19th World Congress of Soil Science
Soil solutions for a changing world
BRISBANE AUSTRALIA 1 – 6 August 2010

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International Union of Soil Sciences

An Invitation to the 19th World Congress of Soil Science

On behalf of the Officers of the *International Union of Soil Science*, we are delighted to extend our personal invitation to you to join us in Brisbane, Queensland Australia for the *19th World Congress of Soil Science* to be held 1-6 August 2010 at the Brisbane Convention and Exhibition Centre.

The conference theme *Soil Solutions for a Changing World* provides a tremendous opportunity for a broad range of presentations – we urge you to share your research, experiences and knowledge with members in Brisbane.

We are very proud to be associated with an outstanding group of professionals who have gathered to form the steering committee for the *19th World Congress of Soil Science*, led jointly by Professor Steve Raine and Mr Mike Grundy.

Please join us and colleagues from throughout the world in what promises to be an outstanding gathering of the Soil Science community.

Roger Swift
President International
Union of Soil Sciences

Neal Menzies
Vice-President
International Union of Soil Sciences

It is our privilege and pleasure, on behalf of the Australian Society of Soil Science Inc., to introduce the *19th World Congress of Soil Science* to be held at the Brisbane Convention and Exhibition Centre, 1 to 6 August 2010.

The Congress, held every four years, presents a global forum at which all those involved in Soil Science can meet with scientists, researchers, academics and professionals to discuss and find *Soil Solutions for a Changing World*.

While you are here we would encourage you and your family to take the time to experience the best of what Queensland has to offer. Brisbane, the capital of Queensland, is a modern, sophisticated city of more than 1.6 million people. Queenslanders enjoy a safe and friendly lifestyle and you will appreciate the reasons why our state is a great place to live, a great place to do business and a great place to visit.

Details of the *19th World Congress of Soil Science* will be regularly updated on this website; please check back often or register your interest to participate and we will keep you informed.

Our Congress Committee is a totally committed group of professionals who are hard at work to present an outstanding conference.

We look forward to welcoming you in 2010 to what we are confident will be the best ever World Congress of Soil Science.

Steve Raine
Co-Chair
19th World Congress of
Soil Science

Patron

Australian Government
Department of Agriculture, Fisheries and Forestry
Department of the Environment, Water, Heritage and the Arts
Grains Research and Development Corporation
Sugar Research and Development Corporation

Mike Grundy
Co-Chair
19th World Congress of
Soil Science

Patron

Queensland Government

Soil-borne phytopathogen and bacterial biocontrol agents using mining tools. The pathosystem *Phytophthora sp-Olea europaea-Bacillus sp.*

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Abstract

Beneficial (e.g. biocontrol, mycorrhizal and rhizobial symbioses, nutrient transformation and uptake) and harmful (e.g. phytopathogens, inorganic and organic phytoxicity, nutrient immobilization, climate change induced stress) interactions and their manipulation are of great topical interest. *Phytophthora* is a soil-borne pathogen against a great plant host number. We aimed *Phytophthora* pathogen of *Olea europaea.* Using data mining tools we obtained information from large databases as EML (Europe), DJJB (Japan) and GenBank (USA). Internal transcribed spacer (ITS) and Internal non-transcribed spacer (IGS) are regions of the DNA used to study taxonomic information in eucariota organisms because of this they are highly conserved in the evolution. Ribosomal 16S DNA was used to obtain taxonomic information about biocontrol bacteria. In our study we looking for the relationship between a large number of *Phytophthora* IGS and ITS sequences deposited into larges databases and the type and place of plant infected. We used a computational platform under GNU/Debian. R and WEKA programs were used for data mining. We obtained information about the relationship that exist between pathogenicity related to geographical point respect to pathosystem *Phythopthora sp* against *Olea europaea L.* Among unsupervised learning hierarchical clustering we obtained a classification from ITS and IGS sequences.

Key Words

data mining, *Phytophthora sp., Olea europaea sp.,* clustering, ITS, IGS

Introduction

The world's population is continuously growing and agricultural production must increase to ensure global access to safe food in sufficient amounts. At the same time, the use of fertilizers and chemical pesticides must be reduced to minimize the deleterious environmental impact of agriculture. In this context, there is a renewer interest in alternative approaches to pest, disease and weed control. The expression 'alternative control methods', meaning alternative to synthetic chemical pesticides, covers a broad array of different approaches based on agricultural practices and the application of 'natural products' and beneficial microorganisms known as biological control agents (BCAs).

