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Mini-Review

Organic versus conventional agriculture: A review from a microorganism's point of view

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ABSTRACT

Although yields from organically managed production systems are lower in general than those from conventional agricultural systems, there are advantages in organic farming in terms of lower energy, fertilizer and pesticide inputs, optimized nutrient utilization, better soil quality, and a lower environmental impact. Higher levels of faunal and floral biodiversity have been found in organically managed farms, but for microbial diversity controversial data is available. One reason for these problems are the methods used for determination of microbial diversity. However, beside qualitative differences in microbial community structures most of the studies show a higher microbial biomass, a higher microbial species richness, a higher biodiversity based on diversity indices and a higher microbial evenness in organic systems. Many plant associated microorganisms are known to have plant beneficial traits. Little is known about the relationship between microbial diversity, plant health and plant growth, and the impact of management on this functional group. Interestingly, results from novel studies indicate an enhancement of plant beneficial microorganisms by organic farming. As an example for this phenomenon the enrichment of microorganisms antagonistic towards plant pathogens in organic vineyards is depicted.

KEYWORDS: microbial diversity, organic farming, productivity, sustainability, plant health, disease suppression

INTRODUCTION

Microbial communities are adapted to certain environmental changes or stress factors. Extreme changes accomplished within a short period of time, as seen in the conversion of natural ecosystems into arable land, will favor dominance of few microorganisms, thus lowering species richness and evenness [1]. Only in a few exceptions the conversion into arable land increases microbial diversity, e.g. when desert soil is converted into agricultural soil in a process called desert farming [2]. But in the most cases, agricultural measures lead to a decrease of biodiversity. Stress factors like pH changes, high salinity, or heavy metal contamination as well as disturbances in humidity decrease catabolic evenness of crop soil microbial communities more dramatically than that of communities from a comparable pasture soil [3]. The process of decreasing diversity has negative implications for agriculture, because a lowered biodiversity is negatively correlated with plant disease suppression, productivity and sustainability of an agricultural system [4, 5, 6]. This correlation was also found for biodiversity of soil microorganisms [7, 8].

The aim of organic farming is to minimize the impact of agricultural measures on the environment by practices such as crop rotation, growing of pathogen resistant cultivars, limited use of

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chemical pesticides and the use of organic manure instead of synthetic fertilizers (Council Regulation of the European Commission No 834/2007 and No 889/2008). By this way it is expected to approach biodiversity conditions in agricultural fields comparable to conditions present in natural ecosystems. From an economic point of view organic farming requires 10-20% more labor input and retrieves lower yields, depending on the crop, than conventional farming in European countries. Nevertheless profits and therefore success of organic farming equals conventional farming due to higher prices for organic products and due to support payments [9]. Costs for corn and soybean equal after some time in both farming systems, but high value crops can be grown less frequently due to organic crop rotation [10]. Although yields from organic farming are lower in general, there are differences between crops. Whereas yields for cereals from organic farming are only 60-70% of yields from conventional farming, yields for vegetables are mostly the same as conventional ones. High variations in yields are found for potatoes [9]. These values are in accordance with results from other studies [11, 12, 13, 14]. Cooper *et al.* [13] correlated yields of winter barley with the factors crop protection and fertilization management, both organic and conventional, and found that conventional crop protection and conventional fertilization led to higher yields than organic treatments. A higher incidence of leaf blotch disease was a crucial factor for the lower yields in organic treatments, whereas a lower incidence of lodging was observed in organic treatments [13]. Incidence of *Septoria* spp. in wheat was enhanced by organic fertilization [15]. These examples show that stability of microbial communities is an important factor for the performance of a farming system. However, some studies show no significant differences in yields from organic and conventional treatments. For example corn yields were not significantly different in a comparison between a conventional system, an organic manure fertilized system and an organic legume fertilized system conducted in a long term study in the USA [16]. Yields and disease incidence in apple production were the same in a five year comparison between an organic, an integrated and a conventional system [17]. Advantages of organic farming are lower inputs in terms of energy, fertilizer and pesticide requirements, lower N losses, better soil quality, and a lower environmental impact [16, 17, 11, 18]. Energy and fertilizer input was reduced 34-53% and pesticide input even 97% in comparison to conventional plots in the long-term field trial DOK [11]. Soil from an organic apple orchard showed lower nitrogen losses in comparison to soil from a conventional orchard due to five times lower rates of nitrate leaching in the organic orchard. Although denitrification rates were higher in the organic orchard, levels of N_2O were not significantly altered [18]. Higher leaching of nitrate also was observed for conventional plots in a long term trial conducted by the Rodale Institute in the US [16].

