APPSA 2nd SCIENTIFIC CONFERENCE

2 - 4 April 2025 | Manthabiseng Convention Centre
Maseru, Kingdom of Lesotho

Harnessing genetic innovations to promote resilient African food systems

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CCARDESA Centre for Coordination of Agricultural Research and Development for Southern Africa

GOVERNO DE ANGOLA

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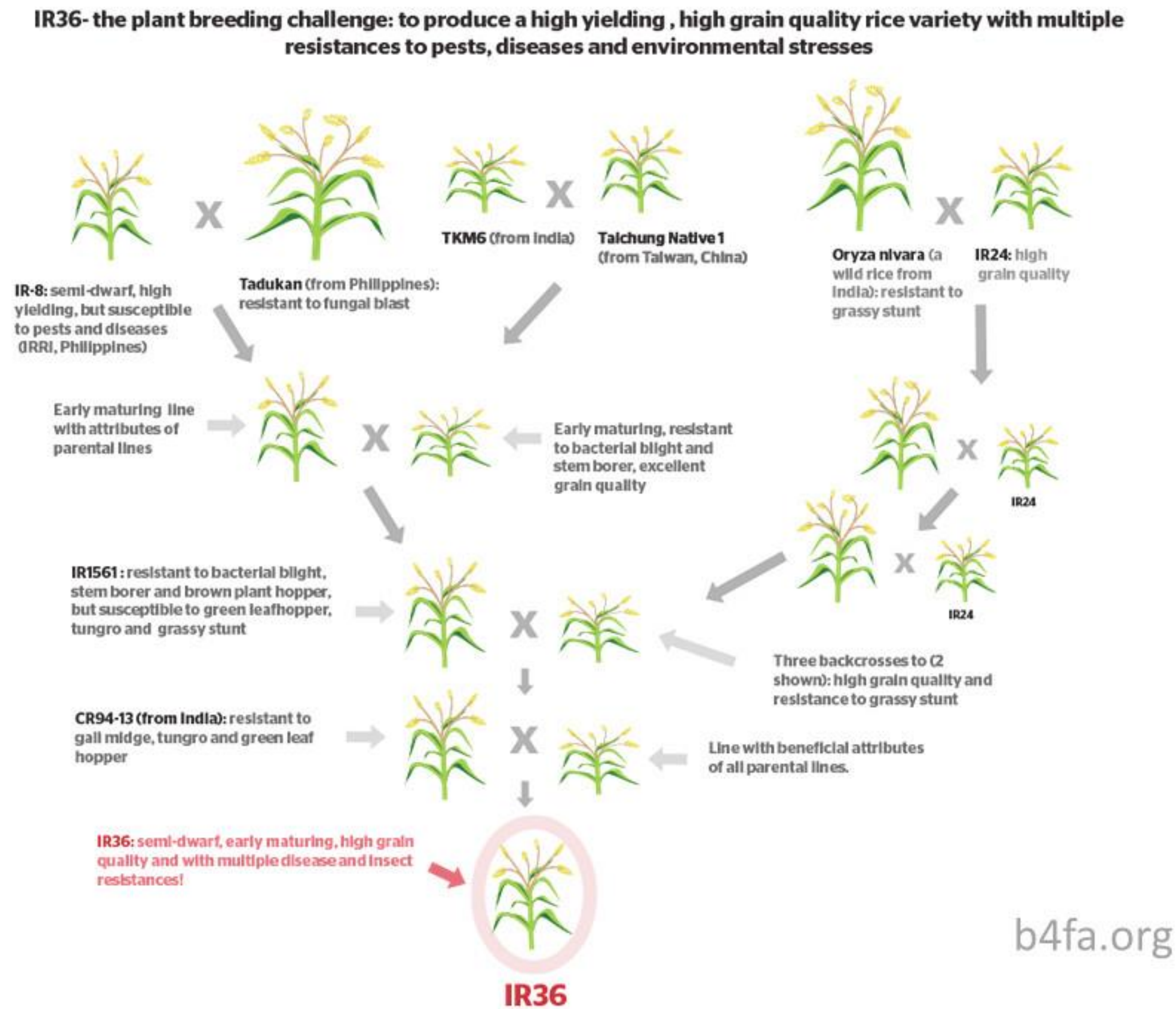
INTRODUCTION

#Crop production form the backborne of most economies in Africa, but productivity is constrained by several biotic and abiotic factors (**<u>plants not fit under these stress conditions</u>**):

#How can farmers respond to this challenge?

- In developing countries, crop production is mostly done by subsistent farmers, who are predominantly resource-poor.
- Cannot make use of these technologies, a phenomenon that coz most of the families to be food insecure, and subsequently leading them into poverty.
- Besides, use of inorganic fertilizers and pesticides is known to negatively impact on ecosystem functions and biodiversity, hence sustainable methods that are accessible to farmers need to be developed.

