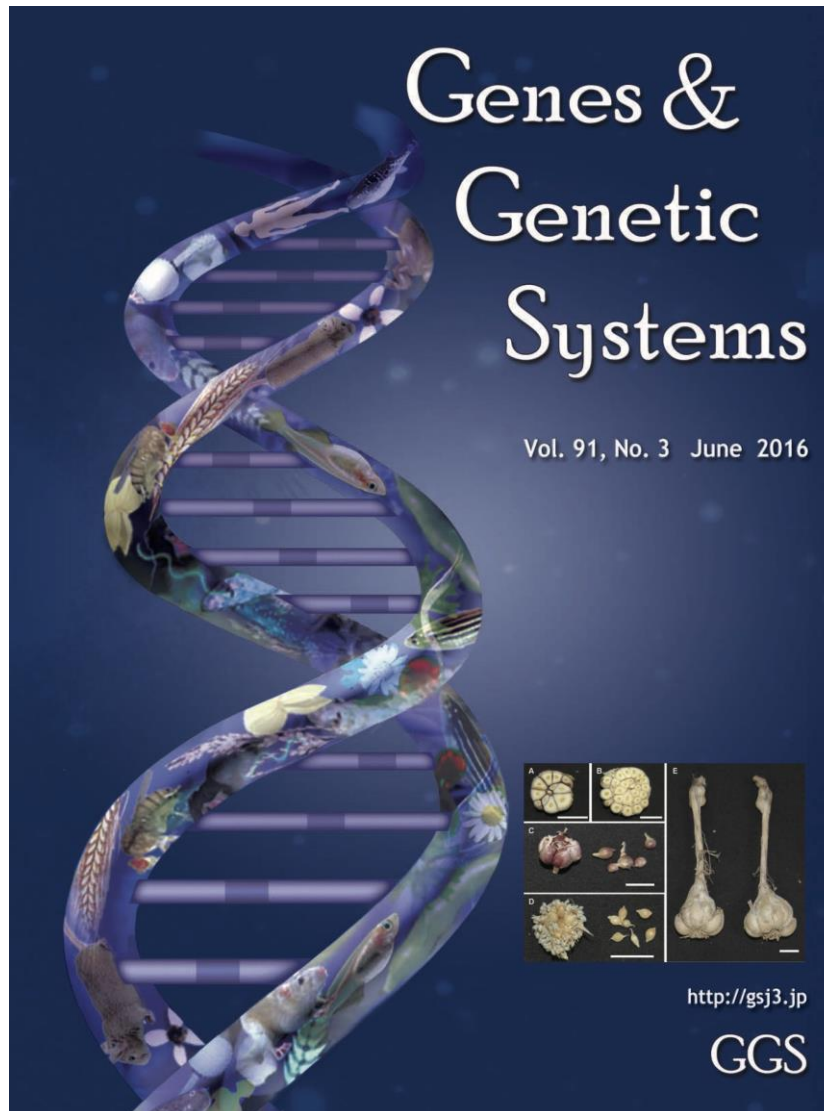




# アジアの遺伝学を主導する 学術雑誌を目指した取り組み

日本遺伝学会編集幹事  
九州大学 舘田英典

# Genes & Genetic Systems (GGS)

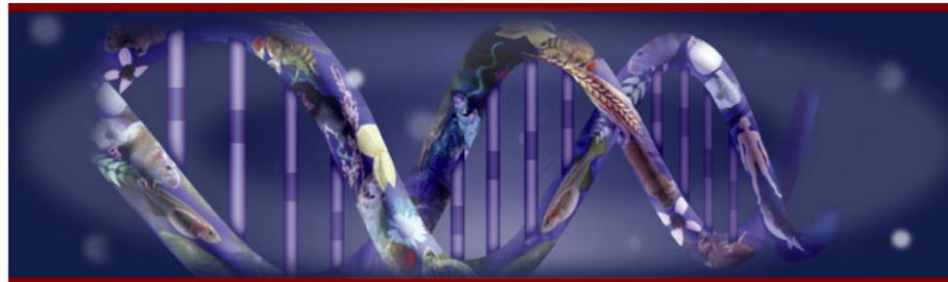


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# GGs home page



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電子ジャーナル

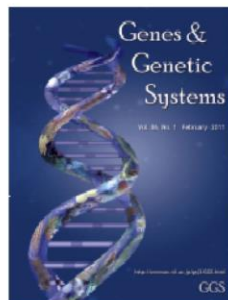
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**Volume And Issue List**  
 Genes & Genetic Systems

- Vol.91(2016)
  - No.2 p.49-**
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- Vol.90(2015)
- Vol.89(2014)
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 The Japanese Journal of

**Genes & Genetic Systems Vol. 91(2016) No. 2**

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**Introduction**

Correlative Gene System: Establishing Next-Generation Genetics P49  
 Sato Fuyuki, Sato Takayama  
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**Special reviews**

