

# Influence of Compost Amendment on Soil Biological Properties and Plants

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## ABSTRACT

Soil has been a source of wealth for humans for thousand of years and it continues at present. As a consequence of this prolonged exploitation, significant tracts of soil have become barren land nowadays. Both mineral and organic amendments have been applied to soil in an attempt to slow down this progressive impoverishment, and compost is one of the most effective amendments. The addition of compost to the soil improves not only physico-chemical properties like aeration, cation exchange capacity, buffer capacity or porosity, but biotic factors too. From a biological point of view, compost can positively affect microbial populations and their enzymatic activities and stimulates the development of plants by means of the presence of growth factors or the increase of antagonistic activity against phytopathogens, among other factors. Moreover, biological activity, mainly microbial activity, plays a key role in soil stability and fertility on account of its participation in structuring processes as well as in biogeochemical cycles. Thus, modifications of biological properties caused by compost amendments have either an indirect effect on physico-chemical conditions. Therefore, benefits of compost in relation to soil restoration are substantial. Due to these positive effects, compost is applied not only for the improvement of agricultural soils, but for the recovery of disturbed soils as a consequence of pollution or fires or soils given to suffer erosion. Nevertheless, since some aspects of the way in which this positive influence is produced remain unclear, a better understanding of the process, mainly from a biological point of view, is needed.

**Keywords:** enzymatic activities, microbial populations, soil fertility

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## INTRODUCTION

Since ancient times, human beings have maintained a very productive relation with soil. Nevertheless, a simple analysis of this relation shows that benefits to soil are not so evident. On the contrary, exploitation of soil has caused progressive impoverishment of land. In order to alleviate such situation, both organic and inorganic fertilizers have been added to soil. Among the first ones, several residual materials produced from different agro-industrial activities have traditionally been applied with this purpose. Nowadays, the overproduction of such kind of wastes promotes this application not only as an attempt to increase organic matter in soils but as an inexpensive strategy to solve the environmental and health risks associated to them (Roig *et al.* 2006; Domene *et al.* 2008). Despite of the potential benefits derived of addition of these organic wastes to soil, these practices can cause some detrimental effects, and their use should be limited. The detrimental effects include the presence of unstable organic matter, heavy metals, organic

pollutants and pathogenic microorganisms the most important (Tejada *et al.* 2006a; Latorre *et al.* 2007). Among the different proposals to prevent this negative impact, composting seems to be one of the most interesting on account of its capacity to stabilize organic matter (Tognetti *et al.* 2007), minimize the toxic effects of both organic and inorganic pollutants (Semple *et al.* 2001; Barker and Bryson 2002) and inhibit the action of pathogenic microorganisms (Suárez Estrella *et al.* 2007).

The addition of compost amendments to soil influences both physico-chemical and biological properties (Odlare *et al.* 2007; Leroy *et al.* 2008). First ones have been traditionally used for estimating the impact of these organic applications on account of the modifications they cause on parameters like aggregate stability, bulk density, porosity, water holding capacity or cation exchange capacity. Nevertheless, the response of such properties to modifications of soil characteristics is very slow and may require long period of time to show significant changes (Ros *et al.* 2003). On the contrary, biological parameters are very sensitive to

changes in soil quality, and they can provide more accurate information in a shorter time as they participate in the biogeochemical cycles and the processes of formation of soil structure (Pascual *et al.* 2000).

From a biological point of view, compost application to soil directly affects both diversity and size of microbial communities (Green *et al.* 2006a; Bastida *et al.* 2008), as well as enzyme activities, since most of the processes in soil are mediated by enzymes from microbial origin (Böhme *et al.* 2005). On the other side, the improvement of soil microbiota in turn influences plant growth by means of the presence of plant growth promoting substances (Keeling *et al.* 2003; Ishii *et al.* 2007) and the increase of nutrient availability (Ros *et al.* 2006b) and suppressive activity (Larkin 2008).

The objective of this paper is to review the influence of compost on soil biology and, in turn, plant development. Although some undesirable aspects may derive from these amendments, mainly if immature products are used, compost affects positively soil microbial activity. The effect of such amendments on soil health, as well as the associated environmental and agronomical applications will be considered.

## SOIL MICROBIOTA: MODIFICATIONS THROUGH COMPOST APPLICATION

Generally speaking, the addition of compost to soil increases both microbial diversity and population (Albiach *et al.* 2000; Lee *et al.* 2004; Ros *et al.* 2006b), although specific results depend on soil characteristics and compost quality and rate of application (Tejada *et al.* 2006b; Pérez-Piqueres *et al.* 2006; Kowaljow and Mazzarino 2007). Taking into account the role that microorganisms play on the maintaining of edaphic fertility and functionality (Gómez *et al.* 2006), this is a quite positive effect in most of the cases.

