



I ENCUENTRO DE INVESTIGADORES EN EL MARCO DEL INSTITUTO DE INVESTIGACIÓN SANITARIA Y BIOMÉDICA DE ALICANTE (ISABIAL) – FUNDACION FISABIO

EGG, «EVOLUTIONARY GENOMICS GROUP»

Universidad Miguel Hernández
Dpto. Producción Vegetal y Microbiología

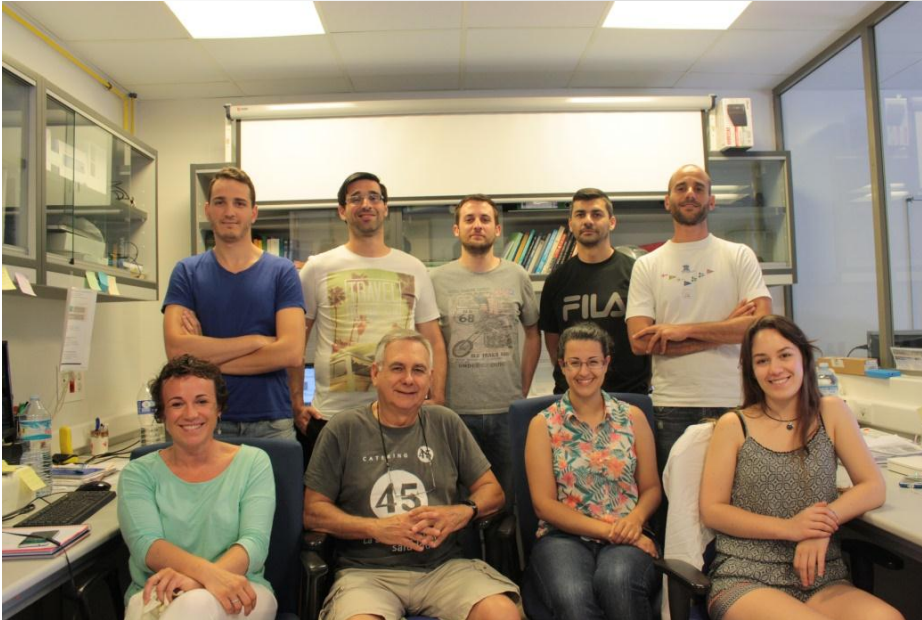
Francisco Rodríguez-Valera

*Hospital General Universitario de Alicante
7 de septiembre de 2016, 16:00 horas*



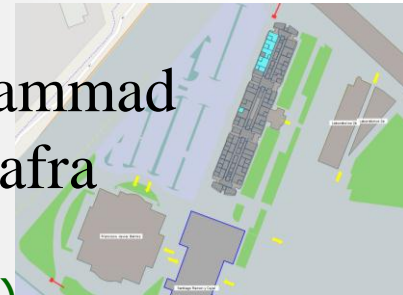
Grupo de investigación

- **Área:** Ciencias Experimentales, Genómica y Ecología Microbiana
- **Investigador principal:**
 - E-mail: frvalera@umh.es



Mario López Pérez
Ana Belén Martin Cuadrado
Riccardo Rosselli
José Manuel Haro Moreno
Pedro J Cabello
Nieves Ramón Marco
Rafael González Serrano

Muhammad
al Shafra



- **Investigadores colaboradores:**
 - Juan Carlos Rodríguez Díaz
(Servicio de Microbiología, Hospital General de Alicante)

Líneas Estratégicas

■ Principales líneas de investigación:

