Understanding the dynamic traits in perennial grasses – an example on drought stress

Kristina Jaškūnė

«Edit Grass 4 Food» kick-off meeting
Riga, 8th October, 2021

Overview

⊙ Phenotyping a dynamic trait

⊙ Modelling leaf growth in response to water deficit

⊙ GWAS for biomass formation under drought

⊙ Elucidating gene regulatory networks
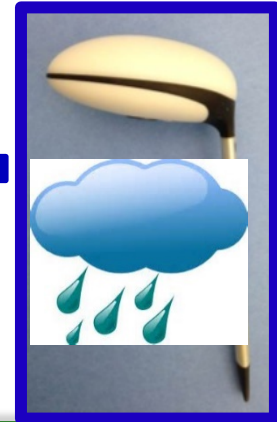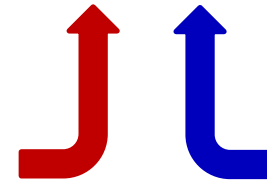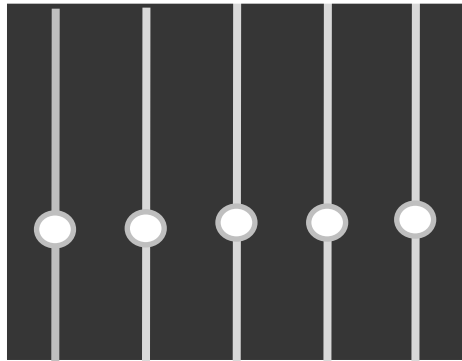
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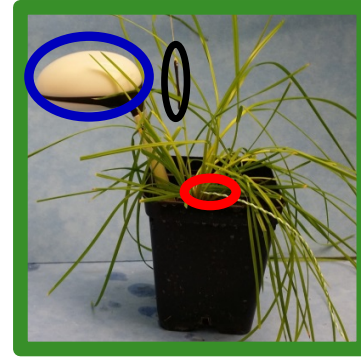
Climate change and drought

- IPPC 2021 report – requiem to fossil fuel and consumerism
- Global warming
- Drought events in last decade:
  - 2015, 2018, 2019, 2021
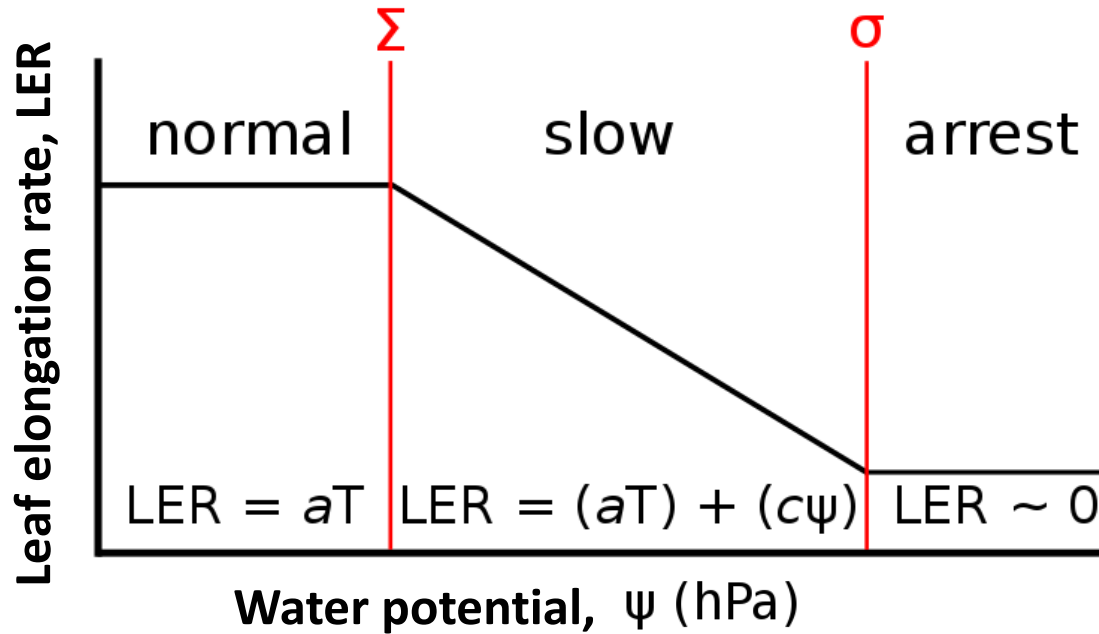- Drought is a major limitation in crop productivity

