Inheritance and programming of parental DNA methylomes in mammals

Supported by the National Natural Science Foundation of China (Grant Nos. 91219104 and 81171902), the research groups led by Dr. Liu Jiang at Beijing Institute of Genomics, CAS and by Dr. Huang Xingxu from Nanjing University, reported their discovery on the inheritance and programming of parental DNA methylomes in mammals in *Cell* (**2014**, 157 (7): 979—991).

DNA methylation is a highly conserved covalent modification of DNA and plays essential roles in development, genome stability, and genomic imprinting. Two waves of demethylation are observed during primordial germ cell (PGC) development and early embryogenesis. Based on the results from cell immunostaining, paternal 5-methylcytosines (5mCs) have been proposed to be actively converted to oxidized bases. These paternal oxidized bases and maternal 5mCs are believed to be passively diluted by cell divisions. However, with single-base resolution, allele-specific DNA methylomes of gametes and early embryos, as well as single-base resolution maps of oxidized cytosines, scientists have revealed that the oxidized derivatives of 5mC present in both maternal and paternal genomes. It has been further proved that paternal methylome and at least a significant proportion of maternal genome undergo active demethylation independent of passive dilution. Besides, all the known imprinting control regions (ICRs) are classified into germline or somatic ICRs. This study not only revised our knowledge on the methylome reprogramming during mammalian early embryogenesis, but also provided invaluable evolutionary insight into genomic imprinting and demethylation.

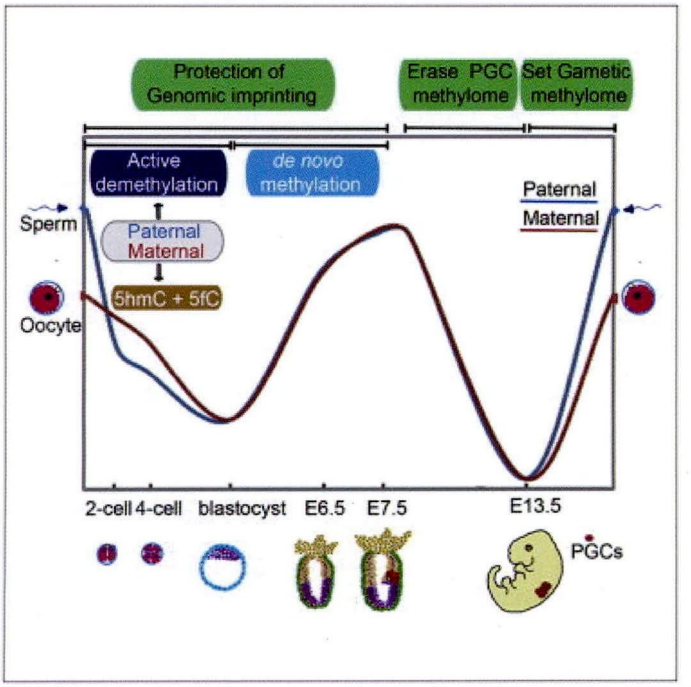

Figure Two waves of genome-wide demethylation in mammals. 5hmC and 5fC present in both maternal and paternal genomes. Genome-wide demethylation is mainly through active demethylation in both paternal and maternal genomes, which is independent of the passive dilution of 5mC or its oxidized derivatives.