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Agroecology = complexity

Cultivated plants in agroecological systems have to cope with many more elements than in industrial farming

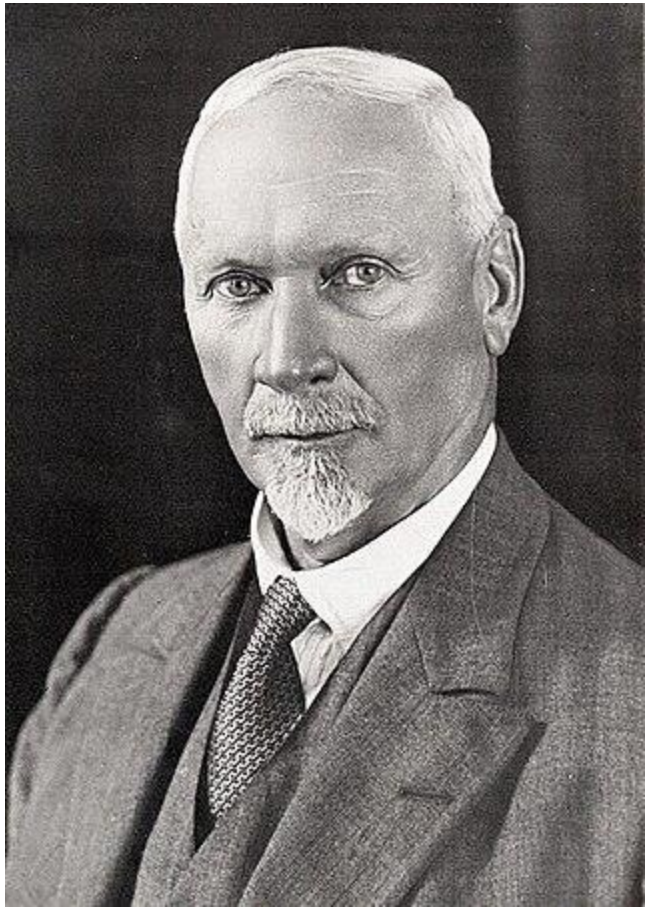
Plants should be ready for that = selected for that

Holistic approach in breeding to address complex plant – environment interactions

What is holistic approach?
Holism by Jan C. Smuts (1926): “the determining factors in nature are wholes . . . which are irreducible to the sum of their parts. ...”

Holism has played a central role in Eastern cultures while it is difficult to understand in the context of Western reductionist science

Nisbett RE, Peng K, Choi I, Norenzayan A. Culture and systems of thought: holistic versus analytic cognition.



Why to develop a holistic approach for breeding in agroecological systems?

Agroecology vision invites to consider all living beings according to their place in the living systems, their evolution and their ability to adapt and to interact

Holobiont
holos, “whole”
bios, “life”
→ natural living entity constituted of a higher, i.e. multicellular, organism called a host, (animal or a plant)
and its microbiota, i.e. the cohort of microorganisms closely associated with it.

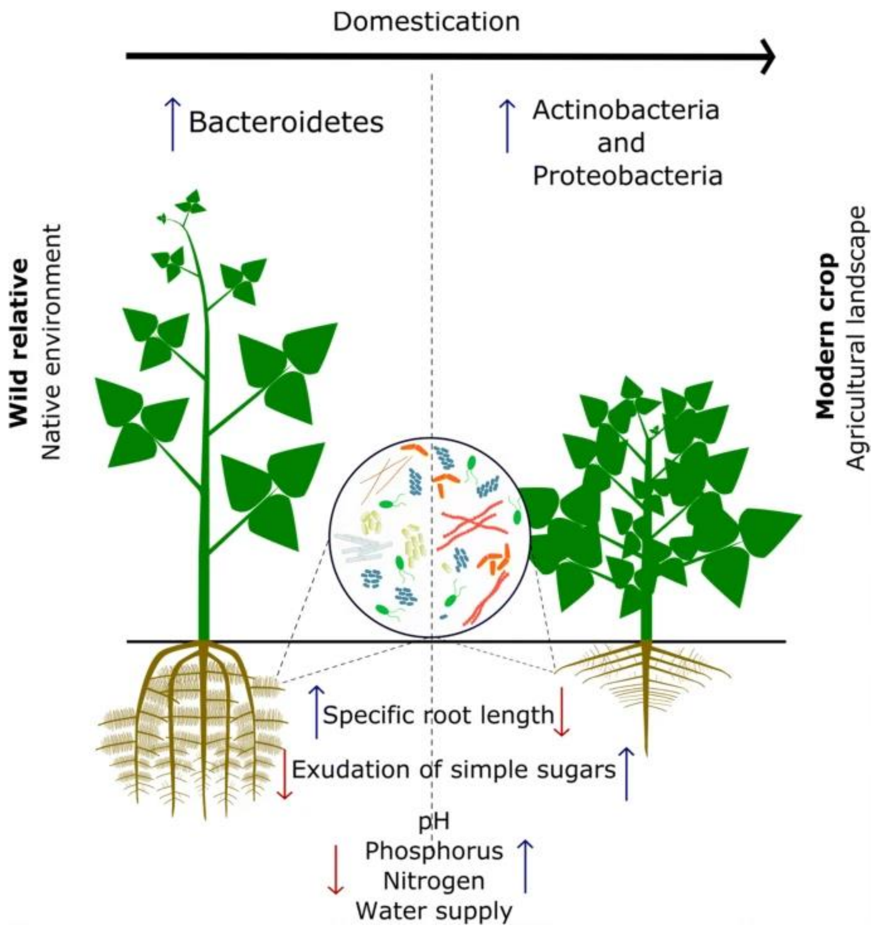
It is a host and all its microbes (for example in the human gut, about 1 to 2 kg per adult).

https://www.lemonde.fr/blog/internetactu/2018/11/30/tous-holobiontes-et-si-letre-humain-etait-un-meta-organisme-plutot-quune-entite-unique/

Impact of domestication on soil management, plant phenotype, plant physiology, and rhizobacterial diversity

-root morphology of the wild relative of bean differs from that of the modern counterpart. Increased availability of nutrients and water led to shallower roots in the modern crop cultivars
-domesticated crop plants presumably also exude more "simple" sugars than their wild relatives
-impact of the domestication process on rhizobacterial community composition → decrease in Bacteroidetes abundance (for slow growth) in favor of Actinobacteria and Proteobacteria (for rapid growth).

