

PHYTOPLASMA DISEASES AND CLIMATE CHANGE

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Phytoplasma associated diseases are long time known world wide as inducing severely economic damages on a variety of cultivated and wild plants. These uncultured parasites are bacteria lacking the cell wall and with transkingdom habitats such as phloem of infected plants and hemolymph of insect vectors. Their genomes are among the smallest of self replicating living organisms due to the drastic genome reduction achieved through a degenerative evolution. The increasing threat of phytoplasma diseases worldwide comes both from emerging diseases in Africa, Latin America and the Caribbean mainly in sugarcane, corn, coconuts, papaya, and vegetables and from devastating epidemics in the rest of the world in grapevines, citrus, forest trees, oil-seed crops, alfalfa, stone and pome fruits. In both cases diseases have the potential to spread to other crop species throughout the world and/or impact of global trade. There are concerns that climate changes resulting from global warming may facilitate the spread of these phytoplasma diseases to new areas and to additional crops, particularly if the vectors become more widespread and able to survive during warmer winters. Phytoplasmas usually do not kill in short time the host plant from which they are strongly metabolically dependent, however unusually cold conditions kill infected plants, while under tropical conditions asymptomatic plant presence is frequent with severe epidemiological consequences. Moreover phytoplasma-infected plants result more susceptible or to infection by other pathogens such as *Venturia inaequalis*, *Spiroplasma kunkelii*, *Acholeplasma palmae*, and very often diverse viruses. Considering the high phytoplasma ability to adapt and colonize new ecological niches, financial losses for world economies can be foreseen if measures are not taken towards an efficient management of these diseases.

Molecular biological studies of phytoplasma-plant-vector interactions (Estudios moleculares de las interacciones fitoplasma-planta-vector)

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Phytoplasmas are bacterial plant pathogens that cause devastating yield losses in diverse low- and high-value crops worldwide (Hogenhout *et al.*, *Mol. Plant Pathol.*, 2008). They are obligate symbionts of plants and insect vectors (leafhoppers) and, in most cases, need both hosts for dispersal in nature. We have examined several molecular biological findings involved in both the plant-phytoplasma and insect-phytoplasma interactions. (i) The complete genomic sequence of a phytoplasma suggested that the genome encodes very few metabolic functions, implying that phytoplasmas are highly dependent on metabolic compounds from their host cells (Oshima *et al.*, *Nature Genet.*, 2004). (ii) An approximately 30-kb region, including glycolytic genes, was tandemly duplicated in the genome of a severely pathogenic phytoplasma (Oshima *et al.*, *Mol. Plant Pathol.*, 2007). The presence of the two glycolytic gene clusters suggested that a higher consumption of the carbon source affects the growth rate of the phytoplasma and causes more severe symptoms directly or indirectly. (iii) Positive selection of Amp, a phytoplasma surface membrane

protein, was recognized (Kakizawa *et al.*, J. Bacteriol., 2006). This positive selection may reflect an interaction between the phytoplasma and the host cytoplasm. (iv) An affinity column assay showed that Amp formed a complex with insect microfilament proteins, which was correlated with the phytoplasma-transmitting capability of leafhoppers, suggesting that the interaction between Amp and insect microfilament complexes plays a major role in determining the transmissibility of phytoplasmas (Suzuki *et al.*, PNAS, 2006). The phytoplasma genome encodes many membrane proteins whose functions are unknown; further analysis of these will provide valuable insights into phytoplasma-plant-vector interactions.

The development of new methods for phytoplasma diagnostics

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Phytoplasmas cause significant diseases in many plant species worldwide and new disease reports are being reported regularly. However, because these wall-less bacteria can not be cultured *in vitro*, molecular methods, and in particular PCR, have become the methods of choice for detection and diagnosis in plants and insect vectors. Most phytoplasma diagnostics and taxonomy has been based upon the 16S rRNA gene which is highly conserved throughout phytoplasma groups, is present in two copies and is easy to amplify using universal primers. Because the titres of phytoplasmas are often low in infected plants, a nested PCR approach is frequently required, which may involve generic primers or group specific primers for the second round of amplification. However, such an approach requires more than one PCR step, increasing the chances of contamination between samples. An alternative to the use of group specific primers is to digest the 16S PCR products with specific restriction endonucleases. The pattern of cut DNA is viewed using agarose or acrylamide gel electrophoresis and can provide a more informative analysis of the phytoplasma present, although it can prove difficult to distinguish between some of the taxonomic groups using this approach. More recently, universal primers for genes other than the 16S rRNA gene have been developed, such as the 23S rRNA gene, the *rp* (ribosomal protein) operon and the *secA* gene. These methods have provided better resolution between the taxonomic groups, and from the additional sequence information, primers and probes have been developed for more sensitive and quantitative detection methods, such as real-time PCR assays and also the terminal restriction fragment length polymorphism (T-RFLP) technique. The development of these methods along with the advantages and disadvantages of using these different approaches will be discussed.

Are phytoplasmas transmitted through seed?

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The principal means of transmission of phytoplasmas between plants is by phloem-feeding insects, although there are many phytoplasmas for which the vectors have yet to be identified. In addition, they can be transmitted experimentally by plant parasitic dodder plants and by grafting infected plant material onto healthy plants. Recently there have been reports in which phytoplasma DNA has been detected in the seed and embryos of plants such as coconuts, alfalfa, tomato, oilseed rape and lime, along with unconfirmed reports of phytoplasmas in progeny plants from this seed. Such a mode of transmission had previously been regarded as unlikely because there is no direct connection between the phloem sieve elements of plants and the developing embryo or seed, but there have been reports of phytoplasmas in companion cells and parenchyma cells. The possibility of seed transmission has wide ranging implications for quarantine services worldwide, since seed is not routinely tested for the presence of phytoplasmas. In this study, we have used nested PCR to detect phytoplasma DNA in peduncles, spikelets, male and female flowers, and 9 out of 52 embryos of West African Tall coconut palms infected with Cape St Paul Wilt Disease in Ghana and also to detect *Candidatus* Phytoplasma asteris DNA in kernels from infected maize plants in Peru. In germination studies, fruits from infected coconut palms had higher germination rates than those from healthy palms indicating that infected fruits retain the ability to germinate. However, no phytoplasmas were detected in seedlings derived through embryo *in-vitro* culture and we have as yet been unable to find any conclusive evidence that these pathogens are transmitted to cause disease in progeny palms.

