CVN CURRÍCULUM VÍTAE NORMALIZADO

María Carmen Marqués Romero

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GOBIERNO DE ESPAÑA
MINISTERIO DE CIENCIA E INNOVACIÓN

FECYT
FUNDACIÓN ESPAÑOLA PARA LA CIENCIA Y LA TECNOLOGÍA

Summary of CV

This section describes briefly a summary of your career in science, academic and research; the main scientific and technological achievements and goals in your line of research in the medium -and long- term. It also includes other important aspects or peculiarities.

phD Mª Carmen Marqués Romero with ID 52643826-T. Born on 05/11/1971. Married with two children.

1989-1997 I graduate at the UPV in Agricultural Engineering (Master Degree), with an average grade of 7.23 and
distinctions in the subjects Genetics and Agricultural Microbiology.

01/03/1997-30/10/1997 I receive a collaboration grant associated with the project "Analysis of harmful fungi in
agriculture" of the M.A.P.A for the analysis of the genetic variability of isolates of Plectosphaerella cucumerina.

12/11/1997 I defend my Final Degree Project entitled “Analysis of Vegetative Compatibility in the Plectosporium
tabacinum phytopathogenic fungus” with High Honors.

01/01/1998-31/12/2001 I obtain a predoctoral research fellowship (FPU) associated with the project "Studies of
remodeling mechanisms of extracellular matrix in plants in response to pathogens" of the MCyT for the
phenotypic, genetic and molecular characterization of mutants of A. thaliana showing alterations in the expression
of defense genes. I also developed molecular markers (SSLPs) to allow the identification and the chromosomal
mapping of mutations.

01/02/2002-31/01/2003 I receive a predoctoral fellowship from the CSIC-Bancaja Foundation to perform a
genomic analysis of the defensive response on an A. thaliana mutant defective in SAR. I used data obtained from
a DNA microarray (Affymetrix) provided by Novartis. This bioinformatic large-scale data analysis was one of the
first genomic studies conducted in Spain.

1999-2003 For four consecutive academic courses I teach the theoretical-practical seminar "Molecular markers
and their applications in biotechnology", of 6 hours each, in the subject Molecular Biology of Plants (5th course of
Agricultural Engineers).

07/14/ 2003-14 /12/2005 I work as a Research Technician in the project "Study of the response to biotic stresses
through functional genomics" of the MCyT for the construction of citrus cDNA libraries and the development of a
high-density cDNA microarray.

09/15/2005 I defend my doctoral thesis "Genetic and molecular characterization of mutants of A. thaliana altered
in the expression of defense genes", obtaining the highest honours of Magna cum laude.

12/15/2005–31/03/2008 I work as a Research Technician in the "Citrus Genome" project of the Ministry of
Agriculture to study the transcriptional responses of different citrus species against infection with the fungus
Phytophthora citrophthora .

07/24/2008–28/11/2011 I work as a phD Researcher in the projects "Identification of mitochondrial diseases
associated with dysfunctions in the process of transporting proteins to mitochondria" and "Genetic and molecular
basis of mitochondrial diseases associated with dysfunctions of the mitochondrial protein transport machinery
"financed by the FIS, in the IPPC. During this period I am in maternity leave for 16 weeks.

02/13/2012-12/31/2015 I work as a Research Technician with phD degree in the project "Role of protein
trafficking in the homeostasis of ions and nutrients in yeast" of the MEyC for the study of post-transcriptional
regulation of the integral plasmatic membrane ATPase Ena1. During this period I am in maternity leave for 16
weeks.

09/15/2016-31/12/2018 I work as a phD Researcher in the AGL2013-47886-R and AGL2016-79825-R projects of
the MEyC for the identification and characterization of miRNAs potentially involved in the stress response in
melon plants

General quality indicators of scientific research

This section describes briefly the main quality indicators of scientific production (periods of research activity, experience in supervising doctoral theses, total citations, articles in journals of the first quartile, H index...). It also includes other important aspects or peculiarities.

WoS RESEARCHER ID: AAC-8432-2019
ORCID: 0000-0001-8392-453X
Citas totales: 368 Citas (5 últimos años): 115 Índice h: 9 Índice i10: 8
Publicaciones con ISSN: 15 Capítulos en libros:1
Publicaciones en Q1: 14 Publicaciones en Q2: 1

María Carmen Marqués Romero

Surname(s):	**Marqués Romero**
Name:	**María Carmen**
ORCID:	**0000-0001-8392-453X**
ResearcherID:	**AAC-8432-2019**
Contact aut. region/reg.:	**Valencian Community**
Email:	**maricarmen_marques@yahoo.es**

Current professional situation

Employing entity: Consejo Superior de Investigaciones Científicas

Type of entity: State agency

Department: Diseño de Biosistemas, Instituto de Biología Integrativa de Sistemas

Professional category: Investigador Doctor

Educational Management (Yes/No): No

City employing entity: Paterna, Valencian Community, Spain

Phone: (+34) 963544171 - 44171

Email: maricarmen_marques@yahoo.es

Start date: 23/07/2020

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241000 - Human biology; 241500 - Molecular biology

Tertiary (UNESCO code): 230102 - Biochemical analysis; 230222 - Molecular pharmacology

Performed tasks: Desarrollo de sistemas de detección de virus, particularmente SARS-COV-2,basados en tecnología CRISPR para su aplicación en la mejora de los sistemas de diagnóstico y seguimiento epidemiológico, adaptándolos a la detección in situ mediante reacciones que no requieran personal ni aparataje especializado.

Identify key words: Natural sciences and health sciences

Field of management activity: General State Administration

Applicability in teaching and/or research: La tecnología basada en los sistemas de reconocimiento/procesamiento mediados por proteínas Cas está en auge dada su gran versatilidad para ser usada no sólo en modificación genética y terapia génica, sino también en sistemas de diagnóstico. Estos últimos están en constante evolución, implementándose con sistemas de amplificación isoterma, que se pueden realizar a temperaturas relativamente bajas y constantes, permitiendo el desarrollo de procesos rápidos, baratos y sencillos que pueden mejorar en gran manera la detección y el seguimiento de epidemias emergentes.

Previous positions and activities

	Employing entity	Professional category	Start date
1	Consejo Superior de Investigaciones Científicas	Investigador Doctor	16/12/2019
2	Consejo Superior de Investigaciones Científicas	Investigador Doctor	01/05/2017
3	Consejo Superior de Investigaciones Científicas	Investigador Doctor	15/09/2015

	Employing entity	Professional category	Start date
4	Universidad Politécnica de Valencia	Investigador Doctor	01/01/2012
5	Centro de Investigación Príncipe Felipe	Investigador Doctor	01/01/2009
6	Centro de Investigación Príncipe Felipe	Investigador Doctor	24/07/2008
7	Universidad Politécnica de Valencia	Investigador Doctor	01/03/2007
8	Universidad Politécnica de Valencia	Investigador doctor	01/03/2007
9	Universidad Politécnica de Valencia	Investigador doctor	15/12/2005
10	Universidad Politécnica de Valencia	Titulado Superior	14/07/2003
11	Universidad Politécnica de Valencia	Titulado Superior	01/02/2002
12	Universidad Politécnica de Valencia	Titulado Superior	01/01/1998
13	Universidad Politécnica de Valencia	Becario de colaboración	01/03/1997

1 **Employing entity:** Consejo Superior de Investigaciones Científicas **Type of entity:** State agency

Department: Redes reguladoras mediadas por ARN no codificante, Instituto de Biología Integrativa de Sistemas

City employing entity: Paterna, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** Yes

Start-End date: 16/12/2019 - 30/05/2020 **Duration:** 5 months - 19 days

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241502 - Molecular biology of plants

Performed tasks: Análisis informáticos de los datos obtenidos de la secuenciación masiva de pequeños RNAs de plantas sometidas a diferentes estreses (empleo de paquetes informáticos de bases de datos (Access), hojas de cálculo (Excel), procesado de secuencias (CutAdapt), análisis estadísticos (Edge, Deseq, Noiseq), y predictivos (miRCat, miRDeep), etc.), para la identificación de miRNAs asociados a la respuesta a estrés en plantas, así como la validación biológica de dichos resultados (stem-loop qRT-PCR, 5’ RLM-RACE, etc.). Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología), máster (Biotecnología Molecular y Celular de Plantas) y doctorado (Biotecnología) durante su fase de prácticas.

Identify key words: Molecular, cellular and genetic biology

Field of management activity: General State Administration

Applicability in teaching and/or research: Applicability in teaching and/or research: El ámbito de estudio de pequeños RNAs no codificantes está en pleno desarrollo y constituye uno de los componentes de las respuestas epigenéticas de los organismos. Se trata de mecanismos de regulación que se escapan de la visión tradicional de gen/proteína pero que tienen una gran relevancia, llegando en algunos casos a producirse modificaciones en el estado de la cromatina que podrían ser heredables. Al tratarse de pequeñas moléculas de ácidos nucleicos, muy estables y específicas, su conocimiento abriría nuevas puertas para la aplicación de la biotecnología en la mejora de las plantas para una adaptación más eficiente al medio y por lo tanto a una agricultura más sostenible. Esos conocimientos podrían también aplicarse en la detección y tratamiento de enfermedades en el ser humano, pues forman parte de un sistema de regulación prácticamente universal.