Emerging links between iron-sulfur clusters and 5-methylcytosine base excision repair in plants P51-62  
 Sato Fuyuki, Sato Takayama  
 Released: October 13, 2016  
 [Advance Publication] Released: September 02, 2016  
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Interspecific hybrids of dwarf hamsters and Phasianidae birds as animal models for studying the genetic and developmental basis of hybrid incompatibility P63-75  
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Gene duplication, silencing and expression alteration govern the molecular evolution of PRC2 genes in plants P85-95  
 Hoshida Y, Yoshida K, Kato Y, Saito Y, Saito Y, Saito Y, Saito Y, Saito Y, Saito Y, Saito Y  
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# 平成25年度 国際情報発信強化申請

JSPS科学研究費補助金（研究成果公開促進費）

「アジアの遺伝学を主導する学術雑誌を目指した取り組み」

- 目的

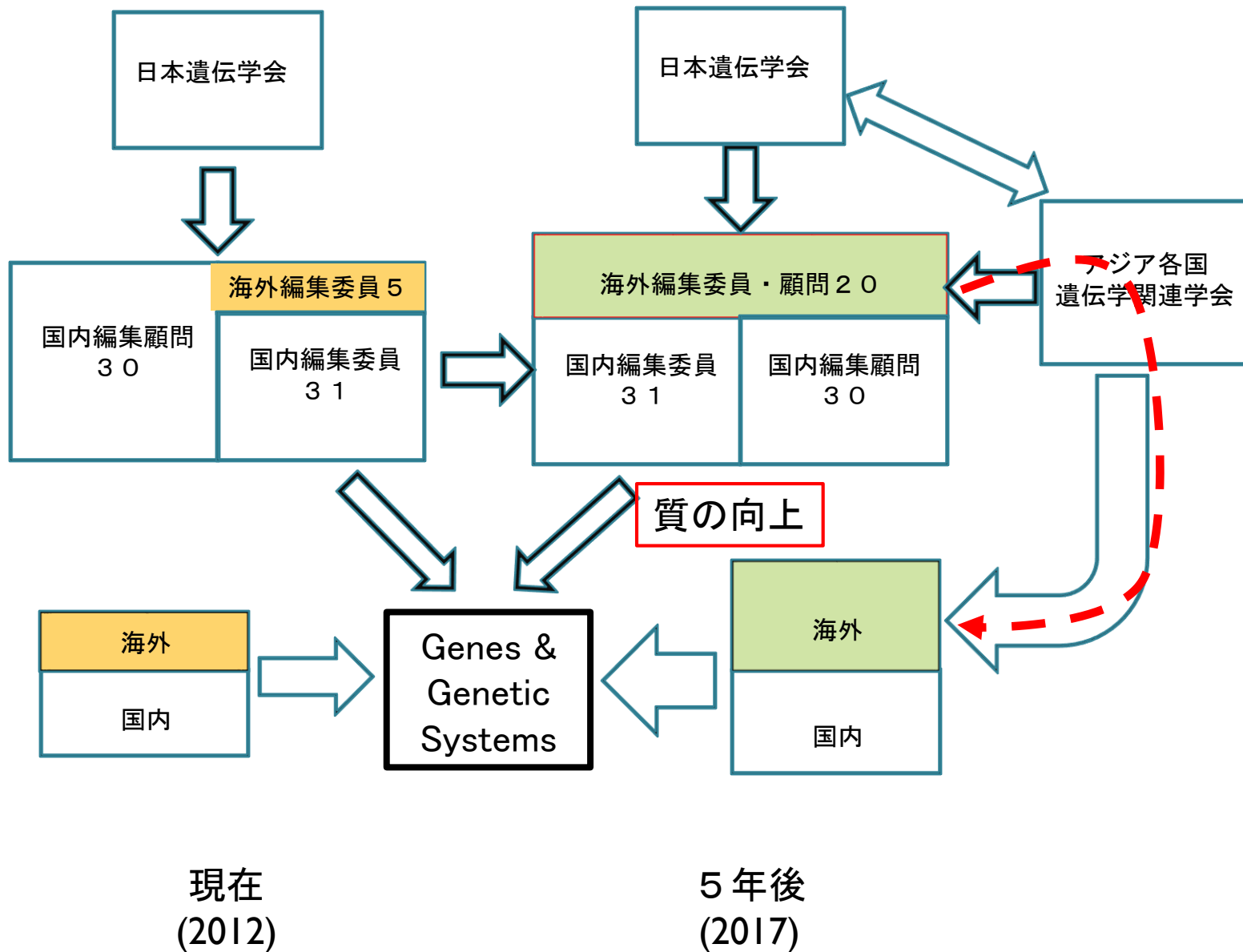
- アジアにおける遺伝学関連の良質の論文を集めて掲載し、アジアにおけるこの分野のトップジャーナルとなる。
  - 投稿数の増加

