



# Genome-wide Analysis Of Transposable Elements In Different Rice Species And It's Association In Plant Disease Resistance (R) Genes In *Oryza Sativa* Nipponbare

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## ABSTRACT

Transposable elements (TEs) are mobile DNA elements which exist in almost all eukaryotic genomes as they have regulatory or coding sequences and often occur in large copy numbers. TEs can cause the transcription or methylation of nearby genes and significantly promote structural variation or genome size expansion. However, TEs are rapidly evolving due to arms races with their host genomes.

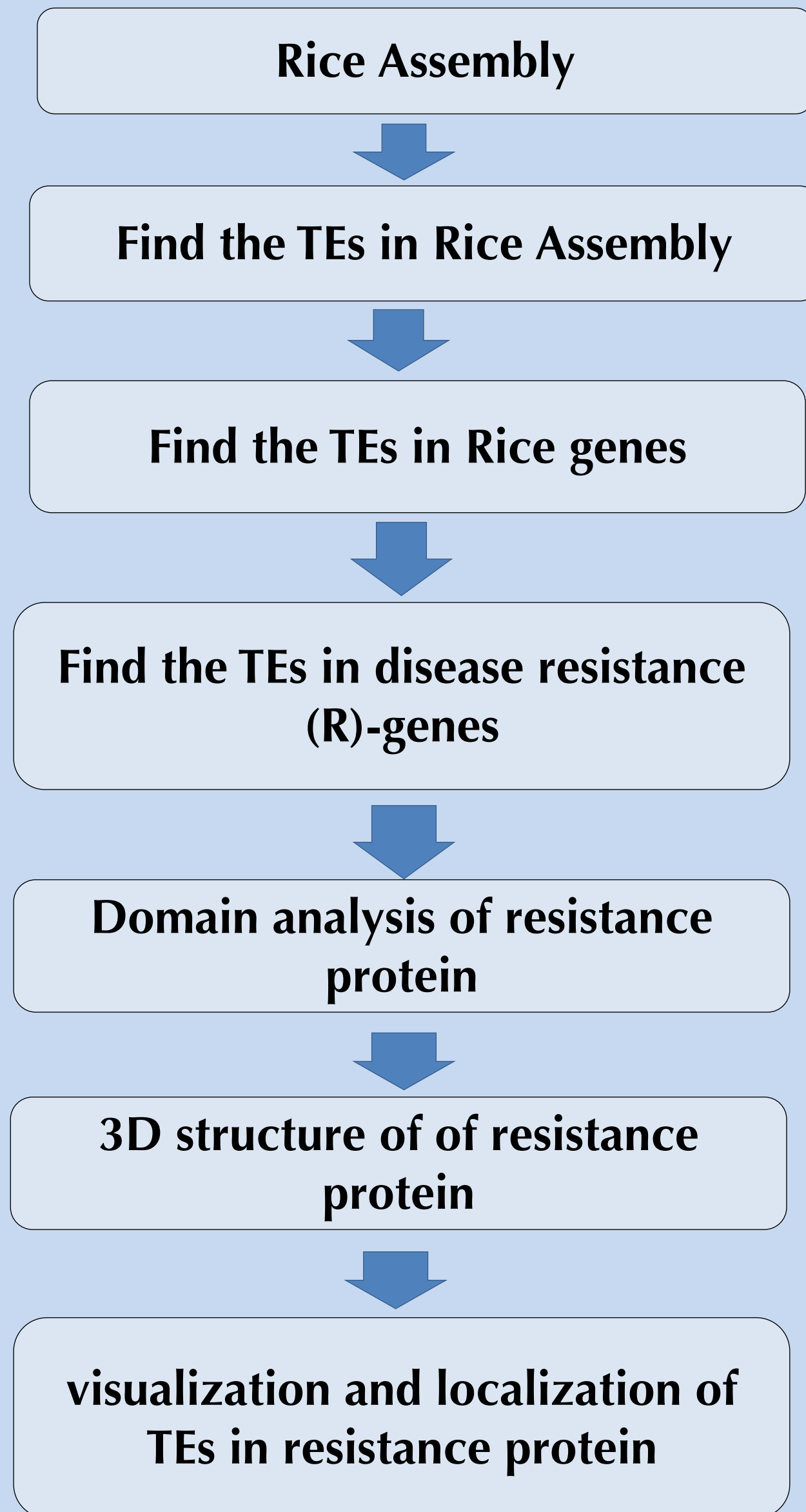
In the present work, we investigated the TEs in Rice (*Oryza sativa* L.) as it is a staple food for more than half of the world's population and it is model organism for genomic research; but can be attacked pathogens Magnaporthe oryzae causes Rice Blast disease, is the most severe diseases of rice that greatly reduces yield up to 65% in susceptible cultivars and grain quality worldwide. Plant disease resistance (R) genes have the ability to detect a pathogen attack and facilitate a counter attack against the pathogen but TEs can affect the expression of these R- genes.

