



**Growth is
natural
with us**



Alltech. 40+ years of consistent growth.

Headquartered in Kentucky, with 95 production facilities and present in over 120 countries.

We are a global leader in biotechnology, animal nutrition and nutritional solutions for agricultural performance.

Our mission is to improve the health and performance of people, animals and plants through scientific innovation.



Agronomic division providing an **innovative biotechnology range** of soil health and plant nutrition, performance and protection products.



- Proven effective, natural-based alternatives to chemicals



- Technology derived from microbial fermentation

PLANT

Bio-solutions
for crop
performance
and quality.



Curiosity is the seed of discovery

Fondation of Alltech by Dr. Pearse Lyons



Launch of Alltech Crop Science. Alltech's Agriculture Division



Yeast fermentation facility in Brazil



ACS Europe



ACS Iberia Europe's leading platform



New Registrations: Biostimulants and biofertilizers



1980

1985

1994

1995

2003

2008

2011

2015

2016

2019

2020

2023

1st Annual International ONE Conference



ACS Brasil first market



Alltech Nutrigenomics Center



Nutrigenomics: ACS Solutions influence the gene expression of plants



Alltech ECO2 Suppressives Soils



New Partnerships I+D+I IDEAGRO

Nutrigenomics

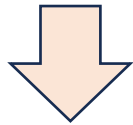
Improving crop quality and
yield

#MaximizeThePotentialOfYourCrop



Nutrigenomics

Two genomic approaches to understand the mode of action of a product

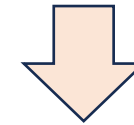


1. Targeted nutrigenomics:

Study of known genes characterized in other works



qPCR



2. Untargeted nutrigenomics:

Sequencing and study of all the genes that are being expressed after a stimulus



RNA sequencing
(transcriptomics)



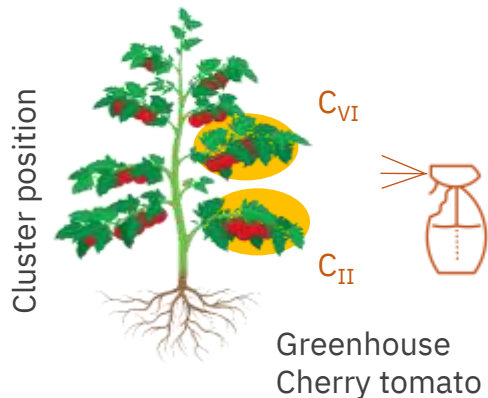
PLANT RESPONSE

Nutrigenomics



APPLICATION PRODUCT

Biostimulant



SAMPLING

Different Moments
Different tissues (roots, stem,
leaves and fruits)



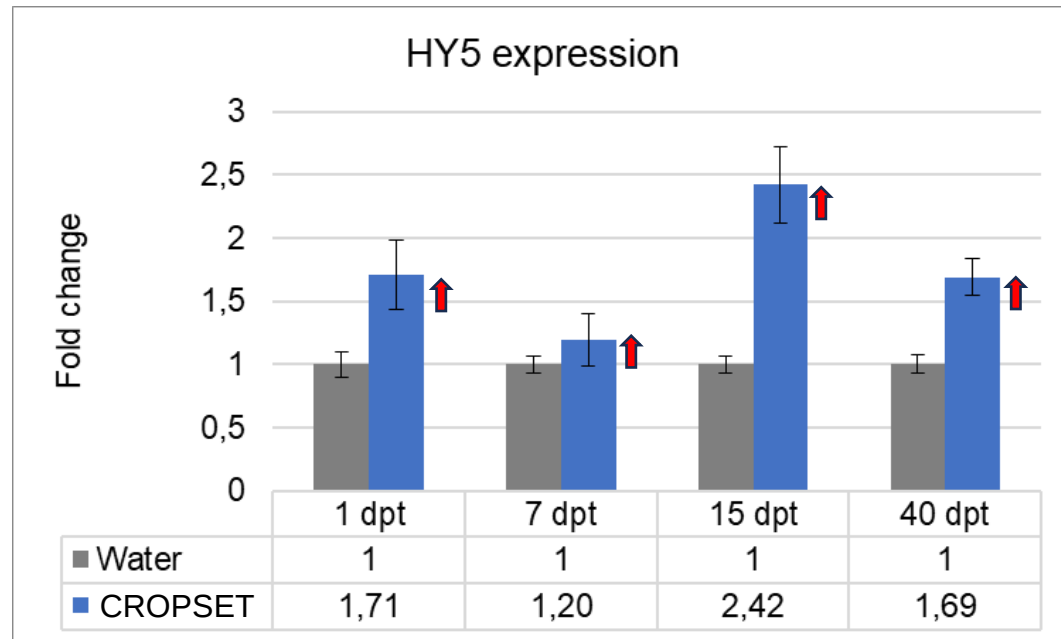
RNA EXTRACTION AND ANALYSIS

What kind of **responses** are observed?
Are there **multiple types** of answers?
Are there **differences** in the answers?
Immediate vs. Delayed responses

GENES INVOLVED IN PLANT DEVELOPMENT AND YIELD



GENES INVOLVED IN DEVELOPMENT AND NUTRIENT UPTAKE



ELONGATED HYPOCOTYL 5 (HY5):

Transcription factor AND master regulator of light-mediated responses.

HY5 binds to the promoter of c. 3000 genes, thereby regulating various physiological and biological processes, including photomorphogenesis, flavonoid biosynthesis, root development, response to abiotic stress and nutrient homeostasis.

Coordinates stem and root growth in response to light.

Regulates the transport of photoassimilates from the stem to sink tissues by activating the expression of different genes



HY5: a key regulator for light-mediated nutrient uptake and utilization by plants

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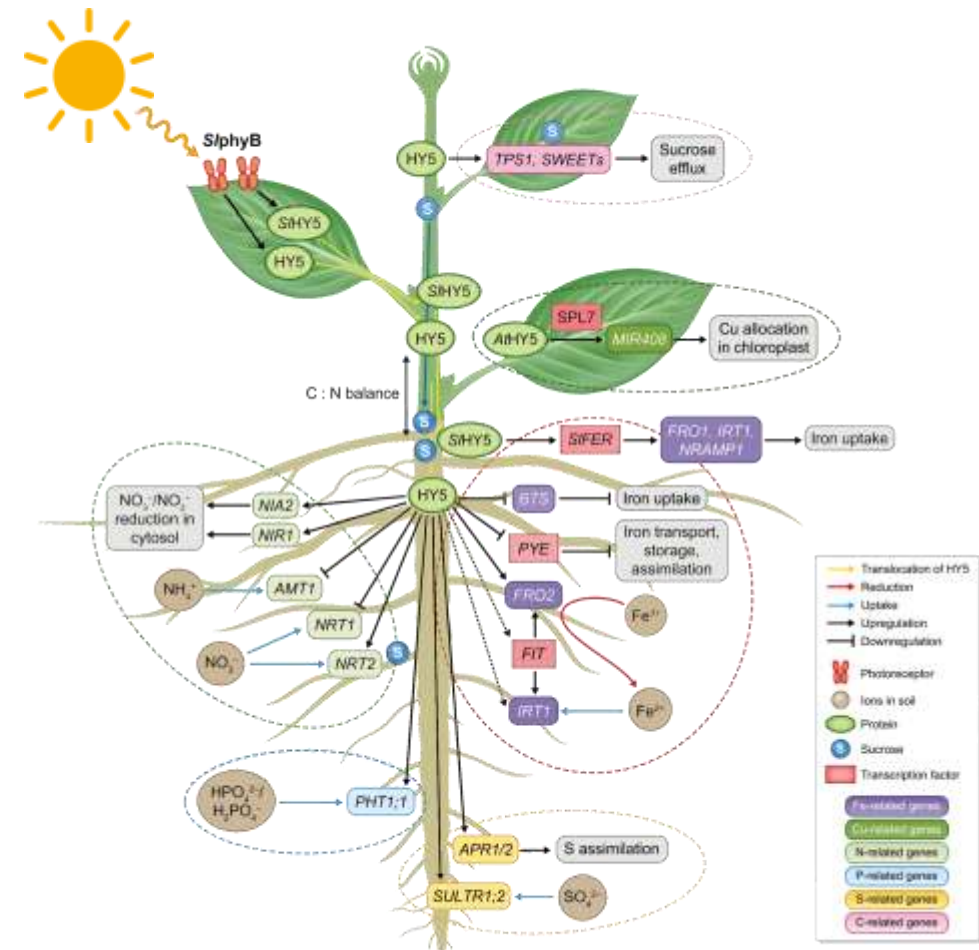


