

Identification and Molecular Characterization of a Phytoplasma Associated with Al-Wijam Disease of Date Palm in Saudi Arabia

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Abstract

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Date palm (*Phoenix dactylifera* L.) has been affected by a disease called Al-Wijam in Saudi Arabia. Main symptoms are leaf stunting, yellow streaking and a marked reduction in fruit and stalk size, which leads to failure in fruit production at harvest. A lethal yellow phytoplasma was identified in Al-Wijam infected date palms growing in the Al-Hassa oasis, Eastern region. More than 30 leaf samples with and without Al-Wijam symptoms and 60 leafhopper samples were collected in a survey in Al-Hassa oasis during 2003-2005. Total DNA was extracted from plants and batches of three insects and indexed by a nested PCR reaction with phytoplasma generic primers P1/P7-R16F2n/R16R2. PCR products were characterized by RFLP and direct sequencing. The 16S rDNA sequences were compared with those of other reference phytoplasmas in the GenBank. Phytoplasma rDNA was amplified from 28 Al-Wijam samples and 16 insect batches. No PCR products were obtained from healthy palms. RFLP patterns for all PCR amplifications were identical with *RsaI*, *HinfI*, *TaqI*, *HpaII*, *KpnI*, *DraI*, *HhaI* and *Sau3AI* enzymes. The 16S rDNA sequences of the phytoplasma identified in date palm (DQ913090) and *Cicadulina bipunctata* (Melichar) (DQ913091) were 100% identical in between and 98% with that of Aster yellows phytoplasma (AF322644) from 16SrI, *Candidatus* Phytoplasma asteris group. This is the first report of a *Ca. P. asteris* phytoplasma associated with a disease in date palm in Saudi Arabia, and the identification of a potential vector of Al-Wijam disease.

Keywords: Aster yellow, *Cicadellidae*, Date palm, *Phoenix dactylifera*, Phytoplasma, Saudi Arabia.

Introduction

Date palm, (*Phoenix dactylifera* L.), is one of the most important cash crops in Saudi Arabia. The area planted with date palm is 150,744 ha where 23 million trees produce 970,488 t of dates annually (5). The Eastern region of Saudi Arabia is one of the most important in the country, growing date palm for centuries with more than 4 million trees located at Al-Hassa oasis.

"Al-Wijam" disease was first reported as widespread in Al-Hassa (18). Symptoms are characterized by a stunting and yellow streaking of the leaves, with fruits and fruit stalks reduced in size (around 30%) and varies based on varieties.

Association of viral, fungal and nematode pathogens with the disease was not consistent (1, 2, 18). A phytoplasma pathogen was suspected to cause Al-Wijam-affected palms following histopathology and antibiotic therapy studies (2). This was further supported by El-Zayat *et al.* (19), who reported a phytoplasma similar to that causing lethal yellow of coconut palm in Florida.

Phytoplasmas are prokaryote organisms of the class *Mollicutes*, which affect more than 700 plant species from tropical to temperate countries (25). They cannot be cultivated *in vitro* and are mainly transmitted by leafhopper or planthoppers of the order *Hemiptera* (30). Phytoplasmas have been associated with diseases in date palm such as white tip die-back (WTD) and Slow decline in Sudan in North Africa (11, 12), yellowing in Kuwait (3), and lethal decline in Texas (23).

Lethal yellowing (LY) and lethal decline (LD) are lethal coconut phytoplasma diseases that are spread in many countries, including these of West and East Africa, including Mozambique and Kenya (33), Tanzania, Ghana (41, 42); the Caribbean and Central America, including Belize (20), Jamaica (44), Honduras (35), Mexico (7, 10), Guatemala (31) and Cuba (29).

Myndus crudus (Van Duzee) (24) is known as the vector of LY (24) in Jamaica and Florida, however, there are reports of other *Hemiptera* species found associated with either LY or LD diseases (15, 33)

The phytoplasma associated with Al-Wijam in Saudi Arabia (19) was found to be similar to that causing lethal yellows in Florida, however, no attempts were made earlier to identify the potential *Hemiptera* vectors out of the disease agent.

In this paper, we report the association of a phytoplasma of 16SrI group, *Ca. P. asteris*, with Al-Wijam in Al-Hassa, Saudi Arabia, and the identification of a cicadellid candidate as the disease vector.