We analyze 30 different rice species by using RepeatModeler and RepeatMasker. The data indicates, the average TE content of rice genome assemblies is 38.79% and different 60 TEs are located within various 103 R-gene loci of *O. sativa* Nipponbare.

## INTRODUCTION

TEs are selfish mobile genetic elements which exist in virtually all eukaryotic genomes [1]. In plants, based on the transposition mechanism the TEs were divided into two classes [2]; Class I (retrotransposons) transpose via an RNA intermediate while class II (DNA transposons) change their location by a cut-and-paste mechanism, characteristic for TEs carrying terminal inverted repeats (TIRs). The Class I TEs are not excised during transposition, which leads to an increase in copy numbers in the host genome. These include retrotransposons with long terminal repeats (LTRs), such as Copia, Gypsy, and non-LTR retrotransposons [3]. LTR retroelements from the significant component of intergenic regions in large plant genomes [4].

## METHODS



## RESULTS

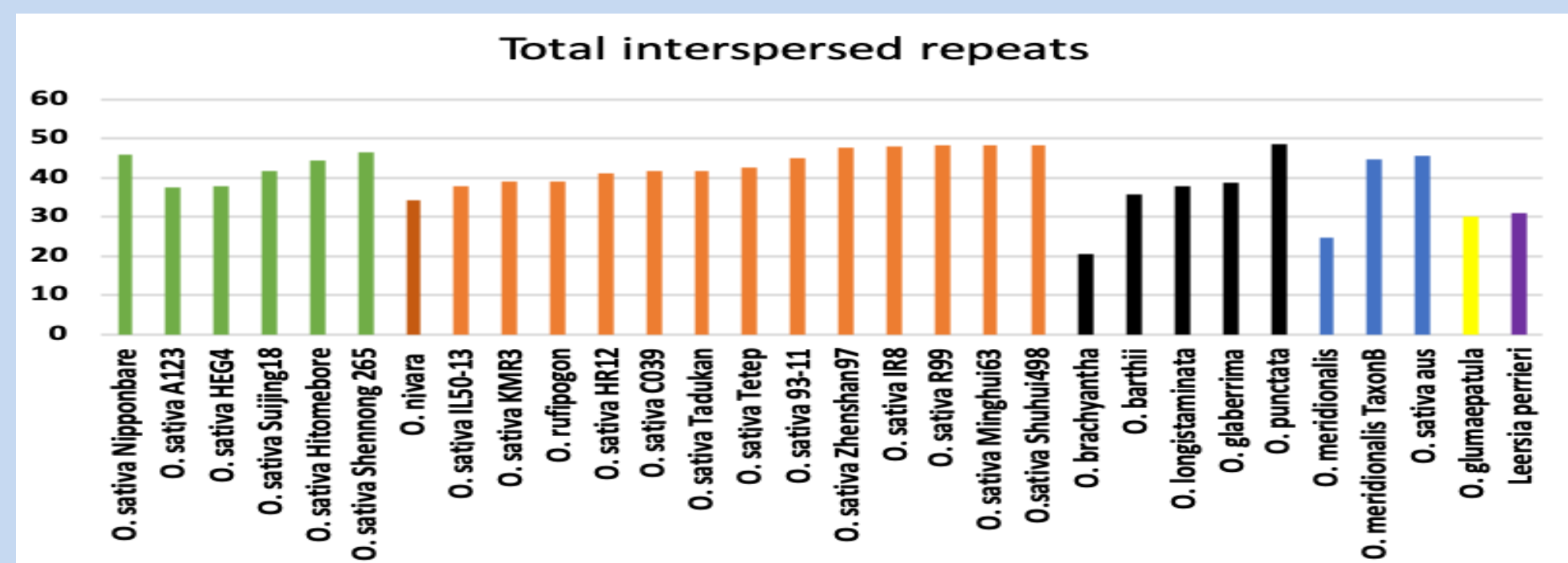


Figure 1. Total interspersed repeats analysis in 30 different rice species

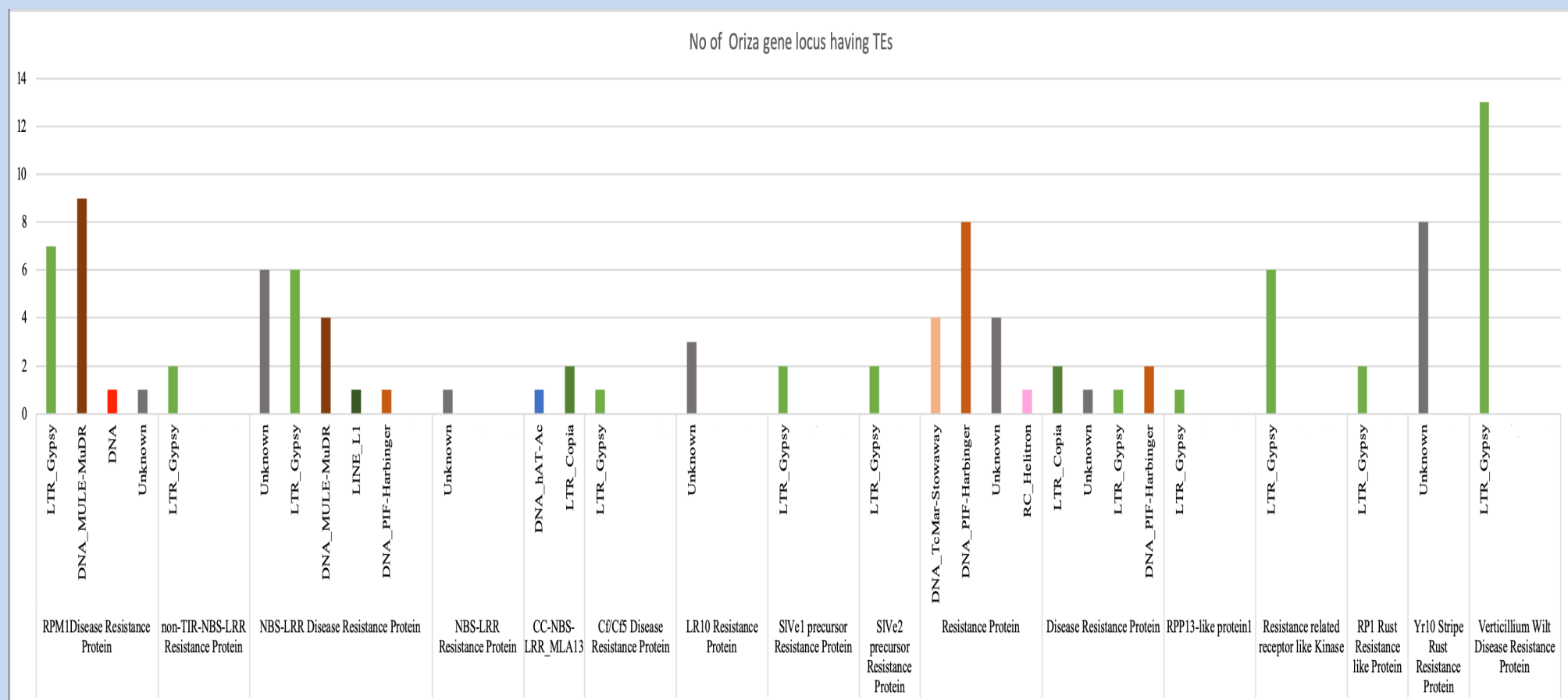


Figure 3. Different TE Classes present in various Plant Resistance (R)-genes loci in *O. sativa* Nipponbare

