

Curriculum Vitae:

Name: Francisco Díez Fuertes.

Year and place of birth: 1982, León. Spain.

Present position:

- 2016-present. Postdoctoral researcher. AIDS Immunopathology Unit, Instituto de Salud Carlos III (SPAIN) in collaboration with Fundación Clinic per la Recerca Biomedica.

Tertiary Education

- 2005. Bachelor in Biology, Faculty of Biology, Universidad de León (SPAIN).
- 2010. PhD in molecular virology. Thesis entitled "*Obtaining of vaccine-products against porcine reproductive and respiratory syndrome by Genetic Engineering techniques*". Department of Animal Health, Faculty of Veterinary Medicine, Universidad Complutense de Madrid (SPAIN).
- 2012. MSc in Bioinformatics and Computational Biology. Degree project entitled "*Molecular epidemiology of HIV-1: phylodynamics, antiretroviral resistances and in silico prediction of coreceptor usage*". Faculty of Chemical Sciences, Universidad Complutense de Madrid (SPAIN).

Positions and employment

- 2006-2010. PhD student (FPI fellowship of the Ministry of Education and Science). Saluvet group, Faculty of Veterinary Medicine, Universidad Complutense de Madrid (SPAIN).
- 2011. Postdoctoral researcher. Saluvet group, Faculty of Veterinary Medicine, Universidad Complutense de Madrid (SPAIN).
- 2011- 2012. Master student. HIV Biology and Variability Unit, Instituto de Salud Carlos III (SPAIN).
- 2013-2015. Postdoctoral researcher (Sara Borrell contract). AIDS Immunopathology Unit, Instituto de Salud Carlos III (SPAIN).

Experience in international institutions

- 2009. Granted stay (6 months) in the Department of Pathobiology, College of Veterinary Medicine, University of Illinois at Urbana-Champaign (USA).
- 2010. Granted stay (4 months) in the Department of Veterinary and Biomedical Sciences. Nebraska Center for Virology. University of Nebraska at Lincoln (USA).
- 2015-2016. Visiting scientist (8 months) in the Single Cell Unit. J. Craig Venter Institute at San Diego (USA).

Teaching activity

- 2014-present. Assistant professor of the Master of Infectious Diseases. Instituto de Salud Carlos III-Universidad de Alcalá (SPAIN)

Research areas of interest:

- Transcriptomic analyses of HIV-infected patients with extreme phenotypes (LTNPs, elite controllers)
- Transcriptome sequencing at Single cell level
- Systems Biology of virus-host interaction
- Evolution and adaptation in HIV-1 genes
- Molecular epidemiology and phylogeography of different genetic forms in HIV-1 pandemic

Involvement in research projects

- Study of genomic, antigenic and pathogenic variations in strains of the Porcine Reproductive and Respiratory Syndrome viruses isolated in Spain. Ministry of Science and Technology. 2006-2007.
- Antigenic characterization of Porcine reproductive and respiratory syndrome virus strains of

different origins and its relevance for the development of effective vaccines. Ministry of Science and Innovation. 2009-2011.

- Recombinant viruses as a method to obtain new vaccines against Porcine Reproductive and Respiratory Syndrome. Ministry of Science and Technology. 2006-2008
- Consolider-Ingenio 2010: Pathogenesis of porcine viral infections (PORCIVIR). Ministry of Education and Science 2006-2011.
- EUROPRISE: Rational design of HIV Vaccines and Microbicides. Commission of the European Communities, European Network of excellence. 2011-2012
- AIDS Research Network (RIS). HIV Immunopathogenesis and vaccine development program: Immunopathogenesis of HIV infection, immunotherapy and vaccine development. Ministry of Economy and Competitiveness. 2013-2016

