AM symbiotic traits can be selected using conventional breeding methods in durum wheat

Chantal Hamel, Asheesh Singh, Ron DePauw, Ron Knox
Semiarid Prairie Agricultural Research Centre

Keywords: Arbuscular mycorrhizal symbiosis, phosphorus acquisition efficiency, durum genotype

Abstract

The management of the arbuscular mycorrhizal (AM) symbiosis, could improve plant's efficiency of fertilizer use. The development and function of an AM symbiosis is largely controlled by the genotype of the host plant. Thus, it may be possible to improve crop nutrient-use efficiency by the selection of genotypes with improve symbiotic effectiveness. Variability in the AM symbiotic development of durum wheat genotypes must be present in breeder plant material for a breeding program to be effective. We tested in the greenhouse under two levels of fertility, the hypothesis that durum wheat genotypes representative of five mapping populations vary in their ability to form the AM symbiosis. We found variations in the influence of the commercial AM fungus *Glomus intraradices* on root colonization, nutrition, and yield of durum wheat. This variation indicates that it is possible to select durum genotypes for improved symbiosis formation using conventional breeding methods.

Introduction

We are in a time of human history where natural resource availability is rapidly diminishing and demand for crops increasing. It becomes important to improve the efficiency of fertilizer use by plants. One way to improve fertilizer use efficiency in crop plants is to manage their AM symbiosis.

It is important to realize that plants never live alone, but are associated with a range of microorganisms that inhabit the surface and the interior of their tissues. Microbial colonization of plants is not random, but largely dependant of the plant itself. Plants cannot walk away from an unhealthy soil environment. Their strategy is to change the soil using a range of chemicals to modify the soil chemical or biological environment. The profile of bioactive chemical produced by plants varies even within a species, thus, it might be possible to select plant genotypes that are better able to form effective symbioses with naturally occuring soil microorganisms such as AM fungi. For selection to be possible, genetic variation must exist. We conducted a greenhouse experiment to define is genetic variation in AM symbiosis formation and effectiveness exists in durum wheat. The hypotheses we tested are: 1) The roots of different durum genotypes develop AM symbioses to different extents and 2) Durum genotypes vary in their biomass and nutrient uptake response to AM symbiosis.

Methods

Treatments of five durum wheat genotypes were grown in 2 L of pasteurized loamy sand containing over 7000 live propagules of *Glomus intraradices* or a control of sterile propagules (autoclaved). A first experiment was conducted under poor soil fertility conditions and a 2nd experiment was conducted under conditions of medium soil fertility. The loamy soil received 0.8 L of a modified Long Ashton nutrient solution in the first experiment, and medium soil fertility condition was created, in a 2nd experiment, by applying or 1.2 L of the nutrient solution. The nutrient solution was added in increasing abundance as plants grew larger. Day/night photoperiod was 16h/8h, and temperature was 15ºC/18ºC for 7 weeks, then 18ºC/21ºC until harvest. Watering was done as needed.
Roots were sampled, cleaned, stained and the level of AM colonization was measured under a dissecting microscope (Giovannetti and Mosse, 1980). Total and grain biomasses were recorded after drying at 40°C until no further reduction of weight occurred on successive dates. Vegetative tissues were ground and analyzed for their nutrient content. Response to AM colonization was expressed as: Response = $(\text{biomass}_{\text{AM}} - \text{biomass}_{\text{control}} / \text{biomass}_{\text{control}} * 100$

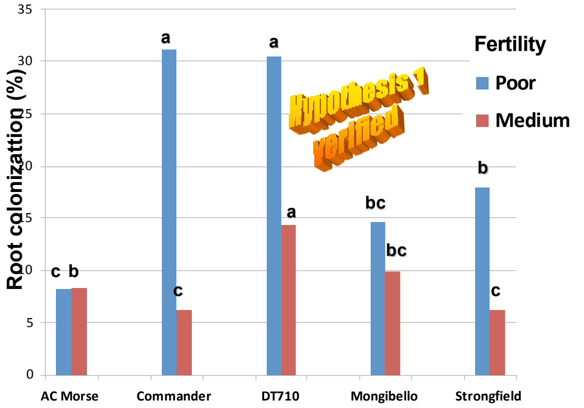

Fig. 1. Level of root colonization by the AM fungus *G. intraradices* as influenced by durum wheat genotype under poor (blue) and medium (red) soil fertility. Bars of the same color and with the same letter are not significantly different (LSD = 0.05).

