



Bespoke microbiome therapy to manage plant diseases

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Information gathered with advanced nucleotide sequencing technologies, small molecule detection systems and computational biology is revealing that a community of microbes and their genes, now termed “the microbiome,” located in gut and rhizosphere, is responsible for maintaining the health of human beings and plants, respectively. Within the complete microbiome a “core-microbiome” exists that plays the pivotal role in well being of humans and plants. Recent studies in medicine have shown that an artificial mixture of bacteria representing the core gut microbiome of healthy person when transferred into gut of diseased person results in re-establishment of normal microflora in the latter leading to alleviation from diseased condition. In agriculture, though not exactly in similar manner as in medicine, success in plant disease management has been achieved through transfer of microbiome by mixing disease suppressive soils with disease conducive soils. A study more similar to artificial gut microbiome transfer in medical field has been recently reported in agriculture, in which transfer of microbiome via soil solutions (filtered and unfiltered) has shown ability to alleviate drought stress in *Arabidopsis thaliana*. However, the exact practice of transferring artificially cultivated core-microbiome as in medicine has not thus far been attempted in plant disease management. Nonetheless, as the gut and rhizosphere microbiome are known to share many common traits, there exists a good scope for accomplishing similar studies in agriculture. Based upon the information drawn from all recent works in microbiome studies of gut and rhizosphere, we propose that tailor-made core-microbiome transfer therapy can be a success in agriculture too and it could become a viable strategy for management of plant diseases in future.

Keywords: microbiome, core-microbiome, plant, disease management, soil, rhizosphere, root, gut

MICROBIOME IN RELATION TO HUMAN AND PLANT HEALTH

The power of next generation sequencing technology is transforming today's biology (Mardis, 2008; Schuster, 2008). Combined with bioinformatics (Lee et al., 2012), it is prising open the microbial “dark matter” and revealing the diversity and functions of microbiome at resolutions unknown hitherto (Forde and O'Toole, 2013; Rinke et al., 2013). It is shedding new light on the role played by the gut microbiome in governing the human health (Turnbaugh et al., 2007; Kinross et al., 2011; Cho and Blaser, 2012; Ottman et al., 2012; Norris et al., 2013), reviving the Metchnikoffian paradigm: colonizing the gut with beneficial microflora could lengthen the human life. The gut microbiota is not only limiting its influence on the human health by its functions in the intestine, it also is impacting the human brain and behavior (Heitz et al., 2011; Cryan and Dinan, 2012; Mulle et al., 2013) as well as social development evidenced by studies in mice (Desbonnet et al., 2013). Remarkably, similar train of evidences is being uncovered in plant world; root microbiome is observed to be tightly linked with the health of the plants (Friesen et al., 2011; Chaparro et al., 2012; Bulgarelli et al., 2013; Gaiero et al., 2013; Mendes et al., 2013). In insects, too, the same story is unfolding (Engel and Moran, 2013). The microbial diversity associated within these ecosystems is being referred to as the “second genome” that is easily 10 times more in scale than the host genome (Grice and Segre, 2012; Turner et al., 2013) and its

impact on regulating human and plant health is becoming more apparent.

CORE MICROBIOME

From among the multitidal microbial communities inhabiting the gut and root, there appears to be a clutch of them which constitute the core microbiome (Tschöp et al., 2009). Core microbiome contains organisms common across the microbiome hypothesized to play a key role in ecosystem function within a habitat (Lederberg and McCray, 2001). Core microbiome of human gut (Turnbaugh and Gordon, 2009; Turnbaugh et al., 2009; Huse et al., 2012; Petrof et al., 2013a,b) and plant (Bulgarelli et al., 2012; Lundberg et al., 2012; Peiffer and Ley, 2013) have been determined at Operational Taxonomic Unit (OTU) levels with small subunit ribosomal RNA genes or random sequencing of all genes. Any changes in the core-microbiome composition or function leads to debilitating or destructive diseases in humans as well as plants (Kinross et al., 2011).