### Influence on microbial communities

Since compost amendments modify both physico-chemical and nutritional properties of soil, microbial populations are affected by this practice (Schloter *et al.* 2003). Most of the studies reported the increase of the microbial biomass as a consequence of the input into soil of the composting organic matter (Chowdhury *et al.* 2000; Selivanovskaya and Latypova 2006; Tejada *et al.* 2008), although no modifications in microbial population have been described in some mid or long-term studies (Calbrix *et al.* 2007; Elfstrand *et al.* 2007). However, this kind of response uses to be mostly related to the presence in the compost of substances which show detrimental effects on microbial growth, such as heavy metals, xenobiotics or salt compounds, as well as the instability of the organic matter (Schloter *et al.* 2003; Courtney and Mullen 2008; Stefanowicz *et al.* 2008).

The mechanisms through which compost enhances microbial growth are evident. On one hand, the application of organic matter with a high degree of stability enhances structural properties of soil, which in turn provides a better habitat for microbial development. Increasing availability of nutrients also contributes to improve conditions for microbial activity (Carrera *et al.* 2007; Kowaljow and Mazzarino 2007). On the other hand, compost possesses its own microbial population, which may join the edaphic microbiota (Pérez-Piqueres *et al.* 2006; Ros *et al.* 2006b; Selivanovskaya and Latypova 2006). Nevertheless, the contribution of this factor to the increases in the size of the microbial population is contradictory, since no significant differences could be observed between the results obtained for compost and sterilized compost (Saison *et al.* 2006), the last obviously with absence of microorganisms.

Besides quantitative aspects, compost input to soil also modifies the structure of microbial communities. As stated previously, physico-chemical and nutritional soil properties are altered as a consequence of compost application, but the extent and quality of this alteration depend on compost cha-

acteristics (Courtney and Mullen 2008). Thus, the addition of several composts to the same soil may produce different responses in terms of microbial activity and functionality (Ros *et al.* 2006b). This is a very interesting tool to be used in environments where action of specific microorganisms is required, as in soil restoration or in bioremediation processes. In such cases, the properties of compost applied may contribute to enhance the populations of those microbial groups involved in the major reactions of such processes (Pérez de Mora *et al.* 2006). Examples of this strategy are the enrichment in polycyclic aromatic hydrocarbons-degrader microorganisms that promotes the treatment of polluted soils with sewage sludge compost (Hamdi *et al.* 2007), the increase in bacterial populations in pesticide polluted soils as a consequence of compost amendment (Moorman *et al.* 2001) or the augmentation of petroleum hydrocarbons degrading microorganisms as a consequence of the treatment of a polluted soil with pig manure compost (Lee *et al.* 2008). Although the impact of this kind of strategy may be short in time because of the disappearance of differences in microbial structure over times (Debosz *et al.* 2002; Ros *et al.* 2006a), it has been proved to be effective, especially if amendments are applied periodically (Pérez de Mora *et al.* 2006; Madejón *et al.* 2009).

One controversial point regarding to compost effect on soil microbial properties is the dose, since conflicted results have been reported in literature about this subject. Thus, while Saison *et al.* (2006) reported the existence of a clear dependence between microbial diversity and the amount of compost applied to soil, Crechchio *et al.* (2001) did not find any significant correlation between these two factors. Anyway, a consensus exists on the benefits of periodic applications of moderate amounts compost for providing improving microbiological properties and supporting soil functionality (Carpenter-Boggs *et al.* 2000; Tejada *et al.* 2007b). About functionality, it seems to be more significant the existence in soil of microbial populations able to achieve the metabolic activity, no matter the degree of biodiversity, than the attribution of such activity to specific microorganisms (Crechchio *et al.* 2004). Then, the functional redundancy existing in the microbial world allows soils with different microbial communities show similar activities, since the same metabolic action can be carry out by different microorganisms. Therefore, microbial biodiversity in soil does not necessarily have to be reflected in functionality (Marschner *et al.* 2003; Barrios 2007).

### Methods for the estimation of the soil microbiota

Soil microbiota can be estimated using many different techniques, both direct and indirect. From traditional methods, like plate count, to the emergent molecular tools, mostly applied for the identification of specific microorganisms or microbial groups, many and diverse methods allow accurately determination of the size and diversity of soil microbial populations.

Direct count of viable cells has some disadvantages, among them the different affinity of microorganisms to soil particles (Mehmannavaz *et al.* 2001), which determine the extractive capacity, or the difficulty of some species to grow in culture systems (Ritz 2007). This drawback can be avoided by using different microscopic methods (fluorescence *in situ* hybridization or live-dead staining), but it is difficult to discriminate between live and dead cells.

