

# Ka와 Ks 값을 이용한 ortholog/paralog 오메가 값 결정 시스템

## WTO: Web Tool to determine Omega value between many ortholog/paralog pairs based on the Ka and Ks values

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### ABSTRACT

In this study, a user can easily determine the values for a user as well as released plant data and get a dot plot representing Ks and Ka values.

## I. Introduction

Orthologs are genes in different species that evolved from a common ancestral gene by speciation. Normally, orthologs retain the same function in the course of evolution. Identification of orthologs is critical for reliable prediction of gene function in newly sequenced genomes and Paralogs are genes related by duplication within a genome and Orthologs retain the same function in the course of evolution, whereas paralogs evolve new functions, even if these are related to the original one.

## II. Implementation

Interspecific and intraspecific homologous regions in genomes are caused by speciation and whole genome duplication, respectively. In the evolutionary study, it is essential to determine the synonymous site rate (Ks) and non-synonymous site rate (Ka) between gene pairs in the homologous regions. In generally, changes in the synonymous sites are accumulated over time whereas changes in non-synonymous sites are affected by several evolutionary events[1][2][3][4]. Thus, aspects of the evolutionary events can be determined by Ka/Ks (omega) value. For example, if the value of a gene pair is higher than 1, the gene pair likely got a positive selection pressure. Most tools to determine the values have been developed for the Linux

command line environment. However, many biologists are not familiar with the environment, and that can be an obstruction in the research. Thus, we have developed a web application, a Web Tool to determine Omega value (WTO). In the WTO, a user can easily determine the values for a user as well as released plant data and get a dot plot representing Ks and Ka values.

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