DISEASE SUPPRESSIVE SOILS AND THEIR MICROBIOME

It is well known that farmers moved soil from one field to another to take advantage of its disease suppression abilities endowed by the soil microbial populations harbored in it (Weller et al., 2002). Soil microbial studies mainly based on cultivation dependent methods lead to the finding of several bacteria

termed plant growth promoting rhizobacteria (PGPR) (Kloepper and Schroth, 1978), particularly the genus *Pseudomonas* spp., in imparting the disease suppressive ability to such soils (Schroth and Hancock, 1982; Haas and Defago, 2005; Mendes et al., 2013). Today, with advanced technologies, studies are generating evidence that it is not an individual or couple of microbes, rather it is “microbiome” (Forde and O’Toole, 2013; Rinke et al., 2013), the complete assemblage of microbial communities of a habitat and their functions, in rhizosphere that is determining plant health (Berendsen et al., 2012; Mendes et al., 2013; Rout and Southworth, 2013). In insects too, the same phenomenon is being observed (Hussa and Goodrich-Blair, 2013). Rhizosphere/core microbiome of *Arabidopsis* (Bulgarelli et al., 2012; Lundberg et al., 2012), desert shrubs *Zygophyllum dumosum* (Zygophyllaceae) and *Atriplex halimus* (Kaplan et al., 2013), and maize (Peiffer and Ley, 2013) have been deciphered and reported to be stable (Lozupone et al., 2012; Lundberg et al., 2012; Li et al., 2013), inheritable (Peiffer et al., 2013) and tightly linked to host tissues (Lee et al., 2013).

ROOT MICROBIOME TRANSFER TO MANAGE PLANT DISEASE

In plant disease management, a simple method of transferring complete microbiome by mixing disease suppressive soils with disease conducive one is practiced. Mendes and colleagues (2011) showed that when soils suppressive to *Rhizoctonia solani*, an important fungal pathogen, is mixed with disease conducive soils at 1:9 ratio (w/w), it successfully suppressed the infection in sugar beet. Metagenomic analysis of the soils using PhyloChip revealed consistent involvement of 17 bacterial communities belonging to Proteobacteria, Firmicutes, and Actinobacteria, considered as core-microbiome, in disease suppression. Other works too, similarly point to the involvement of core-microbiome in soils suppressive to potato common scab (Rosenzweig et al., 2012) and tobacco black root rot (Kyselkova et al., 2009). In all the above mentioned works, Pseudomonadaceae group of bacteria has been suggested as a key player in disease suppressiveness within the core microbiome.

GUT MICROBIOME TRANSFER TO MANAGE HUMAN HEALTH

As with rhizosphere microbiome of plants in agriculture, in medical studies too, the gut microbiome has been found to control the health of the human beings (Turnbaugh et al., 2007; Cho and Blaser, 2012) with a core mainly involved (Tschöp et al., 2009; Turnbaugh et al., 2009; Huse et al., 2012). “Stool transplant” therapy (de Vos, 2013) is one of the several medical practices that is adopted wherein stool taken from healthy person is transferred to diseased person resulting in suppression of many important gastro-intestinal diseases. The principle here is to re-establish normal gut bacteria in the gut of diseased person and bring about positive changes in their health. However, the “stool transplant” therapy is not widely followed since the method is not acceptable to many patients, besides the apprehension that it can transfer pathogenic microbes too. Two recent studies (Petrof et al., 2013a; Ridaura et al., 2013) have found a way to overcome “stool transplant therapy” by using “stool substitute” in which a culturable consortium representing core microbiome is transferred and found to transmit the phenotype

expression aimed for. Petrof and colleagues’ (2013a) work was first of its sort successfully demonstrating that patients suffering from *Clostridium difficile* infection, a debilitating disease of intestine, can be cured when administered with stool substitute mixture comprising a multi-species community of bacteria (RePOOPulate sample) of a healthy individual exhibiting resistance to the disease. Post-treatment metagenomic analysis of the cured patients revealed that the OTU reads from their guts were similar to that of the RePOOPulate sample until six months after its administration even though the microbiota profiles were different. This work was quickly followed by Ridaura et al. (2013) in which they transplanted intact uncultured or cultured human fecal microbiota from each member of a discordant twin pair (one lean and other obese) into separate groups of recipient germ-free mice and found that the obese twin’s fecal microbiota significantly increased the body biomass and adiposity in the germ free mice. It will not, therefore be, contrary to consider that the “stool substitute” transfer consisting of the core-microbiome is an extension of the “stool therapy” and is able to reproduce the expected microbial ecology with desired results. Such successful scientific endeavors are spurring development of new disease management paradigm termed MET: Microbial Ecosystem Therapy (Petrof et al., 2013b).

