Linqing Hu

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EDUCATION

The University of Manchester **09. 2023 – 09.2024**

MSc Bioinformatics and Systems Biology, Grade: **Distinction**

Core modules: Bioinformatics, Computational Approaches to Biology, Experimental Design and Statistics

Project 1: Prof Gisela Orozco's Lab

Title: Using GWAS, RNA-seq and ATAC-seq combined functional genomic annotation to discover the TF-binding regulatory mechanism responsible for Psoriatic Arthritis (PsA)

Summary: Autoimmune diseases (ADs) pose significant global healthcare challenges due to their complex nature and chronic progression. Psoriatic Arthritis (PsA), a subtype of AD, impacts patient quality of life and poses economic burdens. PsA's pathogenesis involves a combination of genetic predispositions and environmental factors. Understanding the role of transcription factors (TFs) in regulating gene expression is crucial for decoding PsA's molecular mechanisms. TFs bind to genetic regulatory elements such as enhancers and promoters, influencing immune responses and inflammation. This study integrates multi-omics data from ATAC-seq, GWAS, and RNA-seq to help identify regulatory elements and provide insight into PsA-related mechanisms, thereby enabling the development of new diagnostic tools and treatment approaches. From the comparison, a new motif was found at the BCL2L11 promoter-associated enhancer SNP rs13401811, which provides a hint at the potential regulatory mechanism of this gene and the pathogenesis of PsA.

Project 2: Prof Simon Hubbard's Lab (the lab is collecting more data for publication)

Title: Co-translational Protein Complex Assembly: integrating structural and quantitative mass spectrometry data to identify candidates

Summary: Multimeric protein complexes assembly through protein-protein interactions are important for cellular functions across all domains of life. Other than the conventional thought that complexes are formed from random collisions of fully synthesised and folded subunits, the process of co-translational assembly (Co-TA) was suggested and found to happen prevalently for both the homomeric and heteromeric complexes. Previous studies have raised three factors (1) the Co-TA processing orders: simultaneous (Co-co) vs sequential (Co-post), (2) the ribosome translation locations: on the same mRNA (cis) vs on different mRNAs (trans), and (3) the subunits assembly orders: directional vs symmetrical that is important to Co-TA, overall, give 6 possible modes of the Co-TA mechanism, and was found favoured by homomeric and heteromeric complexes differently.

Since studies showed that the relative location (either towards the N-terminus or the C-terminus of the protein sequence) of the subunit interactive (buried) surface is evolution-selective and important for the two types of complexes in adopting different modes/mechanisms of Co-TA, this study focused on heteromeric complexes, raised a concept of subunit Moment (M), hypothesised that the Co-TA mechanisms may be distinguishable by the relative location of the buried surfaces in the component subunits of a protein complex through relative Moment (M-rel). Through the use of a novel in vivo experiment, 62 new heteromeric complexes were identified that may undergo Co-TA. By developing a computational method to calculate the relative Moment (M) of subunits by their residual solvent accessibility (ASA) generated from PDB structural data. This study confirmed the potential of using relative M-rel to suggest the possible Co-TA mechanism for complexes and raised its significance in helping tackle diseases.

The University of Edinburgh **09. 2019 - 05. 2023**

BSc Hons Biological Sciences (Biotechnology), Degree: **UK 2:1**

Core modules: Cell Biology; Molecular Biology, Genome and Genetics; Gene Expression and Microbial Regulation, Enzymology and Biological Production, Biotechnology; Novel Approaches, Quantitative Skills

Honours project: Dr Sander Granneman's lab

Title: Performing Differential Gene Expression (DGE) analysis and GO term enrichment analysis of the Nanopore RNA sequencing data to decipher the role of the endonuclease RNase III in regulating Methicillin-resistant *Staphylococcus aureus* (MRSA) gene expression.

Summary: Multimeric protein complexes assembly through protein-protein interactions is important for cellular functions across all domains of life. Other than the conventional thought that complexes are formed from random collisions of fully synthesised and folded subunits, the process of co-translational assembly (Co-TA) was suggested and found to happen prevalently for both the homomeric and heteromeric complexes. Previous studies have raised three factors (1) the Co-TA processing orders: simultaneous (Co-co) vs sequential (Co-post), (2) the ribosome translation locations: on the same mRNA (cis) vs on different mRNAs (trans), and (3) the subunits assembly orders: directional vs symmetrical that is important to Co-TA, overall, give 6 possible modes of the Co-TA mechanism, and was found favoured by homomeric and heteromeric complexes differently. Since studies showed that the relative location (either towards the N-terminus or the C-terminus of the protein sequence) of the subunit interactive (buried) surface is evolution-selective and important for the two types of complexes in adopting different modes/mechanisms of Co-TA, this study focused on heteromeric complexes, raised a concept of subunit Moment (M), hypothesised that the Co-TA mechanisms may be distinguishable by the relative location of the buried surfaces in the component subunits of a protein complex through relative Moment (M-rel). Through the use of a novel in vivo experiment, 62 new heteromeric complexes were identified that may undergo Co-TA. By developing a computational method to calculate the relative Moment (M) of subunits by their residual solvent accessibility (ASA) generated from PDB structural data. This study confirmed the potential of using relative M-rel to suggest the possible Co-TA mechanism for complexes and raised its significance in helping tackle diseases.