Improving drought tolerance

Yield = **Biomass**
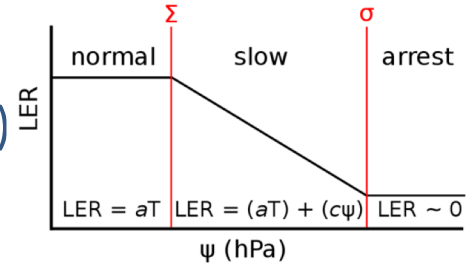
Phenotyping platform

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Leaf growth under water deficit

T = temperature
a, *c* = genotypic response

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Leaf growth under water deficit

The phenotyping approach enables to determine when water potential (Ψ) slows (Σ) and arrests (σ) leaf elongation rate (LER)

Genotypic differencies

a, growth rate
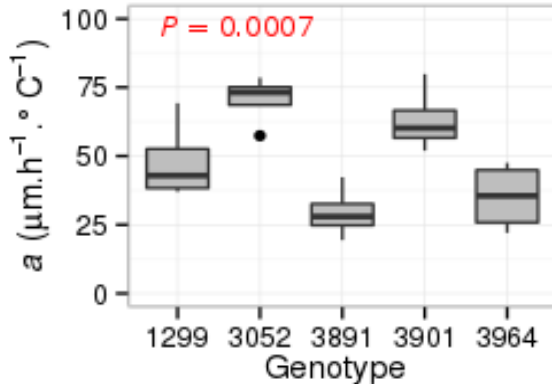
Σ, growth slow

σ, growth stop
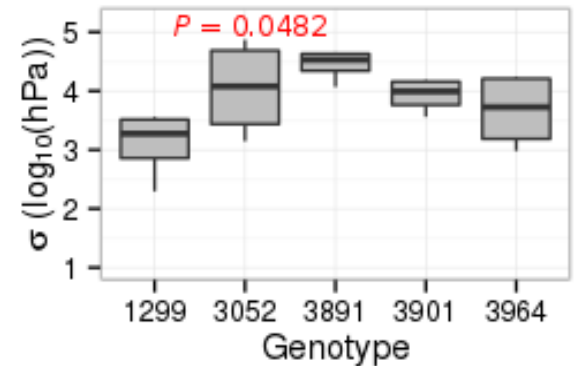
Applicability of the approach

- Determines genotypic response to water stress
- Time independent phenotypic response
- Non-invasive, labour and cost effective
- Adaptable in field
- Can be used in any monocot species
- Applicable to other abiotic stress

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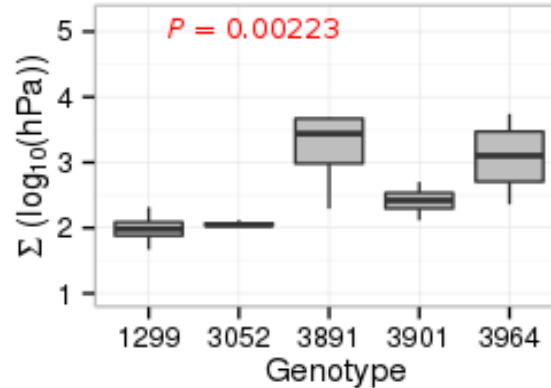# Phenotyping a Dynamic Trait: Leaf Growth of Perennial Ryegrass Under Water Limiting Conditions