STATUS OF DISEASES ASSOCIATED WITH PHYTOPLASMAS IN COLOMBIA AND OTHER LATIN AMERICA AND CARIBBEAN COUNTRIES

(Situación de las enfermedades fitoplásmicas en Colombia y América Latina y el Caribe)

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In the area from Mexico to Argentina including the Caribbean, knowledge of plant diseases caused by phytoplasmas is weak. The area is rich in biodiversity and ecosystems and is the origin of potato, tomato, cocoa and cassava. Diseases associated with phytoplasmas have been reported for important crops such as maize, potato, sugar cane, tomato, coffee, pepper, beans, alfalfa, coconut palms and *Solanum quitoense* (lulo); on trees such as *Gliricida sepium*, *Fraxinus* sp., *Melia azedarach* and *Cordia alliodora* and ornamental plants. Insect vectors have not been identified in the majority of cases. Phytoplasmas are suspected to be the cause of diseases on oil palms, cassava and lupin. Despite an increase in published reports and evidence of losses, most scientists, extension workers and farmers remain unfamiliar with phytoplasma diseases. Common symptoms such as brooming and yellows are often attributed to physiological or nutritional problems or ignored. A low familiarity with symptoms and weak diagnostic capacity (or access to it) in many countries hampers detection and effective control. Molecular techniques are expensive and materials difficult to obtain, though free diagnoses may be available from outside the region (e.g. Global Plant Clinic!). Effective treatment depends on cultural management and use of clean planting material and coordinating responses at a regional or national scale is difficult in countries where farmers are weakly connected to national plant protection organisations. Greater awareness of phytoplasma diseases is needed, beginning with wider knowledge of symptoms and backed up by better access to

diagnostic support. The losses demand better coordinated responses to safeguard food production within countries and guarantee export of quality produce to demanding and competitive international markets.

Comparative analysis of phytoplasma genomes

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Phytoplasmas are insect-transmitted, uncultivable bacterial plant pathogens that cause diseases in several hundreds of economically important plants. They represent a monophyletic group within the class Mollicutes and typically show a small genome with a low GC content and the lack of a firm cell wall. The small genome sizes of the phytoplasmas reflect their highly reduced genomes. Over 500 strains were described, but only four complete genome sequences were published so far.

The analysis of these genomes can just provide a first impression of the functional capacity of these phytopathogenic bacteria.

Three general topics were pointed out for phytoplasma genomics.

(I) Most Mollicutes, including strains of *Candidatus Phytoplasma asteris* and *Ca. P. australiense*, examined so far have circular chromosomes, as it is the case for almost all walled bacteria. However, this general rule is not common for all phytoplasmas as it was shown for *Ca. P. mali*. First hints for the origin and mode of replication of these linear chromosomes will be provided.

(II) Group specific potential mobile units (PMUs) act in the opposite direction responsible for enlarging these reduced genomes in the past at least and influenced the occurrence of genomic re-arrangements. The determination of these PMUs, which are still present in several fragments, appears to be difficult, because reduction also takes part here. Despite these problems, amount and content of these PMUs per genome can be estimated by analysing the paralog groups.

(III) Genome reduction also heavily influences the metabolic capabilities of the organisms, specially the generation of ATP. Glycolysis is the supposed pathway for energy generation in phytoplasmas. The analysis of the *Ca. P. mali* strain highlights again the problem of lacking genes from the central part of the glycolysis. Comparative analysis of phytoplasma genomes and the genome of *Acholeplasma laidlawii* genomes strikes out the influence of genome reduction to this central pathway.

Detection and Differentiation of Phytoplasma in Oman

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In last five years, extensive survey in Oman have yielded more than 25 host plants infected with phytoplasma. These hosts include wild and economically important

species. observed disease symptoms included witches'-broom, stunting, phyllody and virescence. Molecular techniques were adopted for identifying the phytoplasma diseases. Symptoms typical to phytoplasma in lime (*Citrus aurantifolia*) showing witches' broom (LWB) were first reported in Oman during the 1970's. The LWB phytoplasma was classified as belonging to sunhemp phyllody phytoplasma and have been named "*Candidatus* Phytoplasma aurantifolia" according to the sequences of the 16S rRNA gene and 16S-23S intergenic spacer region. Based on RFLP and sequences analyses of 16S rDNA, Phytoplasmas in Oman grouped in Faba Bean Phyllody ribosomal group (16SrII), designated subgroup II-D, Clover proliferation ribosomal group (16SrVI), pigeon pea witches'-broom ribosomal group (16SrIX), '*Candidatus* Phytoplasma aurantifolia' and '*Candidatus* Phytoplasma omanense'. Occurrence of all these groups have been reported from several host plants. The inclusion of non-crop plants, as well as native species with cultivated crop as a result of changes in the sampling the strategy have increase the genetic diversity of phytoplasma types in Oman during the last fives years. Unfortunately control and management strategies of phytoplasma diseases in Oman hamper due to the shortage and lack of information about vectors.

First Report of Group 16SrVI Phytoplasma in Radish from Oman

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Radish (*Raphanus sativus*) which belongs to the family Brassicaceae is important vegetable crops grown in the northern parts of Oman. Traditionally, the Radish leaves are an important part of the daily diet of Omani people and others in the Arabian Peninsula. In December 2007, radish plants were found having phyllody and virescence reminiscent of phytoplasma symptoms. Samples of radish plants were collected from Nizwa and Manah in the interior region located 175 km and 140 km south of the capital Muscat respectively. Total nucleic acid extracted from three symptomatic radish plants were used as template to amplify 16S ribosomal gene of phytoplasma by polymerase chain reaction (PCR) using universal primers (P1/P7) as direct and R16F2n/ R16R2 as nested. The PCR amplifications from all infected plants yielded a product of 1.8 kb by P1/P7 primers and 1.2 kb fragment by nested PCR. No amplicons were evident when DNA extracted from healthy plants was used as template. Restriction fragment length polymorphism (RFLP) profiles of direct PCR products of radish phyllody phytoplasma and other phytoplasma strains belonging to different groups used as positive control with *RsaI*, *AluI*, *Tru9I*, *T-HB8I* and *HpaII* yielded patterns totally different to other phytoplasma which have been recorded in Oman. More than 1640 bp sequence was obtained from direct PCR amplified rDNA for two samples. Sequence homology results on BLAST revealed that Radish phyllody phytoplasma shares >99% similarity with vinca virescence phytoplasma, Potato witches' broom of Alaska and clover proliferation phytoplasma. The BLAST result of 16S rRNA gene sequences confirms that Radish phyllody phytoplasma are members of Clover proliferation ribosomal group (16SrVI). This is the first report of 16SrVI group phytoplasma from Oman and its presence in radish.

