

Project Title:

Single-cell and spatial transcriptomics on plant regeneration

Name:

○Max Minne (1)

Laboratory at RIKEN:

(1) Center for Sustainable Resource Science, Cell Function Research Team

1. Background and purpose of the project,
relationship of the project with other projects

Plants have a remarkable ability to regenerate from tissue damage. However, it is unclear which cells contribute to this process and what genetic regulations support this process. By integrating single cell transcriptomics and spatial transcriptomics we aim to deconvolute the regulatory pathways of wound-induced regeneration in plants.

2. Specific usage status of the system and
calculation method

NA

3. Result

NA

4. Conclusion

NA

5. Schedule and prospect for the future

Integration of large single-nucleus RNA sequencing (snRNA-seq) datasets, integration of snRNA-seq and spatial transcriptomics datasets, automated (machine learning based) cell segmentation of spatial datasets, ...

6. If no job was executed, specify the reason.

We applied to start using the supercomputer just before the annual report deadline and therefore have not executed any jobs yet.