Pérez-Jaramillo, J.E., Carrión, V.J., de Hollander, M. *et al.* The wild side of plant microbiomes. *Microbiome*



Received: 27 April 2021 | Revised: 26 August 2021 | Accepted: 17 September 2021
DOI: 10.1002/pei3.10062

PLANT-ENVIRONMENT INTERACTIONS

RESEARCH ARTICLE

Differentiation of endospheric microbiota in ancient and modern wheat cultivar roots

Solène Mauger[1] | Claire Ricono[1] | Cendrine Mony[1] | Vèronique Chable[2] | Estelle Serpolay[2] | Marine Biget[1] | Philippe Vandenkoornhuyse[1]

Could modern plant breeding and agroecosystems artificialization have altered plants' ability to filter and recruit beneficial microorganisms in its microbiota?

Modern cultivars harbored higher richness of bacterial and fungal **pathogens** than ancient cultivars. The study shows the effect of plant breeding on the microbiota associated plant root.

The domestication process and the development of industrial agriculture, have reduced and shifted the genetic diversity of cereals associated microbiome.
The selection of traits which mainly focused on yield increase caused an increase in pathogen susceptibility and a decrease in nutrient quality.
→ disorders of ecosystems and human health

Reviews: Current Topics

Ancient wheat species and human health: Biochemical and clinical implications

Monica Dinu [a b], Anne Whittaker [c], Giuditta Pagliai [a b], Stefano Benedettelli [c], Francesco Sofi [a b d]

"Biobreeding"

→ breeding technique that take in consideration the whole agroecosystem
→ cultivars that are highly adapted to specific low-input conditions
→ suitability for organic agriculture (in the future, European organic farming will no longer be allowed to use conventional seeds)

Natural crossing between compatible species or varieties

Field cultivation under organic/low-input conditions in different pedo-climatic zones

Participatory observation by farmers and researchers

Selection of plants with better local adaptation, resistance, and quality

Scientific approach to old technique

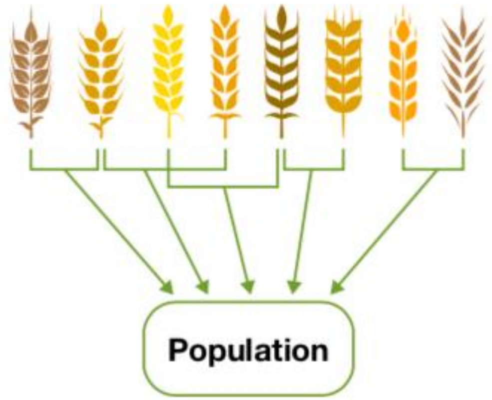
https://www.adriaeco.eu/2024/05/22/biobreeding-e-nuove-varieta-di-cereali-per-lagricoltura-biologica-seminare-il-futuro-mette-a-confronto-esperti-nazionali-ed-internazionali/

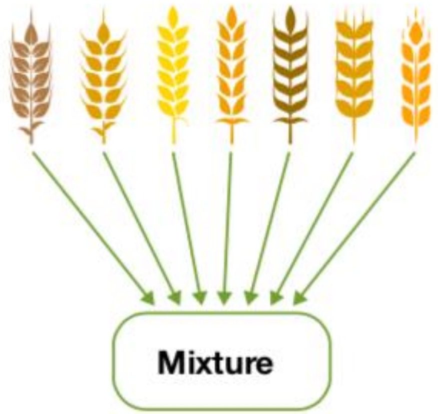
As «biobreeding» requires a lot of time (up to 10/15 years to obtain a stable and uniform variety in field conditions)

variety mixtures and **evolutionary populations** can be used

Variety mixtures: combinations of several varieties grown together → increase resilience, reduce pests and diseases, and stabilize yields

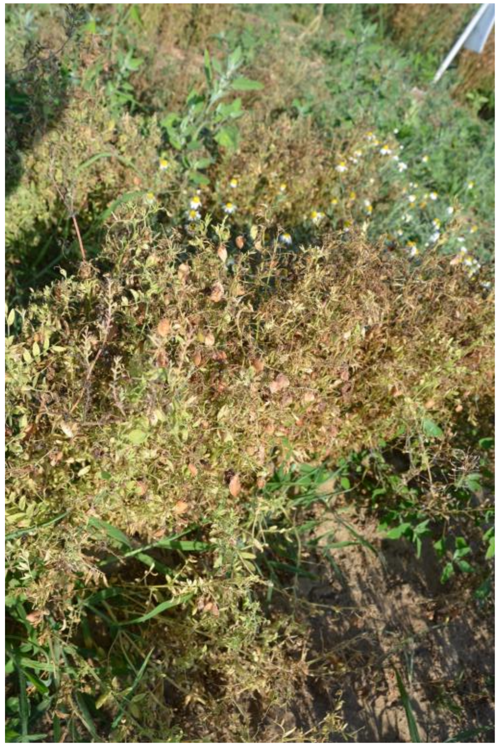
Evolutionary populations: dynamic populations obtained by crossing many varieties or lines → they evolve over time, adapting naturally to local conditions.





Chapter 4

Participatory characterization and genome-wide association study of Italian lentil landraces: unlocking genetic diversity for low input systems and changing climate in the Mediterranean



Hypothesis – Ch 4

Phenotypic and genotypic diversity of Italian lentil landraces and their relationships with collection origin and farmers' preferences

1) Is the diversity of Italian landraces a valuable resource for adapting to low-input systems and changing climates, for future breeding or for composing trait-based cultivar mixtures?