Selected Publications

- Prieto C., Martínez-Lobo J., **Díez-Fuertes F.**, Aguilar-Calvo P., Simarro I., Castro J.M. Immunization of pigs with a major envelope protein sub-unit vaccine against porcine reproductive and respiratory syndrome virus (PRRSV) results in enhanced clinical disease following experimental challenge. *Veterinary Journal* 2011; 189(3):323-9.
- Martínez-Lobo F.J., **Díez-Fuertes F.**, Segalés J., García-Artiga C., Simarro I., Castro J.M., Prieto C. Comparative pathogenicity of type 1 and type 2 isolates of porcine reproductive and respiratory syndrome virus (prrsv) in a young pig infection model. *Veterinary Microbiology* 2011; 154(1-2):58-68.
- Martínez-Lobo F.J., **Díez-Fuertes F.**, Simarro I., Castro J.M., Prieto C. Porcine Reproductive and Respiratory Syndrome Virus isolates differ in their susceptibility to neutralization. *Vaccine* 2011; 9(40): 6928-40.
- **Díez-Fuertes F.**, Vázquez A., Hornillos-Gumiel L., Simarro I., Castro J.M., Martínez-Lobo F.J. Differentiation of type I porcine reproductive and respiratory syndrome virus vaccine and field strains by restriction fragment length polymorphism analysis. *SJAR* 2012; 10(1): 74-77.
- Thomson M.M., Fernández-García A., Delgado E., Vega Y., **Díez-Fuertes F.**, Sánchez-Martínez M., Pinilla M., Castro M.A., Mariño A., Ordoñez P., Ocampo A., Rodríguez da Silva A., Pérez-Castro S., López-Álvarez M.J., Trigo M., Pérez-Álvarez L. Rapid expansion of a HIV-1 subtype F cluster of recent origin among men who have sex with men in Galicia, Spain. *Journal of Acquired Immune Deficiency Syndrome* 2012; 59(3):e49-e51.
- **Díez-Fuertes F.**, Delgado E., Vega Y., Fernández-García A., Cuevas M.T., Pinilla M., García V., Pérez-Álvarez L., Thomson M.M. Improvement of HIV-1 coreceptor tropism prediction by employing selected nucleotide positions of env gene in a Bayesian network classifier. *Journal of Antimicrobial Chemotherapy* 2013; 68(7):1471-85.
- Regidor-Cerrillo J., **Díez-Fuertes F.**, García-Culebras A., Moore D.P., González-Warleta M., Cuevas C., Schares G., Katzer F., Pedraza-Díaz S., Mezo M., Ortega-Mora L.M. Genetic Diversity and Geographic Population Structure of Bovine Neospora caninum Determined by Microsatellite Genotyping Analysis. *PLoS One* 2013; 8(8):e72678.
- Martínez-Lobo F.J., de Lome L.C., **Díez-Fuertes F.**, Segalés J., García-Artiga C., Simarro I., Castro J.M., Prieto C. Safety of Porcine Reproductive and Respiratory Syndrome Modified Live Virus (MLV) vaccine strains in a young pig infection model. *Veterinary Research* 2013; 44:115.
- **Díez-Fuertes F.**, Cabello M, Thomson MM. Bayesian phylogeographic analyses clarify the origin of the HIV-1 subtype A variant circulating in former Soviet Union's countries. *Infect Genet Evol.* 2015; 33:197-205.
- Krishnaswami SR, Grindberg RV, Novotny M, Venepally P, Lacar B, Bhutani K, Linker SB, Pham S, Erwin JA, Miller JA, Hodge R, McCarthy JK, Kelder M, McCorrison J, Aevermann BD, **Díez-Fuertes F.**, Scheuermann RH, Lee J, Lein ES, Schork N, McConnell MJ, Gage FH, Lasken RS. Using

single nuclei for RNA-seq to capture the transcriptome of postmortem neurons. *Nature Protocols* 2016; 11(3):499-524.

- Vega Y, Delgado E, de la Barrera J, Carrera C, Zaballos Á, Cuesta I, Mariño A, Ocampo A, Miralles C, Pérez-Castro S, Álvarez H, López-Miragaya I, García-Bodas E, **Díez-Fuertes F**, Thomson MM. Sequence Analysis of In Vivo-Expressed HIV-1 Spliced RNAs Reveals the Usage of New and Unusual Splice Sites by Viruses of Different Subtypes. *PLoS One*. 2016; 11(6):e0158525.

Other merits

Contribution in scientific meetings:

- Due to my multidisciplinary scientific background I have participated in several international conferences of virology focused in different disciplines such as veterinary, medicine or computational biology. I have contributed during the last 8 years in 21 communications to scientific meetings such as the International symposium on emerging and re-emerging pig diseases, the International Pig Veterinary Society Congress, the International PRRSV Symposium, the Annual Meeting of the European Society for Clinical Virology, the International Conference on Infectious Disease Dynamics, the Spanish National Congress of Virology, the Pacific Symposium on Biocomputing and the NGS Data Analysis and Informatics Conference.

Computer literacy

- Operating systems: Windows, MSDOS, Unix, MAC OS.
- Programming: Perl, SQL and MySQL.
- Statistics: GraphPad Prism 5, SPSS, STATA, R Package.
- Machine learning: Weka3.
- Supercomputing: use of computer clusters to process genetic big data.
- Genetic sequences editing and processing: BioEdit, MEGA4, Jalview, Blast, Psi-blast, ClustalW, Toffee, Muscle, Mafft, blat, phmmer, jackhmmer, hmmbuild, hmmsearch.
- Computational Biology: analyses of data obtained by high throughput sequencing platforms (454, Illumina, Solid) and microarray technologies, protein structure prediction and docking, molecular evolution, phylogenetics, phylodynamics and phylogeographic studies.