Materials and Methods

Sample collection

Leaf samples from 40 date palms with and without Al-Wijam symptoms and 60 specimens of *Cicadellidae*: 42 of *Cicadulina bipunctata* (Melichar) and 18 of *Asymmetrasca decedens* (Paoli) were collected from a survey in Al-Hassa oasis during 2003-2005. DNA of the reference phytoplasma strain of European aster yellows (EAY, 16SrI) from the

phytoplasma collection at Rothamsted Research, UK, was used for direct comparison of restriction fragment length polymorphism (RFLP) patterns.

PCR and RFLP analysis

DNA was extracted from leaf tissue and batches of three insects by the method of Doyle & Doyle, (17). Aliquots of final DNA preparations were used as template for a nested PCR (nPCR) assay with phytoplasma 16S rDNA primers P1 (14) and P7 (37) using a programmable thermocycler (TECHNE, TC-412) following previous described PCR conditions (6). Nested PCR products were digested with restriction endonucleases *RsaI*, *HinfI*, *TaqI*, *HpaII*, *KpnI*, *DraI*, *HhaI* and *Sau3AI* (SIGMA, UK) according to manufacturer's instructions. Digestion products were electrophoresed in 1.5% agarose gels, and visualized after staining with ethidium bromide by UV transillumination. RFLP patterns were compared with previously published patterns (27, 28).

16S rDNA sequencing and phylogenetic analysis

Phytoplasma rDNA amplified by PCR using the primer pair P1/P7 was purified on spin columns (QIAquick gel extraction kit; QIAGEN). The PCR products were sequenced in both directions using primer pair P1/P7 by the Sequencing Service, School of Life Sciences, University of Dundee, UK (<http://www.dnaseq.co.uk>), with Applied Biosystems Big-Dye version 3.1 chemistry on an Applied Biosystems model 3730 automated capillary DNA sequencer. The 16S rDNA sequences of phytoplasmas identified in our study were compared with others in Genbank (Table 1) by BLAST (4). Sequences were aligned and a phylogenetic tree constructed by the program MEGA version 3.1 (26) using 1000 bootstrap datasets to support the branch values. *Acholeplasma palmae* and *A. laidlawii* were used as the outgroups to root the tree.

Results

Sample collection

Newly opened leaves and spathes became stunted and shorter than healthy ones. Stunting and yellowing increase through the years and yellow streaks appear on the petioles. Fruits and fruit stalk were reduced in size by 36-40% in different varieties. In the advanced stages, there was significant stunting and yellowing depending on the variety, until the palm died. Figure 1 shows characteristic symptoms of Al-Wijam disease observed in the Al-Hassa oasis.

PCR and RFLP analysis

Phytoplasma rDNA was amplified from 28 date palm leaf samples showing typical Al-Wijam symptoms, and 16 leafhopper batches: 12 of *C. bipunctata* and 4 of *A. decedens*. Samples were representative with the 1250 bp expected second round PCR amplification (Figure 2). No PCR products were obtained from apparently healthy palms. Except for *TaqI*, the RFLP patterns for all PCR amplicons from date palm and *C. bipunctata* were identical with *RsaI*, *HinfI*, *HpaII*, *HhaI*, *KpnI*, *Sau3AI*, and *DraI* enzymes (Figures 3A and 3B) to that of the reference

control EAY, suggesting these phytoplasmas belong to 16SrI group, *Ca. P. asteris*. In the case of the phytoplasma identified in *A. decedens*, it showed differences when compared to the reference control with *HhaI* and *HinfI* enzymes.

16S rDNA sequencing and phylogenetic analysis

Phytoplasma 16S rDNA sequences from date palm and *C. bipunctata* were 100% identical, and shared 96% identity with 16S rDNA amplified from *A. decedens* phytoplasma.

