Plant–bacteria interactions in the removal of pollutants

Ana Segura and Juan Luis Ramos

Rhizoremediation surged in popularity among scientist as an attractive strategy because plant roots provide a rich niche for bacteria to grow at the expense of root exudates; in turn bacteria act as biocatalysts that remove pollutants. The complexity of the beneficial relationships between plants and bacteria is an exciting area of research which has shown steady progress in the last decade. Despite the advances in the field, specific aspects of the interactions between contaminant-degrading rhizobacteria and plants are still unknown; including the expression of degradation genes in the rhizosphere, the influence of horizontal gene transfer in rhizoremediation, and the possibilities of the selection of specific bacteria by plant rhizosphere. We discuss the recent advances in our understanding of the plant–bacteria interactions during rhizoremediation of organic compounds.

Address
Consejo Superior de Investigaciones Científicas, Estación Experimental del Zaidín, Department of Environmental Protection, E-18008 Granada, Spain

Corresponding author: Segura, Ana (ana.segura@eez.csic.es)

Introduction

During the last thirty years, there has been a very intensive area of research dealing with the identification and characterization of microorganisms able to degrade contaminants. As a consequence, a wide variety of microorganisms are available for the elimination of different types of contaminants from aromatic to linear hydrocarbons, chlorinate compounds, dioxins, explosives, pesticides, and others [1–3]. The bacterial catabolic pathways for the degradation of many compounds are also known (http://umbbd.ethz.ch/index.html; Figure 1) and their regulation has been well characterized [4]. The utilization of laboratory microorganisms in the elimination of soil contaminants using bioaugmentation has been employed with different degrees of success. Unsuccessful bioremediation can be caused by the lack of nutrients in the soil, soil surface properties, toxicity or reduced bioavailability

of the contaminant, inefficient competition of foreign microorganisms with indigenous communities and the failure to express the catabolic functions required for degradation, among others [5]. One of the main problems encountered is the difficulty to establish appropriate numbers of foreign pollutant-degrading bacteria in the contaminated soils and their concomitant persistence. As a solution to overcome some of these limitations, the utilization of rhizospheric bacteria (that are adapted to colonize and compete for space and resources in the rhizosphere) with the appropriate catabolic properties, was thought to be a promising approach [6]. The rhizosphere is a nutrient rich environment that contains higher numbers of microbes (and these are metabolically more active) than bulk soils [7]. Furthermore, some plants secrete compounds that can stimulate the degradation activities required for the elimination of contaminants [8].

Rhizospheric bacteria can establish deleterious, neutral or beneficial interactions with plants. Contaminant-degrading rhizobacteria can be included among the plant-growth promoting rhizobacteria (PGPR) because the presence of contaminants, in general negatively affects the growth of the plant, and the elimination of the inhibiting chemicals will benefit the plant [9]. Although contaminant-degrading strains have been traditionally isolated from various environments, in the last two decades, an increasing number of studies have reported the isolation and identification of rhizospheric bacteria with contaminant-degrading abilities [6,10,11,8].

In this mini-review we will comment on the latest findings in the field of rhizoremediation of organic compounds focusing our attention on the bacteria-plant interactions.

Colonization and adaptation to life in the rhizosphere

Contaminant-degrading rhizobacteria colonize root plants similarly to many other rhizobacteria. Identification of mutants defective in colonization and survival in the rhizosphere has provided some important insight into the processes involved in rhizosphere colonization, such as the implication of chemotaxis, movement toward and attachment to the roots [review in [12]]. The development of the 'In Vivo Expression Technology' (IVET) [13,14] and more recently transcriptional microarrays has allowed researchers to obtain a global image of the processes that take place in the rhizosphere [15]. Proteomic analysis has also been used to explore plant–microbe interactions although many of the studies refer to plant–bacteria interactions in pathogenic and nitrogen fixing

Figure 1

Schematics of several contaminant degradation pathways in bacteria.

bacteria [16,17]. Among the most significant transcriptional responses of bacteria are changes in the transcriptional pattern of catabolic pathways to enable utilization of the chemicals secreted by roots as carbon or nitrogen sources, and the induction of bacterial genes involved in oxidative stress [13,18–20]. These findings indicate that the rhizosphere is a challenging nutritional environment which is oxidatively stressful owing to the formation of reactive oxygen species produced by the respiration of root cells.

Despite these common characteristics, it is becoming clear that plants (root exudates) influence the microbial composition of the root environment [21,22] and select for certain microbes [23,24,25•] and this effect is more clear in endophytic populations [26••,27••]. Interactions between plants, rhizospheric microorganisms and soils have been shaping the terrestrial ecosystems during the Earth's evolution [review in [28]], and specific communication and recognition processes have been established between

plants and microbes through co-evolution. These specific recognition processes have been well studied in pathogens and in some PGPR, but little is known about pollutant-degrading rhizobacteria. Siciliano *et al.* [29] tested the hypothesis that plants living in contaminated environments selected contaminant-degrading bacteria in their rhizosphere. They proved that the enrichment of bacteria with the appropriate catabolic genes in the rhizosphere (and especially in the endophytic root compartment) depended on the type and amount of contaminant and also on the genotype of the plant. Sipilä *et al.* [30] demonstrated that the diversity of ring-cleavage dioxygenases genes in the rhizosphere of birch plants growing in pyrene contaminated soil was higher than that of bulk soil. This higher diversity correlated with the higher pyrene removal observed in planted microcosms compared with that of unplanted microcosms. Many other studies have shown that the plant's genotype has an effect on the outcome of the rhizoremediation through the selective enrichment of the microbial community in the rhizosphere [31•,32,33•].