ROOT CAN FOLLOW THE GUT

In agriculture, a system of manipulating the root environment by artificially inoculating plant and soil beneficial microbes has been followed for long time for improving crop yields. The PGPRs and other plant beneficial microbes (nitrogen fixing and phosphate solubilizing bacteria, *Trichoderma* spp., arbuscular mycorrhizae fungi etc.) isolated from rhizospheres were mass multiplied and artificially inoculated, either singly or in combination of twos, for disease management in plants (Berg, 2009; Lugtenberg and Kamilova, 2009; Chaparro et al., 2012; Qiu et al., 2013). Though this approach has been widely adopted, its success in field conditions have been limited (Bakker et al., 2012). With unequivocal reports coming out indicating that it is not a single taxon, but a consortium of microorganism that is responsible for bringing about diseases suppression in plants (Mendes et al., 2011; Rosenzweig et al., 2012; Trivedi et al., 2012; Klein et al., 2013), the stage is now set for the root to follow gut by adopting the strategy of using “stool substitute” for disease management. Transferring disease suppressive soils has been the only alternate method for transferring the complete rhizosphere/core microbiome in plant protection strategy. Coming closer to “stool substitute” therapy, transfer of microbiome via soil solutions (filtered and unfiltered) has shown ability to alleviate drought stress in *Arabidopsis thaliana*. Pyrosequencing analysis of soils revealed a core microbiome (*Burkholderia*, *Phormidium*, *Bacillus*, *Aminobacter*, *Acidiphilum* among others) involved in alleviating the abiotic stress (Zolla et al., 2013). However, the exact transfer of artificially cultivated core-microbiome as performed by Petrof et al. (2013a) and Ridaura et al. (2013) with gut environment is yet to be attempted in root environment. The possibilities of achieving success is high as there exists a striking similarity between the gut and root microbiota (Berendsen et al., 2012; Ramírez-Puebla et al., 2013). Also, the fact that soil type

plays significant role in the selection and election of microbiome of rhizosphere and root compartment (Berg and Smalla, 2009; Bulgarelli et al., 2012; Lundberg et al., 2012), chances of success for the “rhizosphere substitute” is significantly augmented.

ROOT MICROBIOME CULTURING

In an important meeting convened on topic “culturing a plant-microbiome community” in Rhodes, Greece in 2012, a long-term future research strategy became apparent in which it was suggested that after an initial culture-independent survey of the plant microbiota, the corresponding community members are isolated in collections of pure cultures (Lebeis et al., 2012). Today, by converging information deduced on microbial diversity and functions using next-generation sequencing technologies and multi-species transcriptome analysis (Schenk et al., 2012), molecules/volatile involved in plant-microbe interaction using mass-spectral investigations (Watrous et al., 2012; Badri et al., 2013) combined with power of bioinformatics (Lee et al., 2012), it has become very much possible to culture the appropriate core-microbiome and apply it successfully (Ridaura et al., 2013). To assemble a robust core microbiome of an ecosystem not limited to OTU records alone, Shade and Handelsman (2012) and Lozupone and colleagues’ (2012) suggested collecting the data on (i) OTU membership/ α diversity, (ii) OTU composition/ β diversity, (iii) OTU persistence across time and space and (iv) communication/metabolic networking among the OTUs. Determination of models, particularly of root environment, in which the plants favor the recruitment of antibiotic-producing (and -resistant) bacteria by stimulating interference competition through production of abundant resources, can help improve establishment of the artificially introduced microbiomes (Scheuring and Yu, 2013).

BESPOKE MICROBIOME THERAPY FOR PLANT DISEASE MANAGEMENT

Artificial core-microbiome transfers can decrease the noise intrinsic to any complex communities and are step in right direction in disease management, both for plants and humans, built upon the principles of binary plant/human-microbe interaction in an ecological perspective.

The similarities between the gut and rhizosphere microbiota is striking in many aspects which can encourage emulating experiments carried out in gut with root environment and vice-versa. Based on the increasingly available body of evidences discussed in this article, we propose the model of transfer of bespoke core-microbiome, rather than individual species, as a viable strategy for management of plant diseases in future.