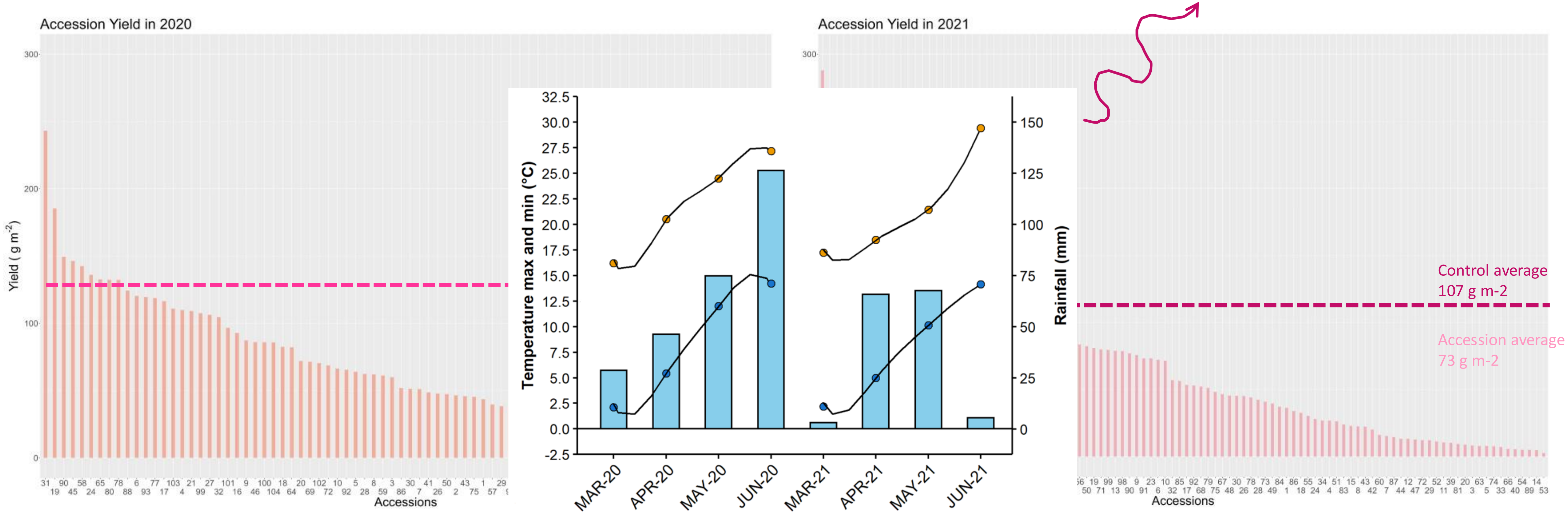
landraces → farmer varieties/heterogeneous material
non-professional breeding processes

control variety → classic breeding programme high-input selection environment

5678	ALTAMUR.	VE 0403		6F	NONAME	7M	3611	
CORELLA	4F	7H	5507		8H	4924 DOP		6H
	VA30	2A	5L	1F		NIS17	6G	2B
2H		4I	8D	4262	4C		BIS1	4E
5502	7P		PAN21	3G	5I	1C		4H
8N	7L	5G		7B	3A	LIN	4944	
8A	6B	5503	6D		5676		8B	7N
	3H	5504	4A	7O		5E	2F	3B
4259		1M	4B	8O	3D		4I	8E
4251	6A		2E	3E	MM15	1E		7D
6E	UST	7C		1G	7A	5F	MT14	
7Q		PAC19	3C		4G	2G	5A	4M
	5B	MAN10	S STEFANO	CAT3		8L	4252	1A
4L		2D	4923	8G	MOD11		5509	8C
4269	PAL20		rimanenza	7R	4258	6C		NENNA
1B	4D	7E		6I	8F	5D	2C	

1) Is the diversity of Italian landraces a valuable resource for adapting to low-input systems and changing climates, for future breeding or for composing trait-based cultivar mixtures?