Sequence similarity between the phytoplasma 16S rDNAs from date palm and *C. bipunctata* to those of previously characterized phytoplasma strains *Ca. P. asteris*, AAY, AshWB, BD, OY was 98%; 95% to *Ca. P. australiense*; 94% to MPV and *Ca. P. japonicum*; 92% to *Ca. P. pyri*, 90% to FCoLY and LDT and less than 89% with other known phytoplasma group, representatives. Sequence similarity of 16S rDNA amplified from *A. decedens* phytoplasma to those of StolSer1, StolSer2, VK and Stolbur was 99%; 98% to *Ca. P. graminis*; 97% to *Ca. P. caricae* and *Ca. P. americanum*; 96% to *Ca. P. fragariae*, 95% to *Ca. P. australiense*, 94% to *Ca. P. japonicum* and MPV, 92% to *Ca. P. pyri*; 90% to FCoLY; 89% to LDT and less than 88% with the rest of phytoplasma groups.

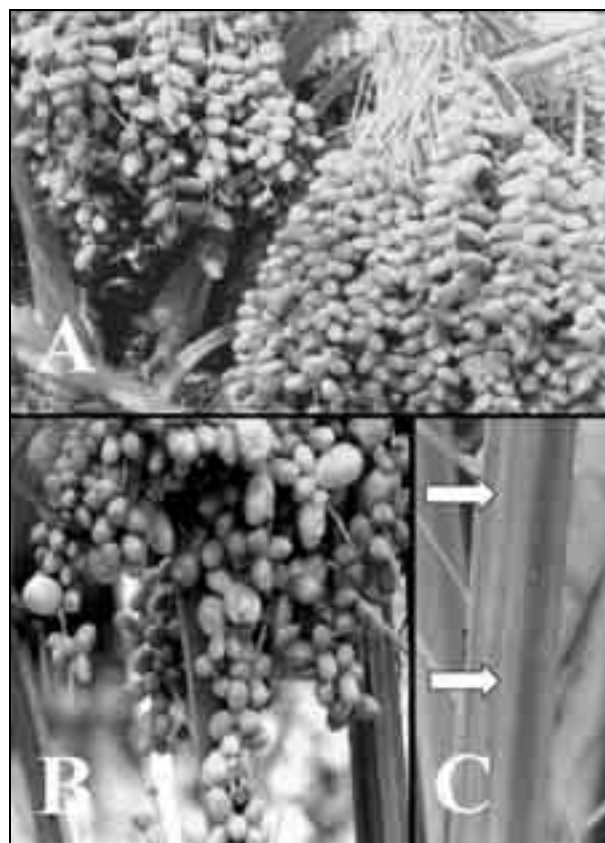


Figure 1. Date in kimir stage. (A) healthy date palm fruit, (B) date from a Al-Wijam affected palm showing stunting symptom, (C) yellow streak on the rachis of leaf from a Al-Wijam affected palm (indicated by arrows).

Table 1. Acronyms GenBank accession numbers of phytoplasma 16S rDNA sequences used to construct the phylogenetic tree.