2 **Employing entity:** Consejo Superior de Investigaciones Científicas **Type of entity:** State agency

Department: Laboratorio de Redes de la Respuesta a Estrés, Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** Yes

Start-End date: 01/05/2017 - 31/12/2018 **Duration:** 1 year - 8 months

Type of contract: Temporary employment contract
Dedication regime: Full time
Primary (UNESCO code): 240000 - Life Science
Secondary (UNESCO code): 240900 - Genetics; 241500 - Molecular biology
Tertiary (UNESCO code): 240992 - Molecular genetics of plants; 241502 - Molecular biology of plants
Performed tasks: Trabajo como Investigador doctor en los proyectos AGL2013-47886-R ("Caracterización de la respuesta a estrés múltiple regulada por ncRNAs en cucurbitáceas. Bases para el diseño de estrategias integrales para la protección de cultivos") y AGL2016-79825-R ("Validación funcional de las redes de sncRNAs que regulan la respuesta a estrés en melón. Análisis de su potencial como fuente de tolerancia a condiciones ambientales adversas") financiados por MINECO PROYECTOS DE I+D+I, Programa Estatal Investigación, Desarrollo e Innovación Orientada a retos de la Sociedad. Me dedico a la identificación y caracterización de miRNAs potencialmente implicados en la respuesta a estrés en plantas de melón, llevando a cabo análisis informáticos de los datos obtenidos de la secuenciación masiva de pequeños RNAs de plantas sometidas a diferentes estreses, así como la validación biológica de dichos resultados. Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología), máster (Biotecnología Molecular y Celular de Plantas) y doctorado (Biotecnología) durante su fase de prácticas. Investigador principal: Dr. Gustavo Gómez (gustavo.gomez@csic.es)
Identify key words: Molecular, cellular and genetic biology
Field of management activity: University
Applicability in teaching and/or research: El ámbito de estudio de pequeños RNAs no codificantes está en pleno desarrollo y constituye uno de los componentes de las respuestas epigenéticas de los organismos. Se trata de mecanismos de regulación que se escapan de la visión tradicional de gen/proteína pero que tienen una gran relevancia, llegando en algunos casos a producirse modificaciones en el estado de la cromatina que podrían ser heredables. Al tratarse de pequeñas moléculas de ácidos nucleicos, muy estables y específicas, su conocimiento abriría nuevas puertas para la aplicación de la biotecnología en la mejora de las plantas para una adaptación más eficiente al medio y por lo tanto a una agricultura más sostenible. Esos conocimientos podrían también aplicarse en la detección y tratamiento de enfermedades en el ser humano, pues forman parte de un sistema de regulación prácticamente universal.

3 **Employing entity:** Consejo Superior de Investigaciones Científicas
Type of entity: State agency
Department: Laboratorio de Redes de la Respuesta a Estrés, Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
City employing entity: Valencia, Valencian Community, Spain
Professional category: Investigador Doctor
Educational Management (Yes/No): Yes
Start-End date: 15/09/2015 - 31/03/2017
Duration: 1 year - 6 months - 15 days
Type of contract: Temporary employment contract
Dedication regime: Full time
Primary (UNESCO code): 240000 - Life Science
Secondary (UNESCO code): 240900 - Genetics; 241500 - Molecular biology
Tertiary (UNESCO code): 240992 - Molecular genetics of plants; 241502 - Molecular biology of plants
Performed tasks: Trabajo como Investigador doctor en los proyectos AGL2013-47886-R ("Caracterización de la respuesta a estrés múltiple regulada por ncRNAs en cucurbitáceas. Bases para el diseño de estrategias integrales para la protección de cultivos") y AGL2016-79825-R ("Validación funcional de las redes de sncRNAs que regulan la respuesta a estrés en melón. Análisis de su potencial como fuente de tolerancia a condiciones ambientales adversas") financiados por MINECO PROYECTOS DE I+D+I, Programa Estatal Investigación, Desarrollo e Innovación Orientada a retos de la Sociedad. Me dedico a la identificación y caracterización de miRNAs potencialmente implicados en la respuesta a estrés en plantas de melón, llevando a cabo análisis informáticos de los datos obtenidos de la secuenciación masiva de pequeños RNAs de plantas sometidas

a diferentes estreses, así como la validación biológica de dichos resultados. Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología), máster (Biotecnología Molecular y Celular de Plantas) y doctorado (Biotecnología) durante su fase de prácticas. Investigador principal: Dr. Gustavo Gómez (gustavo.gomez@csic.es)

Identify key words: Molecular, cellular and genetic biology

Field of management activity: University

Applicability in teaching and/or research: El ámbito de estudio de pequeños RNAs no codificantes está en pleno desarrollo y constituye uno de los componentes de las respuestas epigenéticas de los organismos. Se trata de mecanismos de regulación que se escapan de la visión tradicional de gen/proteína pero que tienen una gran relevancia, llegando en algunos casos a producirse modificaciones en el estado de la cromatina que podrían ser heredables. Al tratarse de pequeñas moléculas de ácidos nucleicos, muy estables y específicas, su conocimiento abriría nuevas puertas para la aplicación de la biotecnología en la mejora de las plantas para una adaptación más eficiente al medio y por lo tanto a una agricultura más sostenible. Esos conocimientos podrían también aplicarse en la detección y tratamiento de enfermedades en el ser humano, pues forman parte de un sistema de regulación prácticamente universal.

4 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Mecanismos de la Respuesta al Estrés en Plantas: Estrés Abiótico-Transporte de potasio en estrés abiótico en plantas y levaduras, Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** Yes

Start-End date: 01/01/2012 - 31/12/2014 **Duration:** 3 years

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 240900 - Genetics; 241500 - Molecular biology

Tertiary (UNESCO code): 240992 - Molecular genetics of plants; 241502 - Molecular biology of plants

Performed tasks: Trabajo en el proyecto “Papel del tráfico de proteínas en la homeostasis de iones y nutrientes en levadura y plantas” (BFU2011-30197-C03-03), bajo la supervisión de la Dra. Lynne Yenush. Realizo un estudio en levaduras acerca del papel que miembros del complejo de secreción de proteínas tienen en la regulación transcripcional y post-traduccional de transportadores iónicos de membrana plasmática, realizando tareas básicas del manejo de levaduras (transformación, mutagénesis, goteos, etc.), así como análisis de co-localización de proteínas marcadas con fluorescencia (microscopía confocal) y detección y cuantificación de proteínas por Western blot, etc. Durante el proceso, utilizando una librería de expresión de Arabidopsis, realizo un escrutinio de interactores (Split-ubiquitin) con el transportador de potasio integral de membrana Kat1, contribuyendo así a la identificación de nuevos mecanismos de regulación de la apertura/cierre de estomas y a su aplicación biotecnológica para la obtención de plantas tolerantes a sequía e infecciones. Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología) Investigadora Principal: Dra. Lynne Yenush (lynne@ibmcp.upv.es)

Identify key words: Molecular, cellular and genetic biology

Field of management activity: University

Applicability in teaching and/or research: Los transportadores iónicos de membrana son elementos esenciales para la regulación de la homeostasis de iones. En particular, participan en la apertura y cierre de los estomas en plantas, con las implicaciones que ello tiene en el control del desarrollo vegetativo, la tolerancia a condiciones de estrés hídrico e incluso la resistencia a determinados tipos de patógenos. El uso de levaduras como organismos modelo nos ha permitido evaluar la importancia de la regulación postranscripcional de estas proteínas integrales de membrana, así como identificar posibles proteínas interactoras que puedan estar implicada en esta función. Los conocimientos generados podrían contribuir al desarrollo de nuevas herramientas de control de la apertura de estomas para ser aplicadas en la producción agrícola.

5 **Employing entity:** Centro de Investigación Príncipe Felipe **Type of entity:** Foundation

Department: Centro de Investigación Príncipe Felipe

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** No

Start-End date: 01/01/2009 - 28/11/2011 **Duration:** 2 years - 11 months

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241007 - Human genetics

Performed tasks: Trabajo en el proyecto “Bases genéticas y moleculares de enfermedades mitocondriales asociadas a disfunciones de la maquinaria mitocondrial de transporte de proteínas” (PI081157), financiado por “Fondo de Investigación Sanitaria. Instituto de Salud Carlos III”, bajo la dirección del Dr. José Hernández-Yago, para la identificación y caracterización de enfermos que presentan deficiencias en el metabolismo mitocondrial debidas a alteraciones en los complejos de transporte de membrana TOMM y TIMM. Mi trabajo se centra fundamentalmente en la búsqueda y localización de las mutaciones responsables y en el estudio de aquéllas que se encuentran en la región promotora. Para ello realizo labores propias del crecimiento y mantenimiento de cultivos celulares primarios (fibroblastos) así como tumorales (A204, HeLa), extractos nucleares, transfecciones (para ensayos de luminiscencia), inmunoprecipitación de cromatina, ensayos de retardo en gel (EMSA), entre otros.

Field of management activity: General State Administration

Applicability in teaching and/or research: Aproximadamente un 70% de las proteínas que tienen como destino las mitocondrias se encuentran codificadas en el ADN nuclear y se sintetizan en el citoplasma, por lo que han de ser transportadas al interior de la mitocondria para ejercer su función. Existen en la membrana mitocondrial complejos multienzimáticos encargados de realizar esta tarea tan fundamental. La mayoría de las enfermedades relacionadas con alteraciones mitocondriales se deben a mutaciones presentes en el ADN mitocondrial. No obstante, algunos pacientes presentan síntomas característicos de deficiencias de la función mitocondrial sin presentar defectos el ADN mitocondrial; en nuestro laboratorio nos encargamos de identificar y caracterizar molecularmente las causas de enfermedad en estos pacientes, especialmente cuando están implicados transportadores de membrana mitocondrial.

