

ABSTRACT

The presence of certain kinesin domains in *Arabidopsis*, *Caenorhabditis elegans* and *Drosophila melanogaster* may suggest new plant subfamilies.

INTRODUCTION

In the past decade, the genetic basis of the *Arabidopsis* genome has been extensively studied. *Arabidopsis* has been the focus of a number of studies including the following:

Arabidopsis is a large and diverse plant species in the family Brassicaceae. It has been cultivated in many parts of the world, including the Middle East, Asia, and North Africa. It is also grown in the USA, Canada, and Europe. The *Arabidopsis* genome is a large collection of DNA sequences, known as mitochondrial DNA (mtDNA) that were obtained from the mitochondrial DNA of the *Arabidopsis* plant (*A. thaliana*). The mitochondrial DNA is the genetic material of the plant and is inherited from both parents.

The *Arabidopsis* genome is composed of three main chromosomes: A In just five years, the genomes of four different eukaryotic organisms have been fully sequenced, including *Saccharomyces cerevisiae*, a unicellular EC2, two multicellular organism *C. elegans*, and *Drosophila melanogaster* and *Arabidopsis thaliana*, which are among the first known examples of complete genome sequencing. By examining predicted gene families in various organisms, including simple single-celled and multicellular cells, it is possible to determine the functions and developmental control pathways of proteins. This study also uncovered the function of zinc-binding genes in bacteria, yeast, and eukaryotes through multiple alignment and parsimony analysis, as well as other techniques. The superfamily of motor proteins known as kinesins has been identified in all eukaryotic organisms, with the aforementioned members having 'superconserved' motor domains. The first kinematic was identified by scientists in squid giant axons, which contain two heavy chain-binding proteins and corresponding tetramer-based motor "domains". Kinesins (human immunodestructive compounds) have been described as subfamilies since 1980s when it is known to perform various tasks by kinesins. Two plant kinesins, PKH and NtKRP125, were identified in tobacco pollen tubes. Another kinesin has been isolated at the molecular level and further characterized at higher levels of biochemistry. The *Arabidopsis* genome was fully sequenced, and it became possible to search the Arabs' database for kinesin-like genes from the conserved motor domain of kinesins. This allowed us to identify the 61 kinematic genes in *Arabidopsis* and their general location on the five *Arabidopsis* chromosomes, which contained the most KBASEs among all eukaryotic genomes that have been sequenced as well as some that may provide insight into their function: all had kinesin domains.

CONCLUSION

Remarkable conclusions Overall, *Arabidopsis* has one of the highest numbers of kinesins among the five completed genomes of all eukaryotic organisms. The majority (60%) of these kinesins in *Arabidopsis* are not classified as subfamilies of known kinematic species such as yeast, *C. elegans* and *Drosophila* and may not even be found in other plants anymore. Additional studies have revealed several intriguing domains within *Arabidopsis* families that aid in understanding their functions. Despite the lack of information on the functions of most *Arabidopsis* kinesins, empirical testing of their function can be achieved through

phylogenetic analysis and functional domain identification. A few knockout mutant libraries obtained by T-DNA insertions in Arabies can also be used to screen for mutations within motor domains.