Soil microbial biomass has been considered as one of the most reliable methods for the estimation of the soil microbiota, especially when the influence of organic amendments needs to be evaluated (Selivanovskaya and Latypova 2006). Nevertheless, its use as indicator is limited due to of the high instability caused both by xenobiotics (Scelza *et al.* 2008) and heavy metals (Aciego Pietri and Brookes 2008). As with microbial biomass, basal respiration, also used for determining indirectly microbial respiration, is affected by heavy metals, although inhibition occurs at higher metal concentrations (Selivanovskaya and Latypova 2006). Other

**Table 1** Molecular methods applied for the estimation of microbial diversity and identification in soils.

| Technique  | Fundamentals   | Applicability  |
|------------|--|--|
| T-RFLP     | Electrophoretic separation of fluorescently labelled terminal restriction fragments on basis of their length   | Analysis of temporal or spatial modifications in microbial communities                               |
| ARDRA      | Similar to T-RFLP, but analysing all the fragments generated during the restriction digestion  | Microbial identification and comparison of microbial communities and dynamics when diversity is poor |
| SSCP       | Discrimination of PCR products according to conformational differences of folded single-stranded DNA   | Study of microbial communities, mutation analysis and typing of isolates                             |
| RAPD       | Electrophoretic separation of PCR products generated from shorter random primers   | Discrimination among microbial groups and analysis of microbial communities                          |
| DNA arrays | Detection of labelled PCR products by hybridization with homologous oligonucleotides on a solid support  | Quantification and identification of microbial species and characterization of microbial communities |
| ARISA      | Amplification with fluorescently labelled primers and electrophoretic separation of the intergenic region between 16S and 23S ribosomal genes  | Analysis of microbial communities  |
| DGGE/TGGE  | Electrophoretic discrimination of small PCR-amplified DNA fragments according to length, GC composition and nucleotide sequence by means of denaturing chemical gradient (DGGE) of temperature gradient (TGGE) | Comparison of microbial communities and monitoring of microorganisms dynamics                        |

Protocols for the application of this molecular methods can be found in the following references: Tiquia *et al.* (2002); Zhang *et al.* (2002); Frankle-Whitle *et al.* (2005); Fracchia *et al.* (2006); Yang *et al.* (2007); Cherif *et al.* (2008); Székely *et al.* (2008).

methods used are CO<sub>2</sub>-production rate, O<sub>2</sub>-consumption rate, substrate induced respiration or adenosine triphosphate (ATP) quantification (Joergensen and Emmerling 2006), all of them based on the determination of activity or biomass rates (Schloter *et al.* 2003).

Recent development of new DNA related tools has led to the proliferation of molecular methods for estimating microbial populations in soil. The quantification can be direct or indirect depending on the cellular lysis. In the first case, cells are lysed *in situ*, which avoid disadvantages derived from extraction, although the purity is lower. In both cases, DNA bound to soil particles after the lysis may be loosed or, on the contrary, extracellular non-viable DNA may be extracted together with DNA released from cells, causing underestimation or overestimation of the DNA results (Taylor *et al.* 2002). In addition, the application of different procedures can affect the total amount of extracted DNA (Stach *et al.* 2001).

Qualitative analysis of microbial communities also can be achieved by both traditional and molecular methods. For traditional methods, several groups of techniques are usually applied to discriminate between bacterial and fungi populations. These include microscopic techniques, biomarkers and isotope-labelling assays, selective inhibition and metabolic activity (Gómez *et al.* 2006; Joergensen and Emmerling 2006). All of them have pros and cons depending on the specific conditions of the assay and the selection of the adequate method or combination of methods on this basis will lead to desired results. Thus, in relation to biomarkers, specificity determines the goodness of the method and can limit its application (Joergensen and Emmerling 2006). Nevertheless, the Phospholipid Fatty Acids Analysis (PLFA) has become one of the most useful techniques among those which study the structure of microbial communities (Malik *et al.* 2008), although the limited complexity of the profiles which produces makes necessary its use in conjunction with other methods (Ringelberg *et al.* 2001; Pombo *et al.* 2005). Regarding to isotope-labelled methods, the availability and affordability of such substrates hamper its applicability (Neufeld *et al.* 2007). The selective inhibition method assumes all microbial groups show the same sensitivity to antibiotics and respond to glucose, which clearly is not true (Bailey *et al.* 2002). Finally, community-level physiological profiles (CLPPs), based on the microbial utilization of different substrates, provides information related to functionality instead of diversity. These methods have overcome the major disadvantage associated with the Biolog<sup>®</sup> system used, the impossibility of detecting non-cultivable microorganisms, with the development of new systems. Additionally, these new systems reduce the time needed for incubation (Chapman *et al.* 2007).