ideagro
an Alltech company

NUTRIGENOMICS

Why HY5?

The gene **ELONGATED HYPOCOTYL 5** regulates growth mechanisms in the plant. **HY5** directly activates the expression of genes involved in both nutrient uptake and utilization in the plant, including nitrogen, phosphorus, iron, sulfur and copper.



NUTRIGENOMICS. Gene selection

Activation of **HY5**



Regulates the assimilation of carbon in the stem.



Is involved in the regulation of the plant's photosynthetic capacity.



Regulates genes involved in chlorophyll synthesis, stomata development, and photosynthesis.

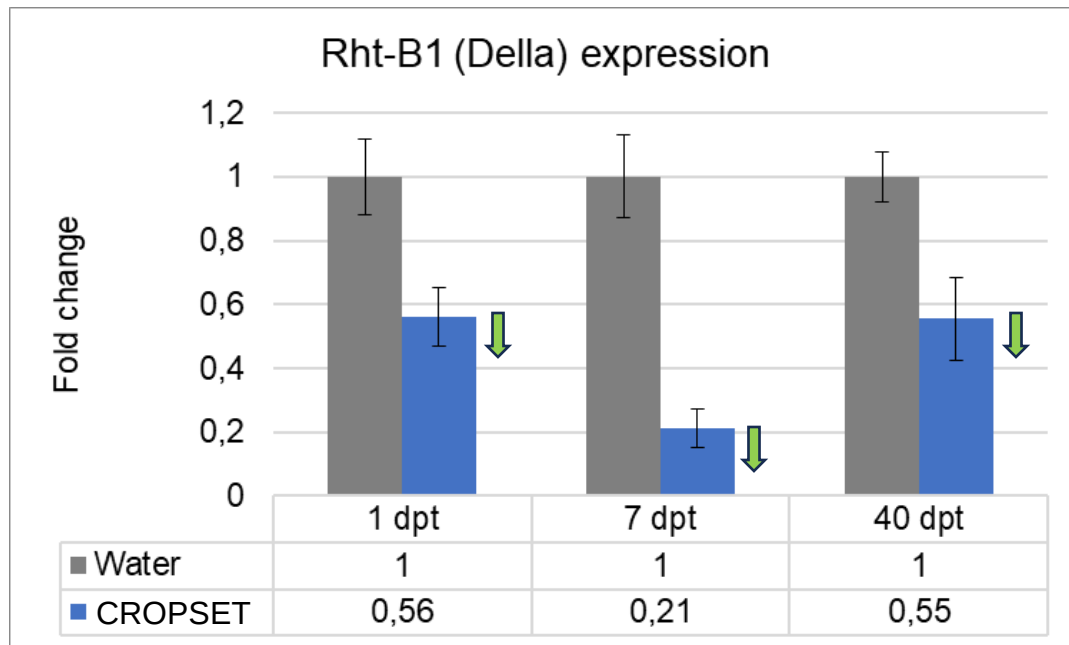


Coordinates stem and root growth in response to light.



Regulates the transport of photo-assimilates from the stem to the sink tissues, activating the expression of different genes.

GENES INVOLVED IN DEVELOPMENT



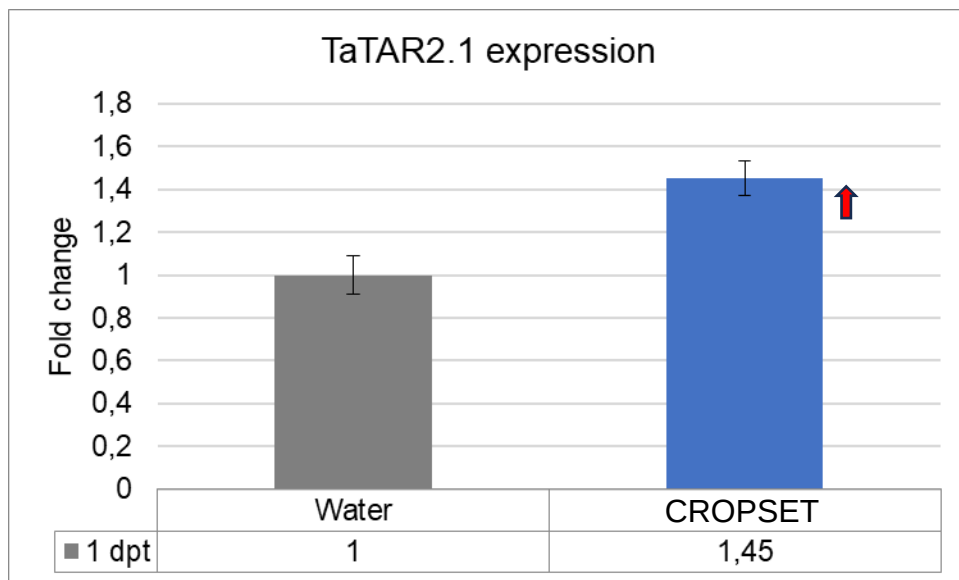
Reduced height-B1b (Rht-B1b) genes encode DELLA proteins, transcriptional regulators that act to **repress** gibberellic signaling.

This class of plant hormones has a well-characterized role in controlling **stem elongation and plant growth**

It has been observed that **a reduction in the expression of the genes that encode DELLA proteins improves the vegetative development of the wheat crop.**



GENES INVOLVED IN AUXIN BIOSYNTHETIC PATHWAY



TRYPTOPHAN AMINOTRANSFERASE RELATED (TaTAR2.1) genes that function in the tryptophan-dependent pathway of auxin biosynthesis.

