Mini-Review Article

The plant microbiome as a resource to increase crop productivity and soil resilience: A systems approach

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Abstract

Climate change along with global population increase pose a challenge to worldwide crop production and soil health. There is a need to intensify agricultural production in a sustainable manner and to find solutions to combat abiotic and biotic stress situations. Plant roots can be colonized by a variety of favorable species and genera that promote plant growth. A systems approach to integrating plant breeding and microbiome via applying novel molecular tools, screening technologies and precision phenotyping has the potential to advance the microbial reproducible application under natural conditions.

Resume

Le changement climatique ainsi que l'augmentation de la population mondiale posent un défi pour la production agricole mondiale et la santé des sols. Il est nécessaire d'intensifier durablement la production agricole et de trouver des solutions pour lutter contre les situations de stress abiotiques et biotiques. Les racines des plantes peuvent être colonisées par une variété d'espèces et de genres favorables qui favorisent la croissance des plantes. Une approche systémique d'intégration de la sélection végétale et du microbiome via l'application de nouveaux outils moléculaires, de technologies de criblage et d'un phénotypage de précision pourrait faire progresser l'application reproductible microbienne dans des conditions naturelles

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Introduction

Climate change has resulted in significant changes in weather pattern, precipitation distribution, and temperature and moisture fluctuations (FAO 2008). Extreme conditions caused by these changes bring about many unexpected and more frequent biotic and abiotic stresses (Bebber, Ramotowski et al. 2013; Bebber, Holmes et al. 2014; Trenberth, Dai et al. 2014; Wallace, Held et al. 2014), in particular, novel combinations of stress severities (Niinemets, Kahru et al. 2017). To feed the increasing world population, total crop production will need to be significantly increased, and from a reduced total area that is liable to more severe environmental stress conditions (Kennedy, Naeem et al. 2002; Tilman, Cassman et al. 2002; Foley, Ramankutty et al. 2011; OECD/FAO 2013; FAO 2014). Drought is expected to expand globally owing to increased evaporation and reduced rainfall or changes in the spatial and temporal distribution of rainfall (Dai 2012). This challenge is particularly acute in sub-Saharan Africa (SSA) and North Africa, as the dryland agriculture contributes significantly to its economy. In addition to decreased agricultural area, the countries face a major concern arising from soil erosion intensified by climate change. This not only reduces soil fertility but contributes to eutrophication of inland and offshore water bodies. Hence the situation calls for novel sustainable agricultural technologies (Dai 2012). It is clear that no single technology can meet all the challenges, or even adequately address a single challenge, such as drought or reduction in soil fertility. In order to reduce vulnerability of agricultural systems to climate change, the applied agricultural technologies should be environmentally friendly, ensure high productivity, and be suitable for farmers' adoption. These goals can be achieved via development and dissemination of innovative interdisciplinary technology combining holistic plant breeding with the native microflora/ microbiome (Timmusk, Behers et al. 2017; Timmusk and Behers 2018).

It is known that plant microbiomes evolve with the host and significantly contribute to environmental adaptation (Timmusk, Paalme et al. 2011; Dai 2012; Timmusk and Behers 2012; Timmusk, Timmusk et al. 2013). Dryland soils have always been affected by several constraints. However, over the millennia dryland communities developed adaptation strategies that enabled them not only to cope with scarcity of water and natural resources, but to encourage the development of flourishing civilizations. Think of the Nabateans in southern Jordan. The recent rapid demographic and socio-economic changes led to intensification processes that were not sustainable, causing extensive soil degradation and undermining the soil capacity to perform its productive and ecological functions, including buffering the impacts of climate variability. In order to re-establish the balance, native microbiome application technologies have to be developed (Timmusk, Behers et al. 2017). Despite their centrality to life on Earth, we apply very little of the native microbiome potential to stressed environments. DNA sequencing technologies have enabled a new view of the ubiquity and diversity of microorganisms, their functions and community dynamics (Alivisatos, Blaser et al. 2015; Hultman, Waldrop et al. 2015; Xu, Naylor et al. 2018). Therefore, manipulation of the native microbiome associated with crops represents a promising strategy for addressing many of the challenges climate change poses to soil health as well as to agricultural productivity.