Steven Yates[1†], Kristina Jaškūnė[2†], Frank Liebisch[3], Sebastian Nagelmüller[3], Norbert Kirchgessner[3], Roland Kölliker[1], Achim Walter[3], Gintaras Brazauskas[2] and Bruno Studer[1*]

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Use of the approach
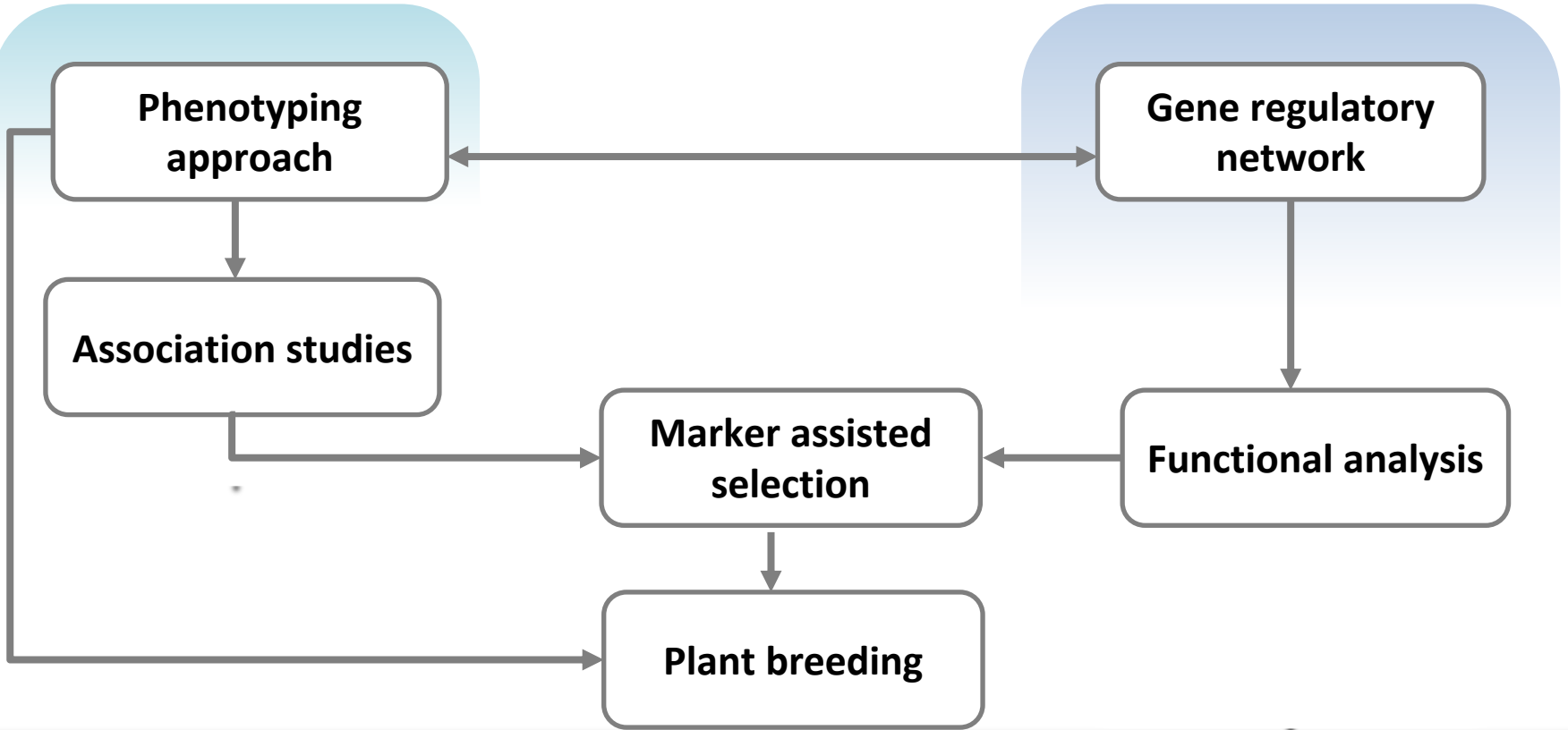
Phenotyping a diverse panel