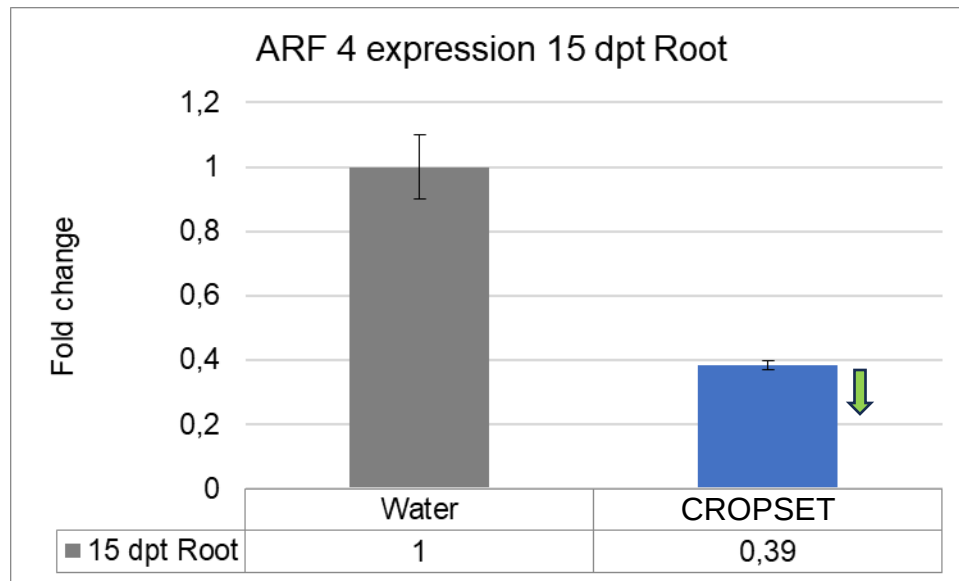
Overexpressing TaTAR2.1-3A in Arabidopsis elevated auxin accumulation in the primary root tip, LR tip, LR primordia, and cotyledon and hypocotyl and increased primary root length, visible LR number, and shoot fresh weight under high- and low-N conditions.

The Auxin Biosynthetic TRYPTOPHAN AMINOTRANSFERASE RELATED TaTAR2.1-3A Increases Grain Yield of Wheat¹

Controlling the major auxin biosynthetic pathway to manipulate auxin content could be a target for genetic engineering of crops with desired traits



GENES INVOLVED IN AUXIN BIOSYNTHETIC PATHWAY



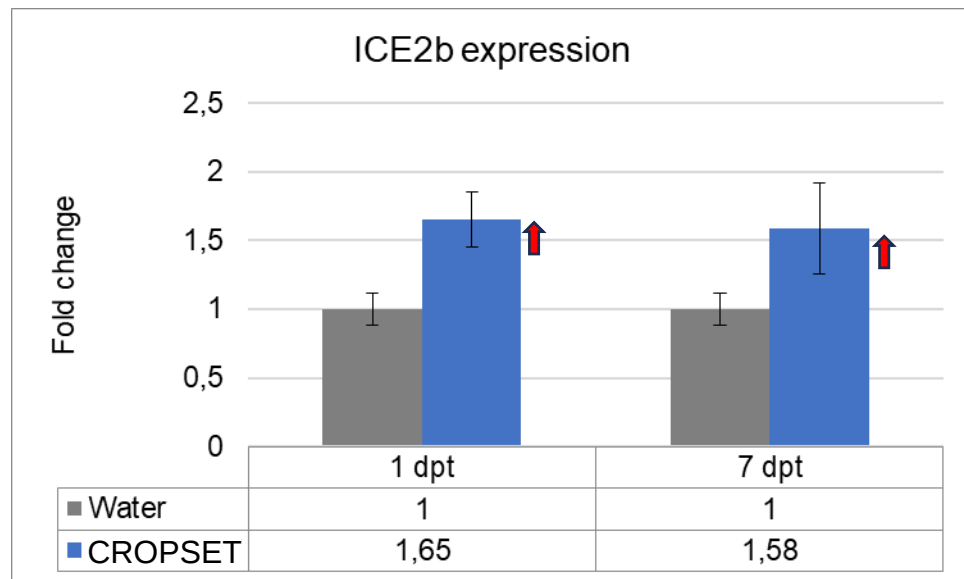
ARF4 (Auxin response factor 4):

Transcription **repressor** factor that participate in the auxin pathway, and affect auxin-responsive gene expression. It has been demonstrated its role in **plant growth and development**.

TaARF4 overexpression led to higher free indole-3-acetic acid (IAA) content. The high free IAA that inhibits apical dominance also reduced primary root length and plant height.



GENES INVOLVED COLD STRESS TOLERANCE



ICE factors are positive regulators of the low-temperature signaling pathway.

ICE factors overexpression can enhance the tolerance of plants to low temperatures.

ICE, CBF and COR are cold tolerance-responding functional and regulatory genes that participate directly or indirectly in defense against low temperature. The ICE-CBF-COR pathway is a universal pathway related to cold stress tolerance in crop species.



Similar results with GRAIN-SET on cereals



The trial was done on wheat, with **GRAIN SET®** being applied at late-tillering stage. 7 different genes known to be involved in key metabolic processes were analysed:

- **HY5**: a **growth promoting gene**, regulating photosynthesis, stem and root growth, carbon absorption and transport.
- **NR2** and **GS2**: involved in **Nitrogen assimilation** (NR2) and **transport** (GS2)
- **DELLA** and **ARF4**: involved in the **regulation of hormones response and balance of the growth**, by repressing responses to gibberelins (for DELLA) and regulation the concentration of auxin (for ARF4)
- **PAL** and **PR2**: **involved in growth and response to stress**, with PAL being key to the salicylic acid pathway and inducing resistance, and PR2 being pathogen-related.



Improves uniformity and precocity of the crop.



Facilitates assimilation of nutrients and soil water.



Increase the quality parameters such as size, density and weight of the grain.



Organic farming according to Regulation (EU) No. 2018/848

Biostimulant Nutrigenomics for your crops

GRAIN SET® is a biostimulant that activates different metabolic processes of the plant, reducing situations of environmental stress.

GRAIN SET® includes micronutrients and fermentation metabolites that allow the plant to concentrate more energy on root growth, allowing better root development and taking advantage of nutrients and soil resources.