PHYTOPLASMAS INFECTING GRAPEVINE IN CHILE: POTENTIAL INSECTS VECTORS AND RESERVOIR PLANTS

(Fitoplasmas asociados a la vid en Chile: potenciales insectos vectores y plantas reservorio)

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Phytoplasmas found in Chilean grapevines showing yellows symptoms were identified as belonging to the ribosomal subgroups 16SrI-B and 16SrI-C ('*Candidatus* Phytoplasma asteris'), 16SrVII-A ('*Ca. P. fraxini*') and 16SrXII-A (stolbur or "bois noir"). The presence of these pathogens in the plants depends from both propagation of infected plants and spreading by different insect species which feed on grapevine and also on the weeds growing near and/or in vineyards. Several *Auchenorrhyncha* species were therefore captured, identified and tested to verify phytoplasma presence; many of them belong to the subfamily *Delthocephalinae* and *Agalliinae* (family *Cicadellidae*) and to the families *Cixiidae* and *Delphacidae*, all known as potential phytoplasma vectors. Several individual insects were positives to the phytoplasmas, in particular 16SrXII-A was detected in insects belonging to the species *Ampliplexus curtulus* Linnavuori & De Long and *Bergallia valdiviana* (Berg.). Different species of weeds were also collected in the vineyards, and 16SrVII-A phytoplasmas were identified in *Convolvulus arvensis* L., *Polygonum aviculare* L., and *Galega officinalis* L. In several cases the grapevine samples, weeds and insects collected in the same vineyard were positives to the same phytoplasma. Assays to verify the phytoplasma transmission ability of the insects carrying phytoplasmas are in progress.

COTTON VIRESCEENCE IN MALI

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Mali and Burkina Faso are the main cotton producers in Sub-Saharan Africa where cotton is the main export commodity. A disease associated with phytoplasmas, cotton virescence, has been reported in Burkina Faso, Ghana and Ivory Coast. The main symptoms are virescence, yellowing and reddening of the leaves and general stunting of the plant. During the early 2000, farmers in the South-Western Mali noticed important damages to cotton production due to a putative cotton virescence disease. The aim of this research was to detect and characterize the cotton disease agent in

Mali, identify alternative host plants, and understand the epidemiology of the disease in the Region.

Field surveys were carried out on July-October 2003-2006 in the cotton-growing areas of Kolondjéba and Yanfolila (Bougouni region). Cotton plants with symptoms were collected and sent to the laboratory for molecular analyses. Weeds were also surveyed for phytoplasma symptoms and samples of *Sida* spp. were analyzed for the presence of phytoplasmas. Potential leafhopper vectors were sweep-collected in different fields in the same areas and stored under ethanol for PCR analyses and species identification. RFLP showed that all amplicons from symptomatic cotton and *S. cordifolia* plants shared the same profile, identical to that of the faba bean phyllody (16Sr-IIc) reference isolate. 170 leafhopper specimens belonged to about 12 species in the subfamily Deltocephalinae (Cicadellidae). Phytoplasma-specific amplicons were obtained from 5 leafhoppers, but their RFLP profiles did not match the one from cotton. Spatial distribution of infected plants and time of symptom appearance suggest that primary infections, due to incoming leafhoppers, are more important than secondary spread, from cotton to cotton.

EFFECTS OF BIOTIC AND ABIOTIC ELICITORS OF PLANT RESISTANCE ON CHRYSANTHEMUM YELLOWS (“*CANDIDATUS PHYTOPLASMA ASTERIS*”) INFECTION.

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Arbuscular mycorrhizal fungi (AM) are naturally present in the roots of most fruit trees. They establish a mutualistic association with the plant, which results in an improved resistance to abiotic and biotic stresses. The presence of non-pathogenic rhizosphere bacteria may also induce a systemic resistance (ISR) in plants. Efficient ISR has been described towards several pathogens, including fungi, viruses and bacteria. Few natural or synthetic compounds, with no obvious deleterious effect on the pathogen, may also induce the activation of the plant defence machinery against several pathogens. ISR may be a useful tool to implement IPM strategies for the control of phytoplasma diseases.

The aim of this work was to assess the activity of biotic and abiotic elicitors of plant resistance on phytoplasma infection. The mycorrhizal fungi *Glomus mosseae* and *G. intraradices*, the rhizobacteria *Pseudomonas putida* S1PF1, *Pseudomonas aureofaciens* 30-84 and *Streptomyces* sp. SB20, and benzo (1,2,3) thiadiazole-7-carbothioic acid S-methyl ester (BTH) have been tested as inducers of resistance against chrysanthemum yellows phytoplasma (CY) infection. *P. putida* alone or in combinations with any of the two *Glomus* species or treatment with 2.4 mM BTH induced a delay of symptom development and protected some plants from CY infection. Combined inoculum of *P. putida* with *G. mosseae* increased the number of root tips and total root length of infected plants. Phytoplasma presence did not interfere with rhizobacteria and mycorrhizal colonization of infected roots. Phytoplasma concentration in elicited and non-elicited plants was compared.

MOLECULAR DIFFERENTIATION OF PHYTOPLASMAS AFFECTING CORN IN COLOMBIA AND SERBIA

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Corn is affected by phytoplasma diseases in some of its cultivation areas where losses of production can be higher than 50%, however in the majority of the cultivations in Americas it is also infected by *Spiroplasma kunkelii*. Moreover it was recently demonstrated that also in corn diverse phytoplasmas can be associated with similar disease symptoms such as stunting, reddening of leaves, early and abnormal ripening, precocious death, poor and shriveled grains in kernels that are in some cases also malformed. While in Americas the leafhopper *Dalbulus maydis* is the vector of both maize bushy stunt phytoplasma, and corn stunt spiroplasma, in the reddening outbreaks reported in Europe the vector role of cixiid(s) was proposed. Phytoplasmas infecting corn in Americas belong to 16SrI-B ribosomal subgroup (aster yellows or ‘*Candidatus* Phytoplasma asteris’), while in Europe they belong to ribosomal subgroup 16SrXII-A (“stolbur”). Strains from both phytoplasmas collected respectively in Colombia, Valle del Cauca and in Serbia, South Banat were further characterized by RFLP analysis and/or sequencing of rpS3, tuf, aminoacid kinase plus ribosomal recycling factor, pseudo helicase, and amp according with the strain. While the stolbur strains collected in Serbia did not show polymorphism when compared to stolbur reference strain, the aster yellows strains from corn collected in Colombia show polymorphisms when compared with 16SrI-B aster yellows phytoplasmas in some of the genes studied. Multiple gene strain differentiation will enable to carry out study towards the best disease management.