- 方法

- アジアの各国の中堅研究者を編集委員や編集顧問に選任
  - 実質的編集作業、編集会議出席、情報発信
- 採択論文の英文校閲

編集委員・編集顧問合同会議

論文投稿数



# 補助金の利用

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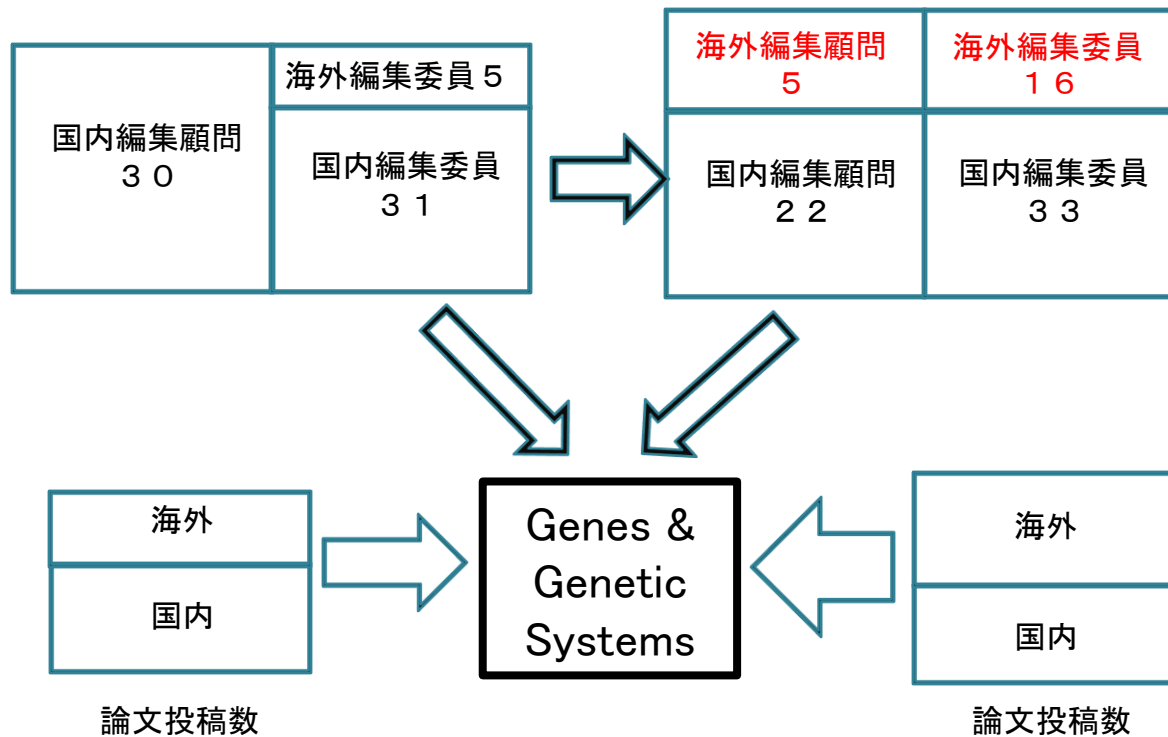
「アジアの遺伝学を主導する学術雑誌を目指した取り組み」