In this review we focus on current knowledge about how microbial diversity can be promoted by the use of organic farming practices. We discuss methodic challenges in assessing microbial diversity and its effects on plant health.

Methods for determining microbial diversity

A detailed review about methods used for determining microbial biodiversity in environmental samples is given by Kirk *et al.* [19]. Biochemical methods are plate counts, physiological profiling of communities, and fatty acid methyl ester analysis but they capture only a very low proportion of the microbial community. Molecular techniques commonly used are measurement of GC content, re-association and hybridization of nucleic acids, microarrays, denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), single strand conformation polymorphism (SSCP), restriction fragment length polymorphism (RFLP), amplified ribosomal DNA restriction analysis (ARDRA), terminal restriction fragment length polymorphism (t-RFLP), and ribosomal intergenic spacer analysis (RISA). Additionally microscopic approaches can be used to study microbial diversity. With unspecific staining methods like for example DAPI staining total cell counts can be obtained independently of cultivation [20]. More detailed information about structure and colonization patterns of microbial communities can be obtained using labeled oligonucleotides specific for certain groups or domains and subsequent laser scanning microscopy, a technique called fluorescence *in situ* hybridization

(FISH) [21]. Microbial communities of several habitats have been investigated using FISH, for example lichens [22], root-associated habitats [23, 24], mosses [25] and leaf surfaces [26]. Fluorescence labeling with genetic markers and subsequent confocal laser scanning microscopy is a powerful instrument for investigating ecological behavior of species or strains of interest. For example colonization patterns of rhizospheric microorganisms have been investigated using this method [27, 28]. Physiological functions of microorganisms can be elucidated *in situ* with stable isotope probing (SIP) [29]. New sequencing technologies have enabled deep insights into the microbial communities of a variety of ecosystems, but so far few studies have elucidated differences in community structure or microbial diversity produced by organic or conventional treatment using these techniques. Metagenomics and amplicon sequencing, favored by a rapid development of new sequencing techniques in the last years, are likely to enable more detailed insights into community structures and will probably provide more accurate ecological data in forthcoming studies. For comparing species richness, diversity indices or evenness estimated from amplicon pyrosequencing it is important to consider experimental methodology, because amplicon length and choice of primer pairs influence amplification efficiency and thus diversity estimates [30].

Investigating microbial diversity comes up with several methodical limitations. The majority of microorganisms present in environmental samples cannot be cultivated by common methods. In soil samples typically the proportion of yet-to-be-cultured bacterial cells lies between 95 and 99.9% [31, 32]. Reasons for this discrepancy are contributed to cells, which are in a physiological state called viable, but not culturable, and to species, which are not cultivated due to special metabolic requirements or due to long generation times under laboratory conditions [19]. The problem of low culturability of microorganisms can be overcome by using molecular techniques based on PCR and subsequent analysis of fragments (e.g. DGGE, t-RFLP). However, estimation of diversity indices from PCR-based methods may not reflect properly the actual diversity present in a sample. This has been shown for t-RFLP analysis of artificial communities, especially when number of species used was high [33]. Using molecular fingerprinting techniques, phylotypes, species, or OTUs of low abundance often cannot be detected [34]. This leads to an underestimation of microbial diversity although the collective abundance of those minor abundant phylotypes may be above the detection limit of the used methods and have important impacts on the functioning of the ecosystem. Another problem is the spatial heterogeneity and the diversity of microhabitats, which raises questions about sample size and sample number [35, 36]. Furthermore the definition of phylogenetic groups among microorganisms is difficult in ecological studies. A critical point in PCR or nucleic acid-based approaches is the extraction of nucleic acids from community samples. For example, extraction of DNA from spores or gram positive bacteria requires harsher conditions than that of gram negative bacteria [37, 19].

