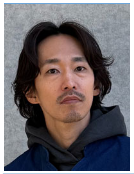
【Grant-in-Aid for Transformative Research Areas（B）】

A New Science for Detecting Evolvability Dynamics: Integration of Bioinformatics, Evo-devo, and Paleontology



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Project Information	Project Number : 25B302 Keywords : evolution, genome, development, fossil record, morphology	Project Period (FY) : 2025-2027

Purpose and Background of the Research

●Outline of the Research

Our understanding on the evolution has been improved through comparative analyses and experiments using extant species. These approaches assume, consciously or unconsciously, uniformity, that ancestral species evolved based on the same properties as extant species. Is this premise really correct?

When we look at various evolutionary histories, we sometimes wonder if the evolvability (capability of evolution) was high in the early stages of evolution but then decreased, in other words, **if evolution slowed down**. However, there is still no framework for scientifically examining this naive question.

To overcome this situation, with the success of physical cosmology in our mind, we believe that in evolutionary biology too, it is necessary to create an integrated research area where theory, experiment, and observation interact with each other.

In our research area, "Detecting Evolvability Dynamics," we suspect the uniformity in evolution at various scales and examine the changes in evolvability between ancestors and descendants (Fig. 1). Here, we aim at accumulating empirical data before constructing a new evolutionary theory, to clarify **whether the decelerating evolution exists due to some mechanism**.

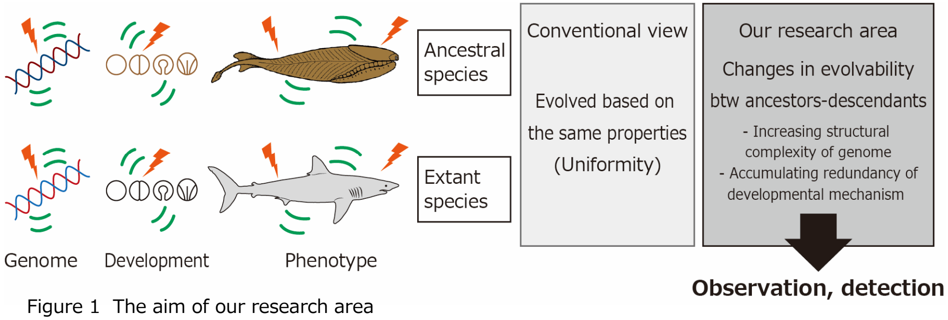

Figure 1 The aim of our research area

●Integration of Bioinformatics, Evo-devo, and Paleontology

Our research area consists of members from different fields of expertise, covering bioinformatics, evo-devo, and paleontology, who share the question above. The mission of our area is to develop researchers who can hold advanced discussions across the boundaries of their fields to come together as a research community that can open a door to a new science.

To promote collaboration, we created our logo, in which a change in evolvability is being detected on a phylogenetic tree through a magnifying glass (Fig. 2).

Figure 2 Our project's logo

Expected Research Achievements

●How to drive our research area

Our area is composed of three planned researches, covering various scales, from species-level to origins of body plans (Fig. 3).

Each of the three projects will obtain unique empirical data on changes in evolvability between ancestors and descendants, which will be compared within the research area to clarify **at what scale** changes in evolvability can be detected. With a hope to constructing a new theory, interactions within the area will lead to narrowing down candidates for the "**universal factors of changes in evolvability**."

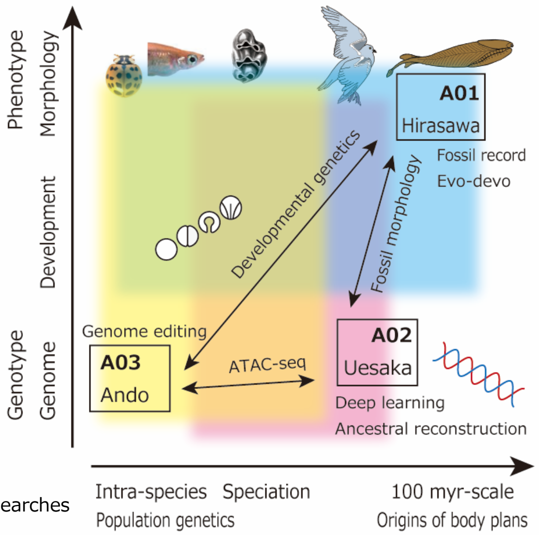

Figure 3 Relationships btw planned researches (blue, A01; red, A02 ; yellow, A03)

●A01: Detecting evolvability dynamics in the vertebrate fossil record

T. Hirasawa (Univ. of Tokyo), Y. Kimura (NSM), H. Higashiyama (SOKENDAI)

Focusing on **the morphological evolution of vertebrates in the fossil record**, A01 will identify the developmental mechanisms behind them, and collect empirical data on the changes in potential of evolutionary novelty emergence (at both 100 myr- and speciation-scales).

Keywords: developmental constraint, intraspecific variation, phenotypic plasticity

●A02: Prediction of ancestral morphological evolvability through deep learning

M. Uesaka (Tohoku Univ.)、T. Nishio (Science Tokyo *Research collaborator)

A02 will develop a method to predict gene regulatory activity and morphological traits from genome sequences alone through **deep learning on gene regulatory regions involved in morphogenesis** and examine changes in morphological evolvability, particularly in the lineage of birds.

Keywords: ATAC-seq, deep learning, ancestral reconstruction, morphogenesis

●A03: Reconstruction of past mutations through genome editing

T. Ando (Kyoto Univ.), S. Anzai (Okayama Univ.)

Using the original technique in **experimental genetics**, A03 will reconstruct mutation patterns in parallel evolving genes in the laboratory and elucidate the factors that cause parallel evolution or overcome the accumulation of mutations at the intra- and inter-specific levels in different animal lineages (insect and fish).

Keywords: genome editing, chromosomal structural changes, mutation

●Expected outcome

Our research area is focusing on empirical data on evolvability dynamics, which, we believe, will lead to the construction of new theory on evolvability in the next step. The creation of such an emerging field should also lead to "**the prediction of the evolution in future**," which has been quite difficult until now.

Homepage Address, etc.	Homepage https://detecting-evolvability-dynamics.com X (in Japanese) https://x.com/Evol_Dynam Bluesky (in English) https://bsky.app/profile/evol-dynam.bsky.social