Plant-associated microorganisms fulfill important functions for plant growth and health. Direct plant growth promotion by microbes is based on improved nutrient acquisition and hormonal stimulation. Diverse mechanisms are involved in the suppression of plant pathogens, which is often indirectly connected with plant growth. Whereas members of the bacterial genera *Azospirillum* and *Rhizobium* are well-studied examples for plant growth promotion, *Bacillus, Pseudomonas, Serratia, Stenotrophomonas,* and *Streptomyces* and the fungal genera *Ampelomyces, Coniothyrium,* and *Trichoderma* are model organisms to demonstrate influence on plant health. Based on these beneficial plant-microbe interactions, it is possible to develop microbial inoculants for use in agricultural biotechnology. Dependent on their mode of action and effects, these products can be used as biofertilizers, plant strengtheners, phytostimulators, and biopesticides. The use of genomic technologies leads to products with more predictable and consistent effects. The future success of the biological control industry will benefit from interdisciplinary research, e.g., on mass production, formulation, interactions, and signaling with the environment, as well as on innovative business management, product marketing, and education. Altogether, the use of microorganisms and the exploitation of beneficial plant-microbe interactions offer promising and environmentally friendly strategies for conventional and organic agriculture worldwide.

On the other hand, plant diseases induced by soil-borne plant pathogens are among the most difficult to control. In the absence of effective chemical control methods, there is renewed interest in biological control based on application of populations of antagonistic microorganisms. Exploring the mechanisms involved in

the protective capability of the bacterial strains is not only necessary for their development as commercial biocontrol agents but raises many basic questions related to the determinism of pathogenicity versus biocontrol capacity in the fungi and protists species complex. The success of biological control depends not only on plant-microbial interactions but also on the ecological fitness of the biological control agents. About informatic methodology using in this paper we know that data mining is a fashionable type of study of data useful to obtain information from large data bases and when traditional statistical methodologies alone can not solve the problem. It use a mixture of traditional statistical and artificial intelligence methodologies.

Methods

Traditional and molecular technologies of microbiology were used in this study to isolate and to identify *Bacillus sp.* strains and *Phytophthora sp.* strains. Bioinformatic tools were used to analyze the results. Our local datasets were composed by sequences obtained from GenBank (USA), EMBL (Europe) and DDBJ (Japan) and information about the origin of the study.

We used a computational platform under GNU/Debian and a processor AMD Turion 64 x 2, with memory 2 Gb and hard disk of 120 Gb. R and WEKA programs were used for data mining analyses. Clustal W, TNT and PAUP were used for data taxonomic classification.

Results

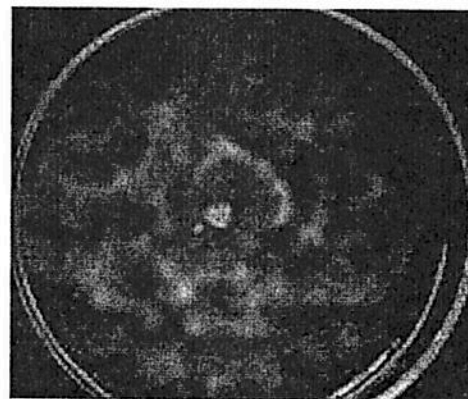Figure 1. *Bacillus sp.* isolated from *Olea europaea* rhizosphere.