EPIDEMIC OCCURRENCE OF WITCHE’S BROOM DISEASE OF IPÊ-ROSA (*Tabebuia pentaphylla*) IN THE CITY OF RIO DE JANEIRO, BRAZIL.

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Tabebuia pentaphylla is a economically important species, being especially adopted as ornamental tree in landscaping of urban areas. It is widely used as ornamental and shade tree in different localities of Rio de Janeiro. In 1982, a disease was first observed on this species, with the following symptoms: hypertrophy of buds and of terminal branches; branch fasciation, usually associated with witches’ broom and leaf chlorosis; development of galls in some cases; and, finally, death of the branches. The disease induces malformation of the aerial part of the trees, reducing, dramatically, the landscaping value of the species. Epidemiological evidences suggested that it was an infectious disease and the symptomatology exhibited by diseased trees suggested that a phytoplasma was associated with the syndrome. The association of a phytoplasma and witches’ broom disease of ipê-rosa was demonstrated in 2007, when tissue samples from hypertrophic buds tested positive for the presence of phytoplasma, through nested PCR. The occurrence of the disease is seen throughout the

city of Rio de Janeiro, in the quarters of Maracanã (Zona Norte), Barra da Tijuca, Recreio dos Bandeirantes and Campo Grande (Zona Oeste), Flamengo and Botafogo (Zona Sul), and Centro. In Zona Sul and Centro of Rio de Janeiro, almost a hundred percent of adult trees exhibit the disease symptoms. The taxonomic characterization of the phytoplasma associated with witches' broom disease of ipê-rosa is under investigation.

DETECCION DEL FITOPLASMA ChWBIII EN SEMILLAS DE *Momordica charantia* L. EN BRASIL. (DETECTION OF ChWBIII PHYTOPLASMA IN SEEDS OF *Momordica charantia* L. IN BRAZIL)

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Momordica charantia L. (Cucurbitácea), utilizada en la preparación de infusiones como medicamento tradicional, especie hermafrodita y con flores unisexuales. Planta hospedera natural del fitoplasma ChWBIII, que causa la enfermedad conocida como "superbrotamiento del chuchuzeiro" en Brasil. Crece en las cercas y sobre la vegetación de la zona costera y en otras ciudades del Brasil. Plantas con síntomas de presencia de fitoplasmas producen frutos pequeños, de consistencia dura, con semillas adheridas fuertemente al endospermo, así como también frutos de tamaño reducido y consistencia mais suave. Las plantas sintomáticas presentan hojas pequeñas y amarillentas, crecimiento abundante de brotes pequeños, entrenudos cortos, flores pequeñas y atrofiamiento. Las semillas de los frutos de plantas sintomáticas estan vazias por dentro sin la presencia del embrión y de las otras estructuras propias de este tipo de semillas. En las localidades de Seropédica y Río de Janeiro, del Estado de Rio de Janeiro, se colectaron muestras de hojas e frutos tanto de plantas sintomáticas como plantas sanas, para determinar la presencia de fitoplasmas. Los ADNs extraídos de las semillas y de los tejidos foliares fueron analizados mediante *nested* PCR con los pares de primers P1/P7 and R16F2n/R16R. Las muestras de las semillas y de los tejidos foliares de las plantas sintomáticas resultaron positivas amplificando bandas de 1.2 kb. y no amplificaron las muestras sanas. Estos resultados demuestran la presencia de fitoplasmas en semillas de *M. charantia* naturalmente infectada con el fitoplasma ChWBIII que ocasiona la malformación de estas y las cuales no germinan.

CURRENT SITUATION OF PHYTOPLASMA DISEASES IN BRAZIL.

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In Brazil, phytoplasma diseases have been described in association with 61 plant species, distributed among 29 botanical families, comprising wild and economically important species. Major symptoms exhibited by naturally diseased plants include witches' broom, phyllody, virescence, color alterations (chlorosis or reddening), and plant stunting. Among the diseases induced by phytoplasmas, the identities of the associated phytoplasmas have not been determined in the following species: *Tetragonia expansa* (Aizoaceae), *Celosia* sp. (Amaranthaceae), *Gomphocarpus* sp.

(Asclepiadaceae), *Tabebuia pentaphylla* (Bignoniaceae), *Ageratum conizoides*, *Ageratum fastigiatum*, *Bidens pilosa*, *Brachiaria plantaginea*, *Callistephus chinensis*, *Chrysanthemum parthenium*, *Solidago microglossa* and *Tagetes minuta* (Compositae), *Ipomoea batata* (Convolvulaceae), *Cucumis sativus* (Cucurbitaceae), *Diospyrus kaki* (Ebenaceae), *Rhododendron* sp. (Ericaceae), *Lisianthus* sp. (Gentianaceae), *Cassia occidentalis*, *Centrosema brasilianum*, *Centrosema pubescens*, *Crotalaria paulinea*, *Desmodium intortum*, *Desmodium leiocarpum*, *Desmodium pabulare*, *Dimorphandra gardneriana*, *Glycine max*, *Phaseolus atropurpureus* and *Phaseolus vulgaris* (Leguminosae), *Sida cordifolia* (Malvaceae), *Eucalyptus* sp. (Myrtaceae), *Cocos nucifera* (Palmae), *Solanum lycocarpum* (Solanaceae), *Waltheria indica* (Sterculiaceae), *Triumfetta bartramia* (Tiliaceae) and *Turnera ulmifolia* (Turneraceae). Classification of phytoplasmas on the basis of 16S rRNA sequences have been achieved for 25 plant species: *Vitis vinifera* (Ampelidaceae), *Catharanthus roseus* (Apocynaceae), *Begonia* sp. (Begoniaceae), *Carica papaya* (Caricaceae), *Erigeron bonariensis* and *Helychrisium bracteatum* (Compositae), *Cucurbita moschata*, *Luffa cylindrica*, *Momordica charantia*, *Sechium edule* and *Sicana odorifera* (Cucurbitaceae), *Brassica oleraceae* var. *capitata* (Crucifera), *Manihot esculenta* and *Euphorbia pulcherrima* (Euphorbiaceae), *Zea mays* and *Saccharum* sp. (Gramineae), *Crotalaria juncea* (Leguminosae), *Hibiscus rosa-sinensis* (Malvaceae), *Bougainvillea spectabilis* (Nyctaginaceae), *Elaeis guineensis* (Palmae), *Passiflora edulis* f. *flavicarpa* (Passifloraceae), *Malus domestica* and *Fragaria* sp. (Rosaceae), *Lycopersicon esculentum* and *Solanum melongena* (Solanaceae). Insect vectors involved in phytoplasmas transmission have not been identified yet, except for *Dalbulus maidis*, the vector of the phytoplasma associated with maize bushy stunt disease.