Acronym	Phytoplasma strain designation	RFLP Group	Accession number
Ca. P. trifolii	' <i>Candidatus</i> Phytoplasma trifolii'	16SrVI	AY390261
Ca. P. fraxini	' <i>Candidatus</i> Phytoplasma fraxini'	16SrVII	AF092209
Ca. P. ulmi	' <i>Candidatus</i> Phyttoplasma ulmi'	16SrV	AFI22910
FD	'Flayescence donée'	16SrV	AF176319
Ca. P. ziziphi	' <i>Candidatus</i> Phytoplasma ziziphi'	16SrV	AY072722
LWB	'Loofah witches' broom'	16SrVIII	L33764
Ca. P. cynodotis	' <i>Candidatus</i> Phytoplasma cynodotis'	16SrXIV	AJ550984
SCWL	'Sugarcane white leaf'	16SrXI	X76432
Ca. P. oryzae	' <i>Candidatus</i> Phytoplasma oryzae'	16SrXI	D12581
FCoLY	'Coconut yellows'	16SrIV	U18747
LDT	'Coconut lethal decline'	16SrIV	X80117
Ca. P. pini	' <i>Candidatus</i> Phytoplasma pini'	16SrIV	AJ310849
Ca. P. castaneae	' <i>Candidatus</i> Phytoplasma castaneae'	16SrIV	AB054986
Ca. P. phoenicium	' <i>Candidatus</i> Phytoplasma phoenicium'	16SrIX	AF515837
PPWB	'Pigeon pea witche's broom'	16SrIX	U18763
VWB	'Vaccinia witche's broom'	16SrIII	X76430
WX	'Western X-disease'	16SrIII	L04682
PYC	'Papaya yellow crinkle'	16SrII	YI0097
PWB	'Peanut witche's broom'	16SrII	L33765
PM	'Papaya mosaic'	16SrII	YI0096
Ca. P. aurantifolia	' <i>Candidatus</i> Phytoplasma aurantifolia'	16SrII	U15442
Ca. P. brasiliense	' <i>Candidatus</i> Phytoplasma brasiliense'	16SrXV	AF147708
Ca. P. mali	' <i>Candidatus</i> Phytoplasma mali'	16SrX	AJ543541
Ca. P. pyri	' <i>Candidatus</i> Phytoplasma pyri'	16SrX	AJ542543
Ca. P. prunorum	' <i>Candidatus</i> Phytoplasma prunorum'	16SrX	AJ542544
Ca. P. spartii	' <i>Candidatus</i> Phytoplasma spartii'	16SrX	X92869
Ca. P. allocasuarinae allocasuarinae	' <i>Candidatus</i> Phytoplasma allocasuarinae'	16SrX	AY13523
Ca. P. rhamni	' <i>Candidatus</i> Phvtoolasma rhamni'	16SrX	X76431
Ca. P. graminis	' <i>Candidatus</i> Phytoplasma graminis'	16SrXVI	AY725228
Ca. P. caricae	' <i>Candidatus</i> Phytoplasma caricae'	16SrXVII	AY725234
StolSer1	'Stolbur, Serbia I'	16SrXII	X76427
Canuum	'Stolbur transmitted from C. anuum'	16SrXII	X76427
StolSer2	'Stolbur, Serbia I'	16SrXII	DQ222972
STOL	'Stolbur, Italy'	16SrXII	AF248959
Ca. P. australiense	' <i>Candidatus</i> Phvtoolasma australiense'	16SrXII	L76865
SGP	'Strawberry green petal'	16SrXII	AJ243044
SLY	'Strawberry lethal yellows'	16SrXII	AJ243045
PDB	'Paoaya dieback'	16SrXII	Y10095
PYL1	' <i>Phormium</i> yellow leaf'	16SrXII	U43569
VK	' <i>V. vinifera</i> phvtoolasma'	16SrXII	X76428
Ca. P. americanum	' <i>Candidatus</i> Phytoplasma americanum'	16SrXII	DOI74122
Ca. P. fragariae	' <i>Candida/us</i> Phytoplasma fragariae'	16SrXII	DQ86423
Asymmetrasca	' <i>A. decedens</i> phvtoolasma'	16SrXII	DQ913092
MPV	'Periwinkle yiarence'	16SrXIII	AF248960
AAV	'American aster yellows'	16SrI	X68373
Ca. P. asteris	' <i>Candidatus</i> Phytoplasma asteris'	16SrI	M30790
AshWB	'Ash witches' broom'	16SrI	AY568302
BD	'Barley deformation'	16SrI	AY734453
OY	'Onion yellows'	16SrI	D12569
Ca. P. japonicum	' <i>Candidatus</i> Phytoplasma japonicum'	16SrI	ABOI0425
Date Palm	'Date palm phytoolasma'	16SrI	DQ913090
Cicadulina	' <i>Candidatus biounctata</i> phvtoolasma'	16SrI	DQ913091
<i>A. oalmae</i>	<i>Acholeplasma palmae</i>	-	L33734
<i>A. laidlawii</i>	<i>Acholeplasma laidlawii</i>	-	M23932

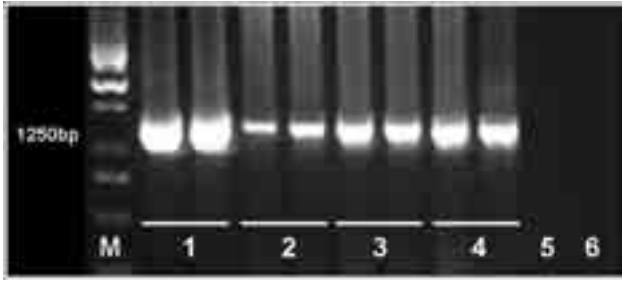


Figure 2. Nested-PCR amplifications with R16F2n/R16R2 primers from Al-Wijam affected date palm and *Cicadellids* associated. Lane 1: EAY reference positive control. Lane 2: *A. decedens*. Lane 3: *C. bipunctata*. Lane 4: leaflet symptomatic. Lane 5: healthy leaflet. Lane 6: water as negative control. Lane M: 1Kb marker (Promega).