6 **Employing entity:** Centro de Investigación Príncipe Felipe **Type of entity:** Foundation

Department: Centro de Investigación Príncipe Felipe

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** No

Start-End date: 24/07/2008 - 31/12/2008 **Duration:** 5 months - 6 days

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241007 - Human genetics

Performed tasks: Trabajo en el proyecto "Identificación de enfermedades mitocondriales asociadas a disfunciones en el proceso de transporte de proteínas a mitocondrias” (PI052356), financiados por “Fondo de Investigación Sanitaria. Instituto de Salud Carlos III”, bajo la dirección del Dr. José Hernández-Yago, para la identificación y caracterización de enfermos que presentan deficiencias en el metabolismo mitocondrial debidas a alteraciones en los complejos de transporte de membrana TOMM y TIMM. Mi trabajo se centra fundamentalmente en la búsqueda y localización de las mutaciones responsables y en el estudio de aquéllas que se encuentran en la región promotora. Para ello realizo labores propias del crecimiento y mantenimiento de cultivos celulares primarios (fibroblastos) así como tumorales (A204, HeLa), extractos nucleares, transfecciones (para ensayos de luminiscencia), inmunoprecipitación de cromatina, ensayos de retardo en gel (EMSA), entre otros.

Field of management activity: General State Administration

Applicability in teaching and/or research: Aproximadamente un 70% de las proteínas que tienen como destino las mitocondrias se encuentran codificadas en el ADN nuclear y se sintetizan en el citoplasma, por lo que han de ser transportadas al interior de la mitocondria para ejercer su función. Existen en la membrana mitocondrial complejos multienzimáticos encargados de realizar esta tarea tan fundamental. La mayoría de las enfermedades relacionadas con alteraciones mitocondriales se deben a mutaciones presentes en el ADN mitocondrial. No obstante, algunos pacientes presentan síntomas característicos de deficiencias de la función mitocondrial sin presentar defectos el ADN mitocondrial; en nuestro laboratorio nos encargamos de identificar y caracterizar molecularmente las causas de enfermedad en estos pacientes, especialmente cuando están implicados transportadores de membrana mitocondrial.

7 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador Doctor **Educational Management (Yes/No):** No

Start-End date: 01/03/2007 - 31/03/2008 **Duration:** 1 year - 1 month

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241502 - Molecular biology of plants

Performed tasks: Trabajo en el proyecto “Genómica funcional de cítricos”, financiado por la Consellería de Agricultura, Pesca y Alimentación, bajo la dirección del Dr. Vicente Conejero y en colaboración con el Dr. Robert Shatters (US Department of Agriculture)., para el estudio de las variaciones en el transcriptoma de cítricos como consecuencia de la alimentación de insectos masticadores (Diaprepes abbreviatus) y chupadores (Brown Citrus Aphid y Asian Citrus Psyllid); realizando labores de hibridación de micromatrices de cDNA de cítricos, adquisición de imágenes (GenePix software) y el posterior análisis estadístico (Acuity software) y bioinformático (GeneCluster, Genesis software, Genevestigator database) para la identificación de posibles marcadores moleculares y su validación biológica (qPCR)

Field of management activity: Spanish Autonomous Region

8 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Professional category: Investigador doctor

Start-End date: 01/03/2007 - 31/03/2008 **Duration:** 1 year - 1 month

9 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Investigador doctor **Educational Management (Yes/No):** Yes

Start-End date: 15/12/2005 - 28/02/2007 **Duration:** 1 year - 2 months - 8 days

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241502 - Molecular biology of plants

Performed tasks: Trabajo en el proyecto “Genómica funcional de cítricos”, financiado por la Consellería de Agricultura, Pesca y Alimentación, bajo la dirección del Dr. Vicente Conejero para el estudio de las respuestas transcripcionales de diferentes especies de cítricos frente al ataque del hongo Phytophthora citrophthora con el fin de identificar posibles mecanismos genéticos de resistencia, realizando labores de hibridación de micromatrices de cDNA y posterior análisis estadístico y bioinformático de los resultados Asimismo actúo como codirectora de la tesis doctoral “Aproximaciones genómicas para el estudio del papel del ácido gentísico en la respuesta defensiva de plantas de tomate”.

Field of management activity: Spanish Autonomous Region

10 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Titulado Superior **Educational Management (Yes/No):** No

Start-End date: 14/07/2003 - 14/12/2005 **Duration:** 2 years - 4 months - 20 days

Type of contract: Temporary employment contract

Dedication regime: Full time

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241502 - Molecular biology of plants

Performed tasks: Trabajo en el proyecto “Estudio de la respuesta a estreses bióticos de cítricos mediante genómica funcional” (GEN 2001-4885-05-01 y GEN 2001-4885-05-02), del Ministerio de Ciencia y Tecnología, bajo la supervisión de los doctores Vicente Conejero y Miguel Ángel Pérez-Amador para la construcción de librerías de cDNA de cítricos de longitud completa y el desarrollo de una micromatriz de cDNA de cítricos de alta densidad (20K), para lo cual pongo a punto un protocolo de amplificación, normalización y clonaje de los transcritos en un vector binario de fácil manipulación (Gateway), que será posteriormente publicado en Methods in Molecular Biology (vol. 815).

Field of management activity: General State Administration

11 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain

Professional category: Titulado Superior **Educational Management (Yes/No):** No

Start-End date: 01/02/2002 - 31/01/2003 **Duration:** 1 year

Type of contract: Grant-assisted student (pre or post-doctoral, others)

Primary (UNESCO code): 240000 - Life Science

Secondary (UNESCO code): 241500 - Molecular biology

Tertiary (UNESCO code): 241502 - Molecular biology of plants

Performed tasks: Disfruto de una beca asociada al proyecto “Bases moleculares de la Interacción Planta-Patógeno” financiado por la Fundación CSIC-Bancaja, en el estudio de las variaciones en el transcriptoma de un mutante de A. thaliana afectado en la regulación del sistema defensivo SAR (Resistencia Sistémica Adquirida) en respuesta a una infección bacteriana. Para ello realizo el análisis estadístico y funcional de los datos provenientes de la hibridación de micromatrices de Affimetrix proporcionadas por Novartis a nuestro grupo, siendo éste uno de los primeros análisis genómicos realizados en España, que formará parte de mi tesis doctoral

Field of management activity: Fundación

12 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University

Department: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera

City employing entity: Valencia, Valencian Community, Spain
Professional category: Titulado Superior **Educational Management (Yes/No):** Yes
Start-End date: 01/01/1998 - 31/12/2001 **Duration:** 4 years
Type of contract: Grant-assisted student (pre or post-doctoral, others)
Primary (UNESCO code): 240000 - Life Science
Secondary (UNESCO code): 241500 - Molecular biology
Tertiary (UNESCO code): 241502 - Molecular biology of plants
Performed tasks: Disfruto de una beca FPU asociada al proyecto “Estudio de mecanismos de remodelación de matriz extracelular en organismos vegetales” (DIGICYT PB96-1055) y en el proyecto “Dinámica de la matriz extracelular de plantas durante el desarrollo y la defensa” (DIGICYT BMC2000-0762) del Ministerio de Ciencia y Tecnología para la caracterización fenotípica, genética y molecular de mutantes de Arabidopsis thaliana con alteraciones en la expresión de genes relacionados con la defensa vegetal frente a patógenos y daño mecánico. Realizo labores de mutagénesis, transgénesis, cruces dirigidos, seguimiento de marcadores genéticos (SSLPs), Northern blot, etc.
Field of management activity: University

13 **Employing entity:** Universidad Politécnica de Valencia **Type of entity:** University
Department: Producción Vegetal, Escuela Técnica Superior de Ingenieros Agrónomos
City employing entity: Valencia, Valencian Community, Spain
Professional category: Becario de colaboración **Educational Management (Yes/No):** Yes
Start-End date: 01/03/1997 - 30/10/1997 **Duration:** 8 months
Type of contract: Grant-assisted student (pre or post-doctoral, others)
Primary (UNESCO code): 240000 - Life Science
Secondary (UNESCO code): 241400 - Microbiology
Tertiary (UNESCO code): 241406 - Fungí
Performed tasks: Disfruto de una beca de colaboración asociada al proyecto “Servicio técnico de laboratorio de diagnóstico fitosanitario: Análisis y determinación de hongos perjudiciales en la agricultura” financiado por la Subdirección General de Sanidad Vegetal del M.A.P.A. en el aislamiento y caracterización de hongos fitopatógenos así como en el análisis de la variabilidad genética de aislados de Plectosphaerella cucumerina por medio del análisis de la compatibilidad vegetativa y de estudios sobre el DNA mitocondrial; que formarán parte de mi Trabajo Final de Carrera.

Education

University education

1st and 2nd cycle studies and pre-Bologna degrees

University degree: Higher degree
Name of qualification: Ingeniero Agrónomo
City degree awarding entity: Valencia, Valencian Community, Spain
Degree awarding entity: Universidad Politécnica de Valencia **Type of entity:** University
Date of qualification: 11/12/1997
Average mark: Good
Prize: Matrícula de honor en Microbiología y Genética

Doctorates

Doctorate programme: Biotecnología
Degree awarding entity: Universidad Politécnica de Valencia **Type of entity:** University
City degree awarding entity: Valencia, Valencian Community, Spain
Date of degree: 15/09/2005
DEA awarding entity: Universidad Politécnica de Valencia
Date DEA was awarded: 2003
European doctorate: Yes
Thesis title: Caracterización genética y molecular de mutantes de A. thaliana alterados en la expresión de genes de defensa
Thesis director: Pablo Vera Vera
Obtained qualification: Magna cum laude
Recognition of quality: Yes
Special doctorate award: No

Language skills

Language	Listening skills	Reading skills	Spoken interaction	Speaking skills	Writing skills
French	A1	A2	A1	A1	A1
English	C1	C2	C1	C1	C1
Catalan	C2	C2	C2	C2	C2
Spanish	C2	C2	C2	C2	C2

Teaching experience

Experience supervising doctoral thesis and/or final year projects

1 **Project title:** Redes de regulación de la respuesta a estrés mediadas por miRNAs
Type of project: Doctoral thesis
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Student: Alejandro Sanz Carbonell
Identify key words: Natural sciences and health sciences
Date of reading: 2020
European doctorate: No
Quality recognition: Yes