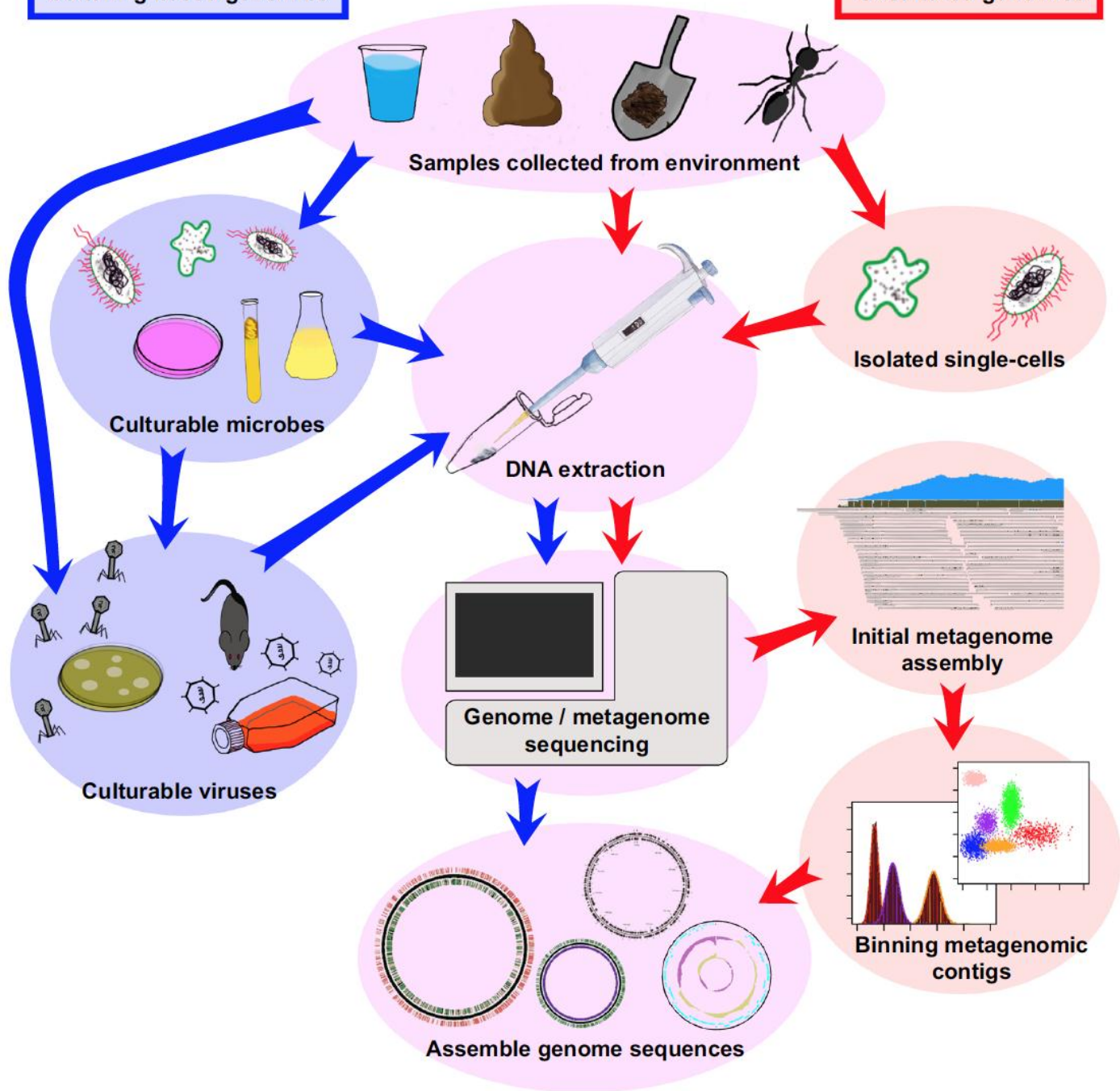
- projects*
- **MEDIMAX:** Third generation microbiology is used to decipher the biology of the microbes living in the Mediterranean DCM.
 - **MACUMBA:** uncover the untold diversity of marine microbes using cultivation-dependent strategies.
 - **AQUAMET:** high throughput metagenomics to solve microbiological water quality for water bodies that supply urban areas, specifically the reservoirs of Tous (Valencia) and Amadorio (Alicante). Different depths and seasons are studied during yearly cycles.
 - **(BAVILON).** Bacteria-virus Interactome Evolution.