課題番号 252006



# 海外編集顧問・編集委員

## 編集委員・編集顧問合同会議



- 合同会議に最低1回出席、討議に参加
- 海外編集委員による編集への実質参加

25年度当初

現在

# 中間評価時（2015年11月）

	投稿数		海外レフリー
	総数	海外投稿数	
2012年	72	31	8.8%
2015年	81	41	21.6%

# 全論文英文校閲

- 文法等
- 読みやすさ

2

## INTRODUCTION

3

Conifers are important tree species in forests and are distributed widely in the temperate,

4

frigid and even subtropical zones, and some of them are also important for commercial purposes. There

5

are 615 species (70 genera) in this group, which have diverse morphologies and ecological traits (Farjon,

6

2010). The genomes of conifers are characterized by large size, among the largest of any nonpolyploid

7

plant species, slow evolutionary rates in coding genes, and accumulations of a large amount of noncoding

8

DNA (Murray, 1998; Ahuja and Neale, 2005; Buschiazzi et al., 2012; Pavy et al., 2012; Ritland, 2012).

9

Recent analyses have revealed that conifer genomes have huge amounts of repetitive sequences (probably

10

non-functional) and low recombination rates in non-coding regions [the red-lettered changes here provide

11

clearer coordination of the sentence, and assume that the two underlined terms are separate features of

12

conifer genomes – is this OK?] (Jaramillo-Correa et al., 2010; Kovach et al., 2010; Liu et al., 2011;

13

Moritsuka et al., 2012). These observations contrast with those of angiosperm genomes reported so far.

14

Unique genomic characteristics of conifers have lately attracted considerable attention as to what makes

15

[or 'causes'?] such differences in these genomic characteristics, and what kind of evolutionary features

16

the conifer genome has; for example, how much intragenome and/or intergenome variation of

