## 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	<i>R-</i> package and R- function
Number of shoots	Integer	early summer	Tussock	Poisson (link = log)	Treatment * Phenological status	1 B	<i>lme4</i> glmer
Plant height (mm)	Numeric	early summer	Shoot	Gaussian	Treatment * Phenological status	1 B/T	<i>nlme</i> lme
Specific leaf area (mm <sup>2</sup> mg <sup>-1</sup> )	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1 B/T/S	<i>nlme</i> lme
Leaf area (mm <sup>2</sup> )	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1 B/T/S	<i>nlme</i> lme
Leaf dry mass (mg)	Numeric	early summer	Leaf	Gaussian	Treatment * Phenological status	1 B/T/S	<i>nlme</i> lme
Occurrence of leaf senescence symptoms	Binary	early summer	Leaf	Binomial (link = logit)	Treatment * Phenological status	1  <b>B</b> / <b>T</b> / <b>S</b>	MASS glmmPQL
Total number of spikelets	Integer	early summer	Shoot (one spike)	Poisson (link = log)	Treatment	1  <b>B</b> /T	<i>MASS</i> glmmPQL
Number of flowering spikelets	Integer	early summer	Shoot (one spike)	Poisson (link = log)	Treatment	1  <b>B</b> / <b>T</b>	MASS glmmPQL
Spike length (mm)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1 B	<i>nlme</i> lme
Mean spikelet length (mm)	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1 B	<i>nlme</i> lme
Mean number of (fertilized / unfertilized) flowers per spikelet	Numeric	late summer/early autumn	One shoot per tussock (spike)	Gaussian	Treatment	1 B	<i>nlme</i> lme