Microbial diversity under organic management

The term ‘organic farming’ implies a variety of measures which aim to reduce the negative impact of agricultural practices on the environment. When studying the impact of organic farming practices on the microbial diversity, this can be done either by comparing the sum of all these measures with a conventionally managed control or by varying single parameters. Table 1 lists a selection of studies, in which the microbial community of agricultural ecosystems in dependence of organic farming practices was investigated. Within the long-term field trial DOK, running since 1978 in Therwil, Switzerland, the parameters fertilization and crop protection are varied within five different systems in a 7-year crop rotation [11]. In this experimental setup, fertilization with farmyard manure had the strongest impact on microbial biomass and biodiversity, whereas type of the previous crop did not have a significant influence [38]. However, type of crop rotation does have significant impacts on the microbial diversity [39]. In comparisons including sites from different regions, the parameter soil type turned out to have the strongest impact on microbial biomass, regardless of management

Table 1. Studies investigating the microbial diversity of organic cropping systems in comparison to conventional systems.

Study	Farming practices investigated or responsible for effects	Target organisms affected
[45]	organic fertilization	higher microbial biomass
[85]	organic fertilization	higher microbial biomass
[60]	organic fertilization	higher microbial biomass
[56]	organic fertilization	higher fungal biomass
[10]	organic fertilization	higher microbial biodiversity, biomass and activity
[59]	organic fertilization (crop residues, sewage sludge, straw)	higher microbial biomass, altered community structures
[86]	organic fertilization	higher activity and species richness of methanotrophic bacteria
[79]	organic fertilization	higher abundance of nitrogen fixing bacteria
[54]	organic fertilization	higher abundance of methanogenic archaea and altered community structures
[52]	organic fertilization	altered community of endorhiza methanotrophs
[87]	organic fertilization	higher abundance and diversity of endorhiza bacteria
[43]	organic manure	higher fungal and bacterial biomass
[38]	organic manure	higher microbial biomass and biodiversity
[18]	organic manure	higher microbial biomass, higher microbial and denitrification activity
[88]	organic manure	lower *Sclerotinia* incidence
[89]	organic manure	lower *Verticillium* and *Streptomyces* incidence
[41]	soil type, organic matter	higher microbial biomass
[49]	organic matter	higher microbial biomass and richness of PLFA patterns
[90]	straw amendment, tillage	lower *Fusarium* incidence
[91]	chitin and laminarin amendment	enhanced Lysis of *Fusarium* chlamydospores
[92]	neem cake, rise husks and sawdust amendments	enhanced Lysis of *Fusarium* chlamydospores
[93]	different organic amendments	lower *Macrophomina* and *Fusarium* incidence
[94]	straw amendments	lower *Rhizoctonia* incidence
[95]	compost and compost spray amendments	increase of systemic acquired resistance in host plant
[62]	low tillage	higher microbial biomass and activity
[96]	low tillage	higher abundances and activities of facultative aerobic, anaerobic and denitrifying bacteria
[97]	low tillage, crop residues	higher microbial biomass
[61]	low tillage, crop rotation	higher microbial biomass
[39]	crop rotation	higher diversity of total bacteria and *nif* genes
[48]	crop rotation	higher species richness of arbuscular mycorrhiza

Table 1 continued..