#How to move towards sustainability in crop production



#Plant breeding is a time-consuming and resource-demanding process

Journal of Agricultural Science; Vol. 10, No. 3; 201
ISSN 1916-9752 E-ISSN 1916-976
Published by Canadian Center of Science and Educatio

Combining Ability for Grain Yield Performance among CIMMYT Germplasm Adapted to the Mid-Altitude Conditions

Casper Nyaradzai Kamutando[1,2], Cosmos Magorokosho[2] & Shorai Dari[1]

Journal of Agricultural Science; Vol. 16, No. 8; 2024
ISSN 1916-9752 E-ISSN 1916-9760
Published by Canadian Center of Science and Education

Potential of Tropically-Adapted Exotic Acid Tolerance White Maize Donor Lines in Sub-tropical Breeding Programmes for Low pH Adaptation

Dibanzilua Nginamau[1,2,3], Casper Nyaradzai Kamutando[4], Cosmos Magorokosho[5], João Constâncio Saraiva[6], Angeline van Biljon[3] & Maryke Labuschagne[3]

Vol. 8(29), pp. 4058-4066, 1 August, 2013
DOI: 10.5897/AJAR2013.7241
ISSN 1991-637X ©2013 Academic Journals
http://www.academicjournals.org/AJAR
African Journal of Agricultural Research

Full Length Research Paper

Exploiting genotype x environment interaction in maize breeding in Zimbabwe

Casper Nyaradzai Kamutando[1,2], Dean Muungani[2], Doreen Rudo Masvodza[3] and Edmore Gasura[1]

agronomy MDPI

Article

Genetic Gains of Grain Yield among the Maize Cultivars Released over a Century from the National Breeding Program of Zimbabwe

Purity Mazibuko [1,2,*], Charles Mutengwa [1], Cosmos Magorokosho [3], Dumisani Kutywayo [2] and Casper Nyaradzai Kamutando [4]

agronomy MDPI

Article

Genetic Potential of New Maize Inbred Lines in Single-Cross Hybrid Combinations under Low-Nitrogen Stress and Optimal Conditions

Fortunate Makore [1], Cosmos Magorokosho [2], Shorai Dari [1], Edmore Gasura [1], Upenyu Mazarura [1] and Casper Nyaradzai Kamutando [1,*]

Euphytica (2024) 220:101
https://doi.org/10.1007/s10681-024-03367-6

RESEARCH

Low pH adaptation of tropical exotic acid tolerance yellow maize donor lines in sub-tropical breeding programs

Dibanzilua Nginamau · Casper Nyaradzai Kamutando · Cosmos Magorokosho · João Constâncio Saraiva · Angeline van Biljon · Maryke Labuschagne

JOURNAL OF CROP IMPROVEMENT
https://doi.org/10.1080/15427528.2021.1974635
Taylor & Francis
Taylor & Francis Group

Check for updates

Participatory variety selection and stability of agronomic performance of advanced sorghum lines in Zimbabwe

