

# Organic breeding should select for plant genotypes able to efficiently exploit indigenous Probiotic Rhizobacteria

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**Abstract** – In order to rapidly achieve crop varieties adapted to organic crop production systems, it is of crucial importance to know plant genotype potential for positive interactions with soil indigenous microflora. In this frame, European research efforts are now considering beneficial non-symbiotic (probiotic) rhizobacteria as an essential factor for sustainable plant breeding. Published findings are beginning to elucidate how probiotic rhizobacteria contribute to plant nutrient assimilation and disease resistance. Future efforts for crop breeding in organic agriculture should take into the right account the capacity of plants to efficiently exploit indigenous probiotic rhizobacteria in low-input cultural conditions.<sup>1</sup>

## INTRODUCTION

The objectives of selection for the development of varieties for organic agriculture differ from those for conventional agriculture. Organic and low-input plant breeding programs are oriented to the selection of plants with both resistance to disease and an efficient nutrient assimilation, in order to keep the productivity, while improving quality and safety by reducing pesticide (Bradshaw et al., 2003) and fertilizer inputs (Gahoonia and Nielsen, 2004).

It is worth noting that the resistance of plants to root diseases, as well as an efficient nutrient assimilation, are profoundly influenced by the presence and activity in soil of beneficial microorganisms. For this reason, organic and low input plant breeding programs take more and more into account the capacity of plants to interact with their own rhizospheric microflora (Picard et al., 2005).

Recent results of breeding programs revealed that it is difficult to select varieties for low-input agriculture by starting from the conventional elite varieties. In fact, plant varieties adapted for organic agriculture often differ from those for conventional agriculture. In particular, crop varieties for conventional agriculture are generally much less sensible to arbuscular mycorrhizal fungi (AMF) than needed for organic agriculture, probably because cultivar development in fully fertilized soils resulted in the selection against genotypes that interact well with AMF (Herrick et al., 1995). Since AMF could actually reduce plant growth in situations where nutrients are not

limiting (*i.e.*, when the cost of maintaining the AMF exceeds the benefit to the host), it may be logical that selection under adequate fertilizer levels has selected for nonmycorrhizal genotypes. On the same way, conventional breeding and crop improvement may have, in some cases, resulted in the loss of host genes important in the *Rhizobium*-legume interaction, and thus in varieties that don't maximize the benefits of this symbiosis. Furthermore, research on the difference among parental plant lines and their progeny for their effect on the rhizobial and AMF microflora indicated that host-controlled nodulation and mycorrhization is inherited through generations, thus demonstrating to have a genetic basis (Rengel, 2002). These inheritance traits are now widely exploited in breeding programs, resulting in the selection of the most part of cultivars for organic agriculture.

On the contrary, in the past, plant breeding programs have not taken into the right account the capacity of crop plants to interact with an other group of beneficial soil microorganisms, known to enhance plant growth by suppressing diseases, fixing atmospheric nitrogen, solubilizing phosphorus, iron and other nutrients, and by producing bioactive compounds that stimulate root proliferation. These microorganisms, generally non-symbiotic rhizobacteria, are called Plant Growth Promoting Rhizobacteria (PGPR) (Kloepper et al., 1980) and, more recently, probiotic rhizobacteria (Haas and Keel, 2003). On the basis of knowledge on rhizobial and AMF interactions, before developing organic programs on the plant interactions with probiotic rhizobacteria, it is primordial to evaluate (1) the possibility or not to select organic varieties among those adapted for conventional agriculture, and (2) the eventual genetic basis of probiotic interaction.

## DIVERSITY OF INTERACTIONS WITH PROBIOTIC RHIZOBACTERIA, BETWEEN VARIETIES FOR CONVENTIONAL AND ORGANIC AGRICULTURE

Several researches indicate that, as for rhizobial and AMF interactions, plant genotypes affect both the performance of root colonisation by probiotic rhizobacteria and their beneficial activity. Differences have been observed, for example, at the cultivar level, as in the case of root colonization in tomato (Smith et al., 1999), cotton (Adams and Kloepper, 2002) and wheat (Mazzola et al., 2004). Even if

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there is no result on the direct comparison between varieties for organic and for conventional agriculture, several researches let to hypothesize that it will be difficult to select varieties presenting high level of interactions with the beneficial rhizobacteria, among the elite varieties selected for the conventional agriculture. In fact, it has been demonstrated that wild rice species and old varieties were more colonized by probiotic rhizobacteria than modern cultivars selected for conventional agriculture (Engelhard et al., 2000). On the same way, probiotic rhizobacteria were found to be more abundant in the rhizosphere of older wheat cultivars than on the roots of newer wheat cultivars (Germida and Siciliano, 2001).

#### GENETIC BASIS OF PLANT INTERACTIONS WITH SOIL PROBIOTIC RHIZOBACTERIA

Recent literature suggested that root colonization by probiotic rhizobacteria is effectively an inherited trait, probably related to heterosis. In particular, Smith et al. (1999) have studied host-linked variations of disease suppression by an inoculated probiotic strain, using a tomato Recombinant Inbred Line (RIL) mapping population. They observed a continuous variation among the RILs for disease suppression by the probiotic strain, and were able to detect three Quantitative Trait Loci (QTL) associated with a host effect on disease suppression.

Concerning probiotic populations naturally present in soils, we have recently observed, by repeated experiments in field conditions, that hybrids of maize can support populations of disease suppressing, root stimulating probiotic rhizobacteria that are more numerous and genetically more diverse than those supported by their parental lines (Baruffa, 2005; Picard et al., 2004; Picard and Bosco, 2005). Furthermore, we also evidenced that hybrid genotypes are more colonized by probiotic rhizobacterial strains with multiple beneficial functions (Picard and Bosco, 2005).

All these findings together suggest that it would be possible to stimulate the diversity of soil indigenous probiotic rhizobacteria from resident populations, by cultivating hybrids obtained by a plant-breeding program directed toward genotypes able to support large and genetically diverse populations of efficient disease suppressors (Picard et al., 2005).

#### CONCLUSIONS

Published and unpublished findings, like those cited above, revealed that future efforts for crop breeding in sustainable low-input and organic agriculture should take into the right account the capacity of plants to positively interact with probiotic and other beneficial soil micro-organisms (Picard et al., 2005). Thus, we propose the development, and the laboratory, field, and biostatistic experimentations, of a breeding strategy directed towards varieties that support large populations of beneficial indigenous probiotic rhizobacteria, as a new approach to the development of sustainable low input and/or organic production systems.

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