Water productivity breeding

Soil water and nutrient availability are the biggest challenges of agricultural production under climate change. Agriculture is the largest water consumer as well as a major source for eutrophication. Intensifying agriculture via expanding to new areas is a limited prospect as it requires more water. Water productivity (WP) is the net return for the water use or the ratio of biomass with the economic value (edible yield) versus the amount of water transpired. Improved nutrient content and WP can be accomplished by breeding water/nutrient -efficient crops. The International Center for Agricultural Research in the Dry Areas (ICARDA) along with internationally recognized academic breeding centers has established a solid platform for WP breeding (Dwivedi, Britt et al. 2015; Ortiz 2015; Lobos, Camargo et al. 2017; Valdiani, Talei et al. 2017). Selected genotypes are better suited to cope with environmental fluctuations and extremes such as drought and heat spells. Whole-genome prediction models estimate all marker effects in all loci and capture small quantitative trait loci (QTL) mapping effects are applied have resulted in impressive advances and became routine in agricultural breeding (Dwivedi, Britt et al. 2015; Ortiz 2015; Lobos, Camargo et al. 2017; Valdiani, Talei et al. 2017). At the phenotype level, improved agricultural techniques and novel high-throughput selection systems are being developed to enable rapid pre-field screening for specific traits. Yet greater unpredictability of weather conditions under climate change makes it clear that plant breeding alone is not able to meet challenges and calls for strategies completing phenotypic plasticity and adaptability without curtailing yield potential.

Plant growth-promoting rhizobacteria

The soil surrounding plant roots is one of the main sources of plant growth promoting rhizobacteria (PGPR) that have metabolic capabilities for growth promotion and protection of different crops from abiotic and biotic stress (Timmusk 2013; Timmusk, El Daim et al. 2014; Timmusk, Kim et al. 2015; Timmusk, Seisenbaeva et al. 2018). The very first report on enhancement of plant drought stress tolerance by rhizosphere bacteria was published in 1999 (Timmusk and Wagner 1999). Later, the discovery was updated with the principally new approach using harsh environment bacteria which have evolved together with the plant roots for thousands of years. Several systems in plants and bacteria have developed in the harsh environments that trigger the available resources and initiate the metabolic growth that is needed in different stress situations in agriculture under climate change. The studies reveal five times greater survival and 78% higher biomass from inoculated plants under drought stress (Timmusk 2013; Timmusk, El Daim et al. 2014; Timmusk, Kim et al. 2015). This is due to the bacterial ability to protect against abiotic stress as well as facilitate nutrient acquisition. As an example the coalescence and self-assembly of TiO_2 nanoparticles on the surface of cell membranes leads to formation of dense and stable biofilms able to improve the survival and function of rhizobacteria. This enhances bacterial attachment to the root and plant biomass (Fig. 1) (Palmqvist, Bejai et al. 2015; Timmusk, Seisenbaeva et al. 2018). In order to be able to reveal the mechanism of action and monitor the fate performance of the strains, strategies for the strains genetic manipulation have been developed and genomes sequenced (Kim and Timmusk 2013). Although the exact mechanisms of plant drought stress tolerance enhancement by the bacteria varies dependent on seedlings age and mode of inoculation, the bacterial biofilm formation on plant roots forms ground to other mechanisms (Timmusk and Wagner 1999; Mayak, Tirosh et al. 2004; Conrath, Beckers et al. 2006; Glick, Todorovic et al. 2007; Dimkpa, Weinand et al. 2009; Sun, Cheng et al. 2009; Yang, Kloepper et al. 2009; Hao, Charles et al. 2011; Timmusk and Nevo 2011; Stearns, Woody et al. 2012; Kim, Glick et al. 2013; Timmusk 2013;