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

Number of shoots Plant heightglmer(Shoot_n-(Treatment) + (1 B), family="poisson", data=matrix, na.action="na.fail")Specific leaf arealme(log(SLA) ~Phenological_status, method = "ML", random=~1 B/T/S, correlation=corCompSymm(0.5,form=~1 B/T/S), data=matrix)Leaf arealme(log(SLA) ~Phenological_status+Treatment, method = "ML", random=~1 B/T/S, correlation=corCAR1(0.5, form=~1 B/T/S), data=matrix)Leaf dry masslme(LDM)^(1/3) ~Phenological_status+Treatment, method = "ML", random=~1 B/T/S, correlation=corCAR1(0.5, form=~1 B/T/S), data=matrix)Occurrence of leaf senescence symptomsglmmPQL(Senescence-Treatment?henological_status, ~ 1 B/T/S, data=matrix)Total number of spikeletsglmmPQL(Total_number_of_spikelets-Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T/S), data=matrix)Number of flowering spikeletsglmmPQL(Number_of_flowering_spikelets-Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T/S), data=matrix)Mean spikelet length unfertilized / unfertilized flowers per spikeletlme(log(Mean_spikelet_length)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), family="poisson", data=matrix)Mean seed mass Reproductive plant height Epigeogenous rhizome dry matter contentlme(log(Total_seed_mass)~Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)Mean seed mass Reproductive plant height Epigeogenous rhizome dry matter contentlme((MDC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)Ime((RDMC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix) <th>Plant traits</th> <th>R script</th>	Plant traits	R script
Plant height Ime(H -Treatment*Phenological_status, method = "ML", random=~1 B/T/S, correlation=corCompSymm(0.5, form=~1 B/T/S), data=matrix)   Leaf area Ime((LA)^(1/3) ~Phenological_status+Treatment, method = "ML", random=~1 B/T/S, correlation=corCompSymm(0.5, form=~1 B/T/S), data=matrix)   Leaf dry mass Ime((LD)^(1/3) ~Phenological_status+Treatment, method = "ML", random=~1 B/T/S, correlation=corCompSymm(0.5, form=~1 B/T/S), data=matrix)   Occurrence of leaf senescence symptoms Ime((LDM)^(1/3) ~Phenological_status+Treatment, method = "ML", random=~1 B/T/S, data=matrix)   Total number of spikelets glmmPQL(Senescence~Treatment*Phenological_status, ~1 B/T, shamily="poisson", correlation=corCans(0.5, form=~1 B/T), data=matrix)   Spike length glmmPQL(Total_number_of_spikelets-Treatment, ~1 B/T, family="poisson", correlation=corCans(0.5, form=~1 B/T), data=matrix)   Mean spikelet length Ime(log(Mean_spikelet_length)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5, form=~1 B), data=matrix)   Mean spikelet length Ime(log(Mean_n_of_flowers)-Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5, form=~1 B), data=matrix)   Mean seed mass glmer(Seed_output-Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")   Mean seed mass glmer(Seed_output-Treatment, method = "ML", random=~1 B, correlation=corCaus(0.5, form=~1 B), data=matrix)   Mean seed mass Ime(log(Total_seed_mass)-Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5, form=~1 B), data=matrix)	Number of shoots	glmer(Shoot_n~(Treatment) + (1 B), family="poisson", data=matrix, na.action="na.fail")
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Leaf area 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), data=matrix)   Leaf dry mass loc(LDM)^(1/3) ~Phenological_status+Treatment,method = "ML", random=~1 B/T/S, data=matrix)   Occurrence of leaf glmmPQL(Senescence~Treatment*Phenological_status, a.a.action="na.fail")   senescence symptoms glmmPQL(Cotal_number_of_spikelets~Treatment,~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)   Number of fowering glmmPQL(Number_of_flowering_spikelets~Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)   spikelets glmmPQL(Number_of_flowering_spikelets-Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)   Mean spikelet length lme(log(Mean_spikelet_length)~Treatment, method = "ML", random=~1 B, data=matrix)   Mean number of (fertilized / unfertilized) flowers spikelet lme(log(Mean_n_of_flowers)~Treatment, method = "ML", random=~1 B, data=matrix)   Seed output glmer(Number_of_flowers)~Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")   Mean seed mass mee(log(Total_seed_mass)~Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)   Mean seed mass lme(log(Total_seed_mass)~Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)   Mean seed mass	Specific leaf area	$lme(log(SLA) \sim Phenological_status, method = "ML", random=~1 B/T/S,$
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Occurrence of leaf senescence symptomsglmmPQL(Senescence~Treatment*Phenological_status, ~ 1 B/T/S, family="binomial", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix, na.action="na.fail")Total number of spikeletsglmmPQL(Senescence~Treatment*Phenological_status, ~ 1 B/T/S, family="binomial", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix, unfertilized flowering spikelet~ 1 B/T/S, family="binomial", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix, lmmPQL(Number_of_flowering_spikelets~Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)Mean spikelet length Mean number of (fertilized / unfertilized) flowers spikeletIme(log(Mean_spikelet_length)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Mean seed massglmer(Number_of_flowers)~Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")Mean seed massglmer(Seed_output~Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")Mean seed masslme(log(Total_seed_mass)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Mean seed masslme(Negrt(Reproductive_plant height Epigeogenous rhizome dry matter contentReproductive plant heightlme((RDMC_pi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Ime((RDMC_pi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Ime((RDMC_pour_youg_hypo_rhiz)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Ime((RDMC_pug_hypo_rhiz)~Treatment, method = "ML", random=~1 B, correlation=corCompS	Lear dry mass	correlation=corAR1(0.5,form=~1 B/T/S), data=matrix)
senescence symptomscorrelation=corCompSymm(0.5,form=~1 B/T/S), data=matrix, na.action="na.fail")Total number of spikeletsglmmPQL(Total_number_of_spikelets~Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)Number of flowering spikeletsglmmPQL(Number_of_flowering_spikelets~Treatment, ~1 B/T, family="poisson", correlation=corCompSymm(0.5,form=~1 B/T), data=matrix)Spike lengthlme(Spike length~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Mean spikelet lengthlme(log(Mean_spikelt_length)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Mean number of (fertilized / unfertilized) flowers per spikeletlme(log(Mean_n_of_flowers)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix, na.action="na.fail")Seed outputglmer(Number_of_flowers-Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")Total seed massglmer(Seed_output~Treatment + (1 B), family="poisson", data=matrix, na.action="na.fail")Mean seed masslme(log(Total_seed_mass-Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)Mean seed masslme(sqrt(Reproductive_plant height) correlation=corCatatio(0.5,form=~1 B), data=matrix)Reproductive plant heightlme((RDMC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Ime((RDMC_poug_hypo_rhiz)/3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Ime((RDMC_poug_hypo_rhiz)/3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm	Occurrence of leaf	glmmPQL(Senescence~Treatment*Phenological_status, ~ 1 B/T/S, family="binomial",
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Reproductive plant heightIme(sqrt(Reproductive_plant_height)~Treatment, method = "ML", random=~1 B, correlation=corRatio(0.5,form=~1 B), data=matrix)Epigeogenous rhizome dry matter contentIme(sqrt(Reproductive_plant_height)~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Young hypogeogenous rhizome dry matter contentIme((RDMC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, data=matrix)Ime((RDMC_young_hypo_rhiz)~Treatment, method = "ML", random=~1 B, data=matrix)Ime((RDMC_young_hypo_rhiz)~Treatment, method = "ML", random=~1 B, data=matrix)	Mean seed mass	Ime(Mean_seed_mass~I reatment, method = $^{\text{ML}}$ , random=~1 B,
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Epigeogenous rhizome dry matter contentIme((RDMC_Epi_rhiz)^3 ~Treatment, method = "ML", random=~1 B, correlation=corCompSymm(0.5,form=~1 B), data=matrix)Young hypogeogenous rhizome dry matter contentIme((RDMC_young_hypo_rhiz)~Treatment, method = "ML", random=~1 B,data=matrix)	Reproductive plant height	correlation=corRatio(0.5 form=~1 B) data=matrix)
Image: space of the space of	Epigeogenous rhizome dry	$lme((RDMC Epi rhiz)^3 \sim Treatment, method = "ML", random=~1 B.$
Young hypogeogenous lme((RDMC_young_hypo_rhiz)~Treatment, method = "ML", random=~1 B,data=matrix)	matter content	correlation=corCompSymm(0.5.form=~1 B), data=matrix)
rhizome dry matter content random=~1 B,data=matrix)	Young hypogeogenous	lme((RDMC young hypo rhiz)~Treatment, method = "ML",
	rhizome dry matter content	random=~1 B,data=matrix)

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