DEVELOPMENT OF NESTED PCR USING GENERIC AND SPECIFIC PRIMERS FOR THE DETECTION OF PHYTOPLASMAS IN VARIOUS HOSTS IN GREECE

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Nested PCR assays were developed for the generic detection of phytoplasmas using degenerate primers that target the 16S rRNA gene and 16S-23S intergenic spacer region. Their efficiency was evaluated using 12 phytoplasma-isolates from different host species belonging to 7 phylogenetic groups: 16SrI (Aster yellows group), 16SrII (Peanut WB group), 16SrIII (X-disease group), 16SrV (Elm yellows group), 16SrVII (Ash yellows group), 16SrX (Apple proliferation group) and 16SrXII (Stolbur group). Additionally, 5 nested primers were designed and evaluated for the specific detection of Aster yellows (AY), Stolbur (STOL), Apple proliferation (AP) and European stone fruit yellows (ESFY). For the identification of phytoplasmas in Greece, 299 samples were collected during 2004-2005 from different crop plants showing symptoms typical of phytoplasma infection. Furthermore, 437 weed samples (with or without symptoms) were collected from affected crops. Some isolates were identified by

sequencing of PCR products or/and by RFLP analysis. Stolbur was detected in tomato, pepper, tobacco and grapevine samples as well as in the arable weeds *Cirsium arvense*, *Xanthium strumarium*, *Convolvulus arvensis* and *Solanum nigrum*. AY was detected in 3,43% of the tested weeds. ESFY is an important plum pathogen, with an incidence ranging from 10-50% in some orchards, which was detected in all collected samples as well as in peach, apricot and almond orchards, though in a lower frequency. Finally, AP was detected in Zagora (Pilio area), in 7,8% of the apple samples showing little fruit symptoms.

Survey of ‘*Candidatus Phytoplasma*’ occurrence in the Canadian Clonal Genebank and commercial plantings.

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In the 1970’s attention become focused on orchard ‘*Candidatus Phytoplasma*’ disease by reports of peach X-disease. As a consequence the host, Eastern chokecherry, *Prunus virginiana*, was eradicated in Southwestern Ontario. In 2008, peach and nectarine material from commercial nursery and orchard stock, reported to have visual symptoms of peach X-disease, was tested for the presence of this ‘*Candidatus Phytoplasma*’ by PCR and was found positive for this pathogen. In addition, several *Malus* and *Pyrus* accessions were tested by ELISA and nested PCR for the presence of ‘*Candidatus Phytoplasma mali*’ and ‘*Candidatus Phytoplasma pyri*’. Some pear accessions resulted positive by these tests. Molecular tests performed independently on the same material gave the same results. Many Sycamore trees (*Platanus occidentalis* L.) planted along roads and gardens showing witches’s broom disease symptoms were tested for the presence of ‘*Candidatus Phytoplasma*’ using PCR and nested PCR and found to be infected. Weather conditions in 2008 appear to be favorable for disease transmission and/ or expression and present a good opportunity to assess disease prevalence.

A HANDBOOK OF LEAFHOPPER AND PLANTHOPPER VECTORS OF PLANT DISEASES (Un manual de saltahojas y saltaplantas vectores de enfermedades de plantas)

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Leafhoppers and planthoppers (Hemiptera: Auchenorrhyncha) are among the most abundant groups of insects, including over 200 well known vectors of phytoplasma, virus and *Xylella*, most found in the family Delphacidae. Around 20,000 out of the 100, 000 putative leafhopper (Cicadellidae) species are described, and there may be around 10,000 planthopper species (Fulgoroidea). Although, many more vectors are expected to be identified because there are more diseases characterized than there are known disease vectors, few comprehensive identification keys are available and

details of pest species are mostly widely scattered in the specialist literature.

This Leverhulme Trust's project will provide a comprehensive and accessible introductory guide to the leafhopper and planthopper vectors of phytoplasma, bacteria and virus diseases through datasheets holding high quality digital images of adult insects (and nymphs where available), taxonomic drawings of morphological features, and text on the biology and pest status of each species, including details of taxonomy, identification, similar species, biology, host plants, distribution, and diseases and bibliography, supporting both professionals as well as workers in developing countries seeking accurate information on identification.

The project will initially compile a database of known plant diseases and their vectors from the various sources available, bringing together knowledge of both phytoplasma and virus diseases with taxonomic and biological vector details, available to both plant pathologists and entomologists. The approach taken of web-based and published handbook will make dissemination easy, flexible and inexpensive from information on known vector species and introductory material provided, to groups generally, as well as, placing emphasis on those that contain pest species.

VARYING SYMPTOMS OF PHYTOPLASMA ESFY IN APRICOT AND PEACH GROWN ON FIFTEEN DIFFERENT *PRUNUS* ROOTSTOCKS

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The visual symptoms displayed by 12 apricot trees and 1 peach cultivar ('Jantze') were monitored after the presence of phytoplasma ESFY was established using nested PCR methods. Fifteen different rootstocks, grown in pots, were then infected by grafting on buds taken from these 13 infected trees. These were: 'MRS 2/5' (*P. cerasifera* × *P. spinosa*), 'AP-1' (*P. cerasifera* × *P. persica*), 'Myrobalan 29C' (*P. cerasifera*), 'MY-KL-A' (*P. cerasifera*), 'Strážovický myrobalan' (*P. cerasifera*), 'Lesiberian' (*P. persica*), 'GF-8-1' (*P. cerasifera* × *P. munsoniana*), 'GF 677' (*P. persica* × *P. amygdalus*), 'GF 31' (*P. cerasifera*), 'GF 305' (*P. persica*), 'VVA-1' (*P. tomentosa* × *P. cerasifera*), 'Shirofugen' (*P. serrulata*), 'St. Julien A.' (*P. insititia*), 'Torinel[®]' (*P. domestica* - hexaploid) a 'M-LE-1' (*P. armeniaca*). Each combination was replicated 15 times and then kept in technical isolation. The symptoms subsequently manifested in the shoots arising from the infected buds, and also in the shoots arising directly from the parent rootstock, were recorded. Symptoms were often species specific and sometimes seen only in specific cultivars too. The primary symptoms of ESFY – chlorotic leaf roll - were recorded in 98% of combinations using the peach cv. 'Jantze', compared to 58% for the apricot cv. 'Poljus Južnyj' and 34% for 'Hargrand_2'. All combinations using the rootstock 'GF-8-1' had symptoms of leaf yellowing, all with 'Torinel[®]' had symptoms of leaf roll and reddening of the leaves, and all with 'GF305' had early leaf cast. Symptoms were also observed after using buds taken from trees known to be ESFY positive but showing no obvious visual symptoms. In the case of infected buds taken from the cv. 'Poyer', 55% of annual shoots showed no visual symptoms and in 36% symptoms of leaf roll were

seen. Chlorotic leaf roll and leaf yellowing were significantly more common than early leaf cast or cases with no obvious symptoms (latent infection).