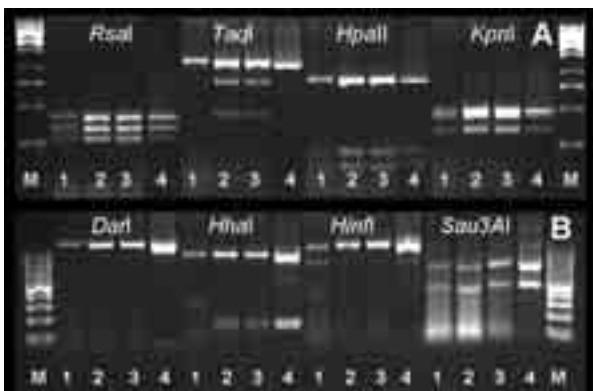


Figure 3. A, B. RFLP analysis of 16S rDNAs amplified by nPCRs with *A. RsaI*, *TaqI*, *HpaII*, *KpnI*, *B. DraI*, *HhaI*, *HinfI* and *Sau3AI* enzymes. Lane 1: *A. decedens*. Lane 2: *C. bipunctata*. Lane 3: leaflet symptomatic. Lane 4: EAY reference positive control. Lane M: 100 bp ladder (MBI Fermentas, Lithuania).

Phylogenetic analysis of 52 phytoplasmas, *A. palmae* and *A. laidlawii* produced the consensus tree illustrated in Figure 4. Phytoplasmas identified in date palm and *C. bipunctata* were embraced in the 16SrI group, *Ca. P. asteris* cluster, which was in agreement with grouping according to RFLP results. However, the phytoplasma identified in *A. decedens* was placed in the phylogenetic branch of phytoplasmas belonging to the 16SrXII group, *Ca. P. solani*.

Discussion

The amplification of phytoplasma DNA from 28/40 date palm plants showing typical Al-Wijam symptoms demonstrates the association of this pathogen with the disease in Al-Hassa oasis as previously described (19).

The phytoplasma identified in date palm and *C. bipunctata* showed RFLP profiles that clearly placed them in the 16SrI group, *Ca. P. asteris*, which is in agreement with sequencing and phylogenetic results (Figure 4).

However, sequence and phylogeny based on the analysis of the 16S rDNA of the phytoplasma identified in *A. decedens*, even sharing similar RFLP profiles with those of the EAY reference control, clearly indicated that this phytoplasma belongs to 16Sr XII group, *Ca. P. solani*.

