Las levaduras: en la intersección entre la Biología de sistemas y la Biomedicina
En memoria del Profesor Julio Rodríguez Villanueva

Yeasts: at the cross-roads of Systems biology and Biomedicine
In memory of Professor Julio Rodríguez Villanueva

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Writing the yeast genome

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Rapid advances in DNA synthesis techniques have made it possible to engineer diverse genomic elements, pathways, and whole genomes, providing new insights into yeast. The synthetic yeast genome project, Sc2.0 is well on its way with seven synthetic *Saccharomyces cerevisiae* chromosomes published and several more completed by a global team. The Sc2.0 genome features several systemic modifications, including deletion of subtelomeres, introns, tRNA genes, transposons and silent mating loci. Strategically placed loxPsym sites enable genome restructuring using an inducible evolution system termed SCRaMbLE (Synthetic Chromosome Rearrangement and Modification by LoxP-mediated Evolution). SCRaMbLE can generate millions of derived variant genomes with predictable structures leading to complex genotypes and phenotypes. The fully synthetic yeast genome provides a new kind of genetics based on variations in gene content and copy number. The 3D structure of synthetic and native chromosomes are very similar despite the substantial changes introduced. We also describe supernumerary designer "neochromosomes" that add new functionalities to cells such as humanization of metabolic pathways and even chromatin. A distinct approach involves karyotype engineering, or the ability to radically restructure genomes, e.g. the reduction of the number of chromosomes in *S. cerevisiae* from 16 to 2 with little apparent effect. Finally, we have automated our big DNA synthesis pipeline (the *GenomeFoundry@ISG*), opening the door to parallelized big DNA assembly, enabling the rapid assembly of a wide diversity of genetic pathways from other organisms.