Landraces shows a better response to stress than commercial cultivar



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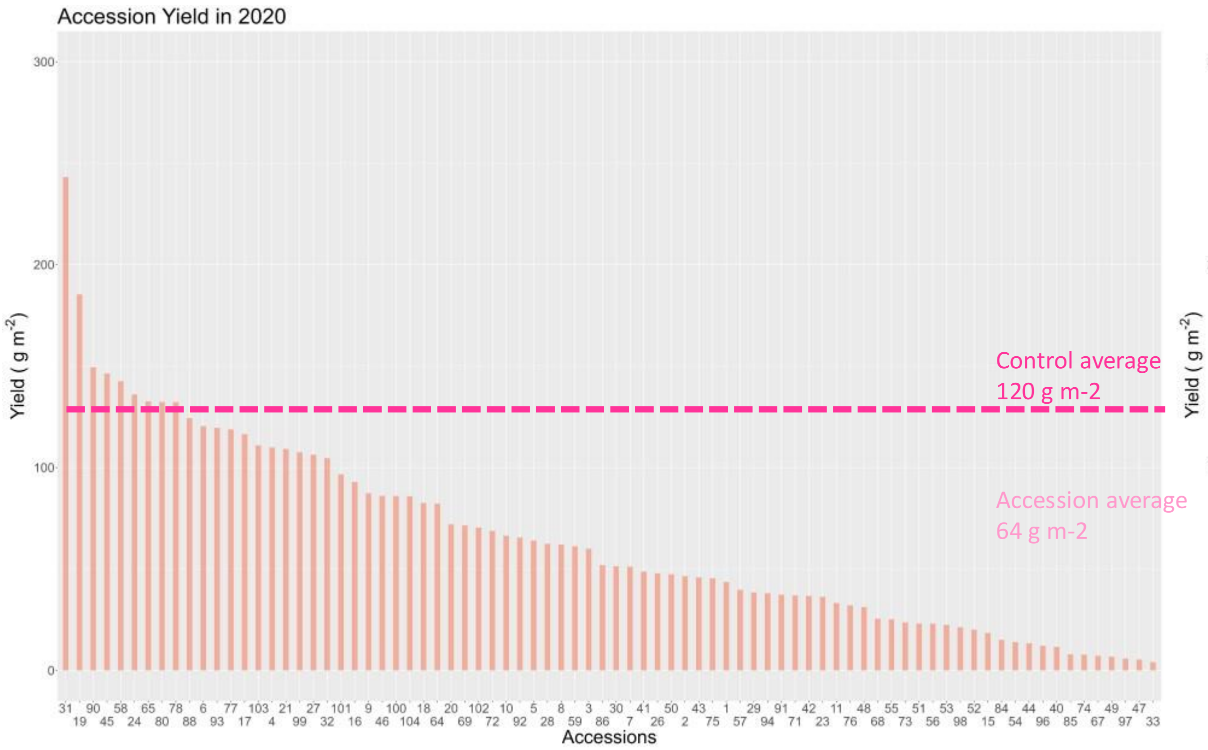
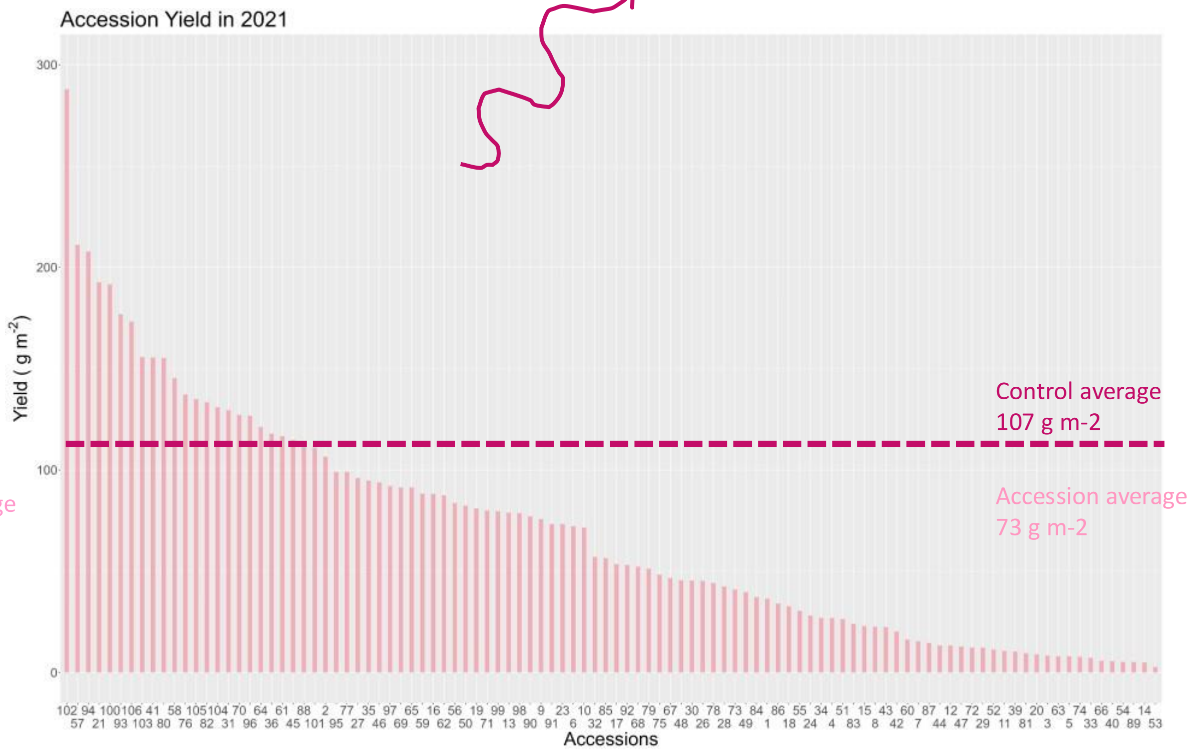
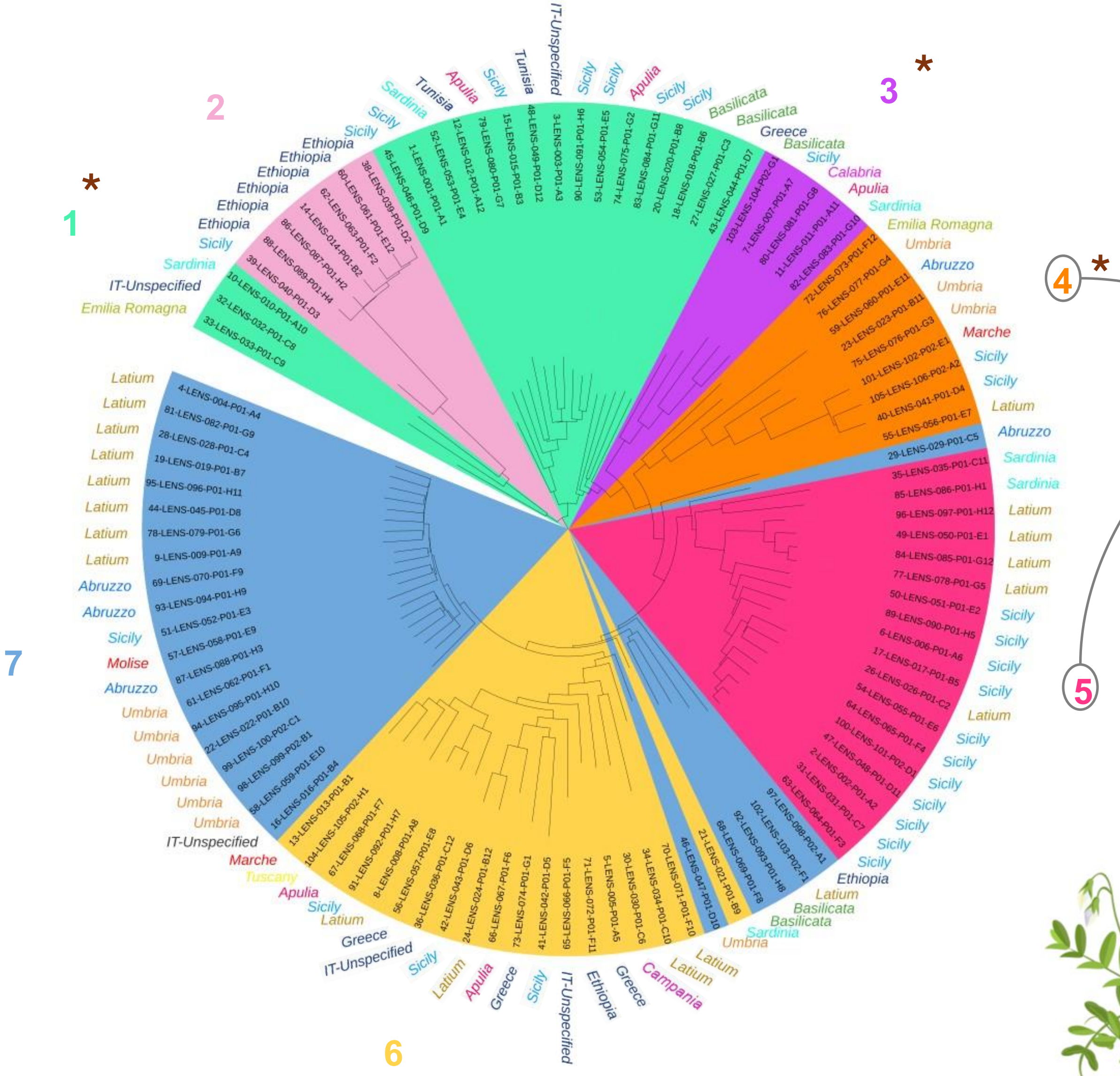






Groups derived from discriminant analysis of principal component (DAPC) based on SNPs

↓

not full correspondence with collection origin!