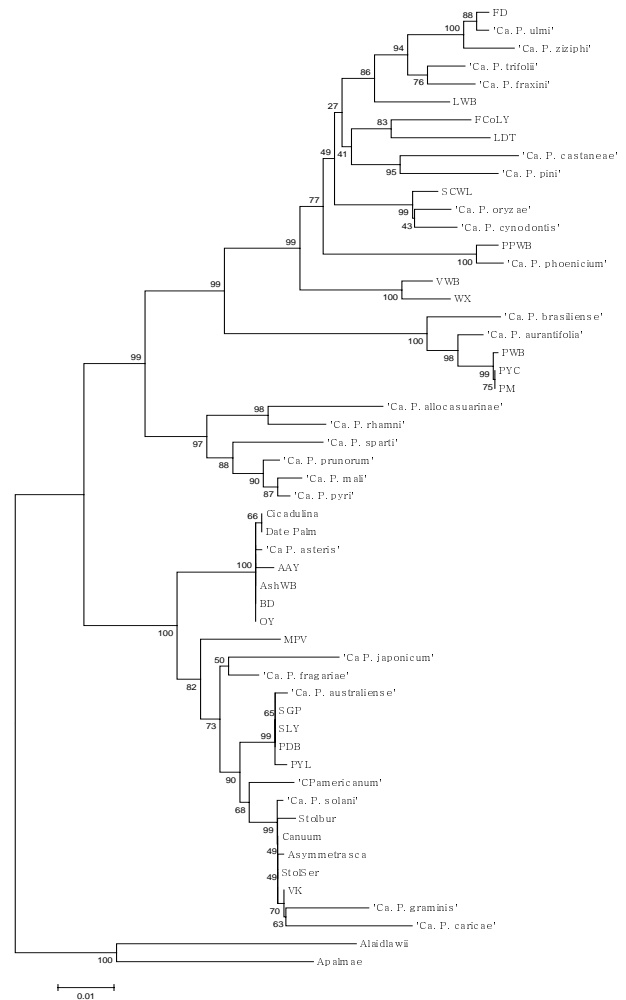


Figure 4. Phylogenetic tree of 16S rDNA sequences constructed by neighbour-joining method showing relationships between phytoplasmas detected in Date palm, *C. bipunctata*, and *A. decedens* with the rest of GenBank reference phytoplasmas analyzed. Numbers above the branches are bootstrap values obtained for 1000 replicates. The branch lengths are proportional to the number of inferred characters state transformation. Abbreviations of phytoplasmas are defined in Table 1.

RFLP analysis has proved to be a simple and rapid tool for the preliminary classification and identification of unknown phytoplasmas in a relatively short time (27, 38). However, it is possible that phytoplasmas belonging to different groups share similar RFLP patterns, whereas, isolates within a given group exhibit distinct RFLP profiles, thus, phytoplasma groups classified on the basis of this method are not always consistent with phylogenetic

grouping (27). Therefore, the sequence of the 16S rDNA gene reflects phylogenetic distance more accurately than restriction patterns which depend on significantly fewer genetic characters (38).

LY and LD type-diseases have been associated with phytoplasmas of 16SrIV group, *Ca. P. palmae* in East Africa (13, 16, 32, 41, 42), North America (22, 23), and Central America and the Caribbean (10, 29, 35, 44). However, other phytoplasma groups, different to 16SrIV, have been associated with phytoplasma diseases in coconut e.g. 16SrXI, *Ca. P. oryzae* and 16SrXII, *Ca. P. solani* with Kalimantan wilt in coconut in Indonesia (43). Recently in India, a possible new phytoplasma has been associated with Kerala wilt disease of coconut palms (39).

The 16SrI, *Ca. P. asteris* is the only phytoplasma group distributed worldwide and the most diverse in plant and insect hosts (28). It has been found in sandalwood in India (36), and safflower and carrot in Israel (34, 36). Results of our experiments extend this to date palms and putative associated species of *C. bipunctata* of Al-Hassa oasis.

Seemüller *et al.* (38) considered phytoplasmas as belonging to the same group if they showed 97% or more similarity between their sequences, while values less than 95% would place phytoplasmas in different groups or subgroups. El-Zayat *et al.* (19), identified a phytoplasma associated with Al-Wijam disease based on an 87% identity of 16S rDNA with that of the Florida lethal yellows phytoplasma; however, the amount of Al-Wijam samples where the phytoplasma was detected was not specified, and additionally it was not found in Al-Wijam affected date palms collected from our surveys.

The phylogenetic tree (Figure 4) reveals that the phytoplasma identified in date palm and *C. bipunctata* are phylogenetically distant from phytoplasmas of 16SrIV group. This phytoplasma showed a 98% identity of its 16S rDNA with that causing aster yellows (AF322644) of 16SrI group, and phylogeny results clearly support that it is a member of this group. This is the first report of the identification of the 16SrI phytoplasma in date palm, and contributes to the knowledge on the biodiversity of phytoplasmas associated with Al-Wijam disease in the

region. The fact that the 16SrXII phytoplasma was only detected in *A. decedens* and not in Al-Wijam affected date palms suggests that *A. decedens* may be an occasional feeder or visitor in the field, and is possibly associated with a disease in other plant host different from Al-Wijam in date palm.

The cixiid *M. crudus* was identified as the primary vector of LY in Florida (24), however, there have been few studies showing other *Hemiptera* species as candidates to vector LY or LD type-diseases. PCR and sequence analysis of the 16S rDNA have identified *Diastrombus mkurangai* and *Meenoplus* spp., (*Delphacidae*) as vector candidates of LD in Tanzania (33). *Sophonia* sp. and *Idioscopus clypealis* (*Cicadellidae*), and *Nisia nervosa* (*Meenoplidae*) have been proposed as the potential vectors for Coconut Kalimantan Wilt in Indonesia (43).