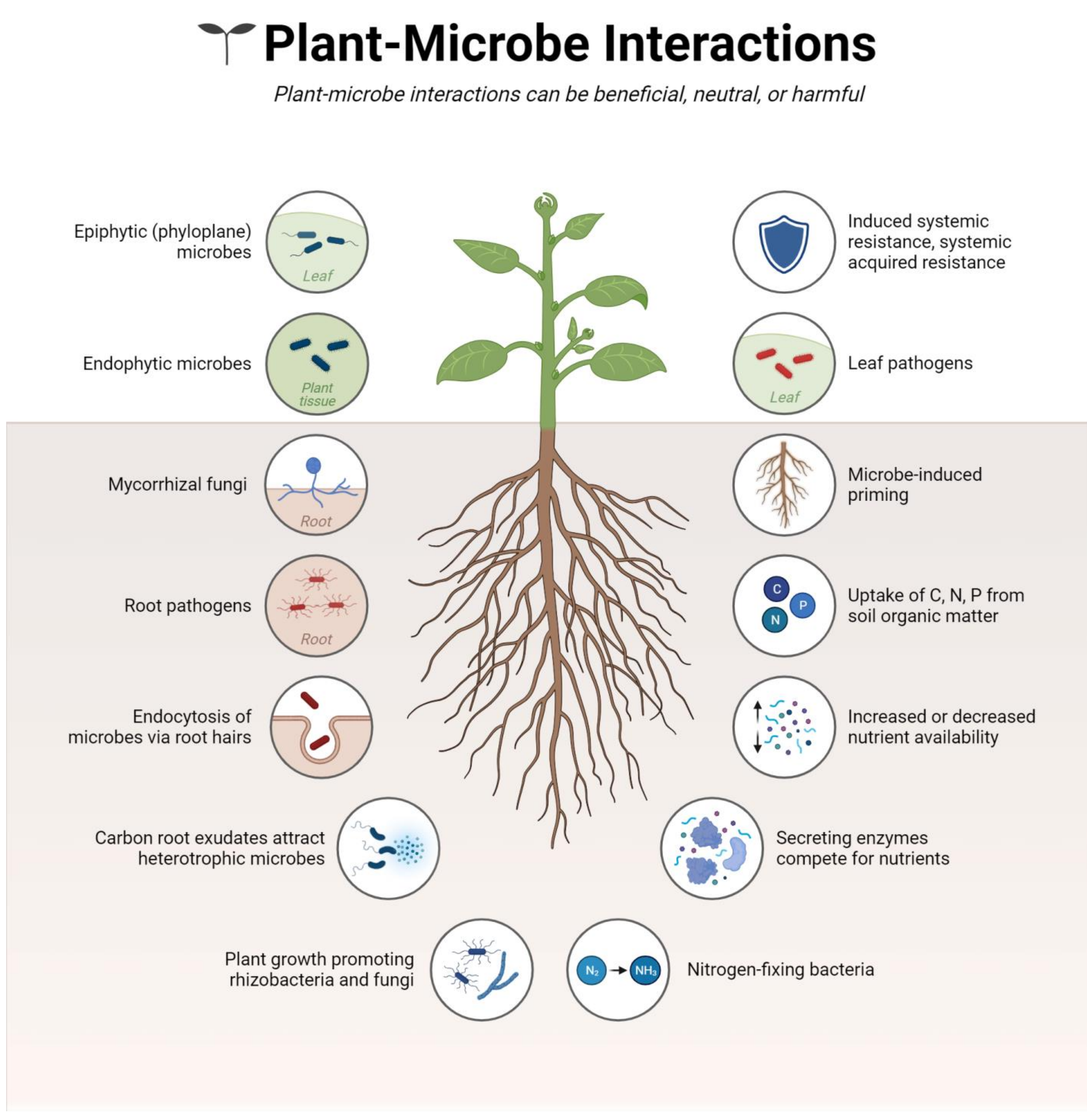
Alec Magaisa[a], Pepukai Manjeru[b], Casper Nyaradzai Kamutando[c], and Martin Philani Moyo[a]

#Any success stories to date?

- Significant progress has been made to date, resulting in commercialization of several crop genotypes adapted to biotic and abiotic stress conditions, as well as harbouring several food and feed quality traits.

- However, under extreme stress conditions, especially in small-holder farming systems, crop productivity has remained averagely low, thereby challenging crop breeders to re-think on their breeding strategies, so that they can enhance crop productivity under the current and the predicted climate change scenarios.

- Microorganisms are postulated to play key roles in stress adaptation (i.e., plant fitness), but their potential contributions, as well as the mechanisms underlying plant-microbe interactions under biotic & abiotic stress conditions are still poorly understood.