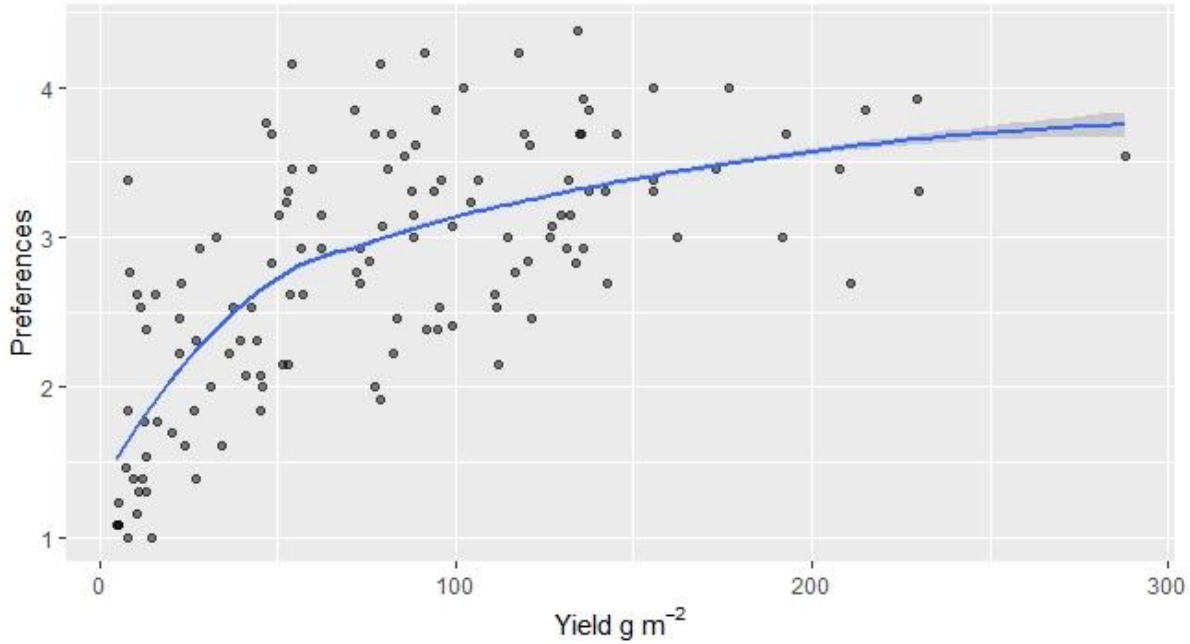
+

collection origin do not explain phenotypic traits

↓

phenology is better explained by DAPC groups

** highest heterozygosity (≈20%)*



rho = 0.73 p < 0.0001

Most preferred traits:
soil cover
canopy homogeneity
plant height
pod number and size
percentage of fruit set
competitiveness
erect habitus

Results – Ch 4

YEAR 2020

Trait	Marker	Chromosome	Position	Pvalue	Qvalue
FLOWERS	90429:38:+	1	397082501	0,00016247	0.0005372
FLOWERS	90429:127:+	1	397082590	0,00015773	0.0005372
FLOWERS	90429:368:+	1	397082831	0,00011816	0.0005372
FLOWERS	458060:75:+	4	475701798	0,00095559	0.0023700
FLOWERS	458060:99:+	4	475701822	0,0012147	0.0024101
FLOWERS	495082:113:-	5	157720761	0,0023692	0.0026115
FLOWERS	495082:59:-	5	157720815	0,0023692	0.0026115
FLOWERS	495082:57:-	5	157720817	0,0023692	0.0026115
FLOWERS	495082:20:-	5	157720854	0,0023692	0.0026115
INFECTION	529715:381:-	5	305000505	0,00040494	0.0021826
INFECTION	529715:378:-	5	305000508	0,000405	0.0021826

YEAR 2021

Trait	Marker	Chromosome	Position	Pvalue	Qvalue
FLOWERS	98844:320:-	1	433291707	0,0066033	0.0196756
FLOWERS	98844:86:-	1	433291941	0,0066033	0.0196756
FLOWERS	98859:65:+	1	433360713	0,012337	0.0196756
FLOWERS	98859:123:+	1	433360771	0,012337	0.0196756
FLOWERS	98859:327:+	1	433360975	0,012554	0.0196756
FLOWERS	98859:260:+	1	433360908	0,012596	0.0196756
FLOWERS	98859:299:+	1	433360947	0,012596	0.0196756
FLOWERS	255866:64:+	2	609565687	0,0096645	0.0196756
FLOWERS	255775:302:-	2	609203846	0,018427	0.0222888
FLOWERS	341352:84:+	3	381248170	0,017425	0.0222888
FLOWERS	347384:79:+	3	408488440	0,022511	0.0249597
FLOWERS	520367:92:+	5	264883488	0,013309	0.0196756
YELLOW1	290218:16:+	3	157976288	0,0018372	0.0311126
YELLOW2	7843:259:+	1	34884375	0,0000165	0.0002578
LODGE	346935:101:-	3	406382818	0,0002025	0.0009075
LODGE	466954:311:-	5	32086743	0,00014906	0.0008907
LODGE	466954:286:-	5	32086768	0,00014906	0.0008907
LODGE	466954:275:-	5	32086779	0,00014906	0.0008907
BRUCHUS	80896:33:+	1	355257873	0,0063775	0.0145883
BRUCHUS	366975:340:-	4	67913853	0,00067558	0.0043810
BRUCHUS	366835:21:-	4	67332586	0,0007661	0.0043810
BRUCHUS	367266:250:-	4	69212691	0,0042085	0.0143101
BRUCHUS	404758:251:-	4	234269759	0,0050047	0.0143101
HEIGHT	162261:373:+	2	184619668	0,010856	0.0347879
HEIGHT	319619:381:-	3	284591913	0,019469	0.0347879
HEIGHT	327474:39:+	3	318588253	0,017743	0.0347879
HEIGHT	415480:66:+	4	281361761	0,012667	0.0347879
HEIGHT	551051:34:-	5	403912287	0,020114	0.0347879
HEIGHT	657273:15:+	6	411433219	0,018552	0.0347879

Interesting for diversification and climate change

GENOME WIDE ASSOCIATION STUDY

11 MTAs in 2020 and 29 MTAs in 2021

flower precocity, susceptibility to disease, leaf yellowing, lodging, susceptibility to Bruchus spp., plant height.