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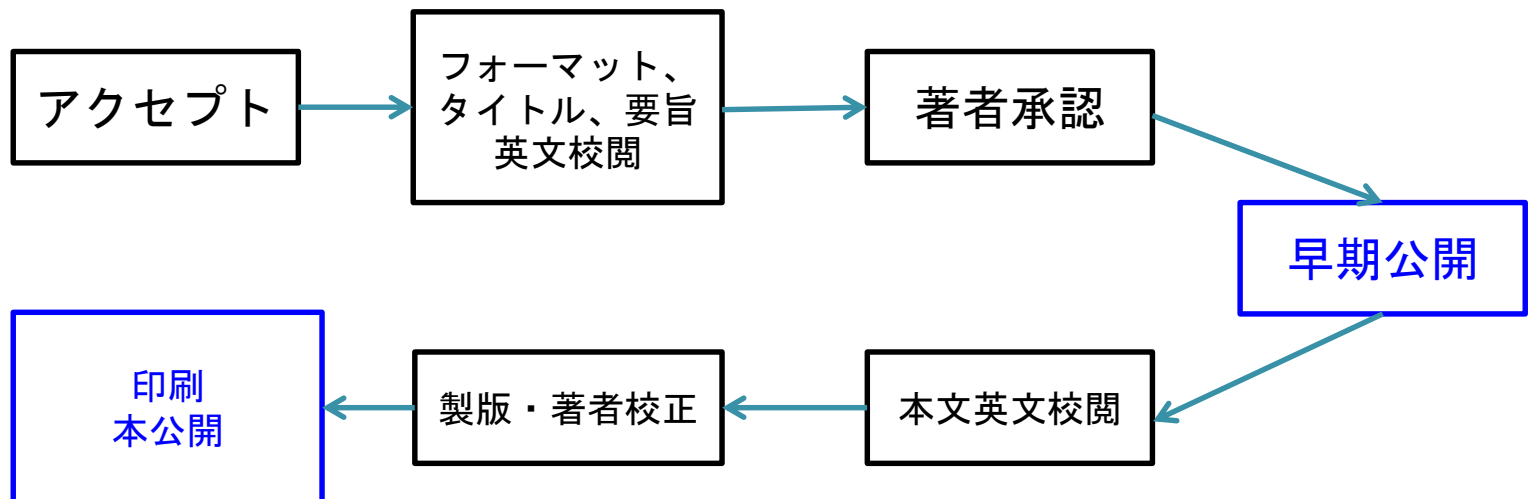
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## 問題点

- 英文校閲をするためにアクセプトから出版まで時間がかかる（～300日）。
- 編集委員長の負担の増大

## 解決

- 早期公開の導入



# 早期公開

Genes & Genetic Systems  
Article ID: 15-00081

Journal

Language: English

DOI <http://doi.org/10.1266/ggs.15-00081>

Advance Publication

**Expression efficiency of NAT2 haplotypes in a Korean population**

[Advance Publication] Released 2016/11/15

Full Text PDF [372K]

Abstracts

Since NAT2 single-nucleotide polymorphisms (SNPs) are responsible for the efficacy of arylamines and hydrazine drugs, defining the effects of these SNPs in various ethnicities is an important factor in the development of personalized medicine. In the present study, we examined the expression efficiency of NAT2 using promoter haplotypes identified in a Korean population. To construct NAT2 promoter haplotypes, seven NAT2 promoter SNPs (*rs4646241*, *rs4646242*, *rs4646243*, *rs4646267*, *rs4345600*, *rs4271002*, and *rs4646246*) were genotyped in a total of 192 Korean subjects. A luciferase assay was performed using the three commonest haplotypes to evaluate enzyme expression level of NAT2 promoter haplotypes. The most common haplotype (TACGAGG) showed the lowest enzyme expression level ( $0.72 \pm 0.06$  relative light units (RLU)/[ $\beta$ -galactosidase]). The second (CGTAAGA) and third (TATAACA) commonest haplotypes showed intermediate and the highest enzyme expression level ( $0.99 \pm 0.05$  and  $1.45 \pm 0.11$  RLU/ $\beta$ -galactosidase), respectively. Haplotype comparison among populations showed that Asian populations had a high proportion of the haplotype for lowest enzyme expression. Haplotype frequencies of Caucasian and African ethnicities were markedly different from those of Korean ethnicity. Results from the present study should contribute to the expansion of our current understanding of the pharmacogenetics field.