2 **Project title:** Análisis de las relaciones funcionales existentes entre la metilación de DNA y la respuesta a estrés por frío
Type of project: End of course project
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Student: Francisco José Gómez López
Obtained qualification: 9
Date of reading: 07/2019

3 **Project title:** Characterization of differentially expressed ta-siRNAs facing stress conditions in melon. Alumno: Luis Cervera Seco
Type of project: End of course project
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Student: Luis Manuel Cervera Seco
Obtained qualification: 10
Identify key words: Molecular, cellular and genetic biology
Date of reading: 07/2018

4 **Project title:** Caracterización funcional de miRNAs específicos de melón relacionados con la repuesta a estrés
Type of project: Minor thesis
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Student: Rafael García López
Obtained qualification: Sobresaliente
Identify key words: Molecular, cellular and genetic biology
Date of reading: 01/2018

5 **Project title:** Caracterización de miRNAs asociados a la respuesta a estrés por salinidad en plantas de melón
Type of project: Minor thesis
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Student: Andrés Sanz Rodríguez
Obtained qualification: Sobresaliente
Identify key words: Molecular, cellular and genetic biology
Date of reading: 10/2016

6 **Project title:** Caracterización de miRNAs asociados a la respuesta a estrés por sequía en plantas de melón
Type of project: Minor thesis
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Student: Pablo Estévez
Identify key words: Molecular, cellular and genetic biology
Date of reading: 10/2016

7 **Project title:** Detección y análisis de miRNAs implicados en la regulación de la repuesta a estrés en melón.
Type of project: End of course project
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Student: Beatriz Fernández Gómez
Obtained qualification: Sobresaliente
Date of reading: 07/2016

8 **Project title:** Aproximaciones genómicas para el estudio del papel del ácido gentísico en la respuesta defensiva de plantas de tomate.
Type of project: Doctoral thesis
Co-director of thesis: Vicente Conejero; Ismael Rodrigo Bravo
Entity: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Student: Mónica Díez Díaz
Obtained qualification: Sobresaliente cum laude
Identify key words: Molecular, cellular and genetic biology
Date of reading: 2009
European doctorate: No
Quality recognition: Yes

Scientific and technological experience

Scientific or technological activities

R&D projects funded through competitive calls of public or private entities

1 **Name of the project:** Rapid ultraspecific and portable SARS-COV-2 diagnostic based on CRISPR-Cas technologies and comercial COV-CRISPIS-COVID19
Entity where project took place: Instituto de Biología Integrativa de Sistemas
City of entity: Paterna, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): Guillermo Rodrigo; Gustavo Gómez; José Antonio Darós
Nº of researchers: 5
Funding entity or bodies:
CENTRO DE ACUSTICA APLICADA Y EVALUACION NO DESTRUCTIVA **Type of entity:** Associations and Groups

Start-End date: 01/06/2020 - 30/05/2021

2 **Name of the project:** Validación funcional de las redes de sncRNAs que regulan la respuesta a estrés en melón. Análisis de su potencial como fuente de tolerancia a condiciones ambientales adversas (AGL2016-79825-R)
Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National
Degree of contribution: Researcher
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): Gustavo Gómez
Nº of researchers: 4
Funding entity or bodies:
MINECO PROYECTOS DE I+D+I, Programa Estatal Investigación, Desarrollo e Innovación Orientada a retos de la Sociedad **Type of entity:** State agency
City funding entity: Madrid, Community of Madrid, Spain

Start-End date: 30/12/2016 - 30/12/2019
Total amount: 154.900 €
Dedication regime: Full time
Applicant's contribution: Análisis informáticos de los datos obtenidos de la secuenciación masiva de pequeños RNAs de plantas sometidas a diferentes estreses (empleo de paquetes informáticos de bases de datos (Access), hojas de cálculo (Excel), procesado de secuencias (CutAdapt), análisis estadísticos (Edge, Deseq, Noiseq), y predictivos (miRCat, miRDeep), etc.), para la identificación de miRNAs asociados a la respuesta a estrés en plantas, así como la validación biológica de dichos resultados (stem-loop qRT-PCR, 5' RLM-RACE, etc.). Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología), máster (Biotecnología Molecular y Celular de Plantas) y doctorado (Biotecnología) durante su fase de prácticas.

3 **Name of the project:** Caracterización de la respuesta a estrés múltiple regulada por ncRNAs en cucurbitáceas. Bases para el diseño de estrategias integrales para la protección de cultivos (AGL2013-47886-R)

Type of project: Basic research (including archaeological digs, etc)

Degree of contribution: Researcher

Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency

City of entity: Valencia, Valencian Community, Spain

Name principal investigator (PI, Co-PI....): Gustavo Gómez

Nº of researchers: 5

Funding entity or bodies:

MINECO PROYECTOS DE I+D+I, Programa Estatal Investigación, Desarrollo e Innovación Orientada a retos de la Sociedad **Type of entity:** State agency

City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member

Start-End date: 01/01/2014 - 30/06/2017

Total amount: 205.700 €

Dedication regime: Full time

Applicant's contribution: Análisis informáticos de los datos obtenidos de la secuenciación masiva de pequeños RNAs de plantas sometidas a diferentes estreses (empleo de paquetes informáticos de bases de datos (Access), hojas de cálculo (Excel), procesado de secuencias (CutAdapt), análisis estadísticos (Edge, Deseq, Noiseq), y predictivos (miRCat, miRDeep), etc.), para la identificación de miRNAs asociados a la respuesta a estrés en plantas, así como la validación biológica de dichos resultados (stem-loop qRT-PCR, 5’ RLM-RACE, etc.). Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología), máster (Biotecnología Molecular y Celular de Plantas) y doctorado (Biotecnología) durante su fase de prácticas.

4 **Name of the project:** Papel del tráfico de proteínas en la homeostasis de iones y nutrientes en levadura (BFU2011-30197-C03-03)

Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National

Degree of contribution: Researcher

Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency

City of entity: Valencia, Valencian Community, Spain

Name principal investigator (PI, Co-PI....): Joaquín Ariño; Lynne Yenush

Funding entity or bodies:

MINECO PROYECTOS DE I+D+I **Type of entity:** State agency

City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member

Start-End date: 01/01/2012 - 31/12/2014

Total amount: 136.730 €

Dedication regime: Full time

Applicant's contribution: Realizo un estudio en levaduras acerca del papel que miembros del complejo de secreción de proteínas tienen en la regulación transcripcional y post-traduccional de transportadores iónicos de membrana plasmática, realizando tareas básicas del manejo de levaduras (transformación, mutagénesis, goteos, etc.), así como análisis de co-localización de proteínas marcadas con fluorescencia (microscopía confocal) y detección y cuantificación de proteínas por Western blot, etc. Durante el proceso, utilizando una librería de expresión de Arabidopsis, realizo un escrutinio de interactores (Split-ubiquitin) con el transportador de potasio integral de membrana Kat1, contribuyendo así a la identificación de nuevos mecanismos de regulación de la apertura/cierre de estomas y a su aplicación biotecnológica para la obtención de plantas tolerantes a sequía e infecciones. Asimismo, realizo labores de dirección y supervisión del aprendizaje de estudiantes de grado (Biotecnología)

5 **Name of the project:** Bases genéticas y moleculares de enfermedades mitocondriales asociadas a disfunciones de la maquinaria mitocondrial de transporte de proteínas (PI081157)
Identify key words: Biomedicine
Identify key words: Molecular mechanism of disease
Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National
Degree of contribution: Researcher
Entity where project took place: Centro de Investigación Príncipe Felipe **Type of entity:** Foundation
City of entity: Valencia, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): José Hernández Yago
Funding entity or bodies:
Fondo de Investigación Sanitaria. Instituto de Salud Carlos III **Type of entity:** Healthcare Institutions
City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member
Start-End date: 01/01/2009 - 31/12/2011
Dedication regime: Full time
Applicant's contribution: Identificación y caracterización de enfermos que presentan deficiencias en el metabolismo mitocondrial debidas a alteraciones en los complejos de transporte de membrana TOMM y TIMM. Mi trabajo se centra fundamentalmente en la búsqueda y localización de las mutaciones responsables y en el estudio de aquéllas que se encuentran en la región promotora. Para ello realizo labores propias del crecimiento y mantenimiento de cultivos celulares primarios (fibroblastos) así como tumorales (A204, HeLa), extractos nucleares, transfecciones (para ensayos de luminiscencia), inmunoprecipitación de cromatina, ensayos de retardo en gel (EMSA), entre otros.

6 **Name of the project:** Identificación de enfermedades mitocondriales asociadas a disfunciones en el proceso de transporte de proteínas a mitocondrias (PI052356)
Identify key words: Biomedicine
Identify key words: Biomedicine
Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National
Degree of contribution: Researcher
Entity where project took place: Centro de Investigación Príncipe Felipe **Type of entity:** Foundation
City of entity: Valencia, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): José Hernández Yago
Funding entity or bodies:
Fondo de Investigación Sanitaria. Instituto de Salud Carlos III **Type of entity:** Healthcare Institutions
City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member
Start-End date: 01/01/2006 - 31/12/2008
Dedication regime: Full time
Applicant's contribution: Identificación y caracterización de enfermos que presentan deficiencias en el metabolismo mitocondrial debidas a alteraciones en los complejos de transporte de membrana TOMM y TIMM. Mi trabajo se centra fundamentalmente en la búsqueda y localización de las mutaciones responsables y en el estudio de aquéllas que se encuentran en la región promotora. Para ello realizo

labores propias del crecimiento y mantenimiento de cultivos celulares primarios (fibroblastos) así como tumorales (A204, HeLa), extractos nucleares, transfecciones (para ensayos de luminiscencia), inmunoprecipitación de cromatina, ensayos de retardo en gel (EMSA), entre otros.