The application of molecular techniques based on the direct analysis of DNA or RNA for the study of microbial

diversity and functionality in environmental samples has led to an increasing knowledge in this area. All of these methods are mostly based on the ribosomal RNA operon because of its ubiquitous distribution and the presence of both variable and highly conserved sequence domains (Justé *et al.* 2008). All of them are culture-independent, fast and can be applied to conserved samples without losing accuracy (Malik *et al.* 2008). Nevertheless some drawbacks related to the recovering and the release of nucleic acids from all genotypes, or the inhibition of the PCR amplification step must be overcome (Jany and Barbier 2008). Among the genetic methods used to obtain microbial communities profiles the following are the most representative: single-strand conformation polymorphism (SSCP), amplified ribosomal DNA restriction analysis (ARDRA), random amplified polymorphic DNA (RAPD), DNA array technology, automated ribosomal intergenic spacer analysis (ARISA), denaturing or temperature gradient gel electrophoresis (DGGE/TGGE) and terminal-restriction fragment length polymorphism (T-RFLP) (Table 1). Most of them are based on the electrophoretic discrimination of PCR products generated from primers of different characteristics according to size or sequence (Ranjard *et al.* 2000). Although these genetic techniques are increasingly displacing conventional methods, they might not be considered as substitutes but as complementary tools, since the application of cross-disciplinary studies provides more completed information.

### Influence on metabolic activities of microorganisms

The influence of microorganisms on soil is mostly achieved by enzymes. These enzymes are involved in nutrient cycling, the establishment of soil structure and even in the restoration of degraded soils (Izquierdo *et al.* 2005; Makoi and Ndakidemi 2008). Taking this into account, probably the enzyme activity analysis provides more accurate information on soil quality and health than determining soil microbial population or soil microbial community diversity. Despite their simplicity, rapidity and low-cost, these methods could be used in conjunction with others to provide a complete vision of the soil *status* (Alkorta *et al.* 2003). On the other hand, the great specificity of the enzymes makes this kind of study difficult, since a relatively high number of them are necessary to obtain valuable information. Considering the enormous quantity of enzymes in soil, just in C and N cycles more than 500 are involved (Schloter *et al.* 2003), a balance between methodological aspects and appropriate information must be reached (Table 2).

Dehydrogenase and fluorescein diacetate (FDA) activities are related to overall microbial activity, while catalase provides information about aerobic microbiota. The first one is a ubiquitous enzyme which, on account of its intra-

**Table 2** Some soil enzymes used as soil quality indicators.

| Enzyme                | Process  | Indicator                                       |
|-----------------------|--|---|
| Dehydrogenase         | Electronic transfer reactions                          | Soil potential to support biochemical processes |
| Catalase              | H <sub>2</sub> O <sub>2</sub> decomposition            | Aerobic microbial activity and soil fertility   |
| Fluorescein diacetate | Ester-cleaving processes                               | Microbial activity                              |
| β-Glucosidase         | β-Glucosides hydrolysis                                | Soil capacity to stabilise organic matter       |
| Cellulase             | Cellulose degradation                                  | Physico-chemical soil properties                |
| Xylanase              | Xylan degradation                                      | Primary litter decomposition                    |
| Phenol-oxidase        | Phenolic compound oxidation                            | Stability of long-term carbon reserves          |
| Urease                | Urea hydrolysis  | Use of urea fertilizer                          |
| Amylase               | Starch Hydrolysis                                      | Soil management practices                       |
| Protease              | N mineralisation                                       | Ecology of microorganisms                       |
| Lipase                | Hydrocarbon degradation                                | Oil-contaminated soils                          |
| Phosphatase           | Hydrolysis of esters and anhydrides of phosphoric acid | Soil fertility                                  |
| Arylsulphatase        | Hydrolysis of sulphate esters                          | Soil fertility                                  |
| Chitinase             | Chitin hydrolysis                                      | Sanitation soil capacity                        |
| Other soil enzymes    | Hydrolytic processes                                   | Degradation of organic matter                   |

Protocols for determining this enzyme activities can be found in the following references: Tabatabai and Bremner (1969); Ladd and Butler (1972); Tabatabai (1982); Schinner and von Mersi (1990); Pati and Sahu (2004); Elfstrand *et al.* (2007); Castaldi *et al.* (2008); Iyyemperumal and Shi (2008); Lee *et al.* (2008); Poulsen *et al.* (2008).

cellular nature, is considered an indirect index of living microbial cells (Taylor *et al.* 2002). Frequently it is used to estimate disruptions produced by organic or inorganic pollutants (Makoi and Ndakidemi 2008), although its high dependency on physico-chemical factors limits its value as overall microbial activity indicator (Ros *et al.* 2003). FDA hydrolysis provides information about such different activities as protease, lipase or esterase, since all of these enzymes can act on fluorescein diacetate (Adam and Duncan 2001). Nevertheless, it is not totally correct to consider this activity as a result of just microbial action, because of the implication of other organism different from microorganisms (Green *et al.* 2006b). Catalase activity is also used as indicator of overall microbial activity, although it is not applicable to anaerobic microorganisms since this enzyme is exclusively in aerobic species (Lee *et al.* 2008).

