NUTRITIONAL GENOMICS: EVALUATING THE IMPACT OF MATERNAL NUTRITION ON THE EPIGENOME OF THE OFFSPRING USING MULTI-OMICS DATA

Peñagaricano F.U.F. Deparment of Animal Sciences, University of Florida, USA.
Email: fpenagaricano@ufl.edu

There is growing evidence that maternal nutrition can induce epigenetic modifications in the fetal genome, such as DNA methylation and histone modifications that alter gene expression, which in turn may lead to permanent phenotypic changes in the offspring with lifelong consequences. These epigenetic modifications depend on the availability of key compounds, such as methyl donors, supplied by different amino acids and vitamins present in the maternal diet. The link between maternal nutrition and subsequent modifications of the fetal genome is one of the molecular mechanisms proposed to explain the phenomenon of fetal programming. The long-term goal of this research is to integrate multiple sources of omics data, including genome-wide DNA methylation and whole transcriptome data, in order to understand the mechanisms underlying the impact that maternal diets have on the offspring epigenome and subsequent overall performance. In particular, this research is intended to respond (1) whether a maternal methyl supplemented diet increases the DNA methylation of the offspring genome, (2) whether these DNA methyl marks are transient or persist across time, (3) whether DNA methylation modulates gene expression, and finally (4) if there are specific functional categories of genes that underlay fetal developmental programming. A deep comprehension of the epigenomic mechanisms underlying the impact that maternal nutrition has on the phenotype of the offspring will benefit not only livestock production but may also have a great impact on human health.

NON-RANDOM DISTRIBUTION OF rDNA SITES IN PLANT CHROMOSOMES

Guerra M. Universidade Federal de Pernambuco (UNIVE), Recife, Brasil.
Email: msfguerra@hotmail.com

5S and 45S rDNA sites are two of the best known chromosome regions of eukaryotic chromosomes and have been mapped in more than a thousand plant species. A meta-analysis of this data strongly suggests that the distribution of these sites in the chromosomes is not randomized but rather biased by the existence of "preferential regions". The 45S rDNA sites have a strong preference for terminal regions of chromosomes, especially in the short arms, whereas the 5SrDNA sites are more commonly found in the proximal regions, mainly in small chromosomes. Surprisingly, the occurrence of both sites in a single chromosome is higher than expected in a random distribution and it is still higher when we consider the occurrence of 5S and 45S sites adjacent to each other. Taking into consideration only the six groups of plants that we have more intensively investigated in the last 10 years [*Citrus*, *Phaseolus*, *Nothoscordum*, *Rhynchospora* (including their related genera), *Cuscuta*, and *Oxalis*] we found evidence that: a) both rDNA sequences are frequently jumping from one position to another; b) closely related *taxa* may have quite different patterns of rDNA site dispersion; c) the 45S sequences are more active travelers than 5S; d) their meeting into close proximity is quite common but it is not preserved during the evolution of the genera. The meaning of these data are discussed and compared with the other repetitive sequences.

QUANTITATIVE GENETICS: CONNECTING THE GENOTYPE, PHENOTYPE AND THE ENVIRONMENT FROM SATELLITES TO GENES

Gutierrez L.[1,2]. [1]Agronomy Department, University of Wisconsin-Madison, USA. [2]Facultad de Agronomía, UDELAR, Uruguay.
Email: gutierrezcha@wisc.edu

Since the advent of agriculture, plant breeding has successfully improved plants for human benefit. Modern plant breeding activities consists in evaluating the genetic merit of lines discerning genetic from environment and noise components. To do so, modern plant breeding relies on the genetics foundations derived from Mendel's work and statistical tools generated afterwards. Plant breeding activities could be grouped in three categories: traditional, marker assisted (MAS), and genomic selection (GS). Traditional plant breeding uses either *per se* phenotypic information, or information from relatives to evaluate their genetic value. MAS on the other hand, involves the identification of markers linked to genes or quantitative traits loci, and then selects individuals based on their marker scores. Finally, GS involves the prediction of the genetic merit of individuals based on their marker scores and a statistical model. All of the three strategies require the evaluation of large number of individuals creating massive amounts of data that needs proper analyses. Our objective was to present some strategies to connect the genotype, the phenotype, and the environment. First, we used novel approaches to improve phenotyping comparing the use of experimental design and spatial corrections in the context of genotypic evaluations. Second, we proposed strategies for modeling genotype by environment interaction in genomic studies. Using all tools available, from satellites to genes, has become a key component in plant breeding activities and large genomic evaluations.