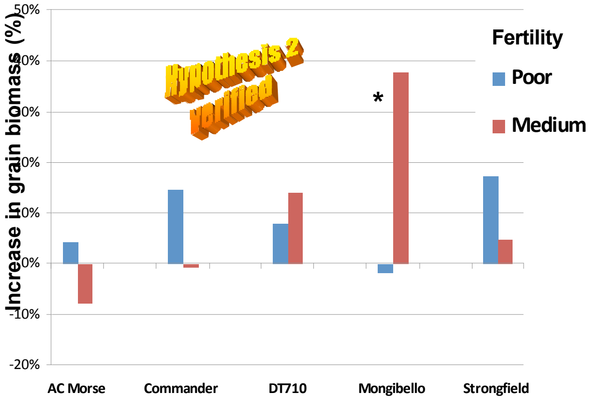

Fig. 2. Response of grain biomass production triggered by inoculation with the AM fungus *G. intraradices*, in different durum genotypes. Values above zero indicate a yield increase. A star on a bar indicates a significant response (LSD = 0.05).

Results

The roots of DT710 developed the most extensive AM colonization, overall (Fig. 3). Commander expressed the most extreme difference for root colonization in poor versus medium soil fertility. AC Morse and Mongibello showed the least differences among the two soil fertility experiments. Non-inoculated plants showed no mycorrhizal association.

There was no response to the AM symbioses under conditions of poor soil fertility, but under conditions of medium soil fertility, Mongibello produced more grain (Fig. 4) and total biomass (Fig. 5).

Among the tested genotypes at poor fertility, the live mycorrhizal treatment differed from the sterile

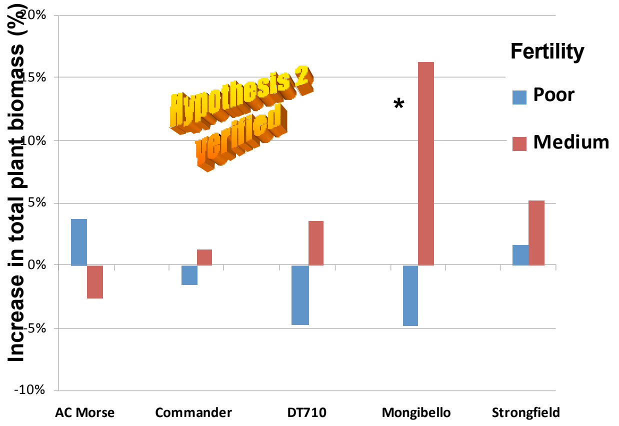

Fig. 3. Response of total biomass production triggered by inoculation with the AM fungus *G. intraradices*, in different durum genotypes. Values above zero indicate a yield increase. A star on a bar indicates a significant response (LSD = 0.05).

control treatment. Grain Mn concentration was higher with AM fungi present and grain cadmium concentration was reduced (Table 1). Except grain Mn, which was higher with AM fungi present under poor fertility conditions, there was no significant effect of mycorrhizal colonization on nutrient concentrations in the vegetative tissues of Mongibello.

Table 1. Influence of the AM fungi on grain nutrient and cadmium concentrations averaged across cultivars under poor soil fertility . Numbers in bold in a column indicates that treatment effect is significant at = 0.01 (**) or 0.001 (***), according to ANOVA.

	N	P	K	Ca	Mg	S	Fe	Mn	Zn	Cd
	(mg g^{-1})	(mg g^{-1})	(mg g^{-1})	(mg g^{-1})	(mg g^{-1})	(mg g^{-1})	(g g^{-1})	(g g^{-1})	(g g^{-1})	(g g^{-1})
G. intraradices	16.4	3.8	5.5	3.5	1.40	1.23	44	**53**	36	**0.172**
Control	17.0	3.8	5.5	2.5	1.35	1.19	46	**47**	36	**0.211**
ANOVA	ns	ns	ns	ns	ns	ns	ns	***	ns	**

Conclusions

Five conclusions can be drawn from these results: (1) The durum wheat genotypes varied in their ability to form the AM symbiosis with *G. intraradices* based on root colonization, (2) the different durum wheat genotypes responded differently in biomass production to the AM symbioses they form with *G. intraradices*, (3) the biomass response to AM symbiosis was not related to the level of AM development in roots, (4) Mongibello was the most responsive genotype with the highest biomass response to the AM symbiosis, and (5) AM reduced Cd concentration in the genotypes tested.

Reference

Giovannetti M, Mosse B (1980) An evaluation of techniques for measuring vesicular arbuscular mycorrhizal infection in roots. New Phytol 84: 489-500.