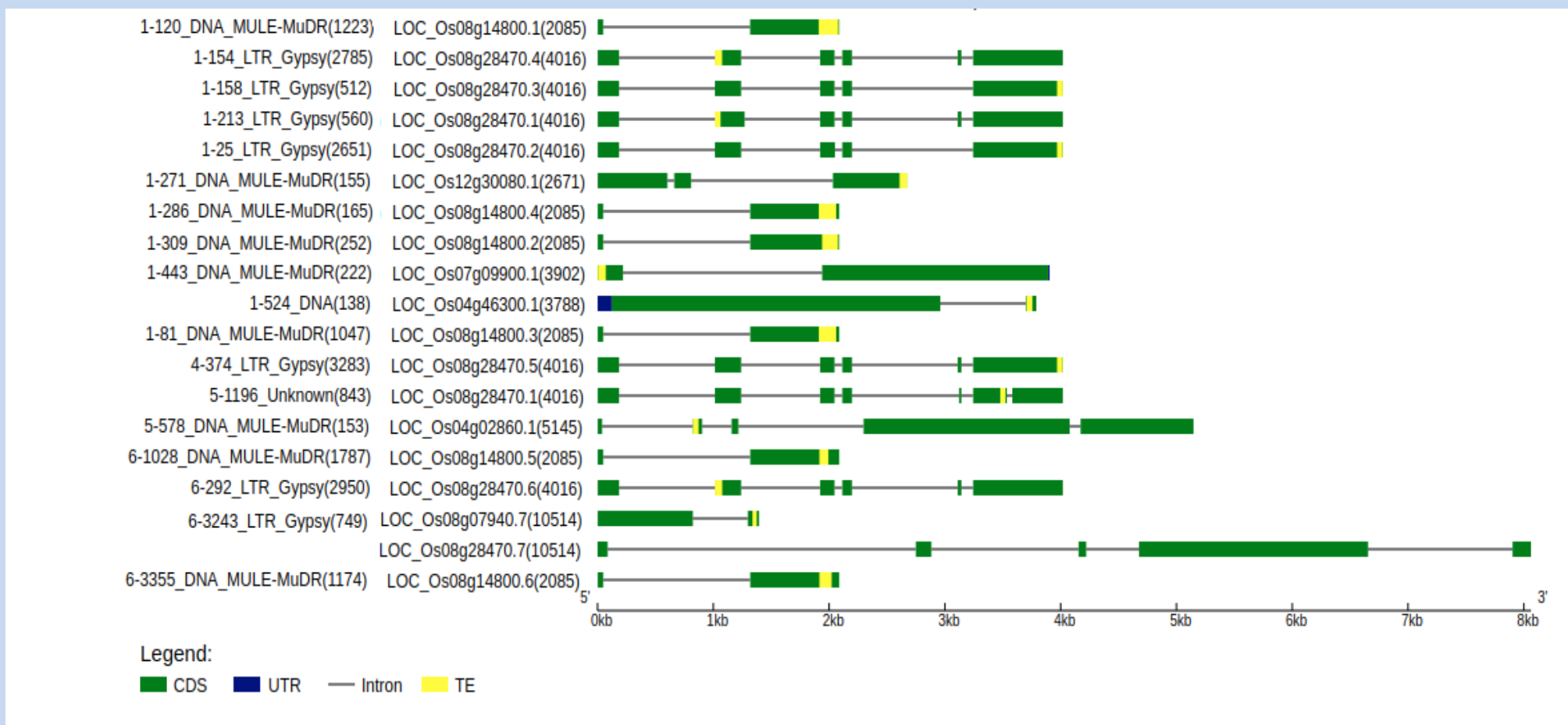


Figure 4. TE footprints in RPM1-Disease Resistance Gene

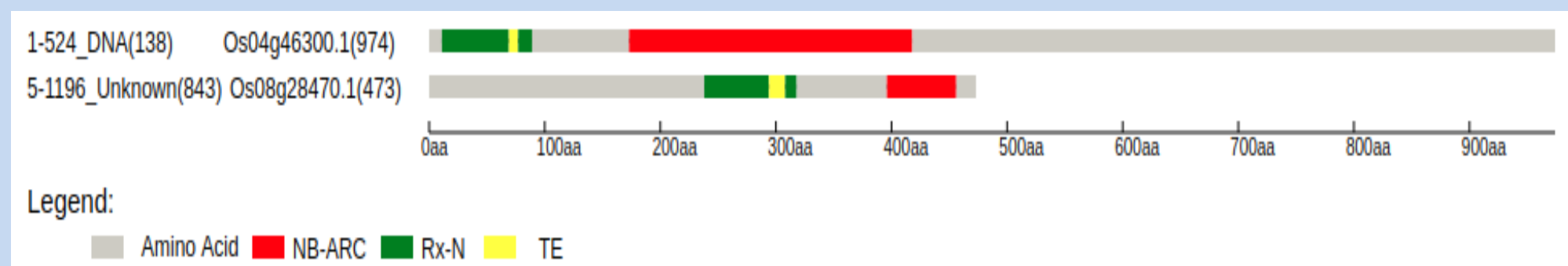


Figure 5. TE footprints in Rx-N domain of RPM1-Disease Resistance Protein

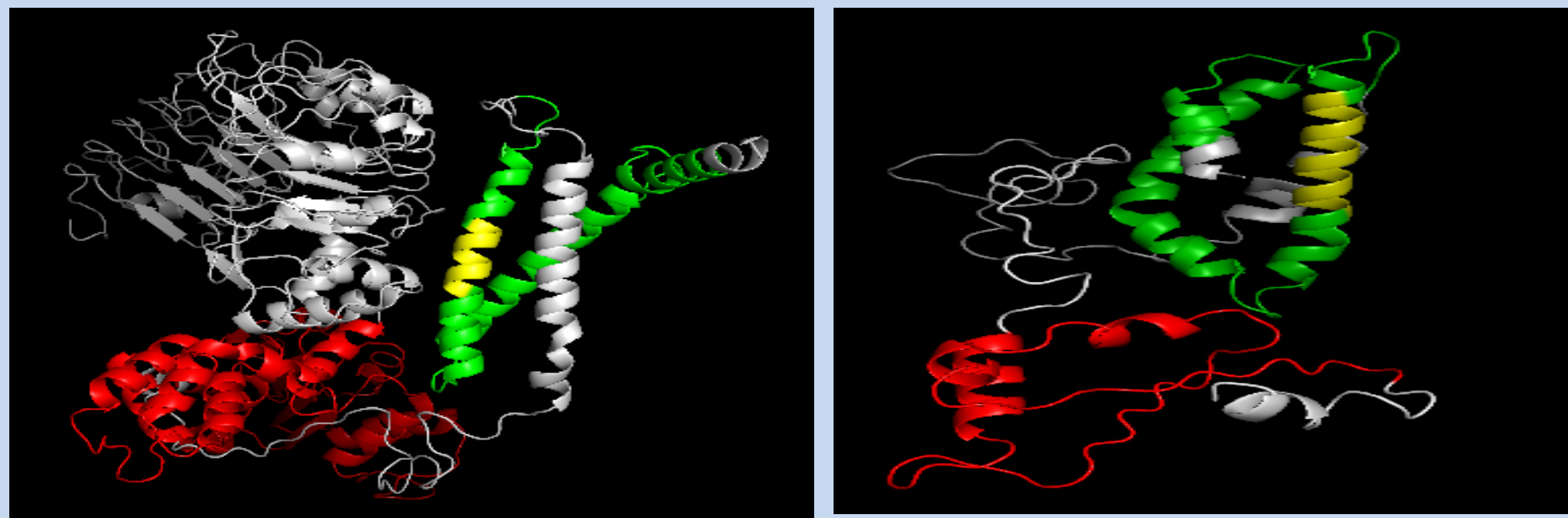


Figure 6. 3D structure of RPM1-Disease Resistance Proteins (A. Os04g46300.1 and B. Os08g28470.1) showing TE footprints inside Rx-N domain

## CONCLUSIONS

- ❖ The average TE content in genome is 38.79%
- ❖ TE content in wild rice *Oryza brachyantha* (wild rice) was low as 20.47% and in *Oryza punctata* (red rice) it is high as 48.55 %
- ❖ Two classes of LTR elements (Ty1/Copia and Gypsy/DIRS1) account for a significant portion of the genome size variations present in the *Oryza* genus
- ❖ It is observed that the different 60 TEs are located within various 103 resistance gene analogs (RGAs), of *Oryza sativa* Nipponbare
- ❖ 16 types of plant disease resistance protein (R) families are associated with 10 different subclasses of TEs
- ❖ Two R-genes (Pi9\_Nbs6) have 10 TEs footprints in rice species *Oryza sativa* Indica 75-1-1127 and Pia\_Os11gRGA4 have one TE footprint in rice *Oryza sativa* Nipponbare.