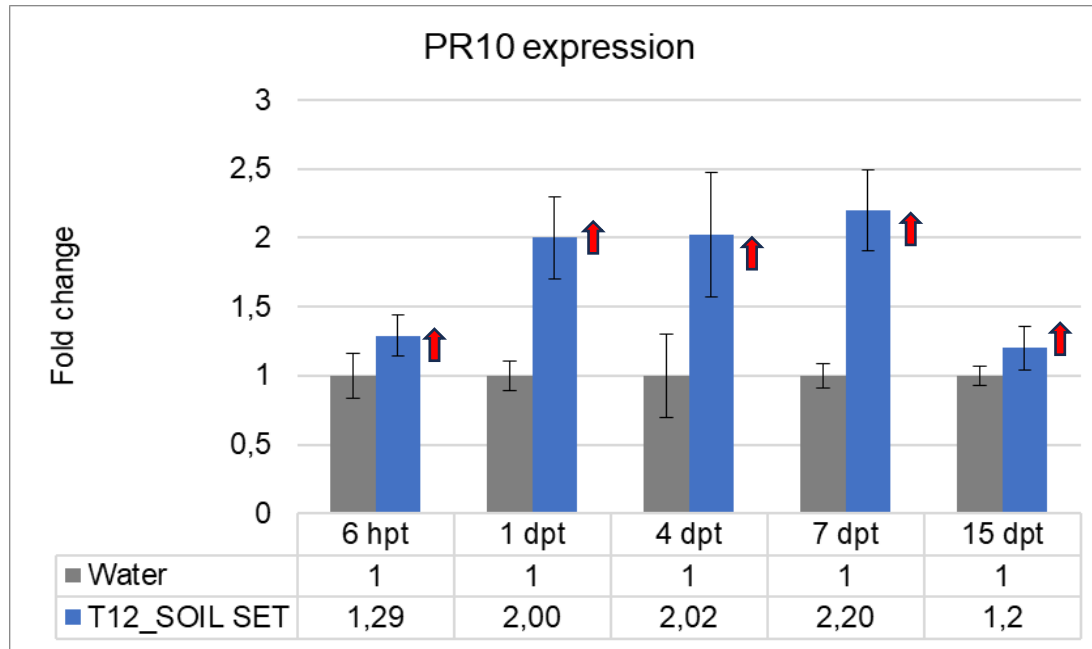
Based on plant
nutrigenomic research



GENES INVOLVED IN STRESS RESPONSES



GENES THAT PARTICIPATE REDUCING VIABILITY AND VIRULENCE OF PATHOGENS



RIBONUCLEASE (PR10) properties and roles in plant defense

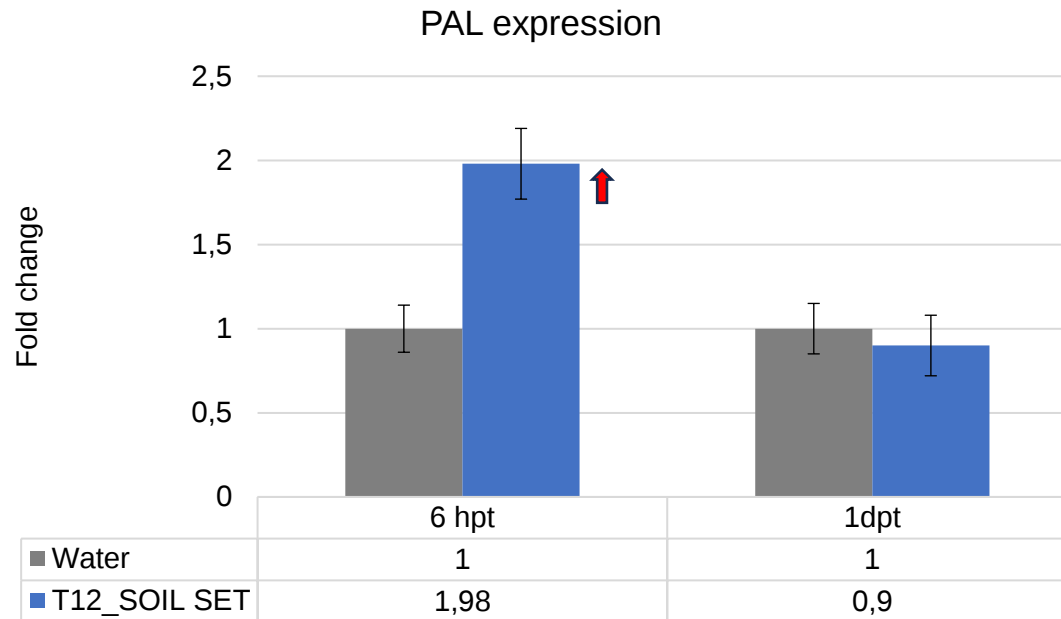
Ribonucleases—degrade RNA

Programmed cell death during hypersensitivity reaction

Antibacterial, antifungal, antinematode and antiviral activity

Salt and cold stress tolerance

GENES INVOLVED IN STRESS AND SECONDARY METABOLITES



Phenylalanine ammonia-lyase
**(PAL) properties and roles in
plant defense**

Plant growth and stress response

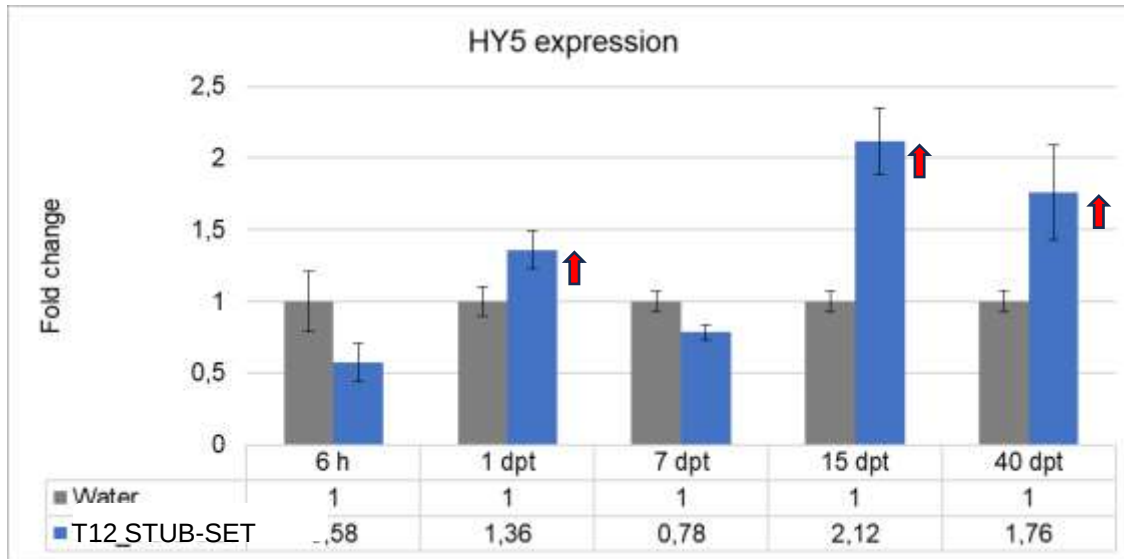
Induces the synthesis of salicylic acid (SA)

Component of many compounds essential for the structure, reproduction, defense and communication of plants.

GENES INVOLVED IN PLANT DEVELOPMENT AND YIELD



GENES INVOLVED DEVELOPMENT AND NUTRIENT UPTAKE

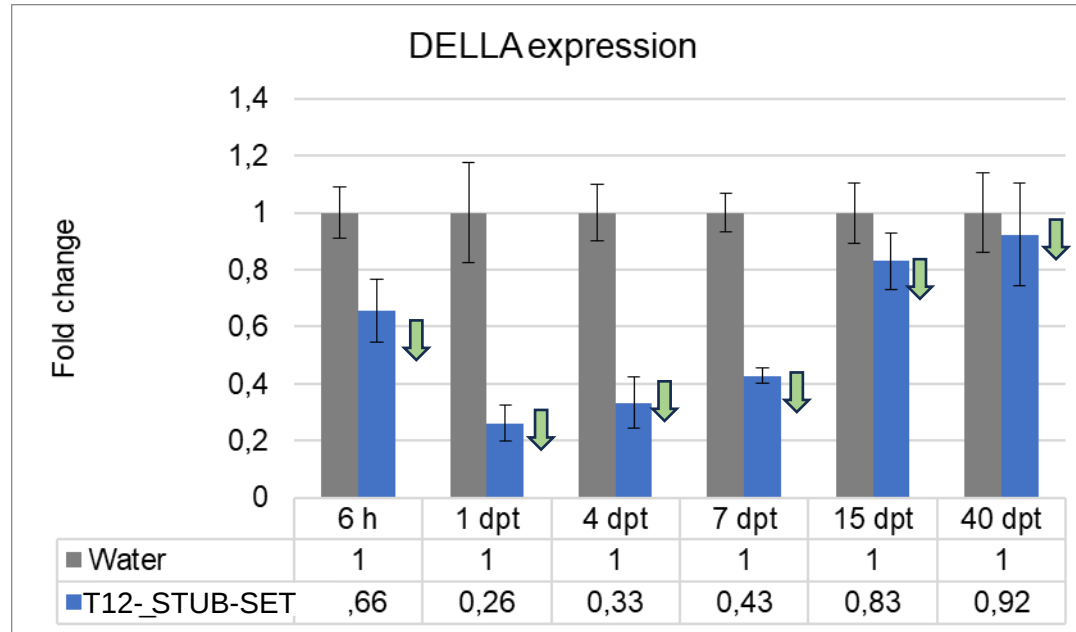


ELONGATED HYPOCOTYL 5 (HY5):

Transcription factor master regulator of light-mediated responses. HY5 binds to the promoter of c. 3000 genes, thereby regulating various physiological and biological processes, including photomorphogenesis, flavonoid biosynthesis, root development, response to abiotic stress and nutrient homeostasis.