Increasing problem

Suggestive significance

	Year 2020				Year 2021			
Trait	Marker	Chr	Pos	p	Marker	Chr	Pos	p
LODGE_1	346792:11:-	3	405793256	0,0425	346935:101:-	3	406382818	0,0002
					346935:6:-	3	406382913	0,0017
LEAF_Y_C_2	513136:93:-	5	234325917	0,0824	515235:324:+	5	243730712	0,0001
YIELD	335413:276:+	3	353678705	1,2228	334317:266:+	3	348248104	0,3684
YIELD	755866:51:+	7	430884993	0,2973	751511:33:-	7	410551159	0,4470

yield = complex trait (environment, multiple small effect loci)

- → limited information in literature
- → suggestive associations may still be relevant

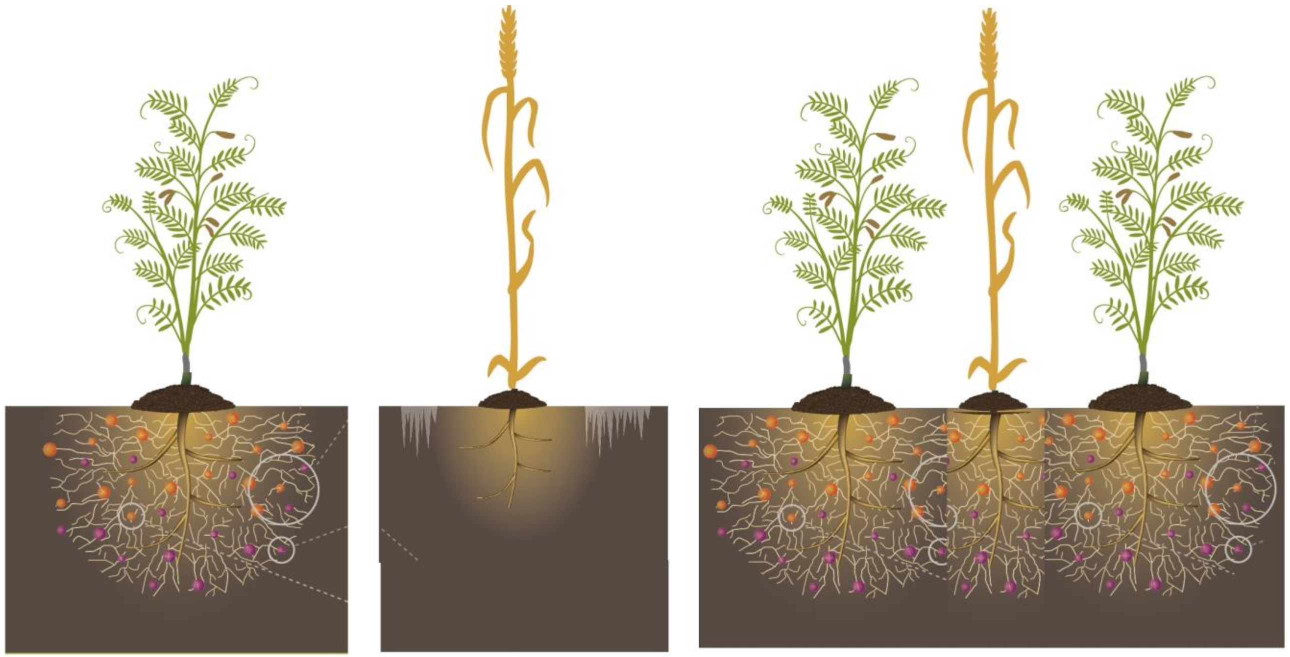
Chapter 5

Intercropping wheat with lentil cultivar mixtures enhances mycorrhizal inoculum potential and promote arbuscular mycorrhizal fungi roots colonization in wheat

Effect of trait-based landrace mixtures and intercropping and on soil microbiota

1) Within lentil cultivar mixtures, can a higher functional diversity elicit a more robust response to environmental stresses (biomass)?

2) Do different lentil cultivar mixtures exhibit different mycorrhizal affinity, with differing impacts on wheat mycorrhization?



Material and methods – Ch 5

Factor 1: intra-specific diversity
Factor 2: inter-specific diversity

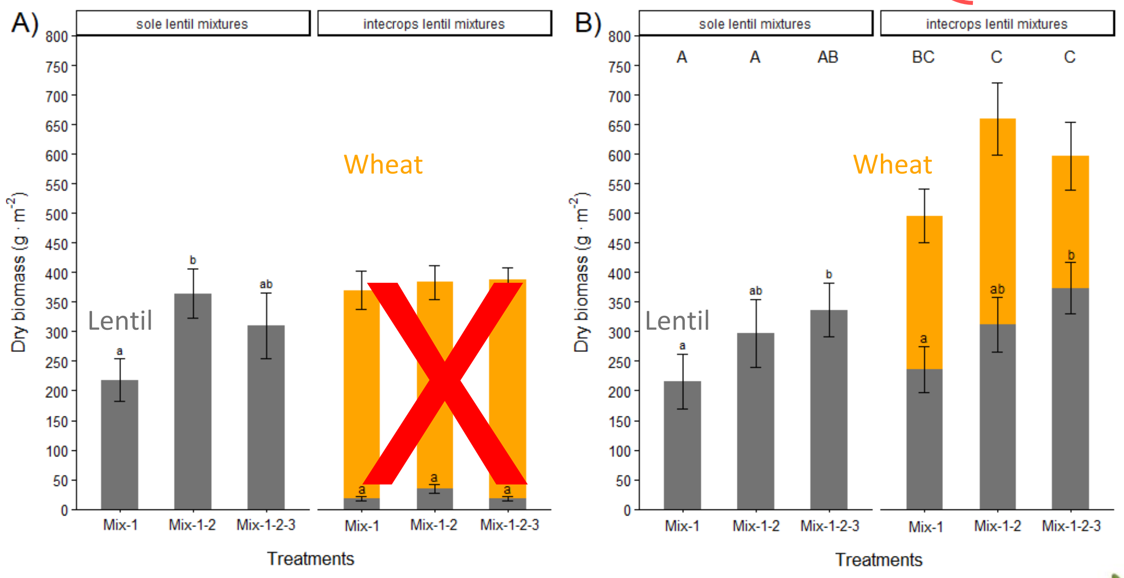
3 levels of mixtures based on functional groups (FG)
-FGs from characterization of chapter 4-