⦿ 197 perennial ryegrass genotypes

- Cultivars – 43 forage and 46 turf
- Ecotypes - 50 maritime and 58 continental origin

Leaf growth   slow   arrest

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Phenotyping a diverse panel

forage cultivars

maritime ecotypes
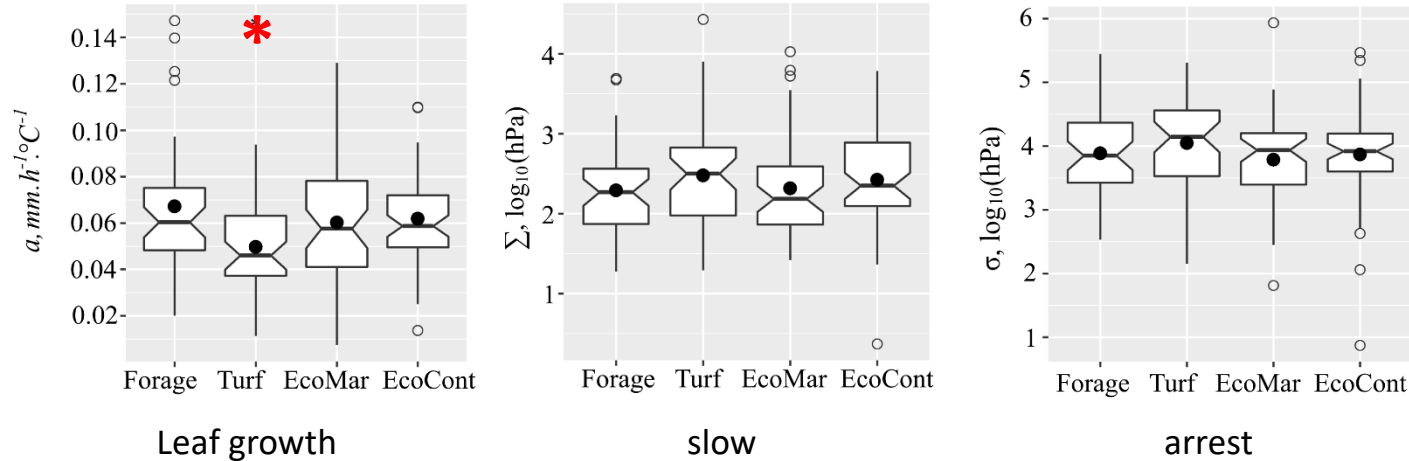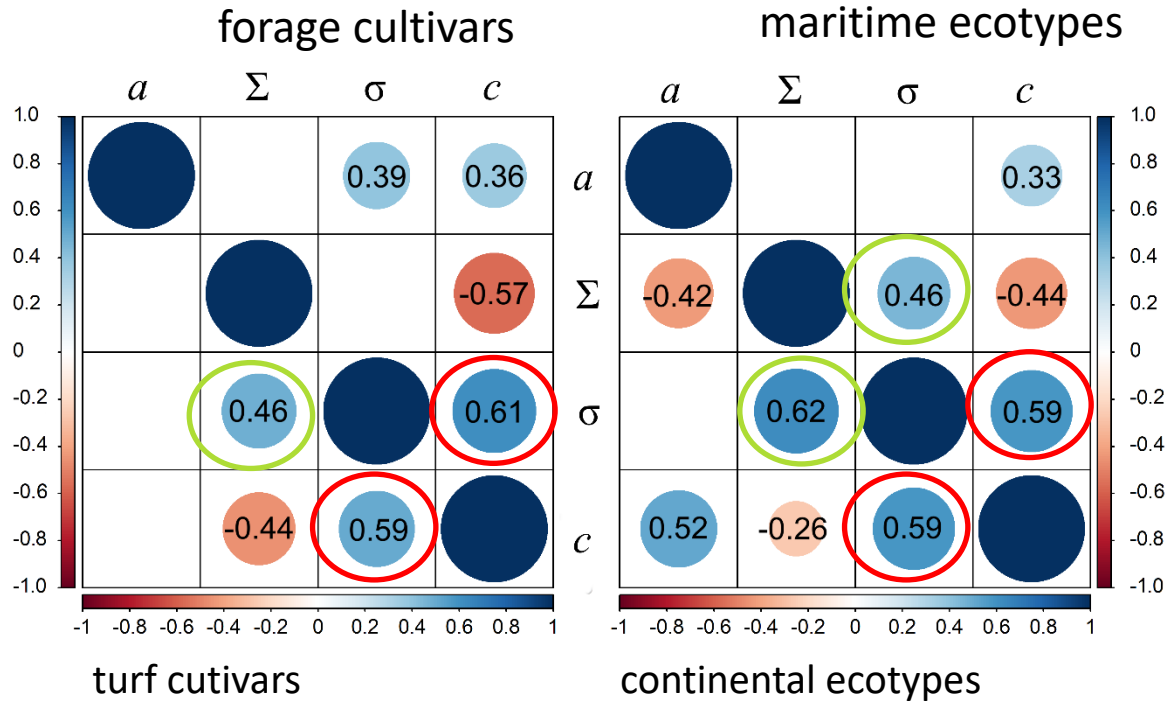
turf cutivars