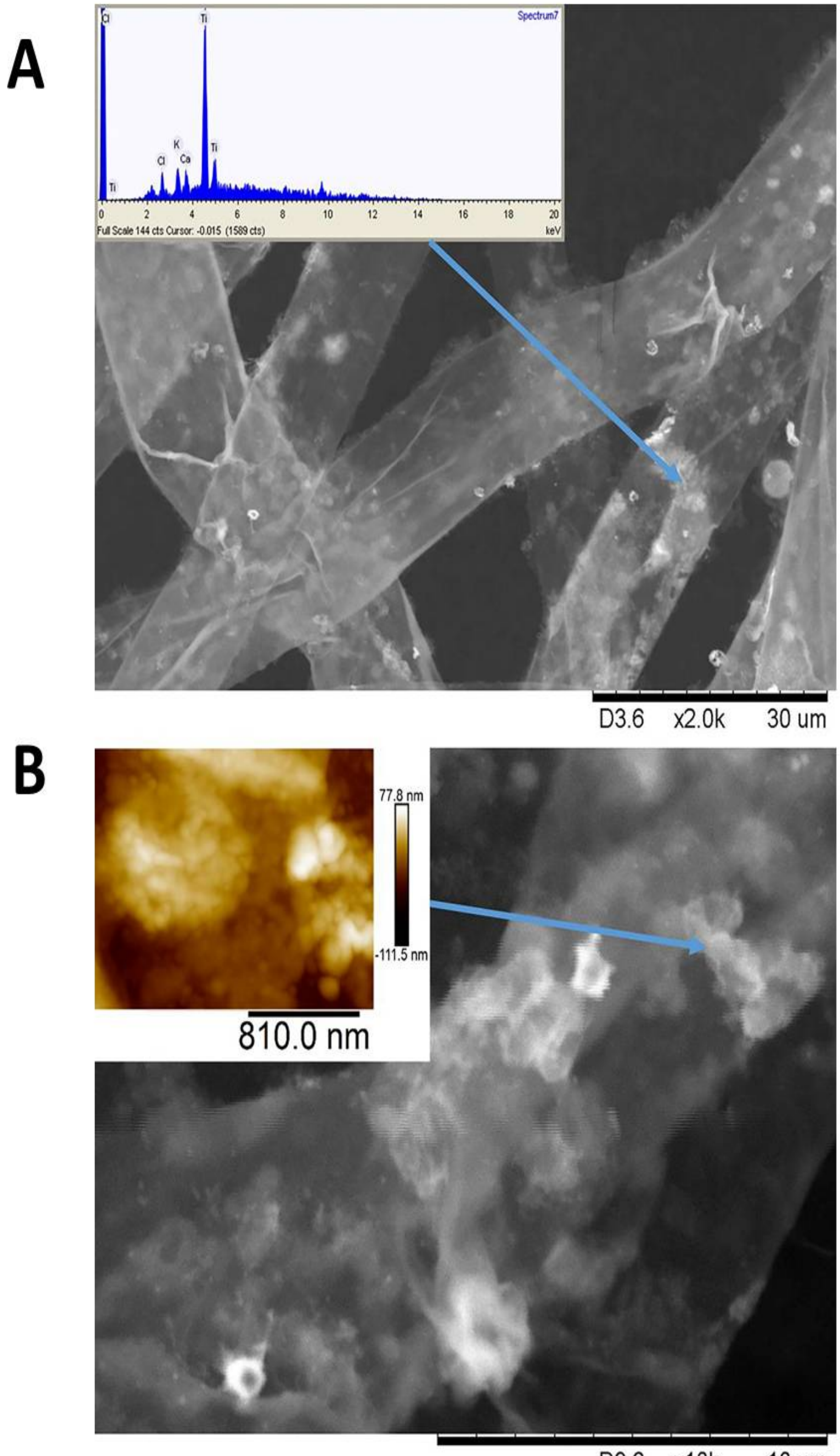

Figure 1 PGPR –nanoparticle (NP) aggregates on plant root.

Typical scanning electron microscopy- energy-dispersive X-ray spectroscopy (EDS) images of PGPR cells grown with NPs for 24 hours on plant root after 6 hours of inoculation (**A**). and the characteristic aggregate sizes of 50–60 nm (**B**). Timmusk et al 2018 Nature, SciRep 10.1038 / s41598-017-18939-x

Timmusk, Copolovici et al. 2018). The dense biofilm matrix limits diffusion of biologically active compounds secreted by bacteria including macro and microelement sequestration from soil. In addition, biofilm formation on root hair substantially improves root-to-soil contact (Yu, Lor et al. 2015), so that biofilm formation per se, importantly contributes to improving plant nutrition. An extracellular matrix formed by bacterial biofilm can provide an almost infinite range of macromolecules beneficial for plant development and growth. Biofilms contain sugars and oligo- and polysaccharides that can play various roles in bacteria-plant interactions, e.g. improving water availability in root medium. The water retention capacity of some polysaccharides can exceed several-fold their mass and even small amounts of the sugars in the biofilm can facilitate maintenance of the hydrated micro-environment (Timmusk, Paalme et al. 2011; Timmusk 2013; Timmusk, Copolovici et al. 2018). Our results demonstrate that the natural soil particles significantly contribute stably attaching PGPRs to plant roots and can be efficiently used for PGPR formulation (Fig. 1). The bacterial layers can be used as a tool for rational design of holobionts in food security programs. Future directions, should aim for combined phenotypic platform i.e bridging the genotype– phenotype gap by improving quantitative and automated selection and screening methods that focus on whole-plant physiology and quality traits.

Conclusion

In order to achieve substantial progress in agriculture and meet the challenges of the 21st century, adoption of systems agriculture is required. This means an integrated approach of plant breeding and microbiome via applying novel molecular tools, screening technologies and precision phenotyping. By manipulating interactions at the root-soil-microbe interface, we may reduce agricultural pesticide, fertilizer, and water use, enrich marginal land, and rehabilitate degraded soils. Hence, a concept integrating plant breeding with the microbiome and rational management of microbial communities has great potential for sustainable precision agriculture.

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