HY5 directly activates the expression of genes involved in nutrient uptake and utilization, including several nitrogen, iron, sulphur, phosphorus and copper uptake and assimilation-related genes.

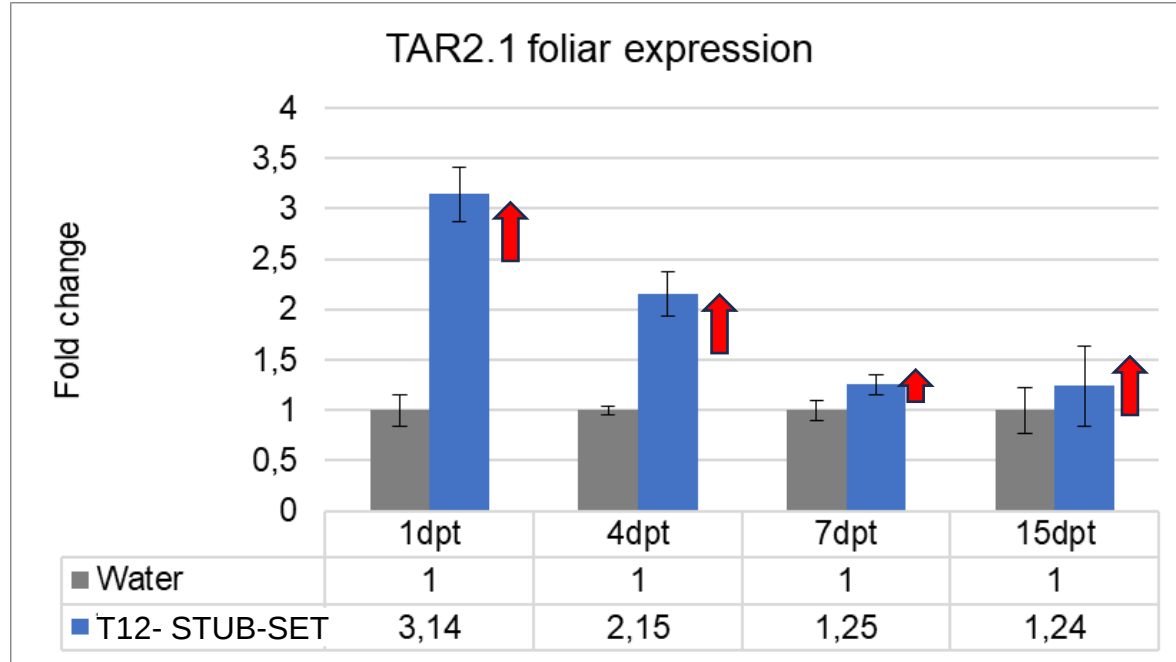
GENES INVOLVED DEVELOPMENT



DELLA proteins (Rht-1B):

Reduced height-B1b (Rht-B1b) genes encode DELLA proteins, transcriptional regulators that act to **repress gibberellic signaling**. This class of plant hormones has a well-characterized role in controlling **stem elongation and plant growth**

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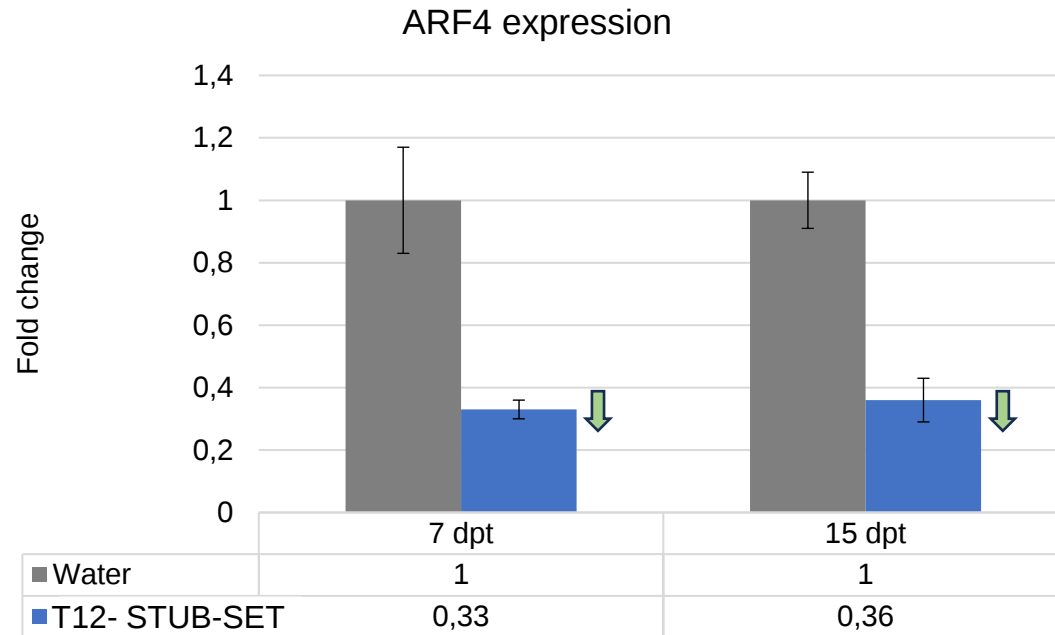
TaTAR2.1 is critical for wheat growth and also shows potential for genetic engineering to reach the aim of improving the grain yield of wheat.

Overexpressing TaTAR2.1-3A in Arabidopsis elevated auxin accumulation in the primary root tip, LR tip, LR primordia, and cotyledon and hypocotyl and increased primary root length, visible LR number, and shoot fresh weight under high- and low-N conditions.

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GENES INVOLVED IN AUXIN BIOSYNTHETIC PATHWAY

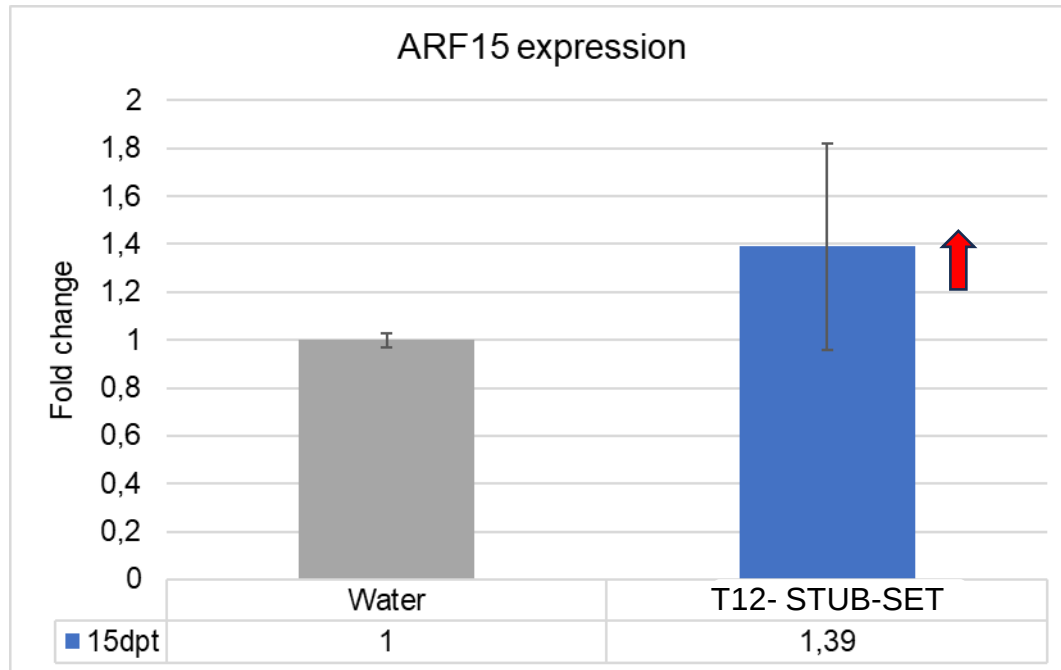


ARF4 (Auxin response factor 4) in ROOTS:

Transcription repressor factor that participate in the auxin pathway, and affect auxin-responsive gene expression. It has been demonstrated its role in plant growth and development.