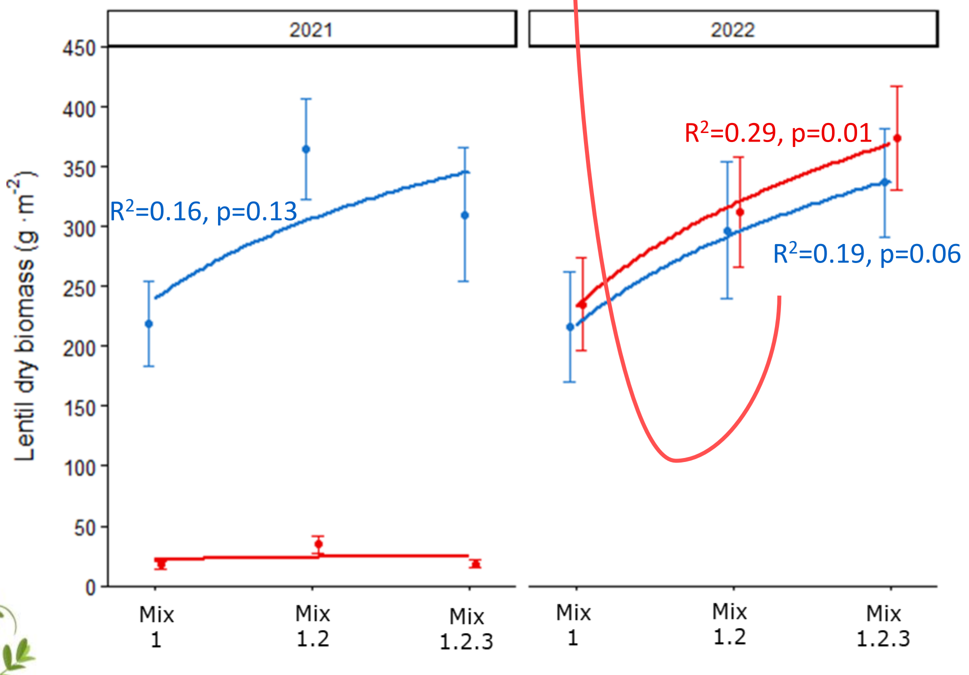
4 levels of intercropping:
wheat lentil intercrop
lentil mixtures
sole wheat control
sole lentil control (commercial variety)

Mixture	Functional Groups	Cultivar
Mix 1	"early cultivar"	ITALY, ITALY -Latium's island LT, ETHIOPIA, ETHIOPIA
Mix 1.2	"early cultivar" + "high biomass"	ITALY, ITALY -Latium's island LT, ETHIOPIA, ETHIOPIA + ITALY -Sicily (Villalba CL, Mussomeli CL, Modica RG, Montagnola PA)
Mix 1.2.3	"early cultivar" + "high biomass" + "high yield"	ITALY, ITALY -Latium's island LT, ETHIOPIA, ETHIOPIA + Sicily (Villalba CL, Mussomeli CL, Modica RG, Montagnola PA) + ITALY -Sicily CL, ITALY -Abruzzo AQ, ITAY -Basilicata PZ, ITALY -Campania

1) Within lentil cultivar mixtures, can a higher functional diversity elicit a more robust response to environmental stresses (biomass)?

In 2022 hypothesis confirmed both at sole crop and intercrop level



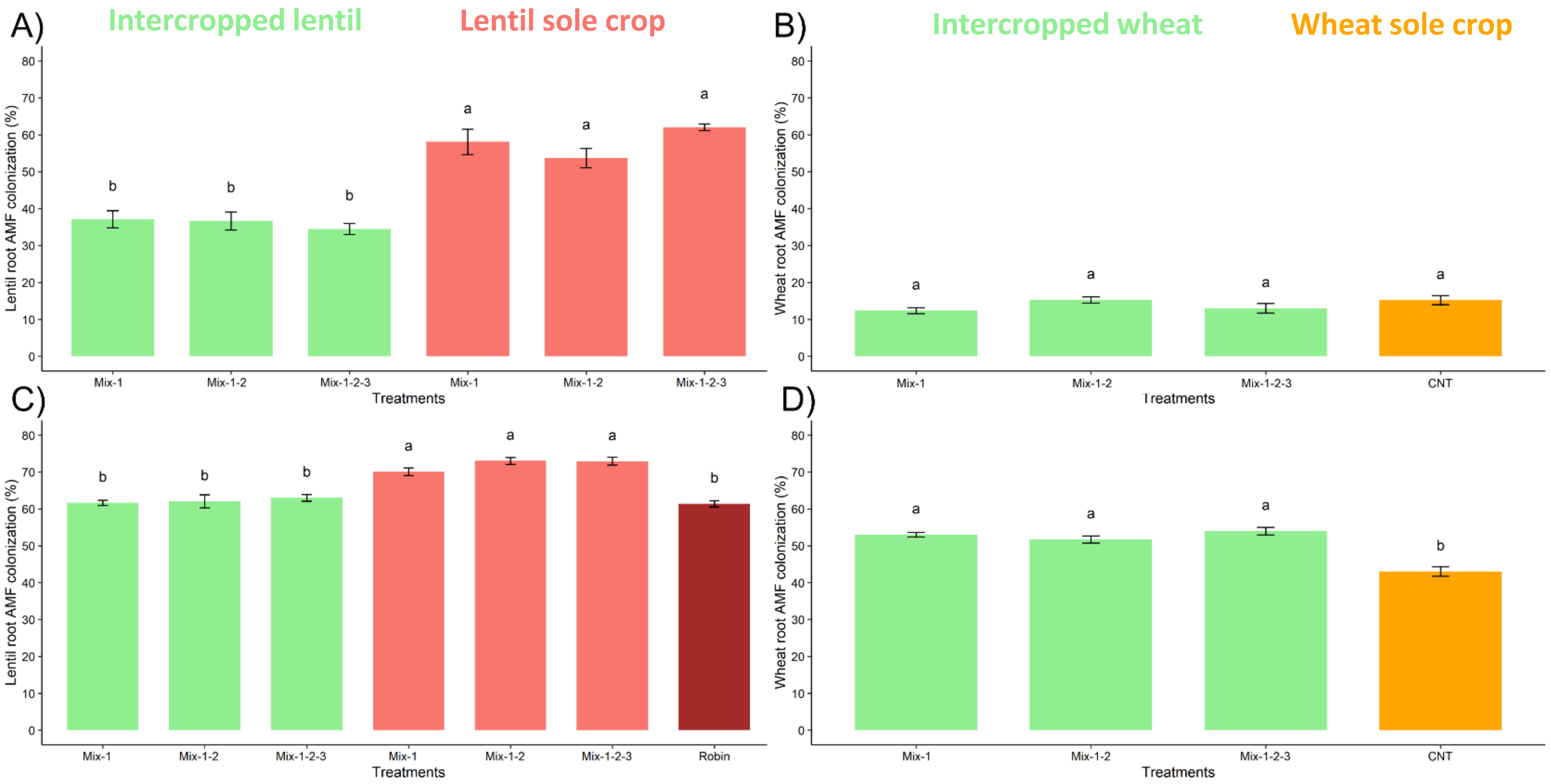


Lentil biomass as intercropped with wheat or sole crop

2) Do different lentil cultivar mixtures exhibit different mycorrhizal affinity, with differing impacts on wheat mycorrhization?