Full Text PDF [372K]

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2016 Page

Expression efficiency of NAT2 haplotypes in a Korean population

Han Sang Noh<sup>1,2</sup>, Jai Seol Lee<sup>1,2,3</sup>, Hyun Noh Chung<sup>1</sup>, Han Sang Shin<sup>1</sup>, The Sun Kang<sup>1</sup>, Hyun-Joo Park<sup>1</sup>, Hyung-Dae Shin<sup>1,2</sup> and Myoung-Woo Chung<sup>1\*</sup>

<sup>1</sup>Clinical Research Division, Toxicological Evaluation and Research Department, National Institute of Food and Drug Safety Evaluation, Chungcheong Health Technology Administration Complex, Cheong, Chungcheong-do, Republic of Korea  
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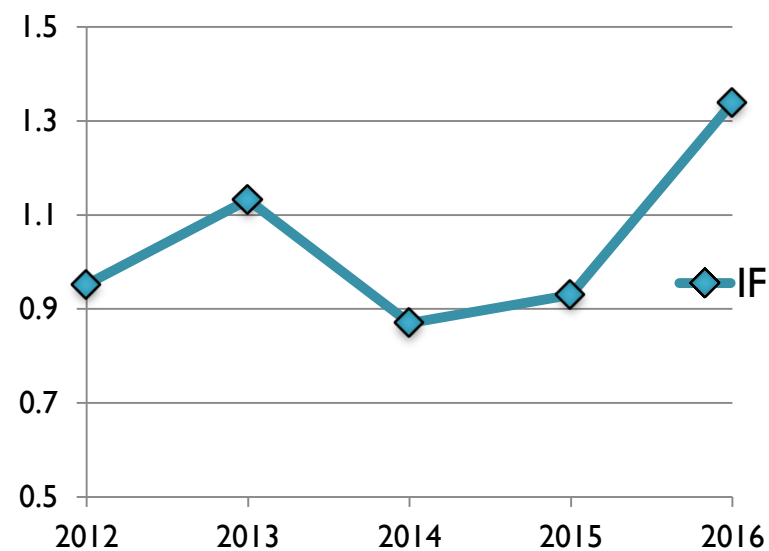
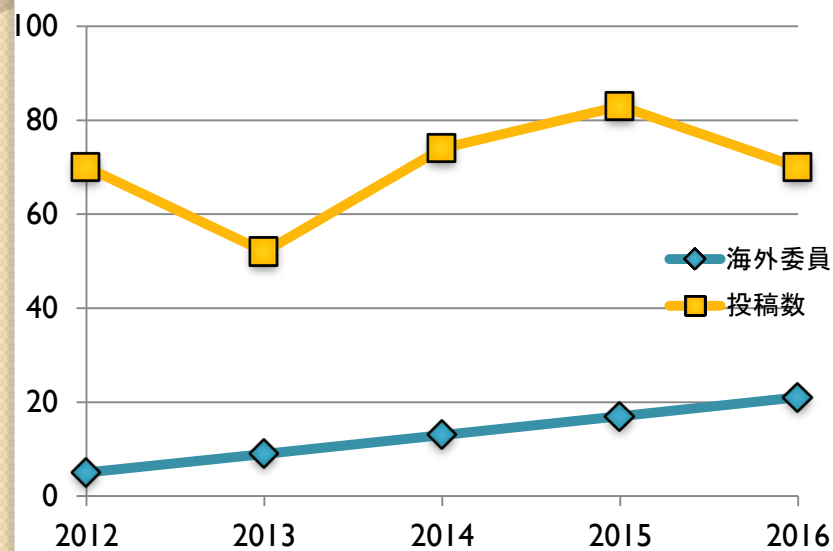
\*These two authors contributed equally to this work.

Short title: Expression efficiency of NAT2 haplotypes

Keywords: N-acetyltransferase 2, expression, haplotypes, polymorphism

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# 海外委員数、投稿数、I F





# GGGSの国際化への取り組み

- 海外編集顧問・編集委員の増加
- アクセプトされた全論文の英文校閲
- 早期公開
- 今後の課題
  - 編集作業の負担増加
  - 投稿数の増加
    - →ホームページの改定（現在進行中）

# 謝辞

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  - J-STAGE（電子ジャーナル、早期公開）
  - EM system（電子投稿システム）