[44]	cover crops	higher diversity of bacterial PLFA patterns
[46]	organic plant protection	higher abundance and diversity of phyllosphere fungi
[57]	organic plant protection	altered fungal community, higher abundance of antagonistic fungi
[40]	cover crops, organic fertilizer, organic plant protection	higher microbial biomass, altered PLFA patterns
[50]	not specified	higher bacterial diversity and activity
[98]	not specified	altered bacterial phyllosphere community
[51]	not specified	higher abundance and diversity of phyllosphere bacteria and fungi
[20]	not specified	higher bacterial and fungal biomass

type [40, 41]. Thus, experimental setup has to be considered when comparing impact factors on microbial communities.

A survey of literature conducted by Hole *et al.* [42] showed that biodiversity of e.g. wild plants, earthworms, spiders, and beetles is higher in organically managed than in conventionally managed farms. Despite of methodical drawbacks in quantitative assessment of microbial diversity, several studies have compared microbial communities of organically and conventionally managed fields. Along with the frequently observed fact that microbial biomass is increased in organic systems, also species richness, diversity indices and evenness tend to be higher. Microbial biomass in soil was shown to be increased due to application of organic manure in several studies using plate counts, microscopy, PLFA extraction and measurement of DNA and organic C contents [43, 44, 40, 45, 20, 38]. Also the phylloplane is colonized by microorganisms in a higher abundance in organic treatments, as shown for apples from organic management [46]. One reason for a higher ability of manure amended soils to build up microbial biomass probably is the increased water holding capacity and porosity [47].

Several studies have compared species richness or diversity indices of microorganisms between organic and conventional treatments. A higher richness among arbuscular mycorrhizal fungi was found by t-RFLP analysis of organically managed maize and potato rhizosphere [48]. Together with this finding higher beta diversity in organically managed fields was detected. Richness of fungal species and, in one case of bacterial species, was higher in organically managed grassland of different soil types [49]. In the long-term trial DOK, the highest biodiversity based on Biolog analysis was found in the biodynamic system, followed by the bioorganic and a conventional system with farmyard manure amendment [11]. The conventional system without amendment of manure showed the lowest biodiversity (calculated as Shannon index of diversity). In a comparison of 13 pairs of farms in the Netherlands, bacterial species richness, but not diversity (both calculated from DGGE microbial fingerprints) was statistically significantly higher in organically managed fields [50]. Leaves and apples of organically managed apple trees harbored a higher number of culturable microorganism species than conventionally managed trees or trees from integrated management [51, 46]. Some studies investigated the influence of farming practices on single groups of microorganisms. For example in the long-term trial NFSC in England, a higher abundance and a higher Shannon index of diversity of *nif*H genes was found in a potato field with an organic crop rotation. In the conventional rotation barley and in the organic rotation bean were the pre-crops of potato. The abundance was assessed with RT qPCR and the index was calculated based on RT DGGE [39]. In the endorhiza of organically managed maize a higher richness of type I Methanotrophs was found based on DGGE fingerprints, showing that also the community of the endosphere can be influenced by farming practices. This effect is contributed to the differences in the fertilizing strategy used in both fields (in the organic system compost was used for fertilization) [52].

Recently it was established that at least in faunal predator-pathogen interactions evenness of both, predators and pathogens, and not species richness is important for maintenance of a sustainable ecosystem [53]. Influence of agronomic practices on microbial evenness in general or on evenness in microbial interaction networks has not yet been subject of many studies. Most studies support presence of differences in community composition rather than evenness between organic and conventional systems. Application of high amounts of cattle manure over a long period of time led to an increase in abundance of archaea, but to a decrease of diversity and evenness [54]. Whereas bacterial species diversity increased with time under organic management, evenness only increased right after change to organic farming and then decreased [50]. Soil community of continuously cropped and rotationally cropped soybean was different in composition, but not in species richness and evenness, assessed by sequencing of clone libraries [55]. Using an extended PLFA analysis, no statistically significant difference in microbial evenness was found between fertilization and crop protection regimes [56]. In the contrary, differences in PLFA patterns were present in this study, suggesting influence of the farming regimes on the microbial community in a qualitative manner. Similar results were obtained using the DNA-based techniques t-RFLP and RISA within the same long term trial [38]. In a long term trial in California, the SAFS project, different PLFA patterns were present between a cover cropped organic, a cover cropped low input, and a conventional tomato field [40]. Differences in the community structure also were present in the phylloplane of organically and conventionally managed grapevine [57]. Whereas significant differences in fungal community structure were revealed using SSCP analysis, differences in bacterial communities were not evident [58].