Cellulases, xylanases, phenol oxidases, amylases and chitinases are involved in the bioconversion of the major carbon polymers present in organic matter: cellulose, xylan, lignin, starch and chitin. Thus, all of them reflect the degree of degradation of the organic matter, as well as other properties according to their specific characteristics. Because of their sensitivity, cellulases provide information about physico-chemical properties of soil (Makoi and Ndakidemi 2008), while xylanases could be an indicator for organic matter losses (Stemmer *et al.* 1999). Phenol oxidases affect the whole decomposition process, since their action influences the availability of carbon by means of the reactivity of the phenolic compounds (Toberman *et al.* 2008). The action of chitinolytic enzymes is noteworthy on the sanitation capacity of soil on account of the structural role of chitin in many phytopathogenic fungal species (Makoi and Ndakidemi 2008). Amylases, as well as β-glucosidases, increase the availability of low molecular weight sugars (Riffaldi *et al.* 2002), which directly affects soil fertility. Lipases, also related to the transformations of macromolecules, plays an outstanding role in soils polluted with hydrocarbons (Lee *et al.* 2008).

Proteases, ureases, phosphatases and arylsulphatases are specifically associated with the biotransformation processes of different nutritional elements. Proteases and ureases, hydrolyse nitrogen compounds, while phosphatases and arylsulphatases take part in P and S cycles, respectively. All of them, therefore, are involved in soil fertility (Makoi and Ndakidemi 2008), while proteases are also useful indicators of heavy metals in soils (Effron *et al.* 2004).

Compost amendments added to soil have an enhancing effect on enzyme activities, which is not surprising if we consider its positive influence on microbial populations and the microbial origin of a great proportion of these molecules. In relation to those activities that reflect global activity, as dehydrogenase, FDA and catalase, the incorporation of stabilised organic matter to soil supports the higher metabolic

activity responsible for the increasing enzyme activities (Bastida *et al.* 2008). This effect can persist in time, causing a residual activity, even higher than initial, as it happens with dehydrogenase activity (Marcote *et al.* 2001). On the contrary, FDA activity does not persist too long after compost amendment, but it is affected to a lesser degree by organic pollutants (Perucci *et al.* 2000). Regarding to catalase activity, an additional factor contributing to the positive effect of compost amendment is the improved soil aeration caused by the higher soil porosity (García-Gil *et al.* 2000).

Enzymes involved in lignocellulose modification are poorly affected by compost amendment, especially if treatments are occasional and short-term effects are considered. Nevertheless, differences are observed depending on quantity and quality of the amendment (Kandeler *et al.* 1999). Example of this is cellulase activity, which increases as higher compost doses are applied to soil (Chang *et al.* 2007). On the other hand, phenol oxidase activity would be decreased due to the inhibitory effect by humic acids on this activity (Allison 2006), and the relatively high proportion of these compounds in a stabilized organic amendment such compost. This inhibitory effect is probably caused by the capacity of humic acids to form complexes with the oxidases and alter their active conformation. On the contrary, xylanolytic enzyme activity is not significantly modified when soil is amended with organic matter (Marschner *et al.* 2003). Similarly to cellulase, amylase activity is directly related to the dosage of organic amendment (Pavan Fernandes *et al.* 2005) and the effect is accumulative (Dinesh *et al.* 2000). In this case, the increasing amylase activity may be consequence of the higher amylase-producers population that follows the organic amendment applications (Mabuhay *et al.* 2006).

β-Glucosidase is affected in major extension by the nature of the organic amendment than by the total carbon added (Pérez de Mora *et al.* 2006). Hence, the availability of readily assimilated carbon enhances this activity, while more recalcitrant compounds do not stimulate it or even decrease it (Ros *et al.* 2006b). In contrast, some residual activity persists after the amendment, although the effect is not as strong as on the dehydrogenase activity, since new compost applications do not increase further the dehydrogenase activity. An interesting characteristic of β-glucosidase is the production of a synergistic effect in conjunction with chitinase enzymes due to the sanitation capacity of the last (Chae *et al.* 2006).