Bibliografía & Colaboraciones Potenciales

- Tres publicaciones, del año 2011 al momento actual, más relevantes para el grupo:
 - Mizuno CM, Ghai R, Saghai A, López-García P, Rodríguez-Valera F. 2016. mBio 7(4):e00805-16. doi:10.1128/mBio.00805-16.
 - A new class of marine Euryarchaeota group II from the Mediterranean deep chlorophyll maximum. Martin-Cuadrado AB, Garcia-Heredia I, Moltó AG, López-Úbeda R, Kimes N, López-García P, Moreira D, Rodríguez-Valera F. ISME J. 2015 Jul;9(7):1619-34. doi: 10.1038/ismej.2014.249.
 - Expanding the marine virosphere using metagenomics. Mizuno CM, Rodríguez-Valera F, Kimes NE, Ghai R. PLoS Genet. 2013 Dec;9(12):e1003987. doi: 10.1371/journal.pgen.1003987. Cited 3 times.

Culturing-based genomics

Uncultured genomics



Mucha experiencia en Bioinformática

EGG. UMH. 2016 (8 servidores)

2.4 TB de RAM

272 procesadores

Almacenamiento: 160 TB

capacidad de cálculo

entre los más altos

de un laboratorio de Microbiología en Europa



Bibliografía & Colaboraciones Potenciales

- Necesidades / Intereses:

- Mayor poder computacional /
Mantenimiento (20.000 €/año)

CHINA. Sunway TaihuLight, 2016. (93 PFLOPS. M\$273)



- Sistemas de secuenciación: Illumina /MiSeq (60.000€)



Bibliografía & Colaboraciones Potenciales

- **Ámbitos complementarios:** Análisis de Genomas de animales (humanos) y plantas

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Human Whole Exome Sequencing Promotion

50X On-target Coverage at
\$399 USD

Advancing Human Whole Exome Sequencing with the State of the Art Agilent Capture Kit

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- **High quality data**
Illumina HiSeq PE150
Q30 > 80%
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- **Latest capture kit**
Agilent SureSelect Human
All Exon V6 KR (88M)
- **Wide-range of samples**
Accepting blood, saliva,
FFPE and fresh samples

Promotion valid until September 30, 2016. Minimum sample amount: 5 Samples
Turnaround time: 22 Working days after samples pass QC (for samples ≤ 20)

ExAC Browser (Beta) | Exome Aggregation Consortium

Search for a gene or variant or region

Examples - Gene: PCSK9, Transcript: ENST00000407236, Variant: 22-46615880-T-C, Multi-allelic variant: rs1800234, Region: 22:46615715-46615880

About ExAC

The [Exome Aggregation Consortium](#) (ExAC) is a coalition of investigators seeking to aggregate and harmonize exome sequencing data from a wide variety of large-scale sequencing projects, and to make summary data available for the wider scientific community.

The data set provided on this website spans 60,706 unrelated individuals sequenced as part of various disease-specific and population genetic studies. The ExAC Principal Investigators and groups that have contributed data to the current release are listed [here](#).

All data here are released under a [Fort Lauderdale Agreement](#) for the benefit of the wider biomedical community - see the terms of use [here](#).

Sign up for our mailing list for future release announcements [here](#).

Recent News

August 8, 2016

- CNV calls are now available on the ExAC browser

March 14, 2016

- Version 0.3.1 ExAC data and browser (beta) is released! ([Release notes](#))

January 13, 2015

- Version 0.3 ExAC data and browser (beta) is released! ([Release notes](#))

October 29, 2014

- Version 0.2 ExAC data and browser (beta) is released! Sign up for our mailing list for future release announcements [here](#).

October 20, 2014

- Public release of ExAC Browser (beta) at ASHG!

October 15, 2014

- Internal release to consortium now available!