SKILLS

Wet lab: Animal and bacterial cells culturing and screening, High-throughput sequencing library preparation, CRISPR-Cas9 library preparation, PCR, Plasmid construction, transmission and DNA assembly, Centrifugation techniques, Spectrophotometer analysis, Agarose gel electrophoresis, Western blotting, Chromatography for protein extraction and purification, ELISA, Light and fluorescence microscopy

Dry lab: Genome, Transcriptome and ATAC-seq data processing; differential expression and GO term enrichment analysis; protein structure analysis; PCA and clustering; Network and logic modelling; Mathematical modelling, Statistics, Machine Learning

Programming language and tools: Python3, R, Bash, Git, PyTorch, Snakemake, DESeq2, TOBIAS

Languages: Mandarin (native), English (professional), Japanese and Korean (basic proficiency)

Others: Affinity Designer2, Adobe Illustrator, Procreate, Adobe Premiere Pro

SELECTED ACADEMIC AWARDS AND HONOURS

2023 SynBioBeta Synthetic Biology Global Conference (Student representative), Oakland, US **2023**

The 12th Summer Research Program on Biomedicine, Medical Facility, Tsukuba University **2022**

Quantitative Biology Summer Training Program, Peking-Tsinghua University Life Science Joint Centre, Peking University **2021**

Silver Award from Intermediate Biology Olympiad, Royal Society of Biology **2018**

Silver Award from Cambridge Chemistry Challenge, University of Cambridge **2018**

SELECTED ACADEMIC EXPERIENCES

iGEM Competition, team ***Edinburgh-UHAS_Ghana*** **06. 2022 - 10. 2022**

Project: Building a biodegradation device containing a PETase and MHETase-involved enzyme cocktail to solve water pollution problem in Ghana; **Awards:** Gold Award, Best Track Nomination.

- **https://2022.igem.wiki/edinburgh-uhas-ghana/index.html**

iDEC Competition, team ***Edinburgh-UHAS_Ghana*** **06. 2022 - 10. 2022**

Project: Random mutagenesis and silver nitrate (AgNO3) based negative selection of different metallothioneins (MTs) exploring the potential for functional MT directed evolution.

- **https://idec-teams.github.io/2022_Edinburgh-UHAS_Ghana/**

Bluepha Co., Ltd. (China), *iGEM team advisor and Summer programs instructor.* **05. 2021 - 08. 2021**

- Supervised 13 high school students on web lab experiments and social engagement activities on the project '**Design an improved ligand-nanoparticle system which utilises pH-sensitive aptamer to improve specificity on targeting HER2 proteins'.** The team achieved a Gold Award. **https://2021.igem.org/Team:GreatBay_SCIE**
- Independently developed teaching materials for teenager-oriented summer programs **'Building a microscope with Lego Bricks'**. Independently taught 4 middle school students on a synthetic biology-based summer school costing £10000 **'Constructing plasmid for fluorescent expression in *E. coli*'** and **'Constructing plasmid to express Polyhydroxyalkanoates (PHAs) biodegradable plastics in *E. coli*'**. My teaching received significant recognition from the students, parents and the company.

SELECTED LEADERSHIP EXPERIENCE AND OTHER AWARDS

British Kendo Association (BKA) Kendo Level 1 Coach **2024**

- Demonstrates a good understanding and dedication to providing professional training in kendo.

Edinburgh University Kendo Club (EUKC), *Health and Safety Officer, Active member* **2021 - 2023**

- Represented the university in local and national competitions and achieved awards.
- Provided training advice and first aid help to club members and maintained a safe training environment.
- Determined, persistent and resilient, has a strong spirit that does not stop until the goal is achieved.

Edinburgh Model United Nations **2023**

- Participated in the 2023 Scot MUN to debate on 'the legitimacy of commercial and altruistic surrogacy and egg donation', great at understanding problems from multiple positions.

High School Jiulian Business Society, *Committee member, President of Central Bank* **2016 - 2017**

- Represented the high school in the 5th National Business Challenge. Assisted in the organisation of the 4th Shanxi province business competition with 120+ attendees.
- Has knowledge in auditing and finance, great at brainstorming and seeking business opportunities.

Professional training in fine art for 5 years **2012 – 2017**

Has a good aesthetic. Skilled in drawing and making designs and figures at the publication level.