# Genome-wide association study reveals escape by delayed growth from aphid herbivory on field-grown *Arabidopsis thaliana*

**Author 1**1  
**Author 2**1,2  
**Author 3**1,3

1 University of Zurich  
2 Ryukoku University  
3 Yokohama City University

# Abstract

Growing number of ecological studies have shown that plant developmental and phenological traits greatly contribute to shaping field herbivory. To reveal genetic bases underlying aphid herbivory, we conducted a genome-wide association study (GWAS) of aphid abundance in a field population of *Arabidopsis thaliana*. Out of a single significant peak on the third chromosome of *A. thaliana*, we isolated *NAME OF THE GENE* (*NOG*) that encoded a ribosomal gene (AT3Gxxxx). Knockout mutants of *nog* exhibited slower growth and ca. x-days later flowering than Col-0. Our laboratory bioassay further showed that a colony of the mustard aphid *Lipaphis erysimi* was difficult to establish on *nog* due to its small rosette size. These findings suggest that side effects of life-history traits on biotic interaction play a more critical role *in natura* than currently appreciated.

# Introduction

Plants are attacked by herbivores across their life cycles in natural environments. While chemical and physical traits have long been a main focus of anti-herbivore defense [1], plant life-history traits also account for herbivory in field environments [2, 3]. For example, phenological shifts can allow plants to escape from seasonal herbivory [4, 5]. Plants’ visibility for herbivores, namely plant apparency [6], often changes from vegetative to reproductive phase, which alters the risk of herbivore attacks across plant ontogeny [3, 7]. By focusing on intraspecific variation within a plant species, several studies have shown that plant apparency shapes heritable variation in herbivory among plant genotypes [8–10], though key genes remain unknown.

Genome-wide association study (GWAS) is increasingly recognized as a promising approach to dissect the genetic architecture of ecologically important traits [11, 12] and identify novel genes from natural phenotypic variation [13, 14]. However, field studies have suggested that controlled laboratory conditions unlikely reflect outdoor environments where interspecific interactions typically occur [15, 16], highlighting the importance of *in natura* study on gene functions [17–19]. For *in natura* understanding of interspecific interactions, it is necessary to conduct GWAS under field conditions.

*Arabidopsis thaliana* is the model plant species distributed in Europe and naturalized around the world. While most accessions of *A. thaliana* bloom in spring, some they are also attacked by xxx during early summer [10, 20]. Of diverse herbivores, aphids are a main herbivore [21]. Phenological traits may play a pivotal role in colonization of other organisms (Horton et al. 2014).

In this study, we discovered a new locus *NAME OF THE GENE* (*NOG*) by using GWAS of aphid herbivory on field-grown *A. thaliana*. To conduct GWAS, we first recorded aphid abundance on 196 *A. thaliana* accessions grown in a field site of Zurich, Switzerland. To validate candidate genes, we then cultivated and released the mustard aphid *Lipaphis erysimi* on *A. thaliana* mutants. The field-based discovery of *NOG* will gain genetic insights into plant apparency on insect herbivory *in natura*.

# Materials & Methods

## Study site (subsection)

Our field survey was conducted in the Irchel-Campus of the University of Zurich….

## Field survey

## Data analysis

### Statistical tests (subsubsection)

We used standard linear models or generalized linear model (GLM) to analyze relationship between the plant height and …

### Figure presentation (subsubsection)

We added trend lines to the bi-plots following the linear regression model:

, where is the response variable; is the explanatory variable; indicates the intercept; represents the regression slope. Because a log link function was used in the Poisson GLM, a regression curve was given by for the number of seeds.

# Results & Discussion

Bolting: pseudo h2 = near to 1.0  
log\_BbLe\_max: pseudo h2 = 0.7  
log\_BbLe\_sum: pseudo h2 = 0.71

Indirect association with herbivory through growth rate Although xxx, the difficulty in plant GWAS (pseudo-correlation, population structure). To solve this issue, xxx.

This study dealt with virtual data and thereby provided no biological significance. Citation Style Language (.csl) is usually available at journal’s page or other repository (<https://github.com/citation-style-language/styles>). If you need a more complex format, HTML or even LaTeX may be required. Try to minimize manual handling until you give up, and export to .docx lastly.

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