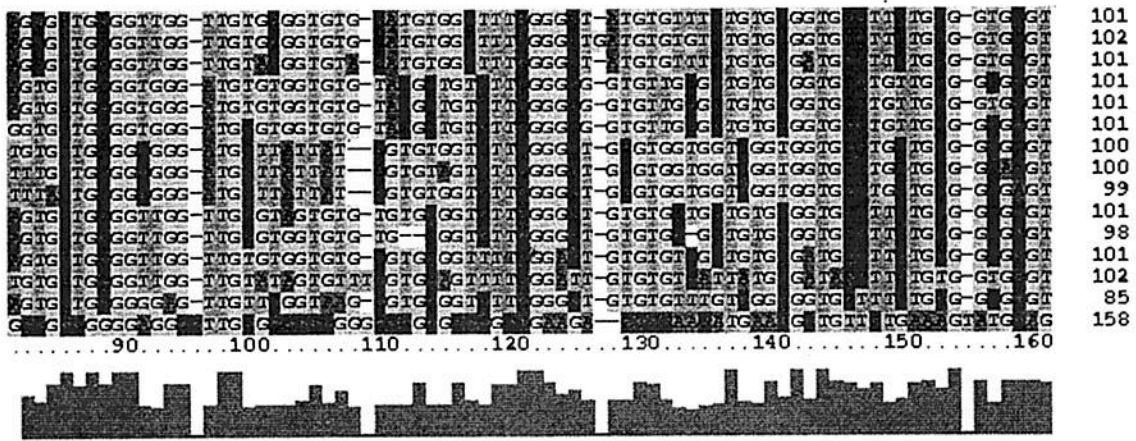Figure 2. *Phytophthora sp.* isolated from *Olea europaea* rhizosphere.

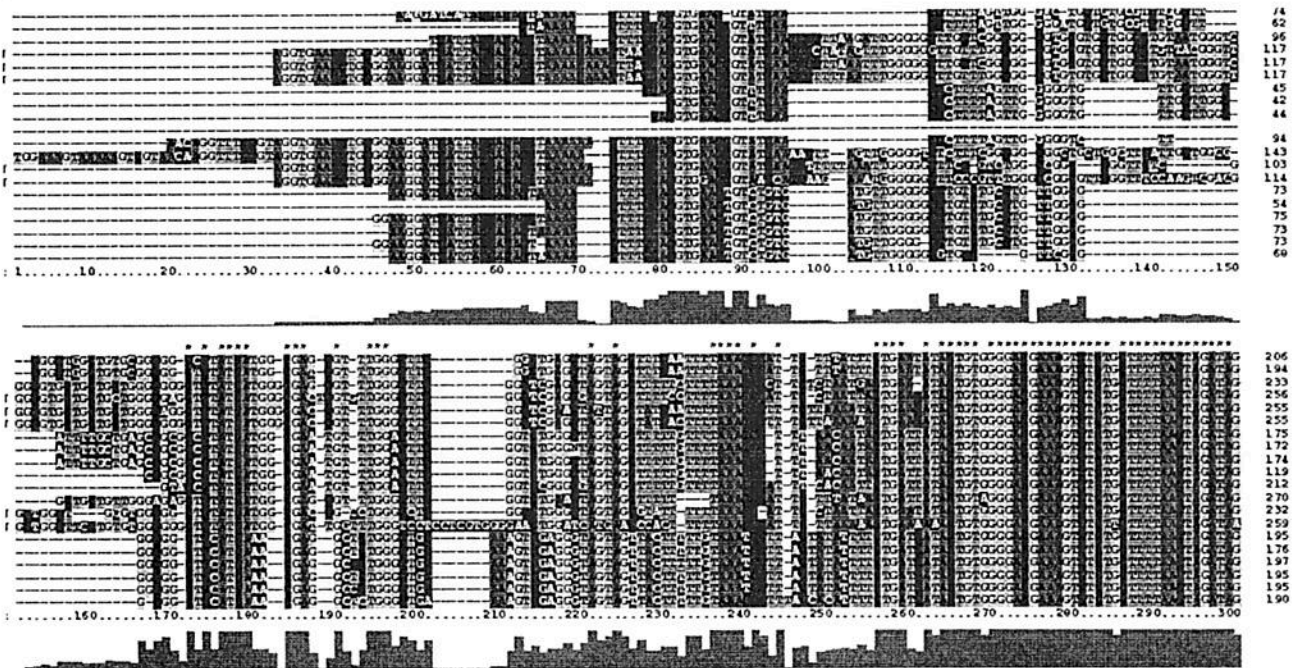Figure 3. Multiple alignment of soil-borne *Bacillus sp.* (rDNA 16S).

Figure 4. Multiple alignment of soil-borne pathogen *Phytophthora sp* internal no transcribed region (IGS).

Conclusion

We obtained information about the relationship that exist between pathogenicity links to geographical point respect to the pathosystem *Phythopthora sp* against *Olea europaea L.*

Actually we are following on the interaction in the pathosystem *Olea europaea-Phytophthora sp-Bacillus sp.* using mining tools.

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