continental ecotypes

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Genotyping-by-sequencing

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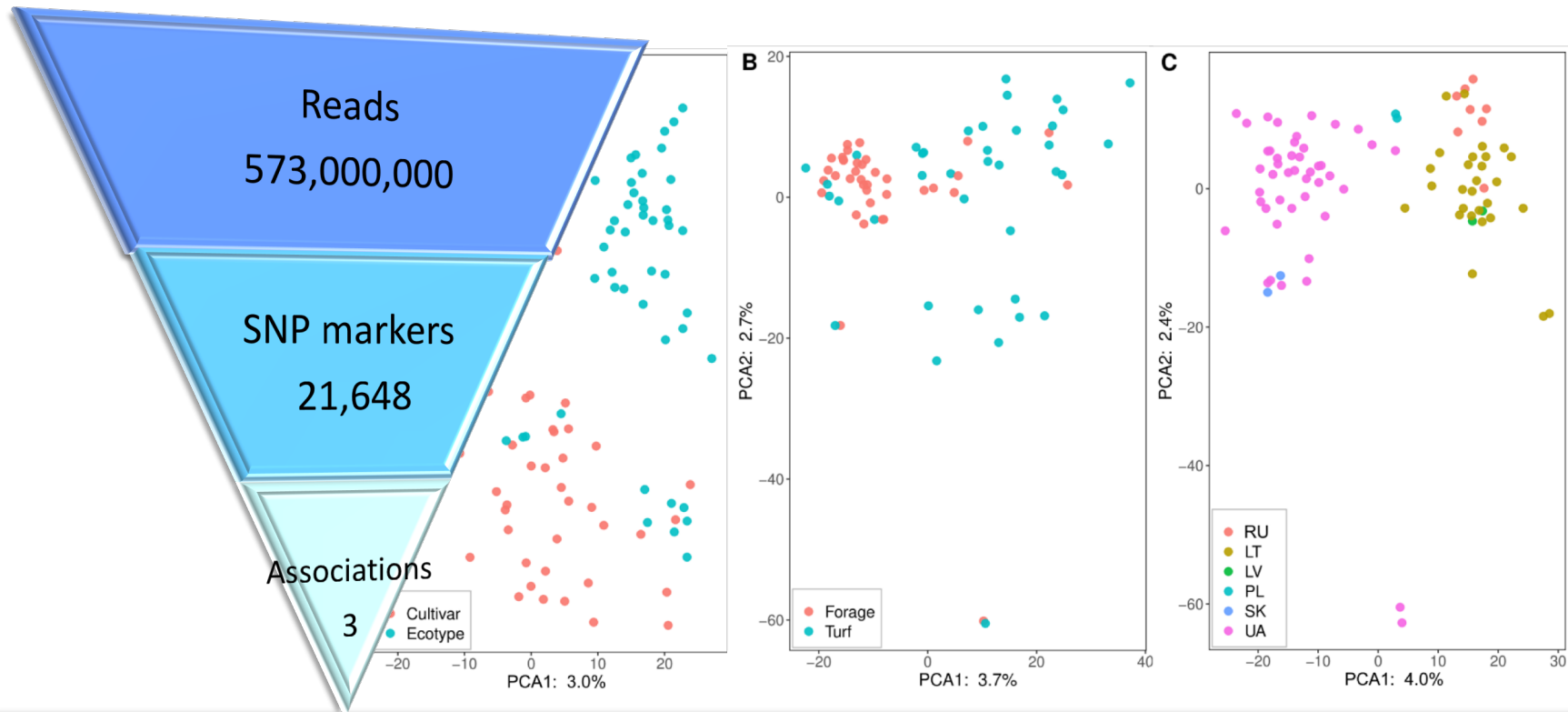
GWAS for biomass formation