REFERENCES

- Badri, D. V., Chaparro, J. M., Zhang, R., Shen, Q., and Vivanco, J. M. (2013). Application of natural blends of phytochemicals derived from the root exudates of *Arabidopsis* to the soil reveal that phenolic related compounds predominantly modulate the soil microbiome. *J. Biol. Chem.* 288, 4502–4512. doi: 10.1074/jbc.M112.433300
- Bakker, M. G., Manter, D. K., Sheflin, A. M., Weir, T. L., and Vivanco, J. M. (2012). Harnessing the rhizosphere microbiome through plant breeding and agricultural management. *Plant Soil* 360, 1–13. doi: 10.1007/s11104-012-1361-x
- Berendsen, R. L., Pieterse, C. M. J., and Bakker, P. A. H. M. (2012). The rhizosphere microbiome and plant health. *Trends Plant Sci.* 17, 478–486. doi: 10.1016/j.tplants.2012.04.001
- Berg, G., and Smalla, K. (2009). Plant species and soil type cooperatively shape the structure and function of microbial communities in the rhizosphere. *FEMS Microbiol. Ecol.* 68, 1–13. doi: 10.1111/j.1574-6941.2009.00654.x
- Berg, G. (2009). Plant-microbe interactions promoting plant growth and health: perspectives for controlled use of microorganisms in agriculture. *Appl. Microbiol. Biotechnol.* 84, 11–18. doi: 10.1007/s00253-009-2092-7
- Bulgarelli, D., Rott, M., Schlaeppi, K., Ver Loren van Themaat, E., Ahmadijnad, N., Assenza, F., et al. (2012). Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. *Nature* 488, 91–95. doi: 10.1038/nature11336
- Bulgarelli, D., Schlaeppi, K., Spaepen, S., van Themaat, E. V., and Schulze-Lefert, P. (2013). Structure and functions of the bacterial microbiota of plants. *Annu. Rev. Plant Biol.* 64, 9.1–9.32. doi: 10.1146/annurev-arplant-050312-120106
- Chaparro, J. M., Sheflin, A. M., Manter, D. K., and Vivanco, J. M. (2012). Manipulating the soil microbiome to increase soil health and plant fertility. *Biol. Fert. Soils* 48, 489–499. doi: 10.1007/s00374-012-0691-4
- Cho, I., and Blaser, M. J. (2012). The human microbiome: at the interface of health and diseases. *Nat. Rev. Gen.* 13, 260–270. doi: 10.1038/nrg3182
- Cryan, J. F., and Dinan, T. G. (2012). Mind-altering microorganisms: the impact of the gut microbiota on brain and behavior. *Nat. Rev. Neurosci.* 13, 701–712. doi: 10.1038/nrn3346
- Desbonnet, L., Clarke, G., Shanahan, F., Dinan, T. G., and Cryan, J. F. (2013). Microbiota is essential for social development in the mouse. *Mol. Psychiatry*. doi: 10.1038/mp.2013.65. [Epub ahead of print].
- de Vos, W. M. (2013). Fame and future of faecal transplantations – developing next-generation therapies with synthetic microbiomes. *Microbiol. Biotechnol.* 6, 316–325. doi: 10.1111/1751-7915.12047
