

【Grant-in-Aid for Specially Promoted Research】

Biological Sciences



Title of Project : The roles and mechanisms of chromatin memory in the robust responses under fluctuating environments

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【Purpose and Background of the Research】

Global warming is expected to drastically alter ecosystems within decades, and perturbations in biological interactions will result in the spread of infectious diseases among both animals and plants. As plants constitute the majority of biomass on earth and stand as the source of the energy flow of ecosystems, it is important to predict how plants will respond to the earth's environmental changes. The prediction should be based on an understanding of the underlying mechanisms of organismal responses. Recent molecular biology has shown the importance of 'chromatin memory', which functions across cell divisions and even across generations.

The trimethylation of the 27th lysine of histone H3 (H3K27me3) plays a key regulatory role in the development of animals; interestingly, in plants, one of its functions is to identify a specific season for reproduction based on temperature. The applicant has shown, using an approach in which multiple histone modifications were monitored biweekly for two years (unpublished), that multiple histone modifications change drastically across seasons and that chromatin memory plays critical roles in many aspects of plant seasonality other than reproduction. Insights obtained from the analyses of these data are expected to reveal the crosstalk between different histone modifications during the formation of chromatin memory and the ecological functions of this memory. Since plant disease and herbivory are the types of factors through which plant fitness is enhanced using chromatin memory, revealing the mechanism and function of such memory will have a large impact on society. Therefore, we have planned an integrative study with the following three aims.

- A. To reveal the novel mechanisms of long-term chromatin memory.
- B. To determine the targets of long-term chromatin memory for responses to novel environmental factors.
- C. To reveal the ecological functions of long-term chromatin memory.

【Research Methods】

We will establish an experimental system in which histone-modification-mediated environmental responses can be introduced on the control of a transgene. By analyzing the system, we will identify a novel mechanism responsible for the accumulation and removal of a repressive histone mark.

Using a molecular genetic approach, the crosstalk between epigenetic modifications will be studied extensively concerning the de novo establishment and inheritance of long-term chromatin memory.

From our long-term field data, we identified a gene that precisely follows the temperature changes, and may regulate its target. We will use this factor as a tool to determine the targets of the novel temperature sensing system. Based on the previous finding that there is seasonality in the gene expression responses of host plants against virus infection. Using the plant-plant virus system, we will determine how histone modifications are altered and identify target genes.

We will further test, using a series of field and growth chamber experiments, how temperature-dependent alterations in histone modification change the defence levels against herbivores, pathogens, and viruses.

【Expected Research Achievements and Scientific Significance】

The project is important because it will effectively identify novel factors and crosstalk between multiple factors in chromatin regulation. By applying single-cell analyses, we will study causal relations between different epigenetic marks, environmental factors, and gene expression. We will also study the functions of chromatin memory in natural environments and thereby bridge chromatin biology and ecology. This is a completely novel step for chromatin biology.

【Publications Relevant to the Project】

- Nishio H, Nagano AJ, Ito T, Suzuki Y, Kudoh H (2020) Seasonal plasticity and diel stability of H3K27me3 in natural fluctuating environments. *Nature Plants* 6: 1091–1097.
- Nishio H, Buzas DM, Nagano AJ, Iwayama K, Ushio M, Kudoh H (2020) Repressive chromatin modification underpins the long-term expression trend of a perennial flowering gene in nature. *Nature Communications* 11: 2065.

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