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Title: A novel MMR pathway in prokaryotes

This seminar was part of the BioInfo4Women series.

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Abstract
Mismatch repair pathway (MMR) is essential to maintain genome stability. While MutS and MutL are essential for performing the initial and steps of the route, those are missing in many Archaea, most Actinobacteria, and other prokaryotes. However, these organisms exhibit similar spontaneous mutation rates to those bearing the MMR proteins.

We have reported NucS, as an endonuclease involved in Mismatch repair (MMR) with no structural homology to known MMR factors. By genetic screenings we found [1] that this protein is required for mutation avoidance and anti-recombination, hallmarks of the canonical MMR in the surrogate model *Mycobacterium smegmatis*, lacking classical MutS-MutL factors. Furthermore, phenotypic analysis of naturally occurring polymorphic NucS in a *M. smegmatis* surrogate model, suggests the existence of *M. tuberculosis* mutator strains.

Structural bioinformatics coupled to evolutionary studies of NucS indicate a complex making-up of the pathway that involved at least two horizontal gene transfers leading to a disperse distribution pattern in prokaryotes. Together, these findings indicate that distinct pathways for MMR have evolved at least twice in nature. Strikingly, the absence of any MMR protein (MutS/L or NucS) on few microoganisms, indicate that additional pathways are yet to be found. The analyses of these findings in the evolutionary context of the classical MMR proteins open novel and intriguing questions in the emergence of the MMR systems.

Short bio

I am a group leader of the Bioinformatics and Computational Biology Group at the Andalusian Center for Developmental Biology (CSIC) as Científico Titular. Biologist by training, I have specialized in Bioinformatics and Computational Biology via postdoctoral training in different labs in the US (as a NASA fellow in R.F. Doolittle's lab at UCSD, as an associate postdoctoral researcher at A. Godzik's lab in The Burnham Institute, San Diego). After almost 6 years of research abroad, I returned to Spain in 2003 to Alfonso Valencia's lab at CNB- CSIC, being a recipient of a Marie Curie International Reintegration Grant until I became independent Group Leader in 2009 in Badalona, at the Institute for Predictive and Personalized Medicine of Cancer (former IMPPC, now merged with IGTP). I moved to the Institute of Biomedicine of Seville in 2013 until July 2018.

Over the last years, my activities within the Group were related to both support and research. Our research interests focus on these lines: (i) emergence and evolution of signaling pathways, (ii) integration and data analyses for comparative genomics, (iii) and estimation of the impact of mutations in the protein function.