Entry No. 8RGS-0060

Category	: 8th Rice Genetics Symposium
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	:
Genome biology Structure Function and Comparison Keyword 2	:
Genome biology Structure Function and Comparison Keyword 3	:
Title of Entry	: Manipulation of meiotic recombination in rice
Presenting author	: Emmanuel GUIDERDONI
Presenting author email	: guiderdoni@cirad.fr
Co author 1	: Delphine Mieulet, Ian Fayos, Julie Petit, Anne Cécile Meunier, Aurore Vernet, Sergi Navarro-Sanz, Brigitte Courtois, Christophe Périn,
Co author 2	: Giacomo Bastianelli, Alain Nicolas, Raphael Mercier
Affiliation presenting author	: Cirad, UMR AGAP, 34398 Montpellier Cedex 5 France and Université de Montpellier, Cirad, Inra, Supagro, 34000 Montpellier, France
Affiliation 1	: Cirad, UMR AGAP, 34398 Montpellier Cedex 5 France and Université de Montpellier, Cirad, Inra, Supagro, 34000 Montpellier, France
Affiliation 2	: Meiogenix, 38 rue Servan, 75011 Paris, France ;Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, Université Paris-Saclay, RD10, 78000 Versailles, France
Select only one type of presentation	: 15 minute oral presentation
Abstract	: Meiotic recombination is hampered by the restricted number of crossovers (CO) between homologous chromosomes and an overall limitation of CO number, the CO homeostasis. Recombination frequency may also vary by 100 fold across regions in large genomes, limiting access to genes of interest in « cold » regions. Here, we present two approaches aiming at either enhancing or redistributing COs in the rice genome. It has been recently shown that FIGL1, FANCM and RECQ4 limit CO formation in Arabidopsis thaliana : Inactivating one or a combination of two of these anti-CO factors conducts to a 3 to 10-fold increase in CO frequency without affecting meiotic progression. RECQ4 and FANCM are highly conserved DNA helicases that resolves recombination intermediates into non CO in a minor CO pathway that normally accounts for 10% of the COs in Arabidopsis. Here, we demonstrate that an Osrecq4l -/- japonica hybrid exhibits an average 3.3-fold CO increase and exhibits normal meiosis progression and seed fertility. A similar approach in an OsfanCM mutant context conducted to a 2.2-fold CO enhancement. This work is being expanded to a distant hybrid background. SPO11 is an essential protein for triggering CO formation at the initiation of meiosis through its capacity to induce with

several partners chromosomal double strand breaks (DSB). Based on a report in yeast, we determined whether the expression of the SPO11-1 coding sequence fused to the GAL4 binding domain (BD) -hereafter referred as SpiX1- can locally enhance CO frequency at GAL4 BD target sites in the rice genome. Genome wide recombination was examined in an aus x Spix1-japonica F2 population. The 4% intervals exhibiting the highest UAS density harbored a significant excess of recombinants in the Spix1 F2 population. Dense genotyping of 5 intervals exhibiting an excess of recombinants in the F2 population localized recombination break points in the vicinity of UAS sites. This approach is now being investigated in a spo11-1 mutant background. Progresses in targeting recombination through the use of a dCas9::SPO11 fusion will be also presented. Altogether, these results indicate that modulating recombination in rice is possible.

Read Less»

Uploaded Files »

No files found.