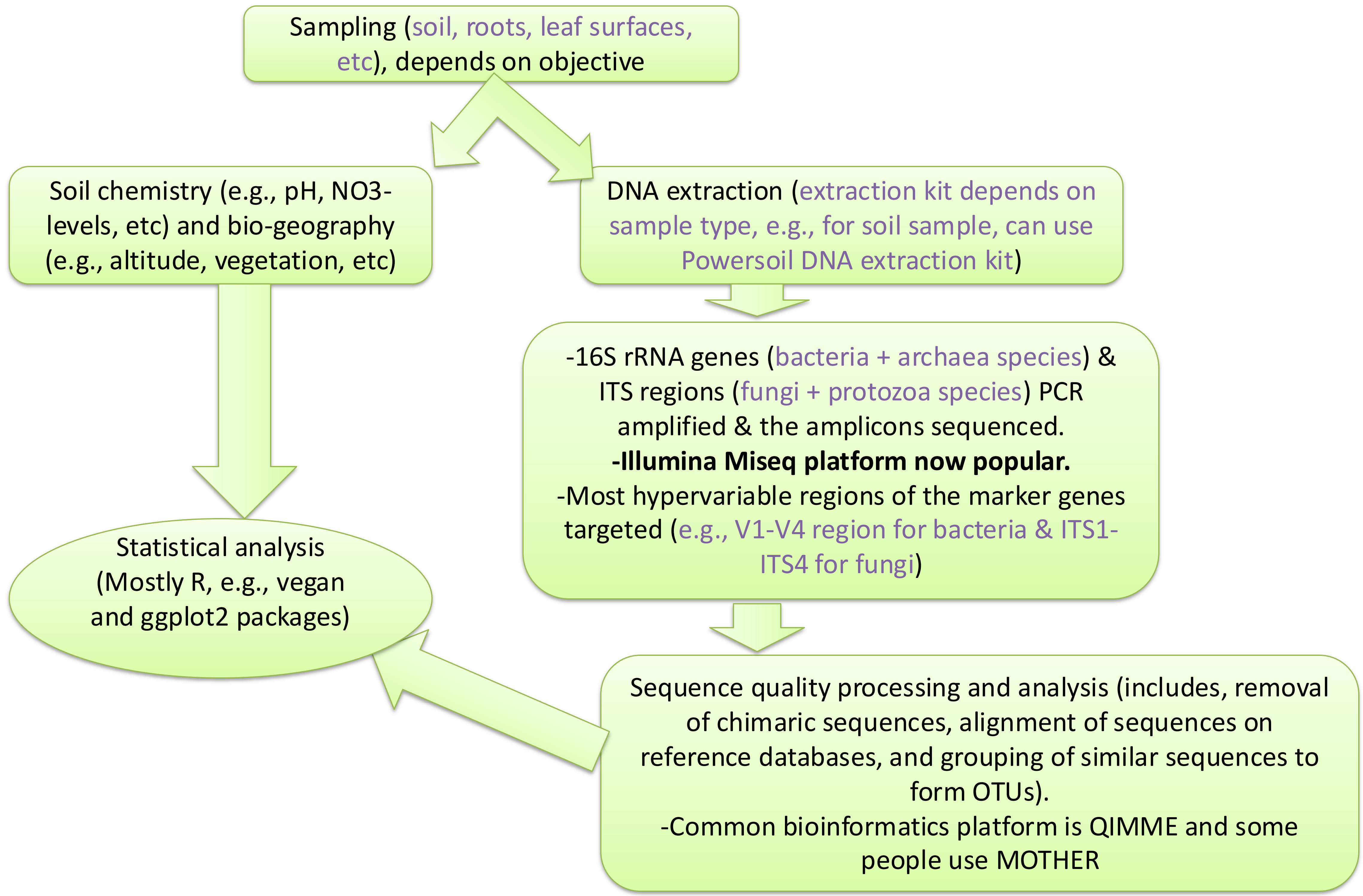
#Which questions can be answered using metagenomics approaches??

1. Who is there (taxonomical identity)?

2. What is she/he doing (functional roles, e.g., plant growth promotion, pathogenicity or nutrient cycling)?

#What then can we do to get the answers???