TaARF4 overexpression in Arabidopsis plants led to low GH3 gene expression and higher free indole-3-acetic acid (IAA) content. The high free IAA that inhibits apical dominance also reduced primary root length and plant height.

GENES INVOLVED IN AUXIN BIOSYNTHETIC PATHWAY



AUXIN REGULATOR FACTOR 15 (TaARF15)_ROOTS

TaARF15 is an ortholog of OsARF5, which regulates the development of rice at different stages (Indoliya et al., 2016).

TaARF15 was expressed in the roots, stems, and leaves of wheat seedling, and its expression levels significantly differed in response to exogenous auxin treatment.

Transgenic *Arabidopsis* containing *TaARF15-A.1* promoted growth of roots and leaves and was overexpressed after auxin treatment



Types of soil microbes/fonction	population growth with STUB-SET 1.2 L/ha
Mobilization of P in the soil	+90%
Filamentous bacteria Degradation of organic residues, forming humus. Also main source of antibiotics.	+81%
micro-fungus (all different kinds)	+70%
Cellulose degrading bacteria	+54%
Pedotrophic micro-flora	+47%
Bacteria fixing mineral nitrogen	+43%
Oligotrophic bacterias various species of bacteria living in low nutrient environment (very efficicent metabolism)	+28%
Ammonifying bacterias decompose N-rich waste into nitrites	+23%
Azotobacter (a free living bacteria fixing N from the air)	+2% -Maximum reached

STUB-SET ON BENEFICIAL MICROBES

National Academy of
Agricultural Science
Ukraine, 2015.

Proven results
for **superior**
harvests.

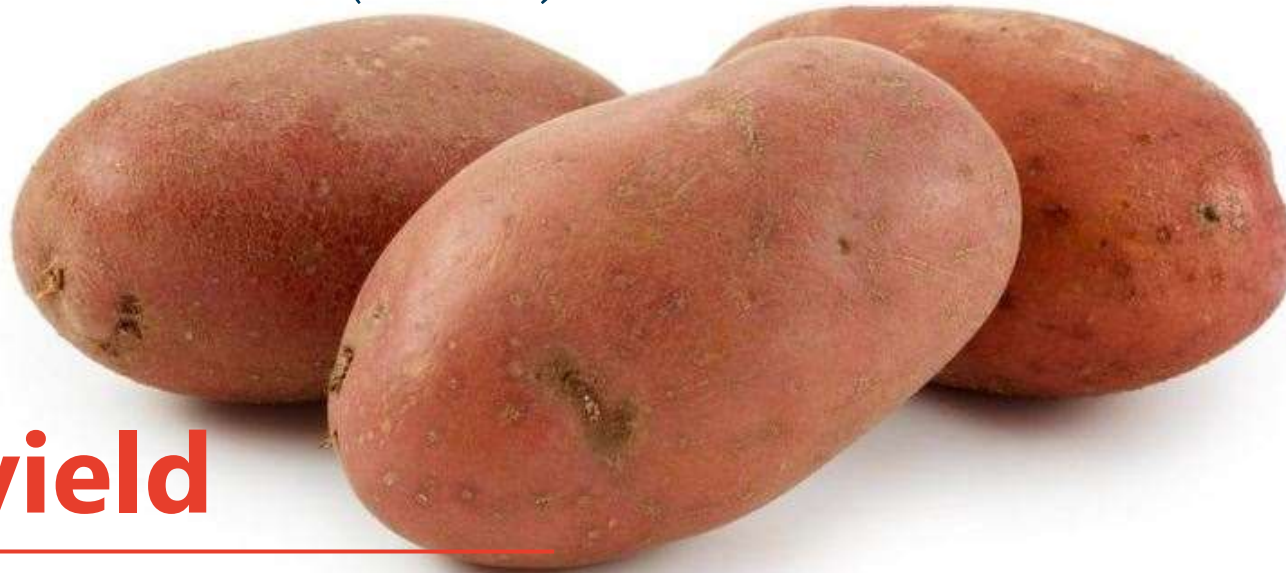
More marketable yield

+8.5 T/ha in 50-75mm (+22%)

Potatoes

Ireland, 2016-2021

Average 13 trials



More yield

+6 T/ha (+12%)