- Engel, P., and Moran, N. A. (2013). The gut microbiota of insects – diversity in structure and function. *FEMS Microbiol. Rev.* 37, 699–735. doi: 10.1111/1574-6976.12025
- Forde, B. M., and O’Toole, P. W. (2013). Next-generation sequencing technologies and their impact on microbial genomics. *Brief. Funct. Genomics.* 12, 440–453. doi: 10.1093/bfpg/els062
- Friesen, M. L., Porter, S. S., Stark, S. C., von Wettberg, E. J., Sachs, J. L., and Martinez-Romero, E. (2011). Microbially mediated plant functional traits. *Annu. Rev. Ecol. Evol. Syst.* 42, 23–46. doi: 10.1146/annurev-ecolsys-102710-145039
- Gaiero, J. R., McCall, C. A., Thompson, K. A., Day, N. J., Best, A. S., and Dunfield, K. E. (2013). Inside the root microbiome: bacterial root endophyte and plant growth promotion. *Am. J. Bot.* 100, 1738–1750. doi: 10.3732/ajb.1200572
- Grice, E. A., and Segre, J. A. (2012). The human microbiome: our second genome. *Annu. Rev. Genomics Hum. Genet.* 13, 151–170. doi: 10.1146/annurev-genom-090711-163814
- Haas, D., and Defago, G. (2005). Biological control of soil-borne pathogens by fluorescent pseudomonads. *Nat. Rev. Microbiol.* 3, 307–319. doi: 10.1038/nrmicro1129
- Heitz, R. D., Wang, S., Anuar, F., Qian, Y., Bjorkholm, B., Samuelsson, A., et al. (2011). Normal gut microbiota modulates brain development and behavior. *Proc. Natl. Acad. Sci. U.S.A.* 108, 3047–3052. doi: 10.1073/pnas.1010529108
- Huse, S. M., Ye, Y., Zhou, Y., and Fodor, A. A. (2012). A core human microbiome as viewed through 16S rRNA sequence clusters. *PLoS ONE* 7:e34242. doi: 10.1371/journal.pone.0034242
- Hussa, E. A., and Goodrich-Blair, H. (2013). It takes a village: ecological and fitness impacts of multipartite mutualism. *Ann. Rev. Microbiol.* 67, 161–178. doi: 10.1146/annurev-micro-092412-155723
- Kaplan, D., Maymon, M., Agapakis, C. M., Lee, A., Wang, A., Prigge, B. A., et al. (2013). A survey of the microbial community in the rhizosphere of two dominant shrubs of the Negev Desert highlands, *Zygophyllum dumosum* (Zygophyllaceae) and *Atriplex halimus* (Amaranthaceae), using cultivation-dependent and cultivation-independent methods. *Am. J. Bot.* 100, 1713–1725. doi: 10.3732/ajb.1200615
- Kinross, J. M., Darzi, A. W., and Nicholson, J. K. (2011). Gut microbiome-host interactions in health and diseases. *Genome Med.* 3, 14. doi: 10.1186/gm228
- Klein, E., Ofek, M., Katan, J., Minz, D., and Gamliel, A. (2013). Soil suppressiveness to *Fusarium* disease: shifts in root microbiome associated with reduction of pathogen root colonization. *Phytopathology* 103, 23–33. doi: 10.1094/PHYTO-12-11-0349
- Kloepper, J. W., and Schroth, M. N. (1978). Plant growth promoting rhizobacteria on radishes. *Phytopathol* 24, 879–882.