1. Who is there (taxonomical identity): The strategy?



#A case study

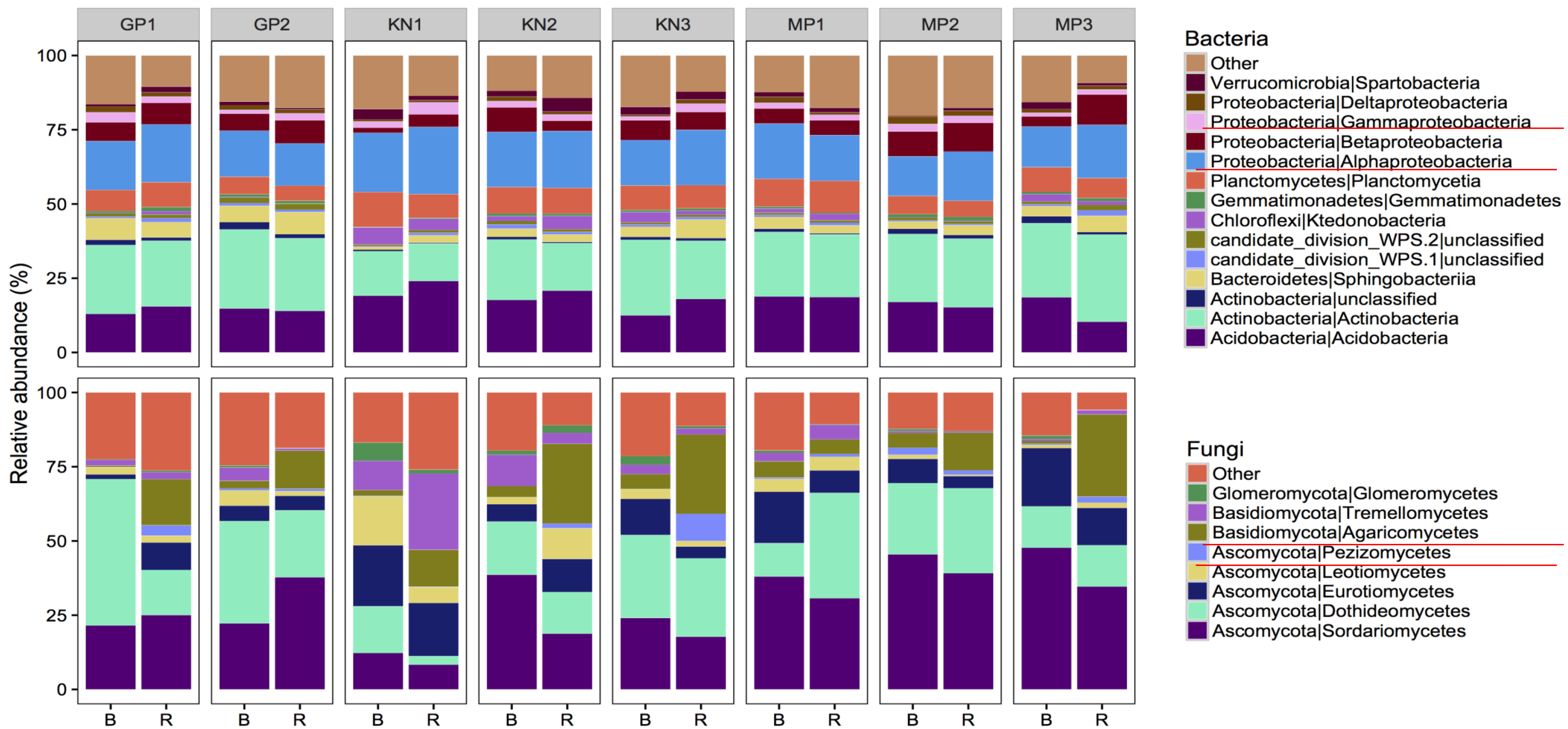
SCIENTIFIC REPORTS

OPEN

Soil nutritional status and biogeography influence rhizosphere microbial communities associated with the invasive tree *Acacia dealbata*

Received: 10 April 2017
Accepted: 20 June 2017
Published online: 26 July 2017

Casper N. Kamutando[1], Surendra Vikram[1], Gilbert Kamgan-Nkuekam[1], Thulani P. Makhalanyane[1], Michelle Greve[2], Johannes J. Le Roux[3], David M. Richardson[3], Don Cowan[1] & Angel Valverde[1]