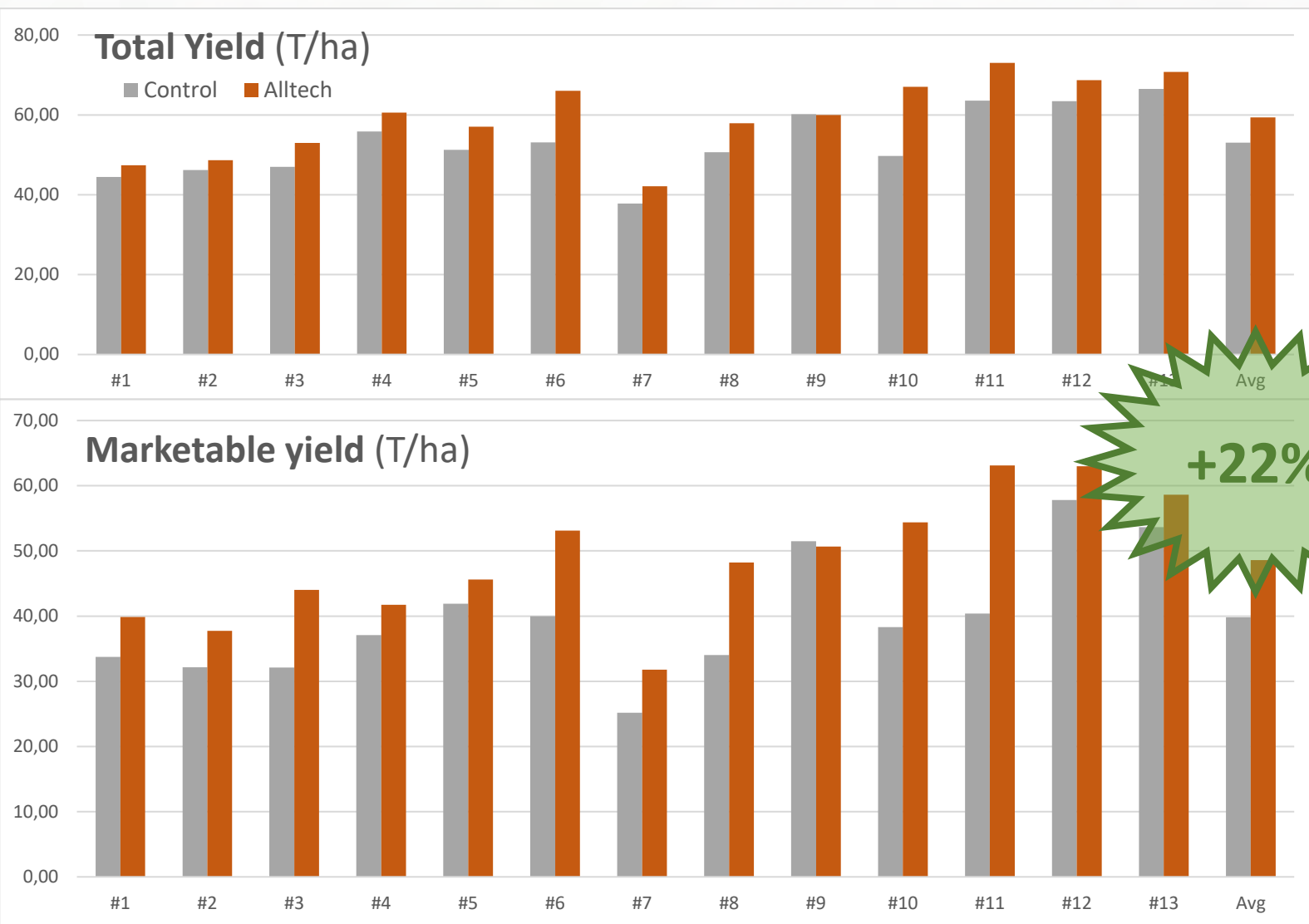
**Increase production
AND quality**

STUB-SET + CROP-SET - IRELAND

- More total yield
- More marketable yield
- More uniformity
- Increase profitability
- Same amount of fertilizer and pesticides
- Reduce waste

List of trial plots, Ireland 2016-2021

#1	2016	Co. Meath	Rooster
#2	2016	Co Meath	M. Piper
#3	2017	Co. Dublin	Rooster
#4	2018	Co. Meath	Rooster
#5	2018	Co. Dublin	Rooster
#6	2018	Co. Londonderry	Rooster
#7	2018	Co. Donegal	Rooster
#8	2018	Co. Meath	Rooster
#9	2018	Co. Wexford	--
#10	2021	Co. Kildare	Rooster
#11	2021	Co. Louth	Rooster
#12	2021	Co. Meath	--
#13	2021	Co. Dublin	Rooster



Onions

Netherlands, 2020

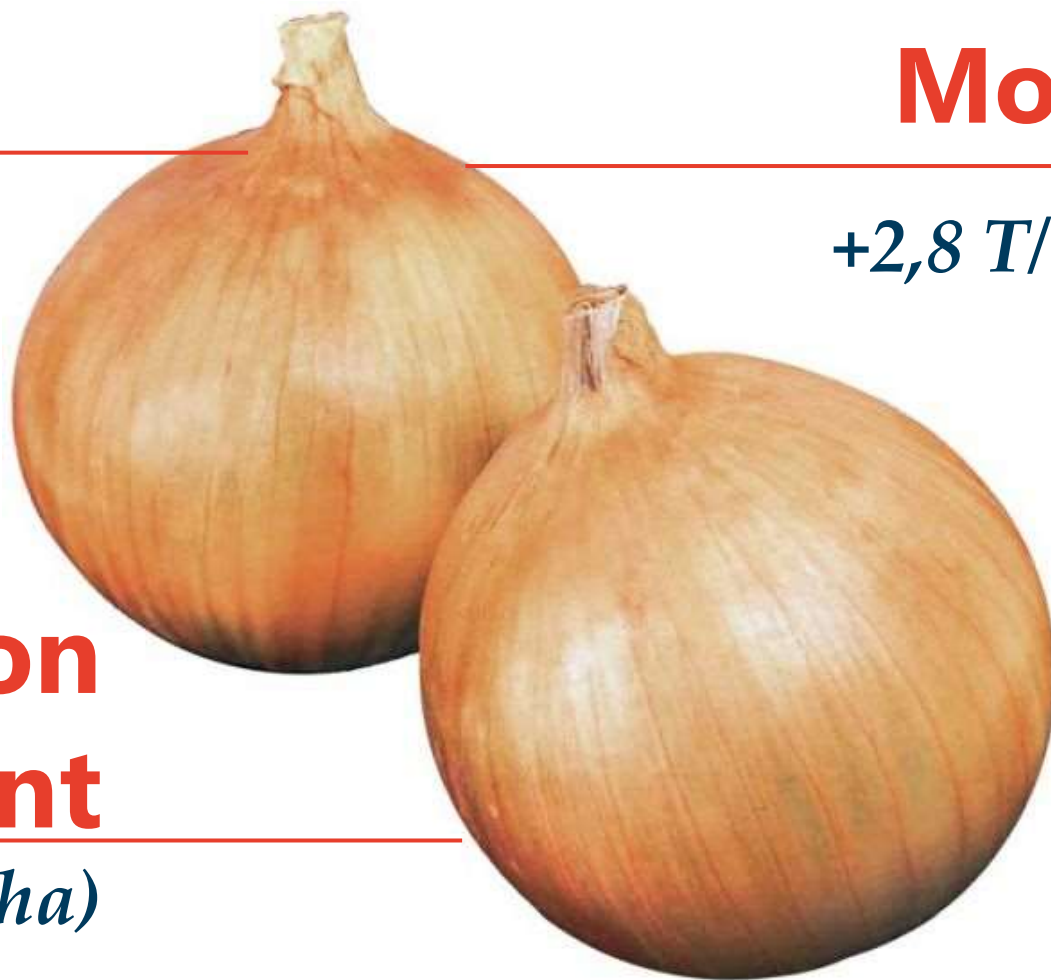
replicated trial

STUB-SET

+CROP-SET

More large onions

+2,8 T/ha in 60-80 mm (+10%)



**Return on
Investment**

5 to 1 (+950 EUR/ha)

**Increase production
AND profitability**

The health of
our soils is the
key to
sustainable
agriculture.



Our objective

SUPPRESSIVE SOILS

- Suppressive soils are characterised by the absence or low level of a disease in a crop susceptible to the pathogen causing the disease, the pathogen being present in the soil and the conditions being favourable for its development.
-Baker y Cook, 1974-
- Ideal environment to optimise the use of our SOIL resources



SOILS SUPPRESSIVE

- Rich in available nutrients
- Biodiversity and a healthy microbiome
- Balanced soil structure

What are the benefits of healthy soil?

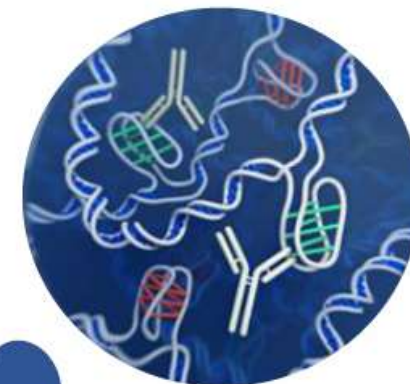
- Reduced impact of stress
- Increased production with fewer inputs.
- Reduced use of chemical fertilisers and synthetic plant protection products.
- Sustainability and profitability

A photograph of a sunset over a dark, flat field. The sky is filled with warm, orange and yellow light from the setting sun, with some clouds visible. The horizon line is low, showing a dark silhouette of trees or a distant shore.