- Kyselkova, M., Kopecky, J., Frapolli, M., Defago, G., Sagova-Mareckova, M., Grundmann, G. L., et al. (2009). Comparison of rhizobacterial community composition in soil suppressive or conducive to tobacco black root rot disease. *ISME J.* 3, 1127–1138. doi: 10.1038/ismej.2009.61
- Lebeis, S. L., Rott, M., Dangl, J. L., and Schulze-Lefert, P. (2012). Culturing a plant microbiome community at the cross-Rhodes. *New Phytol.* 196, 341–344. doi: 10.1111/j.1469-8137.2012.04336.x
- Lederberg, J., and McCray, A. T. (2001). 'Ome Sweet' Omics –a genealogical treasury of words. *Scientist* 15, 8.
- Lee, H. C., Lai, K., Lorenc, M. T., Imelfort, M., Duran, C., and Edwards, D. (2012). Bioinformatics tools and databases for analysis of next-generation sequence data. *Brief. Funct. Genomics* 11, 12–24. doi: 10.1093/bfpg/blr037
- Lee, S. M., Donaldson, G. P., Mikulski, Z., Boyajian, S., Ley, K., and Mazmanian, S. K. (2013). Bacterial colonization factors control specificity and stability of the gut microbiota. *Nature* 501, 426–429. doi: 10.1038/nature12447
- Li, K., Bihan, M., and Methé, B. A. (2013). Analyses of the stability and core taxonomic memberships of the human microbiome. *PLoS ONE* 8:e63139. doi: 10.1371/journal.pone.0063139
- Lozupone, C. A., Stombaugh, J. I., Gordon, J. I., Jansson, J. K., and Knight, R. (2012). Diversity, stability and resilience of the human gut microbiota. *Nature* 489, 220–230. doi: 10.1038/nature11550
- Lugtenberg, B., and Kamilova, F. (2009). Plant-growth promoting rhizobacteria. *Ann. Rev. Microbiol.* 63, 541–556. doi: 10.1146/annurev.micro.62.081307.162918
- Lundberg, D. S., Lebeis, S. L., Paredes, S. H., Yourstone, S., Gehring, J., Malfatti, S., et al. (2012). Defining the core *Arabidopsis thaliana* root microbiome. *Nature* 488, 86–90. doi: 10.1038/nature11237
- Mardis, R. E. (2008). The impact of next-generation sequencing technology on genetics. *Trends Genet.* 24, 133–141. doi: 10.1016/j.tig.2007.12.007
- Mendes, R., Kruijt, K., de Bruijn, I., Dekkers, E., van der Voort, M., Schneider, J. H. M., et al. (2011). Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science* 332, 1097–1100. doi: 10.1126/science.1203980
- Mendes, R., Garbeva, P., and Raaijmakers, J. M. (2013). The rhizosphere microbiome: significance of plant beneficial, plant pathogenic, and human pathogenic microorganisms. *FEMS Microbiol. Rev.* 37, 634–663. doi: 10.1111/1574-6976.12028
- Mulle, J. G., Sharp, W. G., and Cubells, J. F. (2013). The gut microbiome: a new frontier in autism research. *Curr. Psychiatry Rep.* 15, 337. doi: 10.1007/s11920-012-0337-0
- Norris, V., Molina, F., and Gewirtz, A. T. (2013). Hypothesis: bacteria control host appetites. *J. Bacteriol.* 195, 411–416. doi: 10.1128/JB.01384-12
- Ottman, N., Smidt, H., de Vos, W. M., and Belzer, C. (2012). The function of our microbiota: who is out there and what do they do? *Front. Cell. Inf. Microbiol.* 2:104. doi: 10.3389/fcimb.2012.00104
- Peiffer, J. A., and Ley, R. E. (2013). Exploring the maize rhizosphere microbiome in the field: a glimpse into a highly complex system. *Commun. Integr. Biol.* 6:e25177. doi: 10.4161/cib.25177
- Peiffer, J. A., Spor, A., Koren, O., Jin, Z., Tringe, G., Dangl, J. L., et al. (2013). Diversity and heritability of the maize rhizosphere microbiome under field conditions. *Proc. Natl. Acad. Sci. U.S.A.* 110, 6548–6553. doi: 10.1073/pnas.1302837110
- Petrof, E. O., Gloor, G. B., Vanner, S. J., Weese, S. J., Carter, D., Daigneault, M. C., et al. (2013a). Stool substitute transplant therapy for the eradication of *Clostridium difficile* infection: 'Reopulating' the gut. *Microbiome* 1, 3. doi: 10.1186/2049-2618-1-3
- Petrof, E. O., Claud, E. C., Gloor, G. B., and Allen-Vercoe, E. (2013b). Microbial ecosystems therapeutics: a new paradigm in medicine? *Benef. Microbes* 4, 53–65. doi: 10.3920/BM2012.0039
- Qiu, M., Li, S., Zhou, X., Cui, X., Vivanco, J. M., Zhang, N., et al. (2013). De-coupling of root-microbiome associations followed by antagonist inoculation improves rhizosphere soil suppressiveness. *Biol. Fertil. Soils*. doi: 10.1007/s00374-013-0835-1