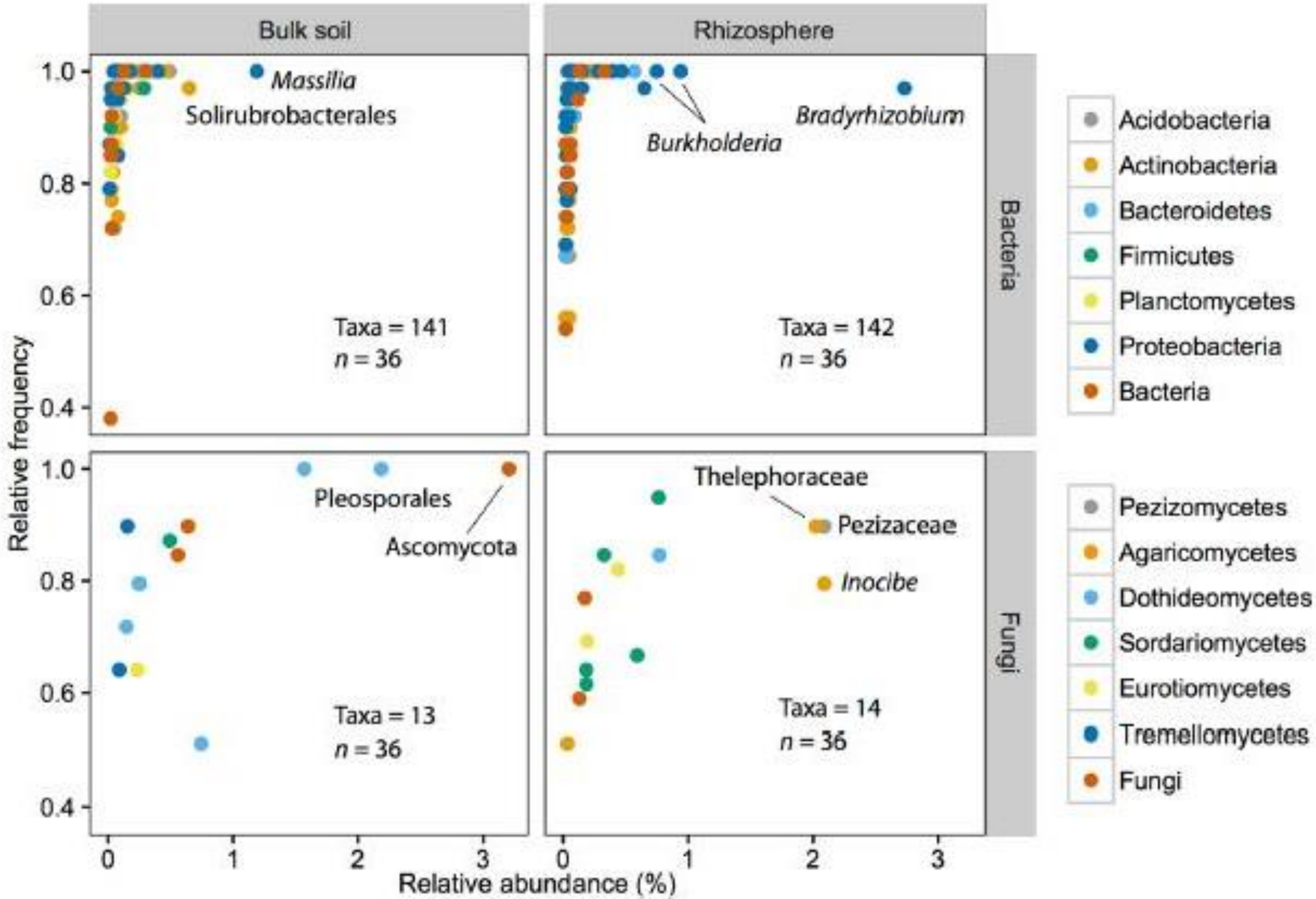


Figure 5. Relative frequency versus relative abundance of biomarker taxa, coloured according to phylum, for bulk and rhizosphere soils (logarithmic LDA score ≥ 2, $P < 0.05$). The number of biomarker taxa (OTUs) and the number of samples (n) are indicated in each plot.

2. What is she/he doing (functional roles, e.g., plant growth promotion, pathogenecity or nutrient cycling)?: The strategy?

Metagenomic DNA samples (usually from at least two different habitants)

Short-gun DNA sequencing

A: ORF prediction/contigs

- ✓ Quality filtering (prinseq)
- ✓ *De novo* assembly (metaSPADES)
- ✓ ORF prediction, contigs > 500 bp (prodigal)
- ✓ ORF alignment, protein database (diamond blastp)
- ✓ Functional/taxonomic annotations (MEGAN community edition)
- ✓ Statistical analysis (STAMP & R)

B: Population genomes

- ✓ Binning, contigs > 1,500 bp (CONCOCT)
- ✓ Bin quality checking (checkM)
- ✓ Bin refinement (Anvio)
- ✓ Bins ≥ 70 % completeness annotations (RAST &KAAS)

#A case study

Microbial Ecology (2019) 77:191–200
https://doi.org/10.1007/s00248-018-1214-0

SOIL MICROBIOLOGY

The Functional Potential of the Rhizospheric Microbiome of an Invasive Tree Species, *Acacia dealbata*

Casper N. Kamutando[1] · Surendra Vikram[1] · Gilbert Kamgan-Nkuekam[1] · Thulani P. Makhalanyane[1] · Michelle Greve[2] · Johannes J. Le Roux[3] · David M. Richardson[3] · Don A. Cowan[1] · Angel Valverde[1,4]