The influence of compost on soil urease activity is a controversial one, since controversial results have been reported. Bastida *et al.* (2008) and Lee *et al.* (2008) described a positive effect, while other authors found no significant changes (Ros *et al.* 2007) or even strong inhibitory effects (García-Gil *et al.* 2000). Two factors are probably the main reasons for this last influence. On one hand, high NH<sub>4</sub><sup>+</sup>

concentrations in compost make unnecessary urease activity and (Ros *et al.* 2006b), on the other hand, the presence of heavy metals depending on the compost characteristics can also inhibit the action of this enzyme (Tejada *et al.* 2007a). Proteolytic activity may be either negatively affected by heavy metals (Lorenz *et al.* 2006), although the existence of proteases of quite different characteristics minimizes this effect. Examples of this diversity are works by Marcote *et al.* (2001) and Ros *et al.* (2003), who found an increase in protease activity determined as caseine, which reflects hydrolysis of high molecular weight proteins, while no influence was reported in relation to proteolytic activity according to N- $\alpha$ -benzoyl-L-arginamide (BAA), which acts upon small and mid-size protein intermediates.

Compost amendments added to soil do not show a clear influence on phosphatase activity, since different results have been reported. As in the case of urease, increasing (Lee *et al.* 2008; Tejada *et al.* 2008) as well as no influential effects (Hamdi *et al.* 2007) have been reported. The availability of phosphorus and the sensitivity of phosphatase activity to pollutants may be mainly responsible for this last effect (Pérez de Mora *et al.* 2006). On the contrary, arylsulphatase activity in soils is positively influenced by periodic compost amendment, as described by different authors (Pérez de Mora *et al.* 2006; Tejada *et al.* 2008).

Since lipase activity is closely related to hydrocarbons degradation, this enzyme is often analyzed in those soils where the concentration of this kind of pollutants is high. In such scenario, the addition of compost use to affect positively the lipase activity (Lee *et al.* 2008).

The estimation of soil enzyme activity, even if different enzymes are analyzed, probably will be not enough to reflect such a complex scenario, but in conjunction with other analysis provide valuable information to shape a real image of soil status, mainly when changes occur (i.e. compost amendment).

### Compost amendment for soil bioremediation

One of the main concerns regarding soil wealth is pollution. Because of wrong agronomical and industrial practices, mining exploitation or occasional polluting discharges, the extension of soil affected by high levels of hydrocarbons, pesticides or heavy metals is significant. Among the diverse proposals for facing this kind of situation, the use of assisted natural remediation processes, (organic amendments, for example) is one of the most appealing one due to low-cost, can be applied on site over large areas and, generally, does not generate by-products (Moorman *et al.* 2001; Madejón *et al.* 2006; Lee *et al.* 2008).

In relation to heavy metals, the high proportion of humic substances contained in compost favours the formation of stable complexes and adsorption processes, which lead to the decrease of these trace elements and, hence, the re-establishment of vegetation (Clemente *et al.* 2006). In contrast, compost addition can enhance the efficiency of phytoremediation processes by increasing the bioavailability of trace elements (Cao *et al.* 2003; Kuiper *et al.* 2004). With respect to pesticides, compost seems to promote sorption processes to organic matter as well as biodegradation by

means of the introduction of non-indigenous microbiota or the stimulation of the native microorganisms (Delgado-Moreno and Peña 2007). Similar mechanisms have been described for the remediation of hydrocarbons (Lee *et al.* 2008), although some drawbacks related to the presence of readily available substrates and the consequent negative influence on biodegradation have been reported (Schaefer and Juliane 2007). On the contrary, the consumption of these easily available compounds can support the build-up of a microbial population able to degrade the contaminant when its availability is poor (Wick *et al.* 2003). An alternative strategy to overcome such disadvantages may be the inoculation with previously remediated contaminated soil, which contributes to increase the proportion of adapted microorganisms (Hwang *et al.* 2001).

### INFLUENCE OF COMPOST AMENDMENT IN PLANT GROWTH AND YIELD

Nowadays soil quality is seriously damaged because of aggressive agricultural practices and the abundance of organic and inorganic pollutants. The worrisome fertility status of soil has led to the search of new nutritional sources that can restore healthier conditions. The incorporation of fresh organic matter to soil may show several disadvantages, among them the instability of the material, the presence of organic and inorganic pollutants and the action of phytopathogenic microorganisms. Composting treatments of these residual materials decrease and even eliminate these risks. Additionally, they provide organic matter with new properties that favour new applications. Thus, during last years compost has been proposed as a component in soilless growing media (Benito *et al.* 2005), tool for the suppression of soil-borne phytopathogens (Noble and Coventry 2005) or material for the reinforcement of highway embankments (Pengcheng *et al.* 2008). Hence, new and promising prospects arise for compost in the future.

### Direct effect on growth and yield of cultures

Mature compost is an easy to disperse and dark-coloured material, with a C:N ratio around 10. After the product is added to soil, microbial communities start to modify the organic matter through a mineralization process, the duration of which depends on climate conditions. In temperate zones, the process progresses slowly, so effects of the amendment can take years to become apparent. In such cases, a significant fraction of the organic matter will be stabilized and integrated into soil humus. On the contrary, in warmer and humid climates, mineralization rate increases such that compost may be completely lost (Albiach *et al.* 2001), and with only mineral nutrients remaining. As a result, periodical compost amendments are needed to promote positive effects.

