Evolutionary Theory for
CONSTRAINED & DIRECTIONAL EVOLUTION
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Grant-in-Aid for Scientific Research on Innovative Areas
新学術領域　進化の制約と方向性

CDE international seminar (online)

2nd: Mar 19th (Fri) 17:00-18:00 (Japan time) [Lang: English]

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Chromosome landscape and positional identity in axolotl limb regeneration

Click this URL for registration (free event)
https://forms.gle/Tzuret4tbAtLhKoRA
(Zoom URL will be sent to you based on the registered information)

- Title & Authors -

Chromosome landscape and positional identity in axolotl limb regeneration

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- Abstract -

Axolotl is a well-known animal model for development, evolution, and regenerative biology. Due to the gigantic axolotl genome size, which is 32Gb (10 times bigger than human and mouse), the genome inspires fascinating questions such as: How is the genome organized and packed in nuclei? How does regulation of gene transcription occur and how is the remarkable regeneration ability governed by large genome regulation.

Recently we successfully assembled the 32Gb axolotl genome at the chromosomal level using a Hi-C assembly strategy. To investigate TAD structures which are known as genome regulatory units upon promoter-enhancer interactions, we constructed Hi-C libraries from an axolotl culture cell line in interphase and mitotic phase. It has been known that interphase chromatin has long-range gene regulation, while mitotic phase chromosomes show only short-range contacts due to highly condensed chromatin structures. The axoltol interphase Hi-C map shows that huge TAD structures, besides, the mitotic Hi-C gave us that the unique chromatin loop structure in the mitotic-phase (Schloissing S+., Kawaguchi A+., Nowoshilow S+., Falcon F+., et al., Under revision in PNAS).

Our new genome assembly gives us the opportunity to address the epigenome regulation during tissue regeneration processes. In contrast to mammals, axolotl limbs are great 3D-tissue regeneration models with three major limb segments. When the axolotl limb is amputated at any position, the remaining limb cells form a regenerating blastema which is full of progenitor cells, and it re-forms a fully patterned limb. How axolotl limb cells maintain and the blastema re-activates a positional identity during regeneration at the chromatin level is elusive. To address this question, we have been examining the regulation of Hox gene clusters as model genes that are well-known for establishing proximo-distal and anterior-posterior identity during limb development. We have been analyzing the ATAC-seq and RNA-seq data in the different limb segments and regenerating blastema.

In the talk, I will discuss our unpublished findings concerning (1) the+., Kawaguchi A+., Nowoshilow S+., Falcon F+., et al., Under revision in PNAS), and (2) the epigenetic regulation of Hox clusters during the limb regeneration (Kawaguchi A., et al., in preparation).

For all of you who are interested in Evolutionary Biology

We are happy to announce open, online international seminar provided by the research project "Constrained and Directional Evolution" (led by Dr. Shigeru Kuratani).
The aim of this open seminar is to share and discuss over the challenging topics in evolutionary biology, such as Evolvability, Constraints, Directionality in phenotypic evolution etc., and to boost interactions between scientists interested in these topics. It's an open seminar with participation free of charge, and we welcome your participation (Students, Postdocs, PIs etc.)

[Greeting from the chair of this project]

How much has our understanding of biological evolution improved in the past half century? Not even the shape of the tiny insect in front of us now can be satisfactorily explained. My understanding of evolution has not changed much since then. I do not think it's the way it should be. it's good enough. At last, it's time we start doing something to solve the mystery.
Why should the shapes of plants and animals be the way they are? How does purposefulness explain the process of these refinement of shapes? This project aims to construct a new theoretical system of evolutionary biology by not only encompassing natural selection and neutral theories but also integrating essential elements that previous theories failed to address. We hope that this attempt will provide a place for gathering bold challengers, and further leads to a new trend in the field of evolutionary biology.
http://constrained-evo.org/greeting.html

進化にご興味のある全ての皆様へ

新学術領域「進化制約方向性（倉谷代表）」公開オンラインセミナーのお知らせです。表現型進化の方向性、拘束、進化可能性といった概念や問題について、考え、議論したり新たな考えや人の相互作用をもたらすための不定期で行う国際オンラインセミナーです（公開。参加費無料）。フランクなオンラインミーティングです。大学院生の方々も広くご参加いただけましたら幸いです。
近くに興味を持たれそうな方がおられましたらお声がけいただけると幸いです。

[領域代表より、抜粋]（原文は HP をご覧ください）

過去半世紀の間、生物の進化についての私たちの理解はどれほど深まっただろうか。いま目の前にいるちっぽけな虫のかたちすら満足に説明してくれない。進化に関する私の理解はあの頃とあまり変わってはいない。さりとて、このままでよいとも思わない。いよいよ謎を解くべく、何かを始めなければならない。動植物のかたちがなぜこのようなものでなければならないのか、そしてそれが洗練されて行く過程にどのように合目的性が入り込むのか、自然選択説や中立説を包含するのみならず、それらが扱うことのできなかった本質的要素を統合することを通じ、本領域は進化生物学の新たな理論体系の構築を目論む。この試み自体、進化生物学領域における梁山泊であり、自ら新たな潮流となり、進化研究を変える第一歩ならんと欲するものである。
http://constrained-evo.org/greeting.html