Characterization of Jamaica phytoplasmas based on RFLP analyses of the 16S rRNA region.

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Despite their economic importance and unique biological features, phytoplasmas remain the most poorly characterized plant pathogens. In characterizing phytoplasmas in Jamaica the conserved 16S rRNA region was probed for variations. Phytoplasma samples collected from three locations, Bachelors Hall, Long Bay and Rowlandsfield, were amplified in P1/P7 PCRs and in nested PCRs using primers LY16Sr-23S/LY16Sf. The characteristic 16S rDNA fragments of 1.8 kb amplified in P1/P7 primed PCRs and of 1.7 kb amplified in nested PCR primed with primers LY16Sr-23S/LY16Sf were digested in single reactions with twelve restriction enzymes. Four enzymes (*Hae*III, *Hinf*I, *Tru* 9 and *Taq* 1) in the Restriction Fragment Length Polymorphism (RFLP) analysis gave differences with the digested samples. The enzyme *Hae* III distinguishes two 'pathotypes' from the Long Bay and Rowlandsfield. *Hinf*I distinguishes three 'pathotypes' from Long Bay, one of which is similar to a 'pathotype' from Rowlandsfield. *Tru* 9 distinguishes three 'pathotypes' from Bachelors Hall. *Taq* 1 enzyme distinguishes two 'pathotypes' from Bachelors Hall. One RFLP pattern obtained from Long Bay is similar to a pattern obtained from Rowlandsfield; suggesting that the 'pathotypes' of phytoplasma are similar. Our results are significant; as this is the first time that variations were detected in 16S rRNA region of the Jamaican LY phytoplasma. The correlations between 'pathotypes' and geographical locations could be significant for epidemiological studies and management strategies of LY disease control.

NEW PHYTOPLASMA HOSTS IN CUBA (Nuevos hospedantes de fitoplasmas en Cuba)

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Phytoplasmas have become a serious threat for agriculture in Latin America and the Caribbean since they have been found in fruit trees, ornamentals, horticultural crops, and weeds. In Cuba, there is an actual policy to plant horticultural crops to increase

the urban and peri-urban agriculture. Phytoplasmas have been associated with diseases in sugarcane, papaya and coconut. However, other crops like tobacco, carrot, reddish, beetroot, cassava and cabbage have been exhibiting typical phytoplasma symptoms, and have been collected from western, central and eastern regions.

Samples were evaluated through nested PCR with phytoplasma primers P1/P7, R16mF2/R1 and fU5/rU3. RFLP with a variety of restriction enzymes were conducted for characterization of isolates. Representative amplicons of each plant species were purified, cloned (pGEMT-Easy Vector, Promega) and sequenced. Sequences were blasted to Genbank, and phylogeny was established using MEGA version 3.1. Two main groups of phytoplasmas, 16SrI, *Ca. Phytoplasma asteris*, and 16SrII, *Ca. Phytoplasma aurantifolia*, have been identified affecting these crops in Cuba, which indicates that both 16SrI and 16SrII alternate between nearby crops. Further studies will be required to identify potential vectors and understand the epidemiology of such diseases.

NAPIER GRASS STUNT AND SMUT IN EAST AFRICA (Enanismo y Carbón de la hierba elefante en África del Este)

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Napier grass (*Pennisetum purpureum*), the most important forage crop in East Africa, has been affected by devastating diseases. Napier Grass Stunt (NGS) is a phytoplasma disease affecting livelihoods of many countries including Ethiopia, Kenya and Uganda, along with Napier grass smut (NHS), caused by a fungus *Ustilago kamerunensis*. Phytoplasmas of groups 16SrIII (X-disease) and 16SrXI (*Candidatus* Phytoplasma cynodontis) have been associated with NGS in Kenya, Ethiopia and Uganda. A serious phytosanitary problem has emerged since those varieties that have been spread among farmers as resistant to NHS are susceptible to NGS. The present paper presents results on the molecular identification and characterization of the NGS phytoplasma, and new insights on NHS. Polymerase chain reaction (PCR)-based assays, using phytoplasma universal primers, in combination with restriction fragment length polymorphism and sequencing analysis of the 16S ribosomal RNA gene were used to analyze NGS-affected samples, including leafhopper specimens identified as potential vectors, and other plant species as alternative hosts. PCR and sequencing assays based on the β -tubuline and ITS regions were used for the molecular identification and characterization of *U. kamerunensis*. Sequences from both NGS phytoplasma and *U. kamerunensis* were compared by BLAST and phylogenetic relationships established. Results point directions towards the development of diagnostic tools for both NGS and NHS diseases, including resistance screening, and the improvement of their management and control.

ALFALFA (*Medicago sativa*) AS A NEW PHYTOPLASMA HOST IN SAUDI ARABIA (Alfalfa (*Medicago sativa*) como un nuevo hospedante de fitoplasmas en Arabia Saudita).

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Phytoplasmas have become a serious threat for agriculture in Saudi Arabia since their detection in date palm and other plant species. Alfalfa is one of the most important forage crop widely used in over the world. Alfalfa plants exhibiting typical phytoplasma symptoms, including witches' broom, leaf yellowing, little leaf, phyllody and virescence were collected from different areas of Alhassa. Other plant species were also surveyed from the alfalfa fields, and leafhoppers were trapped by netting.

Plant and insect samples were subjected to DNA extraction and evaluated through nested PCR with phytoplasma primers P1/P7 and fU5/rU3. RFLP with a variety of restriction enzymes were conducted for partial characterization of isolates. Representative amplicons were purified, cloned (pGEMT-Easy Vector, Promega) and sequenced. Sequences were blasted to Genbank, and phylogeny was established using MEGA version 3.1. The present work discuss about the identification of the phytoplasma associated with alfalfa disease, including alternative reservoirs and potential vectors, and their epidemiological implications for the development of further management strategies.