Leafhoppers, planthoppers and psyllids are the only known insect vectors of phytoplasma diseases (9, 30). Nowadays, research on phytoplasma has focused on the study of phytoplasma-insect vector interactions for further development of strategies to control phytoplasma diseases (8, 40) as it appears that vector control is the most effective if not the only way to stop the spread of phytoplasma diseases (21).

The 16S rDNA of the phytoplasma identified in *C. bipunctata* captured from Al-Wijam-affected date palms in Al-Hassa oasis, has shown a 100% identity with that of the date palm, and accordingly it has been identified as the potential vector of Al-Wijam disease. This is an important contribution for the future control of the disease in Al-Hassa, and points to *C. bipunctata* as the target for future transmission studies to confirm this species as the vector of the phytoplasma causing Al-Wijam disease in Saudi Arabia.

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المخلص

الهديب، خالد عبد الله، يايمان اروشا، م. ولسن وفيل جونس. 2007. الوصف والتشخيص الجزيئي للفيوتوبلازما من مجموعة الاستر المصاحبة لنخيل التمر في المملكة العربية السعودية. مجلة وقاية النبات العربية. 25: 116-122.

يصاب نخيل التمر (*Phoenix dactylifera* L.) بواحة الاحساء بالمملكة العربية السعودية بمرض يدعى الوجام. وتتخلص أعراضه باصفرار مخطط على أنصال الأوراق مترافق مع تقزم في الأوراق الجديدة مما يؤدي إلى انخفاض في إنتاج التمر في المراحل المتقدمة. قام الزيات وآخرون في عام 2002 بوصف المرض على أنه فيوتوبلازما من نوع الاصفرار المميت (Lethal Yellow). وتعتبر حشرة نطاط الأوراق (leafhopper) هي الحشرة الناقلة للفيوتوبلازما ولكن حتى الآن لم تدرس هذه الحشرة. تم جمع أكثر من 30 عينة أوراق نخيل مصابة وغير مصابة بالوجام مع 60 حشرة من المناطق المصابة بواحة الاحساء خلال 2003-2005. وقد تم استخلاص الحمض النووي (DNA) من العينات النباتية والحشرات السابقة وتطبيق تقنية تفاعل السلسلة المتبلورة (nested PCR) عليها وذلك باستخدام بادئات خاصة للتعرف على وجود الفيوتوبلازما (P1/P7-R16F2n/R16R2). تم اختبار الناتج من التفاعل السابق بـ RFLP وفك شيفرة الحمض النووي لـ 16S rDNA ومقارنتها بالفيوتوبلازما الموجوده في بنك الجينات. تم التعرف على وجود الفيوتوبلازما في 18 عينة من أوراق النخيل و 14 عينة تم اختبارها من الحشرات. ولم يكن هناك تفاعل ايجابي مع بعض الأوراق المصابة بنفس الأعراض. وقد كان هناك تطابق واضحاً في اختبار RFLP باستخدام الأنزيمات *Sau3AI* و *HhaI*، *DraI*، *KpnI*، *HpaII*، *TaqI*، *HinfI*، *AluI*، *RsaI*، وقد كانت شيفرة الحمض النووي لـ 16S rDNA للفيوتوبلازما متطابقة

100% مابين شيفرة النخيل (DQ913090) وشيفرة الحشرة الناقلة *Cicadulina bipunctata* (DQ913091)، و 98% مع اصفرار الامتار AF322644 من مجموعة *Candidatus Phytoplasma asteris* 16SrI. ويعتبر هذا التقرير الأول في دراسة مرض الفيتوبلازما التابع لهذه المجموعة كذلك الأول في تشخيص وتعريف الحشرة الناقلة للفيتوبلازما والتي تصيب النخيل بالملكة العربية السعودية. وهذا سوف يساعد في المستقبل في عمل دراسات حول انتقال الفيتوبلازما لنخيل التمر.

كلمات مفتاحية: فيتوبلازما، نخيل التمر، نشاط الأوراق، *Cicadulina bipunctata*، المملكة العربية السعودية
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