7 **Name of the project:** Dinámica de la matriz extracellular de plantas durante el desarrollo y la defensa (DIGICYT BMC2000-0762)

Identify key words: Molecular, cellular and genetic biology

Identify key words: Molecular, cellular and genetic biology

Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National

Degree of contribution: Current university student

Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency

City of entity: Valencia, Valencian Community, Spain

Name principal investigator (PI, Co-PI....): Pablo Vera Vera

Funding entity or bodies:

Ministerio de Ciencia y Tecnología **Type of entity:** State agency

City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member

Start-End date: 01/01/2002 - 31/12/2004

Dedication regime: Full time

Applicant's contribution: Caracterización fenotípica, genética y molecular de mutantes de Arabidopsis thaliana con alteraciones en la expresión de genes relacionados con la defensa vegetal frente a patógenos y daño mecánico. Realizo labores de mutagénesis, transgénesis, cruces dirigidos, seguimiento de marcadores genéticos (SSLPs), Northern blot, etc.

8 **Name of the project:** Estudio de la respuesta a estreses bióticos de cítricos mediante genómica funcional (GEN 2001-4885-05-01 y GEN 2001-4885-05-02)

Identify key words: Molecular, cellular and genetic biology

Identify key words: Molecular, cellular and genetic biology

Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National

Degree of contribution: Researcher

Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency

City of entity: Valencia, Valencian Community, Spain

Name principal investigator (PI, Co-PI....): Vicente Conejero

Funding entity or bodies:

Ministerio de Ciencia e Innovación **Type of entity:** Público

City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member

Start-End date: 01/01/2002 - 31/12/2004

Dedication regime: Full time

Applicant's contribution: Estudio de las variaciones en el transcriptoma de cítricos como consecuencia de la alimentación de insectos masticadores (Diaprepes abbreviatus) y chupadores (Brown Citrus Aphid y Asian Citrus Psyllid); realizando labores de hibridación de micromatrices de cDNA de cítricos, adquisición de imágenes (GenePix software) y el posterior análisis estadístico (Acuity software) y bioinformático (GeneCluster, Genesis software, Genevestigator database) para la identificación de posibles marcadores moleculares y su validación biológica (qPCR)

9 **Name of the project:** Estudio de mecanismos de remodelación de matriz extracellular en organismos vegetales
Identify key words: Molecular, cellular and genetic biology
Identify key words: Molecular, cellular and genetic biology
Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National
Degree of contribution: Current university student
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera **Type of entity:** State agency
City of entity: Valencia, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): Pablo Vera Vera
Funding entity or bodies:
Ministerio de Ciencia y Tecnología **Type of entity:** State agency
City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member
Start-End date: 01/01/1998 - 15/12/2000
Dedication regime: Full time
Applicant's contribution: Caracterización fenotípica, genética y molecular de mutantes de Arabidopsis thaliana con alteraciones en la expresión de genes relacionados con la defensa vegetal frente a patógenos y daño mecánico. Realizo labores de mutagénesis, transgénesis, cruces dirigidos, seguimiento de marcadores genéticos (SSLPs), Northern blot, etc.

10 **Name of the project:** Servicio técnico de laboratorio de diagnostico fitosanitario: Análisis y determinación de hongos perjudiciales en la agricultura.
Identify key words: Plant disease
Type of project: Basic research (including archaeological digs, etc) **Geographical area:** National
Degree of contribution: Current university student
Entity where project took place: Universidad Politécnica de Valencia **Type of entity:** University
City of entity: Valencia, Valencian Community, Spain
Funding entity or bodies:
Subdirección General de Sanidad Vegetal del Ministerio de Agricultura, Pesca y Alimentación
City funding entity: Madrid, Community of Madrid, Spain

Type of participation: Team member
Start date: 01/01/1995
Dedication regime: Full time
Applicant's contribution: Aislamiento y caracterización de hongos fitopatógenos así como en el análisis de la variabilidad genética de aislados de Plectosphaerella cucumerina por medio del análisis de la compatibilidad vegetativa y de estudios sobre el DNA mitocondrial.

11 **Name of the project:** Rapid ultraspecific and portable SARS-COV-2 diagnostic based on CRISPR-Cas technologies and comercial COV-CRISPIS-COVID19
Entity where project took place: Instituto de Biología Integrativa de Sistemas
City of entity: Paterna, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): Guillermo Rodrigo; Gustavo Gómez; José Antonio Darós
Nº of researchers: 5
Funding entity or bodies:
CENTRO DE ACUSTICA APLICADA Y EVALUACION NO DESTRUCTIVA **Type of entity:** Associations and Groups

R&D non-competitive contracts, agreements or projects with public or private entities

1 **Name of the project:** Genoma de cítricos
Identify key words: Molecular, cellular and genetic biology
Type of project: Research and development, including transfer
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Degree of contribution: Researcher
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Name principal investigator (PI, Co-PI....): Vicente Conejero
Participating entity/entities: Instituto Valenciano de Investigaciones Agrarias ; Instituto de Agroquímica y Tecnología de Alimentos ; Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Funding entity or bodies:
Consellería d´Agricultura, Pesca i Alimentació
Type of entity: Público
City funding entity: Valencia, Valencian Community, Spain

Type of project: Coordination
Start date: 01/01/2005
Duration: 3 years
Total amount: 400.000 €

2 **Name of the project:** Bases moleculares de la Interacción Planta-Patógeno
Identify key words: Molecular, cellular and genetic biology
Type of project: Basic research (including archaeological digs, etc)
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Degree of contribution: Current university student
Entity where project took place: Instituto de Biología Molecular y Celular de Plantas Eduardo Primo Yúfera
Type of entity: State agency
City of entity: Valencia, Valencian Community, Spain
Funding entity or bodies:
Fundación CSIC-Bancaja
Type of entity: Foundation
City funding entity: Valencia, Valencian Community, Spain

Start date: 01/02/2002
Duration: 1 year
Identify key words: Molecular, cellular and genetic biology

Scientific and technological activities

Scientific production

Publications, scientific and technical documents

1 Alejandro Sanz Carbonell; Mª Carmen Marqués Romero; Germán Martínez; Gustavo Gómez. Dynamic architecture and regulatory implications of the miRNA network underlying the response to stress in melon. RNA Biology. 17 - 2, pp. 292 - 308. 2020. Available on-line at: <https://www.tandfonline.com/doi/full/10.1080/15476286.2019.1697487>. ISSN 1547-6286

DOI: 10.1080/15476286.2019.1697487

Type of production: Scientific paper
Format: Journal
Position of signature: 2
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee
Total no. authors: 4
Corresponding author: No
Impact source: ISI
Category: Biochemistry and Molecular Biology
Impact index in year of publication: 5.477
Journal in the top 25%: Yes
Position of publication: 44
No. of journals in the cat.: 299

Relevant results: Fourteen stress-responsive miRNAs were identified reactive to seven biotic and abiotic stress conditions in melon at two and four days post-treatment. According to our analysis miRNAs were categorized in three groups showing a broad-, intermediate- or narrow- response range. miRNAs reactive to a broad range of environmental cues appear as central components in the stress-response network. The strictly coordinated response of miR398 and miR408 (broad response-range) to the seven stress treatments during the period analysed here reinforces this notion. Although both, the amplitude and diversity of the miRNA-related response to stress changes during the exposition time, the architecture of the miRNA-network is conserved. This organization of miRNA response to stress is also conserved in rice and soybean supporting the conservation of miRNA-network organization in other crops. Overall, our work sheds light into how miRNA networks in plants organize and function during stress.

2 Antonella Locascio; Mª Carmen Marqués Romero; Guillermo García Martínez; Claire Corratgé Faillie; Lourdes Rubio; José A. Fernández; Anne-Aliénor Véry; José Miguel Mulet Salort; Lynne Paula Yenush. BCL2-ASSOCIATED ATHANOGENE4 Regulates the KAT1 Potassium Channel and Controls Stomatal Movement. Plant Physiology. 181 - 3, pp. 1277 - 1294. American Society of Plant Biologists, 2019. ISSN 0032-0889

DOI: DOI:10.1104/pp.19.00224

Type of production: Scientific paper
Format: Journal
Position of signature: 2
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee
Total no. authors: 9
Corresponding author: No
Impact source: ISI
Category: Science Edition - PLANT SCIENCES
Impact index in year of publication: 6.305
Journal in the top 25%: Yes
Position of publication: 10
No. of journals in the cat.: 228

Relevant results: KAT1 and its homolog KAT2 are the main inward rectifying channelspresent in guard cells, mediating K1influx into these cells, resulting in stomatal opening. To gain further insight into the regulation of these channels, we performed a split-ubiquitin protein-protein interaction screen searching for KAT1 interactors in Arabidopsis (Arabidopsis thaliana). We characterized one of these candidates, BCL2-ASSOCIATED ATHANOGENE4 (BAG4), in detail using biochemical and genetic approaches to confirm this interaction and its effect on KAT1 activity. We show thatBAG4 improves KAT1-mediated K1 transport in two heterologous systems and provide evidence that in plants, BAG4 interacts with KAT1 and favors the arrival of KAT1 at the plasma membrane. Importantly, lines lacking or overexpressing theBAG4 gene show altered KAT1 plasma membrane accumulation and alterations in stomatal movement. Our data allowed us to identify a KAT1 regulator and define a potential target for the plant BAG family. The identification of physiologically relevant regulatorsof K1 channels will aid in the design of approaches that may impact drought tolerance and pathogen susceptibility.

