

<https://molossinus.brc.riken.jp/mogplus/>



我々は実験動物マウスを対象にして、複数の亜種に由来する野生由来近交系統の比較ゲノム解析から見出した4千万種以上の単塩基多型などのゲノム多型情報をデータベースMoG+（モグ プラス： <https://molossinus.brc.riken.jp/mogplus/>）から公開している。MoG+を利用することで、ウェット研究者は多数のマウス系統を対象にして、塩基多型やアミノ酸置換情報を簡単に探索することができる。MoG+にはこれに加えて、遺伝子シンボルを利用したヒト疾患情報へのリンク、疾患モデルマウスの検索機能などが搭載され、理研BRCから入手可能なマウス系統の有無を検索することができる。今回MoG+は、ROIS-DS-JOINTの成果を含む長鎖ゲノム解読などによる構造多型情報を追加して機能向上を行った。MoG+はこれ以外にも、汎用マウス系統の公開ゲノム多型情報、ヒト疾患関連ゲノム多型情報、転写制御に関わる *cis* 制御領域へのリンク機能の向上など、医学生物学分野の研究に資する機能拡張を適宜行っている。

Introduction

Genome Information

- Important for biomedical research, biodiversity and evolution
- Essential for strategic planning of experimental animal science

Laboratory mouse (*Mus musculus*)

- The model organism for mammals and is a complex species containing multiple subspecies
- Genome editing and other genetically engineered animals have been widely used in disease and phenotypic studies

NBRP core facility 「Mice」

Maintains, preserves, and serves over 9,000 mouse strains (@ Experimental animal division)

- Human Disease Models
 - Have common symptoms or common genetic mutations with the disease
- Wild-derived inbred strains established by wild mice around the world
 - Studying the genetic diversity and its role in humanity
- Genetically modified mice
 - Enables visualization of life phenomena by introducing fluorescent and luminescent labels into specific cells and molecules
 - Site-specific genetic manipulation is possible and gene function in cells, tissues and organs can be analyzed

MoG+ (FY2019 -)

Comparison of genomic variations (SNPs, etc.) in the 10 mouse strains analyzed originally and the 37 mouse strains available from public databases.

MSM/Ms

-P--S--I--H--P--A--Q--S--E-
CCATCCATCCATCCAGCACAATCAGAG
CCATCCATCCATCCAGCACAATCAGAG
-P--S--I--Q--P--A--Q--S--E-
Histidine -> Glutamine

Example: Amino acid substitution detection between a reference strain (C57BL/6j) and a Japanese strain (MSM/Ms) in the genomes

MoG+ is being enhanced with the following features

1. Increase the number of links to disease-related information
 - Increase content of information for disease research community
2. Add the information of comparable disease-related variations in humans and mice
 - Assist in selection of best laboratory mouse strains for disease studies
3. Release the latest information of mouse genomic variations
 - Keep database fresh

For the broader research community in biomedical science, population genetics, etc.

1. Upgrading MoG+ information of links to disease-related information

Genome variants and mouse strains available from RIKEN BRC search function of MoG+

By Gene symbol
By Gene symbol
Nucleotide sequence coordinates
Specify a specific position on a chromosome

Example search results for a gene symbol

Links to other DBs
Links to disease-related info.

Genomic variant information for mouse strains available from RIKEN BRC (e.g. Mishima battery strains) and the 37 mouse strains available from public databases (dbSNP).

Variant Table

The unique feature "Wet researcher-friendly DB": Variation search function on important to gene function

Current Access Status

Number of views per month (September, 2024)

22,775 accesses (1131 Unique IP, including unknown)

国	アクセス数	件数
Japan	6,083	11,446
France	5,720	6,623
United States	1,710	2,619
China	497	1,002
Great Britain	266	313
Canada	88	90
Russian Federation	65	317
India	64	106
RW	49	49
Germany	59	41
その他	252	769

2. Adding information of comparable disease-related variations in humans and mice

Assists in the selection of mouse strains for disease studies by listing comparable disease-related variations in humans and mice

An example, TogoVar, a database of Japanese genomic variations and their frequency and association with diseases.

Comparative Genome Analysis

Mouse strains available from RIKEN BRC

Find Mouse Strain Available for Supply

Gene Symbol "Kit"

Strengthening Links to Bioresources

DNA materials

GENE ENGINEERING DIVISION

遺伝子材料開発室

Suggestions best bioresources for your research !

3. Integration of variant information and CRE data

Database Integration Coordination Program (DICP)

Construction of an integrative data platform for transcriptional regulations

February 26, 2024: fanta.bio CRE data version 1.0.0. has been released!

Users can leverage genomic polymorphisms in CRE (cis-regulatory element) regions and explore candidate transcription factors with binding potential

4. Release of New Genome Data for Japanese Inbred Mouse Strains JF1/Ms and MSM/Ms (De Novo Assembly)

The New MoG+ home (Top) and MoG+3.0 (Bottom)

We have recently released genomic data from a de novo assembly of the Japanese inbred mouse strains JF1/Ms and MSM/Ms. This dataset includes genome sequences, structural variations (SV), and other genomic variants.

Visualization of SV Distribution Information (e.g., genomic locations chr8: 111,817,290- 111,990,532).

Summary

MoG+ is

- a genome browser with whole genomes and its variations of mouse strains available from RIKEN BRC (e.g. Mishima battery)
- powered by a genomic variant information data set for "laboratory mouse strains (including original data) "
- to assist users in selecting better laboratory mouse strains for biomedical research

Ongoing enhancements and data additions are being made to add value to the bioresources, to further contribute to human disease research, and to improve the research efficiency of the research community (reducing costs, time consuming, workforce reduction, etc.).

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