



# HOKKAIDO UNIVERSITY

|                     |                                                                                                                                                                                                  |
|---------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Title               | Analysis of Transcriptional and Transpositional Regulation of a Heat-Activated Retrotransposon in <i>Arabidopsis thaliana</i> [an abstract of dissertation and a summary of dissertation review] |
| Author(s)           | 牛, 小瑩                                                                                                                                                                                            |
| Degree Grantor      | 北海道大学                                                                                                                                                                                            |
| Degree Name         | 博士(生命科学)                                                                                                                                                                                         |
| Dissertation Number | 甲第16283号                                                                                                                                                                                         |
| Issue Date          | 2025-03-25                                                                                                                                                                                       |
| Doc URL             | <a href="https://hdl.handle.net/2115/95489">https://hdl.handle.net/2115/95489</a>                                                                                                                |
| Rights(URL)         | <a href="https://creativecommons.org/licenses/by/4.0/">https://creativecommons.org/licenses/by/4.0/</a>                                                                                          |
| Type                | doctoral thesis                                                                                                                                                                                  |
| File Information    | Xiaoying_Niu_abstract.pdf, 論文内容の要旨                                                                                                                                                               |



# 学 位 論 文 内 容 の 要 旨

博士の専攻分野の名称 博士(生命科学) 氏 名 牛 小瑩

## 学 位 論 文 題 名

Analysis of Transcriptional and Transpositional Regulation of a Heat-Activated Retrotransposon in  
*Arabidopsis thaliana*

(シロイヌナズナにおける熱活性型レトロトランスポゾンの制御機構の解明)

Transposon transposition can induce mutations in the genome, potentially causing adverse effects. Therefore, mechanisms that control transposon transposition are essential for maintaining genomic stability in the host. While most transposons are regulated at the transcriptional level through epigenetic modifications such as DNA methylation and histone modifications, the details of post-transcriptional control mechanisms for transposon transposition remain poorly understood. In *Arabidopsis thaliana*, the retrotransposon *ONSEN* is activated by heat stress (HS) at 37°C. In mutants deficient in the RNA-directed DNA methylation (RdDM) pathway, HS triggers transgenerational transposition of *ONSEN*. However, since *ONSEN* transcription levels do not strongly correlate with transposition frequency, RdDM components may have distinct roles in suppressing both transcription and transposition, or other regulatory pathways may act independently of RdDM. This study uses *ONSEN* as a representative model to explore the regulatory mechanisms governing transposons, offering new insights into retrotransposon regulation.

The study is divided into three chapters, each addressing one of these aspects: (1) the relationship between transcription and transposition, (2) the role of epigenetic modification mechanisms, and (3) the identification of novel regulatory mechanisms.

Chapter One focuses on the role of downstream factors in the RdDM pathway in regulating *ONSEN* transcription and transposition. Using mutants, it investigates how these factors contribute to the silencing of *ONSEN* at both the transcriptional and transpositional levels. Among these downstream components, the DDR complex—comprising DRD1, DMS3, and RDM1—and SUVH2 plays a critical role in RdDM. The study primarily highlights the suppressive roles of DDR complexes and SUVH2 in regulating *ONSEN* activity within the RdDM pathway. RdDM-mediated DNA methylation is associated with the suppression of *ONSEN* transcription, but it does not directly affect the silencing of *ONSEN* transposition. The results suggest that SUVH2 and DRD1 contribute to the transpositional silencing of *ONSEN* through a siRNA-dependent pathway. In addition, the independent functions of RdDM factors in inhibiting both the transcription and transposition of retrotransposons, providing new insights into the distinct regulatory mechanisms governing retrotransposon activity. This study proposes that plants, when exposed to adverse environmental stresses, adapt their protective mechanisms to mitigate potential genetic damage caused by these stresses.

Chapter Two examines the relationship between epigenetic modifications and the regulation of transposable

element (TE) activity. Histone acetylation, which is dynamically controlled by the balance between histone acetyltransferases (HATs) and histone deacetylases (HDACs), plays a critical role in transcriptional regulation. To investigate this, an inhibitor affecting histone deacetylation was used to study how these modifications influence TE transcription. This study highlights the complex interplay between chromatin state, DNA methylation, and transcriptional control in regulating TEs during environmental stress. These findings provide new perspectives on the dynamic mechanisms plants use to regulate TE activity, offering insights into how epigenetic processes adapt to external challenges.

Chapter Three investigates new regulatory mechanisms using EMS-induced mutants to uncover novel pathways involved in transposon regulation. I identified an unknown factor involved in *ONSEN* transposition regulation, termed *screen 1*, and explored its genomic location. In *screen 1*, new *ONSEN* insertions were observed, even though *ONSEN*'s transcription level and copy number were equivalent to those in Col. *Screen 1* is likely involved in directly regulating *ONSEN* transposition, bypassing transcriptional control. While the specific genes responsible for *screen 1* remain unidentified, future research will continue to focus on this discovery. Identifying *screen 1* holds the potential for groundbreaking insights into the mechanisms governing TE transposition. This chapter aims to provide insights into previously unknown regulatory processes beyond the RdDM pathway.