| Scaffold	Position	Gene prediction (blastn)	Location	Scaffold position in barley genome	GWAS method	SNP effect	MAF	P-value	P-values FDR	P-values (Bonferroni correction)
scaffold_20866|ref0045961	1878	Transcription factor MYB41 (XM_003573090.4)	outside gene (708 bp)	Hv_chr6H	FarmCPU	-0.548	0.091	4.19E-07	0.009	0.009
					BLINK	NA	0.091	4.15E-07	0.009	NA
					MLMM	NA	0.091	8.16E-07	0.009	0.018
scaffold_4484|ref0039062	32616	Phytochrome B (XM_020328926.1)	intron	Hv_chr4H	FarmCPU	0.739	0.054	1.79E-07	0.019	0.039
					BLINK	NA		1.78E-06	0.019	NA
scaffold_21802|ref0017195	728	NA	intergenic space	NA	MLMM	NA	0.256	4.43E-07	0.009	0.010

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Check for updates

Genome-Wide Association Study to Identify Candidate Loci for Biomass Formation Under Water Deficit in Perennial Ryegrass

Kristina Jaškūnė[1]*, Andrius Aleliūnas[1], Gražina Statkevičiūtė[1], Vilma Kemešytė[2], Bruno Studer[3] and Steven Yates[3]*

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Key candidate genes for leaf growth response under drought

Gene name	Reported biological function
NAC038	involved in gibberellin acid and auxin signaling and regulates cell elongation and proliferation
WSD11	Cuticle wax synthesis in elongating petals
MYB94	Cuticle wax synthesis
TSO1	Inflorescence meristem organization and cell division, cytokinesis
	Control of cell expansion, coordination of growth of adjacent cells, karyokinesis, cytokinesis in flower
	Coordination of cell proliferation and differentiation in root and shoot meristem
MYB4	UV protection
	Chemical volatile production (*Petunia x hybrida*)
HSL1	Seed maturation
WRKY49	Signaling with reactive oxygen species, ethylene, salicylic acid, jasmonic acid in response to fungal pathogen (*Triticum aestivum*)
PRR5	Photoperiod-responsive growth
	Key part of circadian clock

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Improving adaptability and resilience of perennial ryegrass for safe and sustainable food systems through CRISPR-Cas9 technology
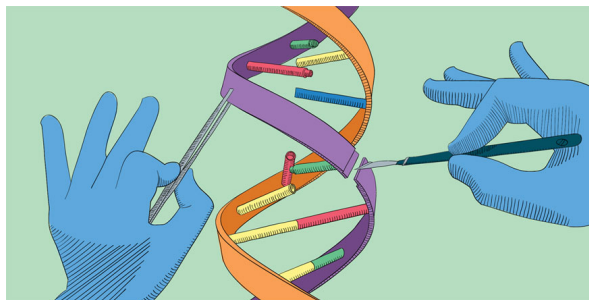
Thanks

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