summer	Shoot	Gaussian	Treatment * Phenological status	1|B/T	*nlme* lme
Specific leaf area (mm² mg⁻¹)	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1|B/T/S	*nlme* lme
Leaf area (mm²)	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1|B/T/S	*nlme* lme
Leaf dry mass (mg)	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1|B/T/S	*nlme* lme
Occurrence of leaf senescence symptoms	Binary	early summer	Leaf	Binomial (link = logit)	Treatment * Phenological status	1|B/T/S	*MASS* glmmPQL
Total number of spikelets	Integer	early summer	Shoot (one spike)	Poisson (link = log)	Treatment	1|B/T	*MASS* glmmPQL
Number of flowering spikelets	Integer	early summer	Shoot (one spike)	Poisson (link = log)	Treatment	1|B/T	*MASS* glmmPQL
Spike length (mm)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme
Mean spikelet length (mm)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme
Mean number of (fertilized / unfertilized) flowers per spikelet	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme

Number of (fertilized / unfertilized) flowers	Integer	late summer/early autumn	One shoot per tussock (spike)	Poisson (link = log)	Treatment	1|B	*lme4* glmer
Seed output	Integer	late summer/early autumn	One shoot per tussock (spike)	Poisson (link = log)	Treatment	1|B	*lme4* glmer
Total seed mass (mg)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme
Mean seed mass (mg)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme
Reproductive plant height (m)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1|B	*nlme* lme
Rhizome dry matter content (mg^{-1}g)	Numeric	late summer/early autumn	Rhizome	Gaussian	Treatment	1|B	*nlme* lme

Table S2. R script of the best model. B – Block; B/T – Tussock nested inside block; B/T/S – Shoot nested inside tussock, nested inside block.

Plant traits	R script
Number of shoots	glmer(Shoot_n~(Treatment) + (1|B), family="poisson", data=matrix, na.action="na.fail")
Plant height	lme(H ~Treatment*Phenological_status,method = "ML", random=~1|B/T, data=matrix)
Specific leaf area	lme(log(SLA) ~Phenological_status, method = "ML", random=~1|B/T/S, correlation=corCompSymm(0.5,form=~1|B/T/S), data=matrix)
Leaf area	lme((LA)^(1/3) ~Phenological_status+Treatment,method = "ML", random = ~1|B/T/S, correlation=corAR1(0.5, form=~1|B/T/S), data=matrix)
Leaf dry mass	lme((LDM)^(1/3) ~Phenological_status+Treatment, method = "ML", random=~1|B/T/S, correlation=corAR1(0.5,form=~1|B/T/S), data=matrix)
Occurrence of leaf senescence symptoms	glmmPQL(Senescence~Treatment*Phenological_status, ~ 1|B/T/S, family="binomial", correlation=corCompSymm(0.5,form=~1|B/T/S), data=matrix, na.action="na.fail")
Total number of spikelets	glmmPQL(Total_number_of_spikelets~Treatment, ~1|B/T, family="poisson", correlation=corRatio(0.5,form=~1|B/T), data=matrix)
Number of flowering spikelets	glmmPQL(Number_of_flowering_spikelets~Treatment, ~1|B/T, family="poisson", correlation=corCompSymm(0.5,form=~1|B/T), data=matrix)
Spike length	lme(Spike length~Treatment, method = "ML", random=~1|B, correlation=corGaus(0.5,form=~1|B), data=matrix)
Mean spikelet length	lme(log(Mean_spikelet_length)~Treatment, method = "ML", random=~1|B, correlation=corCompSymm(0.5,form=~1|B) ,data=matrix)
Mean number of (fertilized / unfertilized) flowers per spikelet	lme(log(Mean_n_of_flowers)~Treatment, method = "ML", random=~1|B, data=matrix)
Number of (fertilized / unfertilized) flowers	glmer(Number_of_flowers~Treatment + (1|B), family="poisson", data=matrix, na.action="na.fail")
Seed output	glmer(Seed_output~Treatment + (1|B), family="poisson", data=matrix, na.action="na.fail")
Total seed mass	lme(log(Total_seed_mass)~Treatment, method = "ML", random=~1|B, correlation=corCompSymm(0.5,form=~1|B), data=matrix)
Mean seed mass	lme(Mean_seed_mass~Treatment, method = "ML", random=~1|B, correlation=corRatio(0.5,form=~1|B), data=matrix)
Reproductive plant height	lme(sqrt(Reproductive_plant_height)~Treatment, method = "ML", random=~1|B, correlation=corRatio(0.5,form=~1|B), data=matrix)
Epigeogenous rhizome dry matter content	lme((RDMC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1|B, correlation=corCompSymm(0.5,form=~1|B), data=matrix)
Young hypogeogenous rhizome dry matter content	lme((RDMC_young_hypo_rhiz)~Treatment, method = "ML", random=~1|B,data=matrix)

Mature hypogeogenous rhizome dry matter content	lme((RDMC_mature_hypo_rhiz)~Treatment, method = "ML", random=~1|B, correlation=corCompSymm(0.5,form=~1|B), data=matrix)