- Ramirez-Puebla, S. T., Servin-Garciduenas, L. E., Jimenez-Marin, B., Bolanos, L. M., Rosenbluth, M., Martinez, J., et al. (2013). Gut and root microbiota commonalities. *Appl. Environ. Microbiol.* 79, 2–9. doi: 10.1128/AEM.02553-12
- Ridaura, V. K., Faith, J. J., Rey, F. E., Cheng, J., Duncan, A. E., Kau, A. L., et al. (2013). Gut microbiota from twins discordant for obesity modulate metabolism in mice. *Science* 341, 1241214. doi: 10.1126/science.1241214
- Rinke, C., Schwientek, P., Sczyrba, A., Ivanova, N. N., Anderson, I. J., Cheng, J.-F., et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature* 499, 431–437. doi: 10.1038/nature12352
- Rosenzweig, N., Tiedje, J. M., Quensen, J. F., Meng, Q. X., and Hao, J. J. (2012). Microbial communities associated with potato common scab-suppressive soil determined by pyrosequencing analyses. *Plant Dis.* 96, 718–725. doi: 10.1094/PDIS-07-11-0571
- Rout, M. E., and Southworth, D. (2013). The root microbiome influences scales from molecules to ecosystems: the unseen majority. *Am. J. Bot.* 100, 1689–1691. doi: 10.3732/ajb.1300291
- Schenk, P. M., Carvalhais, L. C., and Kazan, K. (2012). Unraveling plant-microbe interactions: can multi-species transcriptomics help? *Trends Biotechnol.* 30, 177–184. doi: 10.1016/j.tibtech.2011.11.002
- Scheuring, I., and Yu, D. W. (2013). How to assemble a beneficial microbiome in three easy steps. *Ecol. Lett.* 15, 1300–1307. doi: 10.1111/j.1461-0248.2012.01853.x
- Schroth, M. N., and Hancock, J. G. (1982). Disease-suppressive soil and root-colonizing bacteria. *Science* 216, 1376–1381. doi: 10.1126/science.216.4553.1376
- Schuster, S. (2008). Next-generation sequencing transforms today's biology. *Nat. Methods* 5, 16–18. doi: 10.1038/nmeth1156
- Shade, A., and Handelsman, J. (2012). Beyond the Venn diagram: the hunt for the core microbiome. *Environ. Microbiol.* 14, 4–12. doi: 10.1111/j.1462-2920.2011.02585.x
- Trivedi, P., He, Z., Van Nostrand, J. D., Albrigo, G., Zhou, J., and Wang, N. (2012). Huanglongbing alters the structure and functional diversity of microbial communities associated with citrus rhizosphere. *ISME J.* 6, 363–383. doi: 10.1038/ismej.2011.100
- Turnbaugh, P. J., and Gordon, J. I. (2009). The core gut microbiome, energy balance and obesity. *J. Physiol.* 587, 4153–4158. doi: 10.1113/jphysiol.2009.174136
- Turnbaugh, P. J., Hamady, M., Yatsunenko, T., Cantarel, B. L., Duncan, A., Ley, R. E., et al. (2009). A core gut microbiome in obese and lean twins. *Nature* 457, 480–484. doi: 10.1038/nature07540
- Turnbaugh, P. J., Ley, R. E., Hamady, M., Fraser-Liggett, C. M., Knight, R., and Gordon, J. I. (2007). The human microbiome project. *Nature* 449, 804–810. doi: 10.1038/nature06244
- Tschöp, M. H., Hugenholtz, P., and Karp, C. L. (2009). Getting to the core of the gut microbiome. *Nat. Biotechnol.* 27, 344–346. doi: 10.1038/nbt0409-344
- Turner, T. R., James, E. K., and Poole, P. S. (2013). The plant microbiome. *Genome Biol.* 14, 209. doi: 10.1186/gb-2013-14-6-209
- Watrous, J., Roach, P., Alexandrov, T., Heath, B. S., Yang, J. Y., Kersten, R. D., et al. (2012). Mass spectral molecular networking of living microbial colonies. *PNAS* 109, E1743–E1752. doi: 10.1073/pnas.1203689109
- Weller, D. M., Raaijmakers, J. M., McSpadden Gardner, B. B., and Thomashow, L. S. (2002). Microbial populations responsible for specific soil suppressiveness to plant pathogens. *Ann. Rev. Phytopathol.* 40, 308–348. doi: 10.1146/annurev.phyto.40.030402.110010
- Zolla, G., Badri, D. V., Bakker, M. G., Manter, D., and Vivanco, J. M. (2013). Soil microbiomes vary in their ability to confer drought tolerance to *Arabidopsis*. *Appl. Soil Ecol.* 68, 1–9. doi: 10.1016/j.apsoil.2013.03.007

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 01 October 2013; accepted: 08 November 2013; published online: 03 December 2013.

Citation: Gopal M, Gupta A and Thomas GV (2013) Bespoke microbiome therapy to manage plant diseases. *Front. Microbiol.* 4:355. doi: 10.3389/fmicb.2013.00355

This article was submitted to Plant-Microbe Interaction, a section of the journal *Frontiers in Microbiology*.

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