3 Luis Cervera Seco; Mª Carmen Marqués Romero; Alejandro Sanz Carbonell; Joan Márquez Mollins; Alberto Carbonell; José Antonio Daròs; Gustavo Gómez. Identification and Characterization of Stress-Responsive TAS3-Derived TasiRNAs in Melon. Plant and Cell Physiology. 60 - 11, pp. 2382 - 2393. Oxford Academic, 2019.

DOI: 10.1093/pcp/pcz131

Type of production: Scientific paper | **Format:** Journal

Position of signature: 2 | **Degree of contribution:** Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 7 | **Corresponding author:** No

Impact source: ISI | **Category:** Science Edition - PLANT SCIENCES

Impact index in year of publication: 3.929 | **Journal in the top 25%:** Yes

Position of publication: 23 | **No. of journals in the cat.:** 228

Relevant results: We provide the first comprehensive analysis of computationally inferred melon-tasiRNAs responsive to two biotic (viroid-infection) and abiotic (cold treatment) stress conditions. We identify two TAS3-loci encoding to length (TAS3-L) and short (TAS3-S) transcripts. The TAS candidates predicted from small RNA-sequencing data were characterized according to their chromosome localization and expression pattern in response to stress. The functional activity of cmTAS genes was validated by transcript quantification and degradome assays of the tasiRNA precursors and their predicted targets. Finally, the functionality of a representative cmTAS3-derived tasiRNA (TAS3-S) was confirmed by transient assays showing the cleavage of ARF target transcripts.

4 Alejandro Sanz Carbonell; Mª Carmen Marqués Romero; Antonio Bustamante; Mario A. Fares; Guillermo Rodrigo; Gustavo Gómez. Inferring the regulatory network of the miRNA-mediated response to biotic and abiotic stress in melon. BMC Plant Biology. 19, Springer Nature, 2019. Available on-line at: <https://doi.org/10.1186/s12870-019-1679-0>. ISSN 1471-2229

DOI: 10.1186/s12870-019-1679-0

Type of production: Scientific paper | **Format:** Journal

Position of signature: 2 | **Degree of contribution:** Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 5 | **Corresponding author:** No

Impact source: ISI | **Category:** Science Edition - PLANT SCIENCES

Impact index in year of publication: 3.670 | **Journal in the top 25%:** Yes

Position of publication: 30 | **No. of journals in the cat.:** 228

Relevant results: Pioneering analysis in melon plants in response to seven biotic and abiotic stress conditions. Deep-sequencing and computational approaches have identified twenty-four known miRNAs whose expression was significantly altered under at least one stress condition, observing that down-regulation was preponderant. Additionally, miRNA function was characterized by high scale degradome assays and quantitative RNA measurements over the intended target mRNAs, providing mechanistic insight. Clustering analysis provided evidence that eight miRNAs showed a broad response range under the stress conditions analyzed, whereas another eight miRNAs displayed a narrow response range. Transcription factors were predominantly targeted by stress-responsive miRNAs in melon. Furthermore, our results show that the miRNAs that are down-regulated upon stress predominantly have as targets genes that are known to participate in the stress response by the plant, whereas the miRNAs that are up-regulated control genes linked to development.

5 Antonio Bustamante; Mª Carmen Marqués Romero; Alejandro Sanz Carbonell; José Miquel Mulet Salort; Gustavo Gómez. Alternative processing of its precursor is related to miR319 decreasing in melon plants exposed to cold. Scientific Reports. 8, pp. 15538. Nature, 2018. ISSN 2045-2322

DOI: 10.1038/s41598-018-34012-7

Type of production: Scientific paper | **Format:** Journal

Position of signature: 2

Degree of contribution: Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 5
Corresponding author: No

Impact source: ISI
Category: Multidisciplinary
Impact index in year of publication: 4.011
Journal in the top 25%: Yes
Position of publication: 15
No. of journals in the cat.: 69

Relevant results: We analyzed data obtained by massive sRNA sequencing and 5′ - RACE to explore the accumulation and infer the processing of members of the miR319 family in melon plants exposed to adverse environmental conditions. Sequence data showed that miR319c was down regulated in response to low temperature. However, the level of its precursor was increased by cold, indicating that miR319c accumulation is not related to the stem loop levels. Furthermore, we found that a decrease in miR319c was inversely correlated with the stable accumulation of an alternative miRNA (#miR319c) derived from multiple processing of the miR319c precursor. Interestingly, the alternative accumulation of miR319c and #miR319c was associated with an additional and non-canonical partial cleavage of the miR319c precursor during its loop-to-base-processing. Our results provide new insights regarding the versatility of plant miRNA processing and the mechanisms regulating them as well as the hypothetical mechanism for the response to cold-induced stress in melon, which is based on the alternative regulation of miRNA biogenesis.

6 Maite Castellano; Germán Martínez; Mª Carmen Marqués Romero; Jesús Moreno; Claudia Köhler; Vicente Pallás; Gustavo Gómez. Changes in the DNA methylation pattern of the host male gametophyte of viroid-infected cucumber plants. Journal of Experimental Botany. 2016. ISSN 0022-0957

DOI: 10.1093/jxb/erw353

Type of production: Scientific paper
Format: Journal
Position of signature: 3
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 7
Corresponding author: No

Impact source: ISI
Category: Science Edition - PLANT SCIENCES
Impact index in year of publication: 5.830
Journal in the top 25%: Yes
Position of publication: 14
No. of journals in the cat.: 212

Relevant results: Our results indicate that in the pollen grain, accumulation of HSVd RNA induces a decondensation of the generative nucleus that correlates with a dynamic demethylation of repetitive regions in the cucumber genome that include rRNA genes and transposable elements (TEs). We therefore propose that HSVd infection impairs the epigenetic control of rRNA genes and TEs in gametic cells of cucumber, a phenomenon thus far unknown to occur in this reproductive tissue as a consequence of pathogen infection.

7 Silvia Petrezsélyová; María López Malo; David Canadell; Alicia Roque; Albert Serra Cardona; Mª Carmen Marqués Romero; Ester Vilaprinyó; Rui Alves; Lynne Yenush; Joaquín Ariño. Regulation of the Na+/K+-ATPase Ena1 Expression by Calcineurin/Crz1 under High pH Stress: A Quantitative Study. PloS ONE. 11 - 6, pp. e0158424. 2016.

DOI: 10.1371/journal.pone.0158424

Type of production: Scientific paper
Format: Journal
Position of signature: 6
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 10
Corresponding author: No

Impact source: ISI
Category: Multidisciplinary
Impact index in year of publication: 2.806
Journal in the top 25%: Yes
Position of publication: 15
No. of journals in the cat.: 64

Relevant results: Regulated expression of the Ena1 Na+-ATPase is a crucial event for adaptation to high salt and/or alkaline pH stress in the budding yeast Saccharomyces cerevisiae. ENA1 expression is under the control of diverse signaling pathways, including that mediated by the calcium-regulatable protein phosphatase calcineurin and its downstream transcription factor Crz1. We present here a quantitative study of the expression of Ena1 in response to alkalinization of the environment and we analyze the contribution of Crz1 to this response.

Experimental data and mathematical models substantiate the existence of two stress-responsive Crz1-binding sites in the ENA1 promoter and estimate that the contribution of Crz1 to the early response of the ENA1 promoter is about 60%. The models suggest the existence of a second input with similar kinetics, which would be likely mediated by high pH-induced activation of the Snf1 kinase.

8 Mª Carmen Marqués Romero; Sara Zamarbide Forés; Leda Pedelini; Vicente Llopis Torregrosa; Lynne Yenush. A functional Rim101 complex is required for proper accumulation of the Ena1 Na+-ATPase protein in response to salt stress in Saccharomyces cerevisiae. FEMS Yeast Reseach. 15 - 4, pp. fov017. Oxford University Press, 2015. ISSN 1567-1356

DOI: 10.1093/femsyr/fov017

Type of production: Scientific paper
Format: Journal
Position of signature: 1
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee
Total no. authors: 5
Corresponding author: No
Impact source: ISI
Category: Applied Microbiology and Biotechnology
Impact index in year of publication: 2.479
Journal in the top 25%: No
Position of publication: 61
No. of journals in the cat.: 161

Relevant results: The maintenance of ionic homeostasis is essential for cell viability, thus the activity of plasma membrane ion transporters must be tightly controlled. Previous studies in Saccharomyces cerevisiae revealed that the proper trafficking of several nutrient permeases requires the E3 ubiquitin ligase Rsp5 and, in many cases, the presence of specific adaptor proteins needed for Rsp5 substrate recognition. Among these adaptor proteins are nine members of the arrestin-related trafficking adaptor (ART) family. We studied the possible role of the ART family in the regulation of monovalent cation transporters. We show here that the salt sensitivity phenotype of the rim8/art9 mutant is due to severe defects in Ena1 protein accumulation, which is not attributable to transcriptional defects. Many components of the Rim pathway are required for correct Ena1 accumulation, but not for the accumulation of other nutrient permeases. Moreover, we observe that strains lacking components of the endosomal sorting complexes required for transport (ESCRT) pathway previously described to play a role in Rim complex formation present similar defects in Ena1 accumulation. Our results show that, in response to salt stress, a functional Rim complex via specific ESCRT interactions is required for the proper accumulation of the Ena1 protein, but not induction of the ENA1 gene.