The positive effect on physico-chemical and biological properties of compost amendments promotes ideal conditions for plant growth and, in turn, improve yield. There are many studies that support this influence (Table 3). A wide diversity of raw materials have been used in these studies, although a combination of different wastes is recommended

**Table 3** Some studies of plant yield improvement by compost amendment.

| Plant     | Compost amendment  | Treatment                  | Yield improvement                  | Reference                    |
|-----------|--|----------------------------|------------------------------------|------------------------------|
| Barley    | Spent mushroom compost                                       | 100 t ha <sup>-1</sup>     | 59% higher grain yield             | Courtney and Mullen 2008     |
| Wheat     | Composted sugarcane bagasse                                  | 15 Mg ha <sup>-1</sup>     | 23% higher grain yield             | Barzegar <i>et al.</i> 2002  |
| Sorghum   | Composted household refuses, animal manure and crop residues | 10 Mg ha <sup>-1</sup>     | 238% higher grain yield            | Ouédrago <i>et al.</i> 2001  |
| Maize     | Biogenic-municipal waste                                     | 10 g kg soil <sup>-1</sup> | ≈ 300% shoot/root C                | Muhammad <i>et al.</i> 2007  |
| Bean      | Sewage sludge compost  | 4.5 Mh ha <sup>-1</sup>    | 70% higher productivity            | Garrido <i>et al.</i> 2005   |
| Pigeonpea | Cattle manure compost  | 330 kg H ha <sup>-1</sup>  | 181% higher total plant dry weight | Akhtar 1999                  |
| Tomato    | Sugar mill by-products compost                               | 45 g per plot              | 87% higher shoot weight            | Meunchang <i>et al.</i> 2006 |
| Lettuce   | Tobacco waste compost  | 50 t ha <sup>-1</sup>      | 25% higher yield                   | Okur <i>et al.</i> 2008      |
| Rice      | Crushed cotton gin compost                                   | 20 t ha <sup>-1</sup>      | 9.5% higher yield                  | Tejada and González 2006     |
| Corn      | Sewage sludge compost  | 150 kg N ha <sup>-1</sup>  | 12% higher dry matter yield        | Warman <i>et al.</i> 2005    |

to prevent some detrimental properties of specific materials, which might hamper the composting process, and obtain of a better and balanced final product from an agronomical point of view (Sánchez-Arias *et al.* 2008; Sellami *et al.* 2008). However, compost quality is not the only factor to be considered for the success of the amendment. Soil properties also play an important role (Ouédrago *et al.* 2001; Muhammad *et al.* 2007), which makes necessary the adaptation of compost characteristics to the specific soil demands. Sometimes, these demands are better met not by means of improved physico-chemical or nutritional compost properties but through the action of microbial inoculants (Postma *et al.* 2003; Grandlic *et al.* 2008).

The assessment of compost influence on plant growth can be achieved through different parameters, among them yield, productivity, dry weight of plant, weight and number of fruits, length and weight of stem, shoot and root carbon, N or P uptake capacity, etc. (Garrido *et al.* 2005; Warman and Termeer 2005; Tejada and González 2006; Muhammad *et al.* 2007).

### Compost as a suppressive soil-borne pathogen tool

One of the major advantages of compost in relation to fresh organic matter is practically the absence of biological contaminants. The conditions during the composting process as well as the presence of antagonistic compounds and microorganisms promote the elimination of pathogenic species (Vinnerås *et al.* 2003; Suárez-Estrella *et al.* 2007). Obviously, the environmental (temperature) sanitation capacity of the composting process is not conserved in compost, but on the contrary, the suppressive effects of antagonistic microorganisms and compounds are responsible for are preserved (Malakandri *et al.* 2008) and favoured the sanitation soil capacity against diseases caused by both nematodes (Widmer *et al.* 2002) and microorganisms (Tilston *et al.* 2002). Nevertheless, several mechanisms are involved in this phenomenon, most of them attributed to the presence of antagonistic microorganisms. Hence, competition for nutrients and ecological niches, nutrient availability, parasitism, production of cell-wall hydrolytic enzymes of antibiotic compounds and induction of host resistance contribute in different extent to this capacity (Kavroulakis *et al.* 2005; Ntougias *et al.* 2008).

