

gest that the non-random movement to one pole is indicative of normally occurring non-random segregation of chromosomes. Conclusions: There are two suggestive pieces of evidence that there is non-random segregation in *Mesostoma* spermatocytes. Our experiments add a third piece of evidence. We hope to test further for non-random segregation using micromanipulation techniques to move chromosomes around in the cell, and to mate our strain with European strains of the same species that have different chromosome configurations.

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Common and distinct roles of the isoforms of histone variant H2A.Z in transcriptional regulation

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Nucleosomes consisting of DNA and core histones are the basic units of chromatin and play central roles in the regulation of genome functions. Histone variants are structurally similar to canonical histones, and the ex-

change of canonical histones to their variants contributes to chromatin modulation and various epigenetic regulations. H2A.Z is an evolutionarily conserved H2A variant reportedly involved in the regulation of genome functions, including chromosomal segregation and transcriptional regulation. However, molecular mechanisms of H2A.Z functions have not been fully elucidated. In particular, molecular functions of two isoforms of vertebrate H2A.Z (H2A.Z.1 and H2A.Z.2) have not been analyzed specifically. On the other hand, when considering the biological phenomena, only H2A.Z.2 reportedly has a role in driving malignant melanoma (Vardabasso *et al*, *Mol Cell*, 59, 2015). To investigate molecular functions of the H2A.Z isoforms, we established gene knockout cells for H2A.Z.1- or H2A.Z.2-regulated genes with chicken DT40 cells (Z.1-KO or Z.2-KO cells, respectively). We found that some, but not all, genes are differently dysregulated in Z.1-KO and Z.2-KO cells. Genes for transcriptional regulators, including cancer associated genes, are differently dysregulated in Z.1-KO and Z.2-KO cells, especially under oxidative stress conditions. Chromatin immunoprecipitation analysis revealed that H2A.Z.1 and H2A.Z.2 have common and distinctive roles in the regulation of these genes. Our study showed that H2A.Z.1 and H2A.Z.2 have common and distinctive functions in epigenetic regulation.

Reference: Vardabasso, C., Gaspar-Maia, A., Hasson, D., Pünzeler, S., Valle-Garcia, D., Straub, T., ... Bernstein, E. (2015). Histone Variant H2A.Z.2 Mediates Proliferation and Drug Sensitivity of Malignant Melanoma. *Molecular Cell*, 59(1), 75–88. <https://doi.org/10.1016/j.molcel.2015.05.009>