9 José Miquel Mulet Salort; Vicent Llopis Torregrosa; Cecilia Primo Planta; Mª Carmen Marqués Romero; Lynne Yenush. Endocytic regulation of alkali metal transport proteins in mammals, yeast and plants. Current Genetics. 59, pp. 207 - 230. Springer Nature, 2013. ISSN 0172-8083

DOI: 10.1007/s00294-013-0401-2

Type of production: Scientific paper
Format: Journal
Position of signature: 4
Degree of contribution: Author or co-author of review
Total no. authors: 5
Corresponding author: No
Impact source: ISI
Category: Genetics and Heredity
Impact index in year of publication: 2.682
Journal in the top 25%: No
Position of publication: 76
No. of journals in the cat.: 167

Relevant results: The relative concentrations of ions and solutes inside cells are actively maintained by several classes of transport proteins, in many cases against their concentration gradient. These transport processes, which consume a large portion of cellular energy, must be constantly regulated. Many structurally distinct families of channels, carriers, and pumps have been characterized in considerable detail during the past decades and defects in the function of some of these proteins have been linked to a growing list of human diseases. The dynamic regulation of the transport proteins present at the cell surface is vital for both normal cellular function and for the successful adaptation to changing environments. The composition of proteins present at the cell surface is controlled on both the transcriptional and post-translational level. Post-translational regulation involves highly conserved mechanisms of phosphorylation- and ubiquitylation-dependent signal transduction routes used to modify the cohort of receptors and transport proteins present under any given circumstances. In this review, we will summarize what is currently known about one facet of this regulatory process: the endocytic regulation of alkali metal transport proteins. The physiological relevance, major contributors, parallels and missing pieces of the puzzle in mammals, yeast and plants will be discussed.

10 José Hernández Yago; Mª Carmen Marqués Romero; Abelardo Solano; Carles Marco; Jesús Ángel Prieto Ruiz; José Rafael Blesa. NRF-1 and GABP (NRF-2) transcription factors collaborate in regulating the expression of the human TOM7 gene. FEBS Journal. 278, pp. 251 - 252. 2011. ISSN 1742-464X

Type of production: Scientific paper
Format: Journal
Position of signature: 2
Degree of contribution: Author or co-author of article in journal without external admissions assessment committee
Total no. authors: 6
Corresponding author: No
Impact source: ISI
Category: Science Edition - BIOCHEMISTRY & MOLECULAR BIOLOGY
Impact index in year of publication: 3.790
Journal in the top 25%: No
Position of publication: 89
No. of journals in the cat.: 290

11 Mª Carmen Marqués Romero; Hugo Alonso Cantabrana; Javier Forment; Raquel Arribas; Santiago Alamar; Vicente Conejero; Miguel Ángel Pérez Amador. A new set of ESTs and cDNA clones from full-length and normalized libraries for gene discovery and functional characterization in citrus. BMC Genomics. 10, pp. 428. Springer Nature, 2009. ISSN 1471-2164

DOI: 10.1186/1471-2164-10-428

Type of production: Scientific paper
Format: Journal
Position of signature: 1
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee
Total no. authors: 7
Corresponding author: No
Impact source: ISI
Category: Science Edition - BIOTECHNOLOGY & APPLIED MICROBIOLOGY
Impact index in year of publication: 3.759
Journal in the top 25%: Yes
Position of publication: 28
No. of journals in the cat.: 152

Relevant results: We developed an integrated method to generate a new normalized EST collection enriched in full-length and rare transcripts of different citrus species from multiple tissues and developmental stages. We constructed a total of 15 cDNA libraries, from which we isolated 10,898 high-quality ESTs representing 6142 different genes. Percentages of redundancy and proportion of full-length clones range from 8 to 33, and 67 to 85, respectively, indicating good efficiency of the approach employed. The new EST collection adds 2113 new citrus ESTs, representing 1831 unigenes, to the collection of citrus genes available in the public databases. To facilitate functional analysis, cDNAs were introduced in a Gateway-based cloning vector for high-throughput functional analysis of genes in planta. Herein, we describe the technical methods used in the library construction, sequence analysis of clones and the overexpression of CitrSEP, a citrus homolog to the Arabidopsis SEP3 gene, in Arabidopsis as an example of a practical application of the engineered Gateway vector for functional analysis.

12 María Ángeles Martínez Godoy; Nuria Mauri; José Juárez; Mª Carmen Marqués Romero; Julia Santiago; Javier Forment; José Gadea. A genome-wide 20 K citrus microarray for gene expression analysis. BMC Genomics. 9, pp. 318 - 329. Springer Nature, 2008. ISSN 1471-2164

DOI: 10.1186/1471-2164-9-318

Type of production: Scientific paper
Format: Journal
Position of signature: 4
Degree of contribution: Author or co-author of article in journal with external admissions assessment committee
Total no. authors: 7
Corresponding author: No
Impact source: ISI
Category: Science Edition - BIOTECHNOLOGY & APPLIED MICROBIOLOGY
Impact index in year of publication: 3.926
Journal in the top 25%: Yes
Position of publication: 24
No. of journals in the cat.: 144

Relevant results: We have designed and constructed a publicly available genome-wide cDNA microarray that include 21,081 putative unigenes of citrus. As a functional companion to the microarray, a web-browsable database [1] was created and populated with information about the unigenes represented in the microarray, including cDNA libraries, isolated clones, raw and processed nucleotide and protein sequences, and results of all the structural and functional annotation of the unigenes, like general description, BLAST hits, putative Arabidopsis orthologs, microsatellites, putative SNPs, GO classification and PFAM domains. We have performed a Gene Ontology comparison with the full set of Arabidopsis proteins to estimate the genome coverage of the microarray. We have also performed microarray hybridizations to check its usability.

13 Javier Forment; José Gadea Vacas; Mª Carmen Marqués Romero; Vicente Conejero. Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies. BMC Genomics. 57 - 3, pp. 375 - 391. Springer Nature, 2005. ISSN 0167-4412

DOI: 10.1007/s11103-004-7926-1

Type of production: Scientific paper

Format: Journal

Position of signature: 30

Degree of contribution: Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 53

Corresponding author: No

Impact source: ISI

Category: Science Edition - PLANT SCIENCES

Impact index in year of publication: 3.328

Journal in the top 25%: Yes

Position of publication: 14

No. of journals in the cat.: 144

Relevant results: A functional genomics project has been initiated to approach the molecular characterization of the main biological and agronomical traits of citrus. As a key part of this project, a citrus EST collection has been generated from 25 cDNA libraries covering different tissues, developmental stages and stress conditions. The collection includes a total of 22,635 high-quality ESTs, grouped in 11,836 putative unigenes, which represent at least one third of the estimated number of genes in the citrus genome. Functional annotation of unigenes which have Arabidopsis orthologues (68% of all unigenes) revealed gene representation in every major functional category, suggesting that a genome-wide EST collection was obtained. A Citrus clementina Hort. ex Tan. cv. Clemenules genomic library, that will contribute to further characterization of relevant genes, has also been constructed. To initiate the analysis of citrus transcriptome, we have developed a cDNA microarray containing 12,672 probes corresponding to 6875 putative unigenes of the collection. Technical characterization of the microarray showed high intra- and inter-array reproducibility, as well as a good range of sensitivity. We have also validated gene expression data achieved with this microarray through an independent technique such as RNA gel blot analysis.

14 Paloma Abad Campos; Ana Pérez; Mª Carmen Marqués Romero; Mª José Vicente; B Bruton; José García Jiménez. Assessment of vegetative compatibility of Acremonium cucurbitacearum and Plectosphaerella cucumerina isolates from diseased melon plants. EPPO Bulletin. 30 - 2, pp. 199 - 204. Wiley Online Library, 2000. ISSN 1365-2338

Type of production: Scientific paper

Format: Journal

Position of signature: 3

Degree of contribution: Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 6

Corresponding author: No

Relevant results: One of the most important disease complexes of melon in Spain has been referred to as collapse, sudden wilt or vine decline. Acremonium cucurbitaceaum and Plectosphaerella cucumerina (anamorph Plectosporium tabacinum) are two of the fungi implicated in this disease complex. Genetic diversity among populations of these two plant pathogens has been approached by the assessment of vegetative compatibility using nitrate non-utilizing auxotrophs. In A. cucurbi- tacearum, with a host range limited to Cucurbiraceae and found in Spain and USA (California and Texas), 10 vegetative compatibility groups have been identified. Plectosphaerella cucu- merina has worldwide distribution and wide plant-host range. From a collection of P. cucumerina isolates with different plant and geographical origins, only four pairs have developed complementary heterokaryons when pairings of phenotypically distinct nit mutants (nit1 x NitM) were conducted. Each of the four vegetative compatibility groups consists of two members with close geographical origin and all the isolates were from diseased melon plants. Of the remaining P. cucumerina isolates, two did not produce nit mutants, two were self- incompatible and the others were vegetatively incompatible among themselves, suggesting that this fungal species may have wide genetic diversity in nature.

15 Esther Mayda; Mª Carmen Marqués Romero; Vicente Conejero; Pablo Vera Vera. Expression of a Pathogen-Induced Gene Can Be Mimicked by Auxin Insensitivity. Molecular Plant-Microbe Interactions. 13, pp. 23 - 31. APS Publications, 2000. ISSN 0894-0282

Type of production: Scientific paper **Format:** Journal

Position of signature: 2 **Degree of contribution:** Author or co-author of article in journal with external admissions assessment committee

Total no. authors: 4 **Corresponding author:** No

Relevant results: Following perception of a pathogenic attack, plants are able to develop a strong response with the corresponding activation of a plethora of defense-related genes. In this study we have characterized the mode of expression of the CEVI-1 gene from tomato plants, which encodes an anionic peroxidase. CEVI-1 expression is induced during the course of compatible viral and subviral infections, like many other defense-related genes, but is induced neither in incompatible interactions nor by signal mole-cules such as salicylic acid, ethylene, or methyl jas-monate. Additionally, CEVI-1 is induced in detached leaf tissues following a pathway distinct from that related to the classical wound response. We also describe the char-acterization of the structural CEVI-1 gene and compare the mode of expression in different transgenic plant spe-cies harboring a CEVI-1::GUS construct. Furthermore, we have isolated mutants in Arabidopsis, called dth mu-tants, that are deregulated in the control of expression of this gene. From the initial analysis of some of these mu-tants it seems that activation of CEVI-1 gene expression correlates with a defect in the perception of auxins by the plant. All these results may suggest that, during sys-temic infections with viruses, auxin homeostasis is one of the components participating in the regulation of the overall defense response.