Received: 24 March 2018 / Accepted: 28 May 2018 / Published online: 9 June 2018

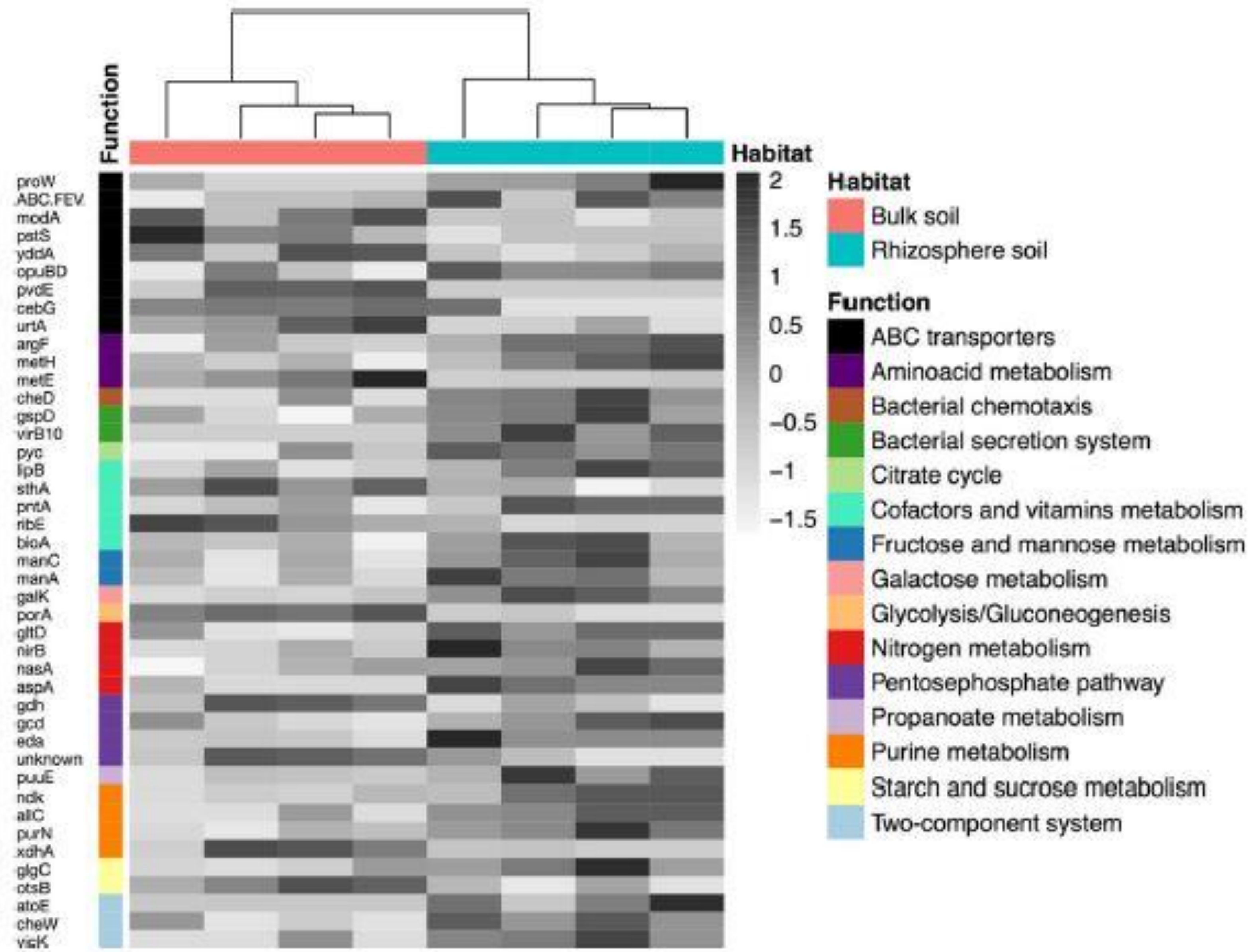


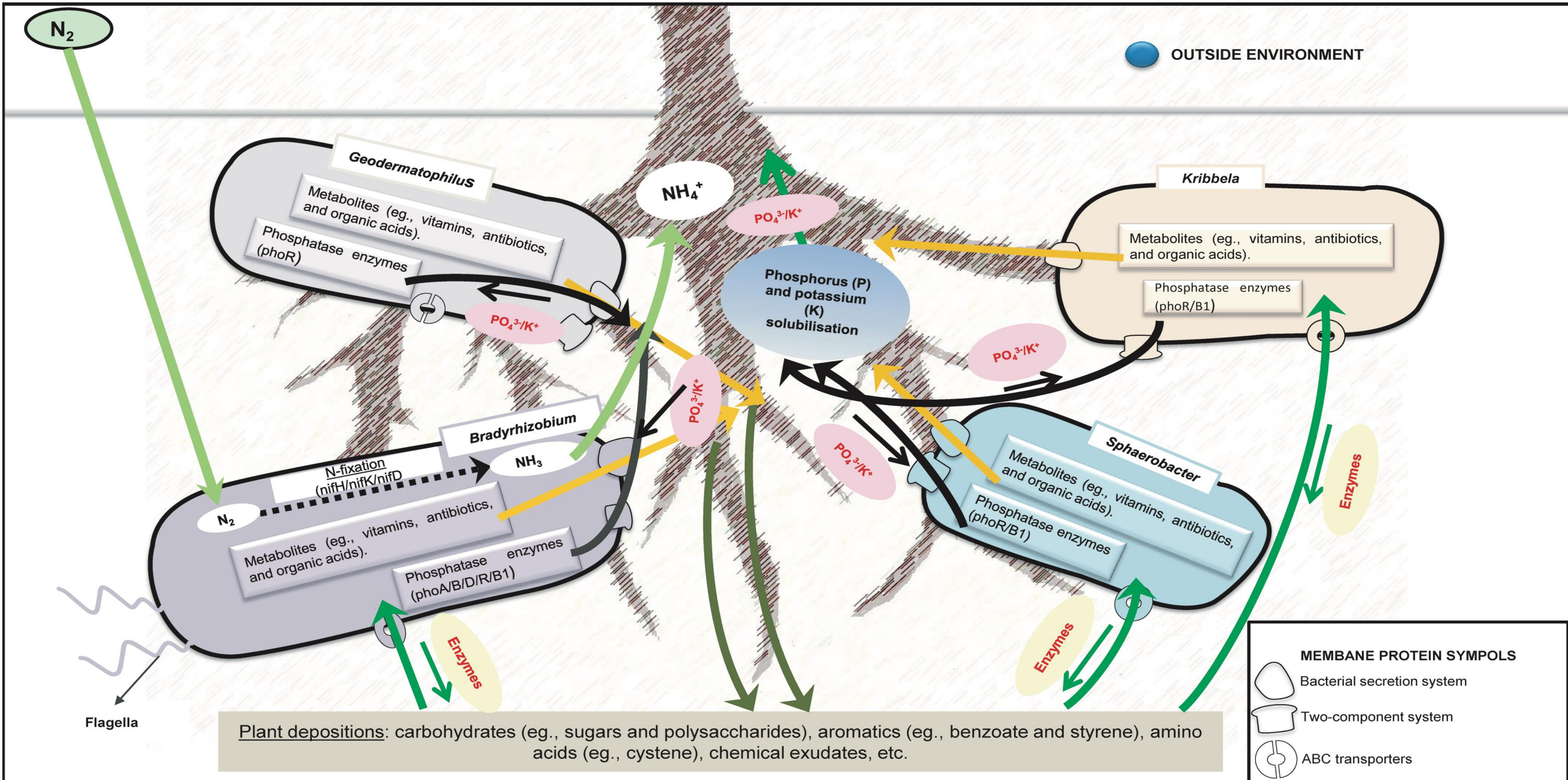
Fig. 2 Heat map of differentially abundant plant growth-beneficial functions, as revealed by STAMP statistical analysis. Genes associated with a similar function are represented by one colour; for example black denotes genes associated with ABC transporters. Each row was scaled so that the mean of each gene across samples was calculated and coloured by the corresponding *z*-score of each cell. Clustering of the samples was done using the UPGMA method with correlation distances. Individual genes associated with a specific function are shown on the left side of the figure