Phytoplasma diseases in Argentina. Current situation (FITOPLASMAS EN ARGENTINA. SITUACIÓN ACTUAL)

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En Argentina existen dos situaciones marcadas en lo que respecta a infecciones por fitoplasmas. En algunos casos la enfermedad se da de manera recurrente y sistemática en cultivos, nativas y malezas produciendo daños que podrían ser cuantificables, en cambio en otros la aparición es aleatoria, en pocos ejemplares, lo que solo permite el estudio del patógeno. Se está trabajando en el diagnóstico y caracterización de fitoplasmas y aspectos epidemiológicos de estas enfermedades. Se utilizan técnicas de Microscopía Electrónica, PCR utilizando cebadores universales y específicos, RFLP sobre los productos de amplificación, y secuenciación de genes 16Sr, y de proteínas ribosomales. Se ha logrado identificar fitoplasmas del grupo 16Sr I (*Aster yellows*) subgrupo B; 16SrIII (*X-disease*) subgrupos B y J, 16Sr VII (*Ash yellows*) subgrupo B y del nuevo subgrupo C y también del grupo 16Sr XIII (*Mexican periwinkle*) subgrupo C, sumando nuevos grupos y subgrupos *rrpp*. Se evalúa incidencia y prevalencia de la enfermedad llamada “*Tristeza del ajo*” en *Allium sativum* L., el MBS en maíz (*Zea mays* L.), la “*Escoba de bruja de la alfalfa*” (*Medicago sativa* L.), el “*Declinamiento del paraíso*” (*Melia azedarach* L.), se están iniciando los estudios en frutilla (*Fragaria x ananassa*), en nativas como lagaña de perro (*Caesalpinia gilliesii* Wall. Ex Hook), romerillo (*Heterothalamus alienus* Spreng. Kuntze) y malezas como rama negra (*Coniza bonariensis* L.) y artemisa (*Artemisa* spp). La prevalencia en general es elevada y la incidencia variable según la enfermedad, con alto índice de mortalidad sobre el material afectado. Se están estudiando poblaciones de hemípteros para determinar que especies estarían involucradas en la transmisión.

OCURRENCIA Y DISTRIBUCIÓN GEOGRÁFICA DE FITOPLASMAS ASOCIADOS CON ENFERMEDADES DE PAPA EN MÉXICO

(Occurrence and geographical distribution of phytoplasmas associated with potato diseases in Mexico)

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El cultivo de la papa es uno de los más importantes de México y en los últimos años ha sido afectado por enfermedades causadas por fitoplasmas, como la punta morada (PPT) y brote de hilo (PHS) de la papa, ocasionando severos estragos en las regiones productoras del país. En estudios previos se identificaron y caracterizaron fitoplasmas asociados con las enfermedades PPT y PHS. El objetivo de este trabajo de investigación fue determinar la ocurrencia y distribución geográfica de fitoplasmas en las principales regiones productoras de papa del país. 2994 muestras (tubérculos y follaje) colectadas en las principales regiones paperas de México como Sinaloa (SIN), Sonora (SON), Chihuahua (CHI), Guanajuato (GTO), Coahuila (COAH), Jalisco (JAL) y Baja California (BC) durante el periodo 2003-2006 fueron analizadas por PCR anidado con oligonucleótidos universales para fitoplasmas (R16MF2/R16MR2 y R16F2n/R16R2). Los productos de PCR fueron clonados, secuenciados y analizados con los programas MegAlign y pDRAW32. Se encontró al grupo del amarillamiento del aster (16Sr-I) distribuido en todas las regiones productoras, mientras que el grupo de la escoba de bruja del cacahuete (16Sr-II) se encontró solamente en GTO, el grupo de la enfermedad X del durazno (16Sr-III) en GTO y COAH y el grupo de la virescencia de la teresita Mexicana (16SrXIII) se encontró recientemente en Sinaloa. Este es el primer reporte de fitoplasmas del grupo 16SrXIII infectando papa en México.

SITUACIÓN ACTUAL SOBRE ENFERMEDADES FITOPLASMICAS EN HORTALIZAS EN MÉXICO

(Current situation of phytoplasma diseases in vegetable crops in Mexico)

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La horticultura representa una de las actividades agrícolas más importantes en México, tanto como alimento como por la cantidad de mano de obra requerida y las divisas generadas por su exportación. se considera que uno de los factores limitantes para la producción de hortalizas en México son las enfermedades causadas por fitoplasmas, con un mayor impacto en el cultivo de papa. La punta morada de la papa y *Bactericera cockerelli* han causado severos problemas a la producción de papa en

las zonas productoras del centro y noreste del país, presentándose pérdidas de hasta el 100% en algunos lotes. En los últimos 6 años nuestro grupo de investigación ha realizado un escrutinio nacional sobre enfermedades relacionadas con fitoplasmas en cultivos hortícolas con énfasis en aspectos epidemiológicos (vectores y hospederos). Mediante estudios de PCR anidado, PCR múltiple con oligonucleótidos específicos, PCR en tiempo real, análisis RFLP-PCR y secuenciación se ha confirmado la presencia de fitoplasmas en los cultivos de chile, papa, tomatillo y tomate. También se han identificado como malezas hospederas a *Rhynchosia minima*, *Ludwigia octovalvis*, *Cissus Sycloides*, *Parthenium hysterophorus* y *Polygonum hydrapiper*. Los fitoplasmas encontrados ampliamente distribuidos en cultivos hortícolas de nuestro país pertenecen a los 16SrI, 16SrII, 16SrIII y 16SrXIII. Durante varios años se había asociado altas poblaciones de *B. cockerelli* a enfermedades fitoplásmicas del cultivo de papa; pero fue hasta recientemente que nuestro grupo de trabajo confirmó a *Bactericera cockerelli* como transmisor de estos fitoplasmas.

EL AMARILLAMIENTO LETAL DEL COCOTERO EN CUBA.