*"A nation that destroys its soil
destroys itself".*

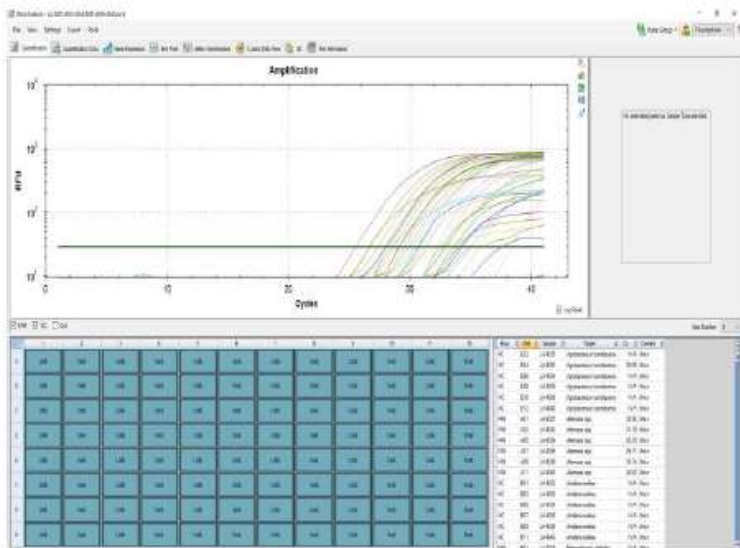
—Franklin Delano Roosevelt

PLANT PATHOGENS MULTIDETECTION



Plant pathogens multidetection

- Molecular analysis by real-time PCR (qPCR)
- FUNGI, BACTERIA AND VIRUSES
- **SIMULTANEOUS DETECTION** of different pathogens (up to 45)
- Samples of soil, plant tissue, water and biostimulants
- Detection kits already available for **290 MICROORGANISMS**
- Kits designed to detect the main pathogens of 17 GROUPS OF CROPS



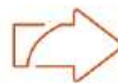
qPCR plate type I:
6 samples * 32 pathogens/sample



Results:
192 pathogens detected/1 hour

New qPCR Real-time system

qPCR plate type II:
24 samples * 32 pathogens/sample



Results:
768 pathogens detected/ 1 hour

 **24h-48h**
Results

Plant pathogens multidetection



Color legend: semi-quantitative quantification



High concentration
Ct < 25,00

Medium concentration
25 < Ct < 30

Low concentration
Ct > 30,00

Fungi

Parámetro	Resultado	Ct	Procedimiento
<i>Alternaria spp.</i>	Presencia	25,26	Sonda específica qPCR
<i>A. radicina</i>	Ausencia	-	Sonda específica qPCR
<i>Botrytis cinerea</i>	Presencia	28,37	Sonda específica qPCR
<i>Cylindrocarpon spp.</i>	Ausencia	-	Sonda específica qPCR
<i>Erysiphe polygoni</i>	Ausencia	-	Sonda específica qPCR
<i>Fusarium spp.</i>	Presencia	21,94	Sonda específica qPCR
<i>Fusarium equiseti</i>	Presencia	25,97	Sonda específica qPCR
<i>Fusarium oxysporum</i>	Presencia	28,83	Sonda específica qPCR
<i>Fusarium solani</i>	Presencia	18,06	Sonda específica qPCR
<i>Geotrichum candidum</i>	Ausencia	-	Sonda específica qPCR
<i>Itersonilia pastinaceae</i>	Presencia	22,03	Sonda específica qPCR
<i>Leveillula spp.</i>	Ausencia	-	Sonda específica qPCR
<i>Macrophomina phaseolina</i>	Ausencia	-	Sonda específica qPCR
<i>Phytophthora spp.</i>	Ausencia	-	Sonda específica qPCR
<i>Pythium spp. (I)</i>	Ausencia	-	Sonda específica qPCR
<i>Pythium spp. (II)</i>	Ausencia	-	Sonda específica qPCR
<i>Rhizoctonia solani</i>	Presencia	24,13	Sonda específica qPCR
<i>Rhizopus stolonifer</i>	Ausencia	-	Sonda específica qPCR
<i>Sclerotinia sclerotiorum</i>	Ausencia	-	Sonda específica qPCR
<i>Sclerotium rolfsii</i>	Ausencia	-	Sonda específica qPCR
<i>Verticillium spp.</i>	Ausencia	-	Sonda específica qPCR

Bacteria

Parámetro	Resultado	Ct	Procedimiento
<i>Candidatus liberibacter subsp. solanacearum</i>	Presencia	24,48	Sonda específica qPCR
<i>Erwinia carotovora subsp. atroseptica</i>	Ausencia	-	Sonda específica qPCR
<i>Erwinia carotovora subsp. carotovora</i>	Ausencia	-	Sonda específica qPCR



Fungi and bacteria multidetection

Solanaceae



Microorganism	
1 <i>Alternaria</i> spp.	21 <i>Phytophthora cryptogea</i>
2 <i>Botrytis cinerea</i>	22 <i>Phytophthora infestans</i>
3 <i>Candidatus liberibacter</i> subsp. <i>solanacearum</i>	23 <i>Phytophthora parasitica</i>
4 <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i>	24 <i>Phytophthora</i> spp.
5 <i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	25 <i>Pseudomonas corrugata</i>
6 <i>Colletotrichum coccodes</i>	26 <i>Pseudomonas syringae</i> pv. <i>tomato</i>
7 <i>Colletotrichum gloeosporioides</i>	27 <i>Pyrenochaeta lycopersici</i> (Raza 1)
8 <i>Colletotrichum</i> spp II	28 <i>Pyrenochaeta lycopersici</i> (Raza 2)
9 <i>Corynespora cassicola</i>	29 <i>Pythium</i> spp. (I)
10 <i>Didymella lycopersici</i>	30 <i>Pythium</i> spp. (II)
11 <i>Erwinia carotovora</i> subsp. <i>atroseptica</i>	31 <i>Ralstonia solanacearum</i>
12 <i>Erwinia carotovora</i> subsp. <i>carotovora</i>	32 <i>Rhizoctonia solani</i>
13 <i>Fusarium oxysporum</i>	33 <i>Sclerotinia minor</i>
14 <i>Fusarium oxysporum</i> f. sp. <i>lycopersici</i>	34 <i>Sclerotinia sclerotiorum</i>
15 <i>Fusarium oxysporum</i> f. sp. <i>radicis-lycopersici</i>	35 <i>Sclerotium rolfsii</i>
16 <i>Fusarium solani</i>	36 <i>Stemphylium</i> spp.
17 <i>Fusarium</i> spp.	37 <i>Streptomyces scabies</i>
18 <i>Helminthosporium solani</i>	38 <i>Thielaviopsis basicola</i>
19 <i>Olpidium brassicae</i>	39 <i>Verticillium albo-atrum</i>
20 <i>Phytophthora capsici</i>	40 <i>Verticillium dahliae</i>

sos

Safeguard Our Soils

POWERED BY

Alltech[®]
CROP SCIENCE

ideagro

#SoilHealthExperts



#SOS—Safeguard Our Soils: An Initiative for Soil Health and Sustainability

Soil health is key to sustainable agriculture, supporting food production, environmental preservation, and biodiversity.

However, around the globe soils face increasing challenges such as erosion, compaction, and nutrient loss, threatening agricultural productivity and the ecosystems that sustain life on Earth. Protecting and regenerating soil is critical to maintaining fertility and ensuring the production of healthy and nutritious food for current and future generations.





WORKING TOGETHER FOR A
Planet of Plenty