On account of the different mechanisms by which compost can induce suppressiveness, differences are expected among composts (Thermosuizen *et al.* 2006). Even same type of compost may differ on its influence depending on maturity degree, location, storage conditions, timing of application and type of pathogen to be controlled (Postma *et al.* 2003; Ntougias *et al.* 2008). Other factors related to the previous composting process, such as properties of the raw material, type of composting process or microorganisms that re-colonized the wastes after the thermophilic stage, also affect the level of disease control (Alabouvette *et al.* 2006). This variability makes difficult to predict the specific effect of compost on one or more pathogens and, therefore, makes necessary to study case by case. Nevertheless, attempts have been made to look for valuable parameters in predicting the suppressive potential of compost, most of them related to microbial aspects (Diab *et al.* 2003; Noble and Coventry 2005; Pérez-Piqueres *et al.* 2006).

Depending on the factor responsible for the action against pathogens, two different mechanisms can be differentiated: general and specific suppressiveness. The first one is associated to the activity of the whole compost microbiota (Ntougias *et al.* 2008) and the competitive effect antagonistic microorganisms exert, with no major intervention of specific microorganisms. This kind of suppressive action is determined by the amount of available decomposable organic matter, which in turn is depending on the dosage amended (Veeken *et al.* 2005). An example of disease controlled by this kind of mechanism is that caused by *Fusarium oxysporum*, a very sensitive microorganism to

competition processes, which is inhibited by most of compost no matter their properties (Alabouvette *et al.* 2006).

The other suppressive mechanism implies the action of specific microorganisms. Since the efficacy of such mechanism depends on the presence in compost of the active microorganism against the pathogen to be suppressed, variability is quite higher in these cases. A possible solution for this drawback is the enrichment of compost in specific bio-control agents (BCAs) by means of external supplementation (Hoitink *et al.* 2006), although results depends on compost origin and maturity degree as well as plant pathosystem (Postma *et al.* 2003).

BCAs show two major mechanisms for conferring protection to plants against pathogenic microorganisms. First and simpler, they can control the growth of such species by means of competence processes in the rizosphere (Malakandri *et al.* 2008). The second one, which shows greater complexity, implies the endophytic growth of the BCA. This mechanism favours growth since the BCA find little or no microbial competition and, more important, suppressive action can also affect to vascular diseases (Nejad and Johnson 2000).

One of the most interesting mechanisms of the BCAs suppressive effect is the so-called systemic induced resistance (SIR), which increases protection against foliar diseases (Kavroulakis *et al.* 2005). This effect, one of the last mechanisms to be recognized as part of the suppressive action of the compost amendments (Kuc 1987), is mediated by microbial species, both pathogenic and non-pathogenic, or certain chemical agents (Vallad *et al.* 2003). The recognition of these intermediates by the plant promotes a cascade of signals which results in the synthesis of defence molecules, mostly pathogenesis-related proteins, and the reinforcement of cell walls (Alabouvette *et al.* 2006). Since efficiency of SIR is higher when the inducing agent acts previously to the plant-pathogen contact, no contact between pathogenic microorganism and BCA is needed. The presence of the BCA induces some physiological reactions that contribute to protect the plant, among them production of H<sub>2</sub>O<sub>2</sub>, Ca<sup>2+</sup> influx or pH increase (Alabouvette *et al.* 2006) and promotes the action of plant defence enzymes, such as  $\beta$ -1,3-glucanase,  $\beta$ -1,4-glucosidase, peroxidase or chitinase (Vallad *et al.* 2003). Among the different BCAs that have been described to induce systemic resistance in plants, *Pseudomonas* and *Trichoderma* species have proved to be the most efficient (Bolwerk *et al.* 2003; Harman *et al.* 2004; Ongena *et al.* 2004).

### CONCLUSION

The use of organic matter to improve soil properties has been an usual practice for a long time. Manure, biosolids, crop residues and other organic wastes have been used for this purpose. Nevertheless, these fresh materials not only provide carbon and other nutritional elements but pollutant and phytotoxic compounds as well as pathogenic microorganisms either. The processing of such materials prior to their incorporation to soil minimizes these risks while increases their degree of stability. One of the techniques that promote these characteristics is composting. Compost amendment added to soil improves both physico-chemical and biological properties, which in turn contributes to restore degraded soils and improves the agronomic quality of soils. Biological properties are especially significant on account of their influence on soil status. Microorganisms and their enzymes exert a beneficial effect in soil quality and, consequently, in plant growth since their activities increase nutrient availability and promote suppressiveness as well as stimulate the degradation of different type of pollutants. Thus, compost also prevents or reduces the use of environmentally dangerous chemical products traditionally applied for crops sanitation by means of this suppressive action. In this sense, compost added can contribute to reduce CO<sub>2</sub> emissions by sequestering carbon and modifying agronomic practices that favour such emissions. In summary, compost

nowadays is an indispensable material for increasing the sustainability of agriculture and promoting the restoration of disturbed soils, through the improving of soil biological properties.

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