(Coconut lethal yellowing in Cuba)

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Dentro de las enfermedades que afectan al cultivo de cocotero se encuentra el amarillamiento letal del cocotero. En este trabajo se propuso evaluar la diversidad de los aislados de fitoplasmas encontrados a partir del estudio de la región no-ribosomal del genoma. La comparación de las secuencias de los aislados cubanos respecto a las de otros fitoplasmas procedentes de jamaica evidenció una alta homología, Por otra parte se seleccionó la localidad de Playa Duaba en Baracoa, foco activo de la enfermedad para realizar los análisis de la enfermedad. Se realizó la detección de los fitoplasmas presentes en plantas con síntomas a través de la PCR con los iniciadores P1/P7 y LYF1/LYR1, se inventariaron los posibles insectos vectores, se registró la vegetación acompañante, así como los ecotipos de cocotero presentes. A partir de la amplificación del segmento 16S rRNA y de la región no-ribosomal se obtuvieron fragmentos de 1.8kb y de 1.0kb, respectivamente. Se colectaron los insectos: *Omolicna* sp. (Hemiptera: Fulgoridae), *Cedusa* sp (Hemiptera: Fulgoridae), *Nymphocixia caribbea* Fennah (Hemiptera: Cixidae), *Saccharosydne* sp (Hemiptera: Fulgoridae). De la vegetación característica de la zona se colectaron las especies: *Stachytarpheta jamaicensis*, *Cleome ginandria*, *Emilia fosbergii* y *Jatropha gossypifolia*, entre otras. Los ecotipos más representativos son los cocos criollos, los indios verdes, dorados, amarillos y rojos, de los cuales los criollos fueron los más afectados.

Estado actual del conocimiento de los cicadélidos (Hemiptera:Cicadellidae) de interés económico para Cuba. Marta M. Hidalgo-Gato y Rosanna Rodríguez-León
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En Cuba existe un estimado de 401 especies de hemípteros auquenorrincos, distribuidas en 14 familias y 75 géneros. Entre las familias mejor representadas, se encuentra Cicadellidae, con 56 géneros y 164 especies que representan 40,8 % del total. Esta constituye además, una de las de mayor importancia, porque algunos de sus integrantes constituyen vectores de enfermedades a diferentes plantas y cultivos. El objetivo de este trabajo es recopilar información sobre las especies de cicadélidos de interés económico en Cuba. Los resultados que se exponen proceden de proyectos de investigación, revisión de la colección entomológica del Instituto de Ecología y Sistemática y de la literatura. Dentro de la familia Cicadellidae, 33 especies habitan en plantas económicas de Cuba y 16 son registradas como transmisores reales ó potenciales de enfermedades a las plantas, en diferentes países América y las Antillas. Las especies que viven en plantas económicas de Cuba, pertenecen a las subfamilias Typhlocybinae (14 spp.), Deltocephalinae (9 spp.), Cicadellinae (6 spp.), Agallinae (3 spp.) y Xerophloeinae (1 sp.); mientras que las especies que constituyen vectores potenciales de enfermedades para Cuba, pertenecen a las subfamilias Deltocephalinae (7 spp.), Agallinae (4 spp.), Cicadellinae (3 spp.), y Typhlocybinae (2 spp). En el ecosistema cañero, se listaron 12 especies de cicadélidos de importancia económica, mientras que en los ecosistemas naturales: 3 especies en la Sierra de los Órganos, 13 en la Sierra del Rosario, 6 en Topes de Collantes, 12 en el Archipiélago de Sabana Camagüey y 1 en la Altiplanicie Sagua-Baracoa.

SITUACIÓN ACTUAL DE HEMIPTERA: FULGOROMORPHA EN CUBA. ESPECIES DE IMPORTANCIA EN LA TRANSMISIÓN DE ENFERMEDADES A LAS PLANTAS.

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Los Fulgoromorpha (planthoppers) están representados en todas las regiones del mundo pero se les encuentra principalmente en los trópicos, sus integrantes son responsables de muchos de los estragos más importantes en los grandes cultivos de cereales en el mundo: arroz, maíz, trigo, sorgo, los cuales son ocasionados durante la puesta, la alimentación, o por la transmisión de diferentes fitopatógenos. En Cuba, 23 especies de 7 familias están presentes en diferentes hábitats, tanto en agroecosistemas como en ecosistemas naturales. Es objetivo de este trabajo brindar información actualizada sobre las especies de Hemiptera Fulgoromorpha presentes en agroecosistemas y ecosistemas naturales de Cuba, con énfasis en la situación taxonómica y distribución geográfica de las especies transmisoras de enfermedades en cultivos de interés económico. Entre estas especies de importancia se destacan los delfácidos: *Saccharosydne saccharivora* en la caña de azúcar, *Peregrinus maidis* en el maíz y *Tagosodes orizicola* en el arroz y los cíxidos: *Myndus crudus* y *Nymphocixia caribbaea* en cocoteros. La información compilada procede de resultados científicos obtenidos por las autoras en Proyectos de Investigación realizados en áreas naturales y en agroecosistemas de Cuba, de la revisión de la Colección Entomológica del IES y de la literatura especializada. Los resultados expuestos pueden servir de base para la

investigación y el control sobre estos insectos y las enfermedades que transmiten en el país.

TRANSMISIÓN DE TRES GRUPOS DE FITOPLASMAS POR *Bactericera cockerelli* A PLANTAS DE CHILE, PAPA Y TOMATE EN SINALOA, MEXICO

(Transmission of Three Phytoplasmas Groups by *Bactericera cockerelli* to Pepper, Potato and Tomato Plants in Sinaloa, Mexico)

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Los cultivos hortícolas son de suma importancia en Sinaloa, México para el consumo local, industrial y de exportación. Sin embargo, su producción ha sido limitada por insectos plaga y enfermedades causando severas pérdidas económicas. Recientemente se han observado síntomas asociados con enfermedades fitoplásmicas en cultivos de chile, papa y tomate. *Bactericera cockerelli* se ha asociado con éstas enfermedades en Norte América y México; sin embargo, no se ha reportado como vector de fitoplasmas. Mediante trampas amarillas se confirmó la presencia de *B. cockerelli* en estos cultivos durante los ciclos 2004 al 2006 en Sinaloa. Estudios sobre la dinámica poblacional revelaron que durante el ciclo 2005-2006 el número de insectos fue 30 veces mayor que durante el ciclo 2004-2005. Individuos de *B. cockerelli* fueron alimentados en plantas sanas hasta obtener una colonia libre de fitoplasmas. Para los bioensayos de transmisión se utilizó como inóculo una planta de chile infectada. Insectos infectados fueron alimentados en plantas sanas de chile, papa y tomate confinadas en jaulas individuales con malla antiáfidos, por triplicado y usando como control negativo insectos sanos. La transmisión de fitoplasmas se determinó por PCR anidado. Mediante PCR múltiple con oligonucleótidos específicos, análisis RFLP-PCR y secuenciación se confirmó que los fitoplasmas transmitidos pertenecen a los grupos 16SrI, 16SrII y 16SrXIII. Este es el primer reporte de transmisión de tres grupos de fitoplasmas por *Bactericera cockerelli* en México.