16 Mª Carmen Marqués Romero; Miguel Ángel Pérez Amador. Construction and analysis of normalized and full-length cDNA libraries from citrus.Functional Genomics: Methods and Protocols. 815, pp. 51 - 66. Springer Nature, 2012. ISSN 1064-3745

Type of production: Book chapter **Format:** Book

Position of signature: 1 **Degree of contribution:** Author or co-author of chapter in book

Total no. authors: 2 **Corresponding author:** No

Relevant results: We have developed an integrated method to generate a normalized cDNA collection enriched in full-length and rare transcripts from citrus, using different species and multiple tissues and developmental stages. Interpretation of ever-increasing raw sequence information generated by modern genome sequencing technologies faces multiple challenges, such as gene function analysis and genome annotation. In this regard, the availability of full-length cDNA clones facilitates functional analysis of the corresponding genes enabling manipulation of their expression and the generation of a variety of tagged versions of the native protein. The development of full-length cDNA sequences has the power to improve the quality of genome annotation, as well as provide tools for functional characterization of genes.

Works submitted to national or international conferences

1 **Title of the work:** Characterization of miRNA-mediated response to multiple stress conditions in Cucumis melo.

Name of the conference: Small Molecules in Plant Research: Chemistry and Biology Come Together Symposium

Type of event: Conference **Geographical area:** European Union

Type of participation: Participatory - oral communication **Reasons for participation:** Open access

Corresponding author: No

City of event: Valencia, Valencian Community, Spain

Date of event: 10/12/2019

End date: 11/12/2019

Luis Manuel Cervera Seco; Joan Márquez Molins; Alejandro Sanz Carbonell; Gabriel Fernández Guzmán; Mª Carmen Marqués Romero; Gustavo Gómez. "Characterization of miRNA-mediated response to multiple stress conditions in Cucumis melo.".

2 **Title of the work:** Functional implications of stress-dependent miRNA misprocessing in Cucumis melo plants.
Name of the conference: Small Molecules in Plant Research: Chemistry and Biology Come Together Symposium
Type of event: Conference
Geographical area: European Union
Type of participation: Participatory - oral communication
Reasons for participation: Open access
Corresponding author: Yes
City of event: Valencia, Valencian Community, Spain
Date of event: 10/12/2019
End date: 11/12/2019
Gabriel Fernández Guzmán; Alejandro Sanz Carbonell; Joan Márquez Molins; Luis Manuel Cervera Seco; Gustavo Gómez; Mª Carmen Marqués Romero. "Functional implications of stress-dependent miRNA misprocessing in Cucumis melo plants.".

3 **Title of the work:** Inferring the relationship between differential methylation and siRNAs alterations in melon plants exposed to cold stress
Name of the conference: Small Molecules in Plant Research: Chemistry and Biology Come Together Symposium
Type of event: Conference
Geographical area: European Union
Type of participation: Participatory - oral communication
Reasons for participation: Open access
Corresponding author: No
City of event: Valencia, Valencian Community, Spain
Date of event: 10/12/2019
End date: 11/12/2019
Joan Márquez Molins; Luis Orduña; Luis Manuel Cervera Seco; Gabriel Fernández Guzmán; Mª Carmen Marqués Romero; Alejandro Sanz Carbonell; Gustavo Gómez. "Inferring the relationship between differential methylation and siRNAs alterations in melon plants exposed to cold stress".

4 **Title of the work:** Inferring the regulatory network of the miRNA-mediated response to stress in melon.
Name of the conference: Meeting Bioinformatics@Valencia
Type of event: Conference
Type of participation: 'Participatory - poster
Corresponding author: No
City of event: Valencia, Valencian Community, Spain
Date of event: 12/07/2018
End date: 12/07/2018
Alejandro Sanz Carbonell; Antonio Bustamante; Mª Carmen Marqués Romero; Gustavo Gómez.

5 **Title of the work:** MiRNA-dependent Regulatory Network Involved in Global Stress-response in Melon Plants
Name of the conference: XVI Solanacea and III Cucurbitacea Joint Conference
Type of event: Conference
Type of participation: 'Participatory - poster
Corresponding author: No
City of event: Valencia, Valencian Community, Spain
Date of event: 03/09/2017
End date: 06/09/2117
Alejandro Sanz Carbonell; Antonio Bustamante; Mª Carmen Marqués Romero; Wilson Davi Dávila; Manuel Gorritz; Belén Picó; Antonio Monforte; José Miguel Mulet Salort; Mario Fares; Gustavo Gómez.

6 **Title of the work:** Deciphering the post-transcriptional mechanisms underlying Ena1 accumulation in response to salt stress.
Name of the conference: 30th Small Meeting on Yeast Transport and Energetics.
Corresponding author: No
City of event: Salamanca, Castile and León, Spain
Date of event: 09/07/2012
End date: 12/07/2012
Mª Carmen Marqués Romero; Sara Zamarbide Forés; Leda Pedelini; Vicent Llopis Torregrosa; Lynne Paula Yenush.

7 **Title of the work:** NRF-1 and GABP(NRF-2) transcription factors collaborate in regulating the expression of the human TOM7 gene.
Name of the conference: 36th FEBS
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Turin, Italy
Date of event: 25/06/2011
End date: 30/06/2011
Mª Carmen Marqués Romero; Abelardo Solano; Carles Marco; Jesús Ángel Prieto Ruiz; José Rafael Blesa; José Hernández Yago.

8 **Title of the work:** A transcriptomic approach to study the response of different species of citrus plants to the infection with Phytophthora citrophthora.
Name of the conference: XIV International Congress on Molecular Plant-Microbe Interactions.
Type of event: Conference
Type of participation: 'Participatory - poster
Corresponding author: No
City of event: Quebec, Canada
Date of event: 19/07/2009
End date: 23/07/2009
Mª Carmen Marqués Romero; Laura Abizanda; Mónica Díez Díaz; José Gadea Vacas; Gisbert, A.; Hinarejos, C.; Pilar López Gresa; Mira, J.; Ismael Rodrigo; José Tuset; Vicente Conejero.

9 **Title of the work:** NRF transcription factors regulate the human genes encoding the subunits of the mitochondrial protein translocases.
Name of the conference: 34th FEBS
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Praga, Czech Republic
Date of event: 04/07/2009
End date: 09/07/2009
José Rafael Blesa; Jesús Ángel Prieto Ruiz; Abelardo Solano; Mª Carmen Marqués Romero; José Miguel Hernández; Carles Marco; Abraham, B.A.; Harrison, B.J.; Hegde, A.A.; José Hernández Yago.

10 **Title of the work:** Functional study of genes potentially involved in juvenile-to-adult transition in citrus plants identified by expression profiling.
Name of the conference: 11th International Citrus Congress
Type of event: Conference
Type of participation: 'Participatory - poster
Corresponding author: No

City of event: Wuhan, China
Date of event: 26/10/2008
End date: 30/10/2008
Gema Ancillo; Mª Eugenia Gas; José Gadea Vacas; Javier Forment; Juárez, J.; Mª Carmen Marqués Romero; Pina, J.A.; Luis Navarro.

11 **Title of the work:** Gentisic acid as a signal molecule in the defensive response of tomato plants.
Name of the conference: Reunió Conjunta de Genòmica i Proteómica de la Xarxa valenciana i la Xarxa catalana, i de la Secció de la SCB.
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Peñíscola, Spain
Date of event: 07/03/2008
End date: 08/03/2008
Mónica Díez Díaz; Mª Carmen Marqués; Antonio Granell; José Gadea Vacas; Ismael Rodrigo Bravo; Vicente Conejero.

12 **Title of the work:** Gentisic acid as a signal molecule in the defensive response of tomato plants.
Name of the conference: 6th Plant Genomics European Meetings
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Tenerife, Spain
Date of event: 03/10/2007
End date: 06/10/2007
Mónica Díez Díaz; Mª Carmen Marqués; Antonio Granell; José Gadea Vacas; Ismael Rodrigo Bravo; Vicente Conejero.

13 **Title of the work:** Transcriptomic analysis to study the role of gentisic acid as a signal molecule in the defensive response of tomato plants.
Name of the conference: 2nd International Workshop on: PR-proteins and Induced Resistance against Pathogens and Insects.
Type of event: Conference
Type of participation: Participatory - oral communication **Reasons for participation:** Open access
Corresponding author: No
City of event: Doorn, Holland
Date of event: 10/05/2007
End date: 14/05/2007
Mónica Díez Díaz; Mª Carmen Marqués Romero; Antonio Granell; José Gadea Vacas; Ismael Rodrigo Bravo; Vicente Conejero.

14 **Title of the work:** The Arabidopsis obi1 mutant as a tool for the analiysis of the local response to pathogens.
Name of the conference: XIII Internacional Conference on Arabidopsis Research
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Sevilla, Andalusia, Spain
Date of event: 28/06/2002
End date: 02/07/2002

Mª Carmen Marqués Romero; Brigitte Mauch Manni; Pablo Vera Vera.

15 **Title of the work:** Assessment of vegetative compatibility of Acremonium cucurbitacearum and Plectosporium tabacinum isolates from melon diseased plants.
Name of the conference: EPPO/MPU Conference on Cucurbitaceous and Solanaceous Vegetable Diseases in the Mediterranean Area.
Type of event: Conference
Type of participation: 'Participatory - poster **Reasons for participation:** Open access
Corresponding author: No
City of event: Kerkyra, Greece
Paloma Abad Campos; Ana Pérez; Mª Carmen Marqués Romero; Vicente, M.J.; Bruton, B.D.; José García Jiménez.