Plant health and microbial diversity

Organic agronomic measures lead to increased soil organic carbon content and to an elevated microbial biomass in comparison to soils under conventional management. Especially incorporation of organic manure or compost contributes to this difference [43, 40, 59, 56, 60, 54]. But also zero tillage or soft tillage operations develop soils with higher microbial mass and activity than heavily tilled systems [61, 62]. The higher microbial biomass in organic systems is traced back to the community's ability to convert organic matter to biomass more readily and with lower costs of energy than communities present in conventional soils [11]. The presence of a functionally diverse microbial community therefore ensures more efficient resource utilization in organic systems with advantages for plant growth and health. This is also reflected in lower nitrogen losses found in organic management systems [16, 18].

It is shown by Crowder *et al.* [53] that biodiversity indices and species richness need not necessarily be a crucial factor for the health status of an ecosystem. Experiments in potato field plots revealed that, with a larger evenness of predators and (insect) pests, biomass production and mortality of pest species increased [53]. Evenness of microbial communities plays a crucial role for stress tolerance of physiological functionality, which has been shown in microcosm experiments [63]. Resource availability and concentration of toxic compounds are important factors influencing functional diversity and microbial evenness [64, 65]. To our knowledge there has not been any study that showed direct associations between increased plant health or plant growth and increased microbial diversity or evenness.

Little is known about the influence of agronomic practices on the communities of plant beneficial microorganisms or their functional activities. Many plant-associated microorganisms, and especially those associated with the rhizosphere of plants, are known to exhibit traits and functions beneficial to plant health [66, 67]. These functions include production of plant growth hormones, provision of nutrients (e.g. sulfate oxidation, phosphate solubilisation), induction of plant's systemic resistance, and antagonism to plant pathogens. Microorganisms present in the endosphere of plants can exhibit plant beneficial functions such as biosynthesis of plant growth stimulating substances and antagonism to phytopathogens [68, 69]. Saprophytic microorganisms residing on aerial parts of plants are known to inhibit germination of fungal conidia due to nutrient competition [70].

Results from several studies suggest that a higher microbial biodiversity also harbors a higher potential of plant beneficial traits. A higher suppressiveness towards growth of the plant pathogenic fungus *Rhizoctonia solani* was found in soil from pristine grassland than in soil from arable land under oat/maize/potato rotation as well as under continuous maize cultivation [71]. Microbial diversity was higher in the grassland soil, whereas no significant differences in diversity and suppressiveness were present between the two arable soils. In general, the phenomenon of suppressiveness of soils to certain plant diseases is more frequently found and more pronounced in organically managed soils [72, 73]. In barley and wheat the higher suppressiveness to take all decline in organically managed fields was contributed to a lower native abundance of fluorescent *Pseudomonas*, key factors of take all decline [74]. Species of *Pseudomonas* play an important role in plant health. Several species are known to elicit plant beneficial traits, e.g. *P. fluorescens*, *P. putida* and *P. chlororaphis*, and environmental conditions on the field as well as certain farming practices can alter the abundance of biocontrol *Pseudomonas* [75, 76, 77]. For example compost amendments increased the abundance of biocontrol *Pseudomonas* in the rhizosphere of crop plants [77]. Organic measures have less adverse impact on arbuscular mycorrhizal fungi, which have positive effects on plant nutrition and plant pathogen defense, than conventional farming methods [78]. Nitrogen fixation is an important physiological process especially in semiarid, nutrient poor soils. By usage of organic fertilizers the abundance of nitrogen fixing bacteria was increased in sorghum fields on semiarid soils [79]. Pyrosequencing of rhizospheric soils from organic and conventional farming systems revealed striking differences in the structure of bacterial communities of canola and wheat fields (Li, R. and Fernando, D. Department of Plant Science, University of Manitoba, Winnipeg, Canada; unpublished data). Under organic systems, abundance of *Proteobacteria*, a phylum which comprises important plant growth promoting rhizobacteria, was nearly twice as high as in conventional fields. Sequences of these bacteria were assigned to genera such as *Pseudomonas*, *Stenotrophomonas*, and *Burkholderia* - genera, which are known to establish positive plant-microbe interactions [80, 66].