Genome reconstruction

Composite genomes (≥70% completeness) characteristics

Parameters	Bin12.2	Bin15.1	B17.1	Bin20.1	Bin21
Closest taxonomic neighbour	*Koribacter*	*Bradyrhizobium*	*Geodermatophilus*	*Kribbela*	*Sphaerobacter*
Sequence size (bp)	4,912,472	7,476,157	3,911,194	6,607,702	2,363,288
Shortest contig size	1501	1530	2523	2203	1662
Median sequence size	4644	7822	14308	19673	4680
Mean sequence size	5918.6	9785.5	17778.2	26751.8	5908.2
Longest contig size	30361	49996	84287	122199	26027
No. of contigs with protein-encoding genes (PEGs)	830	764	220	247	400
No. of subsystems	299	476	345	390	229
No. of coding sequences	4417	7052	3796	6324	2442
No. of RNAs	57	47	49	33	32
GC content (%)	53.7	63.9	68.5	69.5	66.3
N50 value	5926	8817	21074	40710	4887
L50 value	274	266	62	51	154
Genome completeness (%)	80.17	89.56	83.64	85.11	73.49
	Sequence coverage values (no. of reads mapped back to the composite genomes)				
34R *(Rhizosphere)*	4	346699	48	906	0
43R *(Rhizosphere)*	10	3342	114	117	94458
21R *(Rhizosphere)*	15	21915	334833	1043984	8
51R *(Rhizosphere)*	17	12035	57	1569	107
Rhizosphere total	**46**	**383991**	**335052**	**1046576**	**94573**
1C4 *(Bulk soil)*	51	2989	82	638	6
2C3 *(Bulk soil)*	214753	1013	166	582	21
8C4 *(Bulk soil)*	43	3006	146	1081	49
4C3 *(Bulk soil)*	27	4256	5517	1334	82
Bulk soil total	**214874**	**11264**	**5911**	**3635**	**158**

Putative PGP roles of bacteria residing in the rhizosphere of *Acacia dealbata* plants in South Africa.



CONCLUSIONS

- Although a lot of progress has been made in development of crop genotypes adapted to some biotic and abiotic yield constraining factors, farmers, especially those in developing countries are still experiencing yield loses.

- Frequency of occurrence and intensity of climate change-induced abiotic stresses, especially drought and heat stress, is expected to increase, thereby warranting plant breeders to modify their breeding objectives and strategies so that crops that can cope with the present and future climate scenarios are developed.

- Selecting for crops with enhanced ability to recruit beneficial soil microbiota in their rhizosphere can be a possibility and maybe key in enhancing crop adaption and productivity under severe stress conditions.

End-Thank you for listening!