AMF in 2021

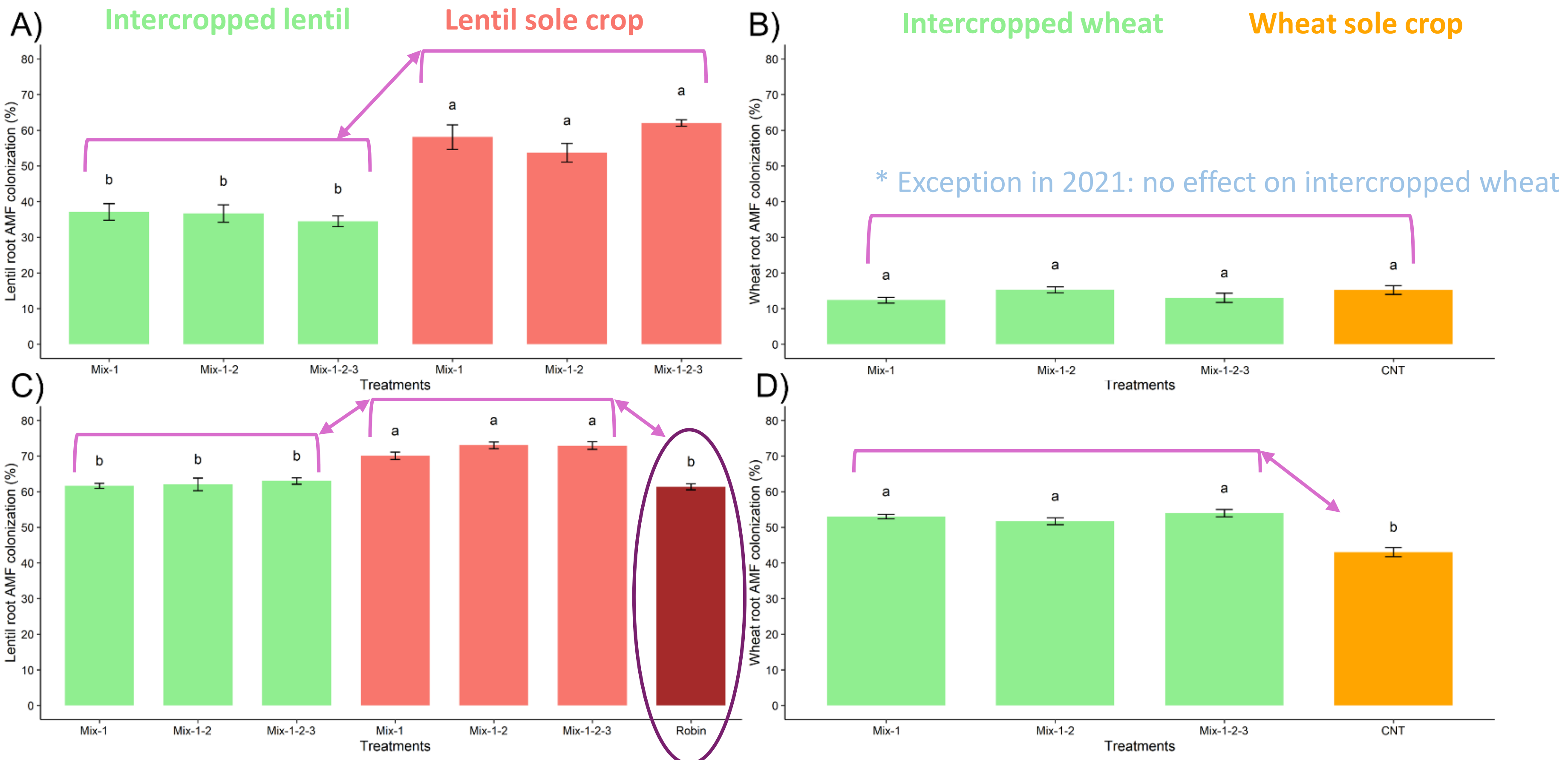
AMF in 2022



Significant effect between intercrop and sole crop
Significant effect between mixtures and commercial cv.
No effect between mixtures

AMF in 2021

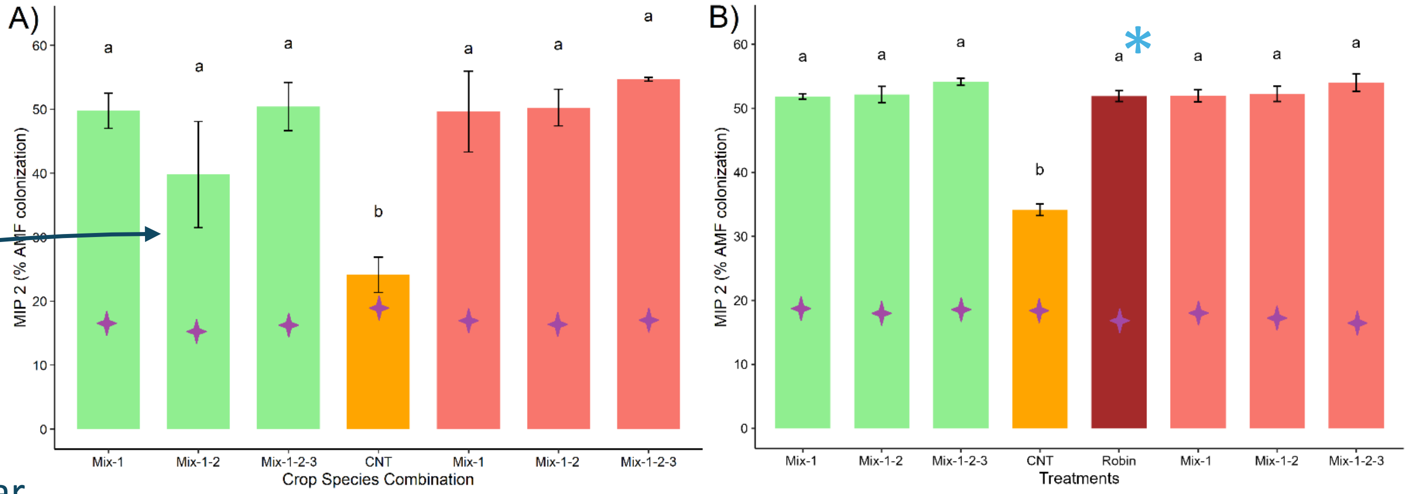
AMF in 2022



Commercial cultivar!

2) Do different lentil cultivar mixtures exhibit different mycorrhizal affinity, with differing impacts on wheat mycorrhization?

* Lower AMF in commercial cultivar is not explained by lower MIP



Despite low biomass clear effect of lentil on MIP in 2021: Residual effect?