Case study: Microbial community of grapevine phyllosphere

An example for the enrichment of plant beneficial microorganisms due to organic farming practices was found in the pathosystem grapevine - *Botrytis cinerea*. In a comparative study between organic and conventional vineyards in Austria, a higher percentage of fungi with antagonistic activity towards the grapevine pathogen *Botrytis cinerea* was present in phyllosphere samples of organic samples [57]. The majority of antagonistic fungal isolates from organic samples was identified as *Aureobasidium pullulans*. Enrichment of this fungus was verified by molecular fingerprints and quantitative real time PCR. Strains of *A. pullulans* are known for its antiphytopathogenic activity [81]. Plant protection measures in this study conducted in the organic plot mainly consisted of application of sulfur and copper as well as natural substances such as fennel oil and aluminum sulphate, whereas in the conventional plot fungicides and botryticides were used. Isolates of *A. pullulans* are known to exhibit tolerance to heavy metals like copper [82, 83]. Furthermore *A. pullulans* is highly resistant to sulfur and is able to oxidize it, which may enable this fungus to optimize growth in oligotrophic environments [84]. These physiological properties of *A. pullulans* suggested that agronomic measures of organic viticulture led to the enrichment of this fungus and therefore to an enrichment of the antiphytopathogenic potential elicited by microorganisms. Whether enrichment of *A. pullulans* also increased resistance of grapevine plants towards plant pathogenic fungi in the field needs to be clarified. Furthermore, it remains to be investigated, if the increased abundance of antagonistic fungi may be caused by the overall higher abundance of fungi in the organically treated grape plants. Another study comparing the microbial flora of apple fruits from organic and integrated farming in Switzerland revealed similar results [46]. Also in this study, *A. pullulans* was found to be enriched in organically produced apples.

CONCLUSIONS

Although yields are lower and labor input is higher in most organically grown crops, there are several advantages of organic farming. Higher microbial biomass and a higher microbial diversity are frequently found in the rhizosphere but also in the phyllosphere of organically managed crops. The higher microbial biodiversity, which can develop under organic farming, leads to more stable physiological networks and thus ensures more effective resource utilization. Furthermore, a higher microbial diversity increases the potential of plant beneficial microbial effects, for example plant disease suppressiveness. Therefore, more focus should be addressed to integration of elements from organic agriculture into existing production systems and their impact on microbial biodiversity and microbial community functions. Most crop cultivars are bred for conditions present in conventional agriculture. Therefore, these cultivars often are not adapted properly to conditions provided by organic farming. Plant breeding with the aim to develop cultivars better adapted to organic farming conditions would improve performance in organic agriculture and thus may reduce the gap between organic and conventional yields.

Decrease in biodiversity caused by agronomic practices is a dangerous threat to sustainability, soil and plant health, and productivity of agricultural systems. In order to face lowered microbial diversity in agricultural ecosystems it is important to understand the impacts of human activities on microbial communities and to identify measures that increase biodiversity and favor emergence of microorganisms with beneficial traits like antagonism towards plant pathogens, nitrification or phosphate solubilisation.

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