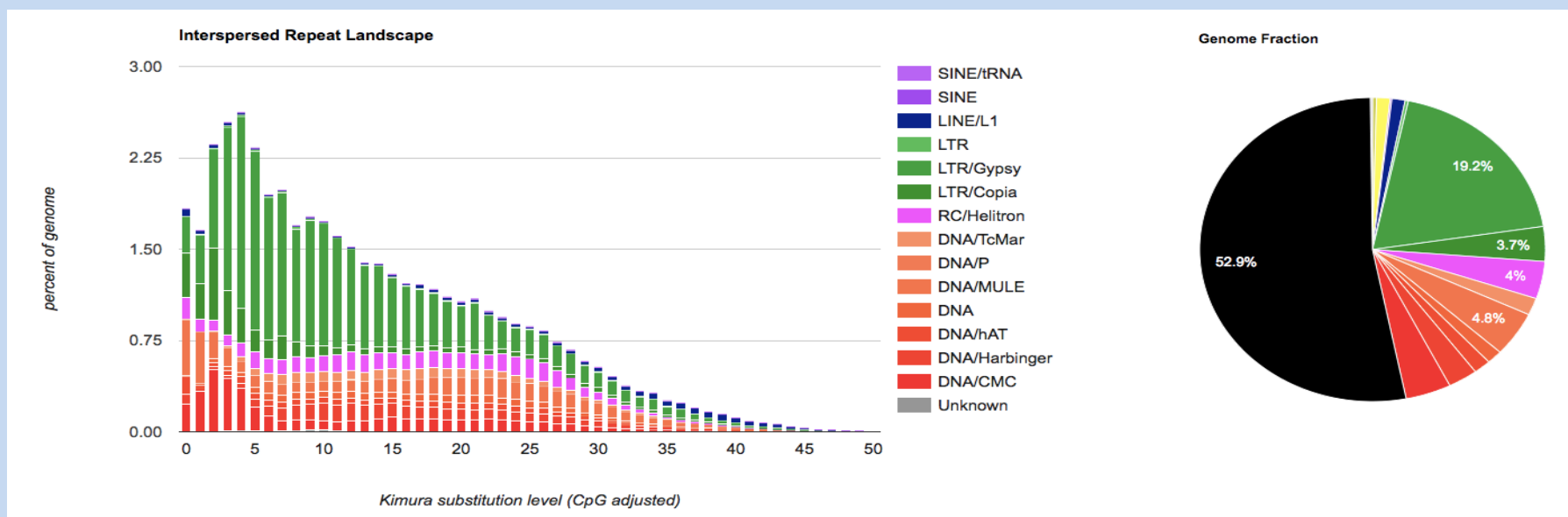


Figure 2a. TE fraction in *O. sativa* Nipponbare (46%)

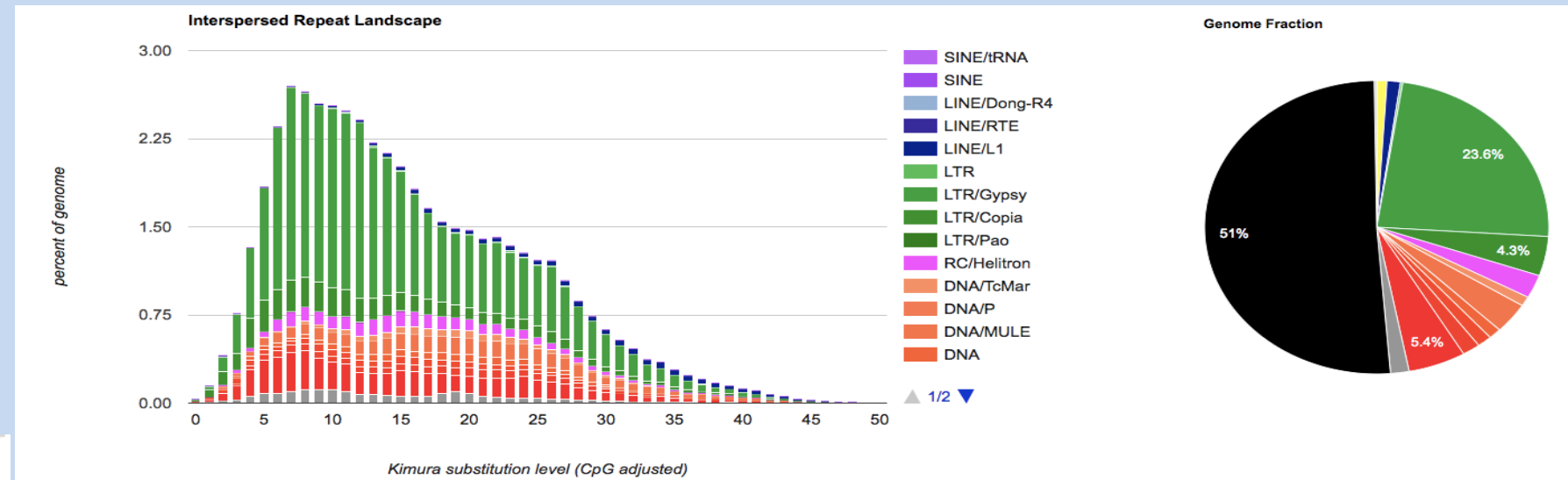


Figure 2b. TE fraction in *O. brachyantha* (20.47%)

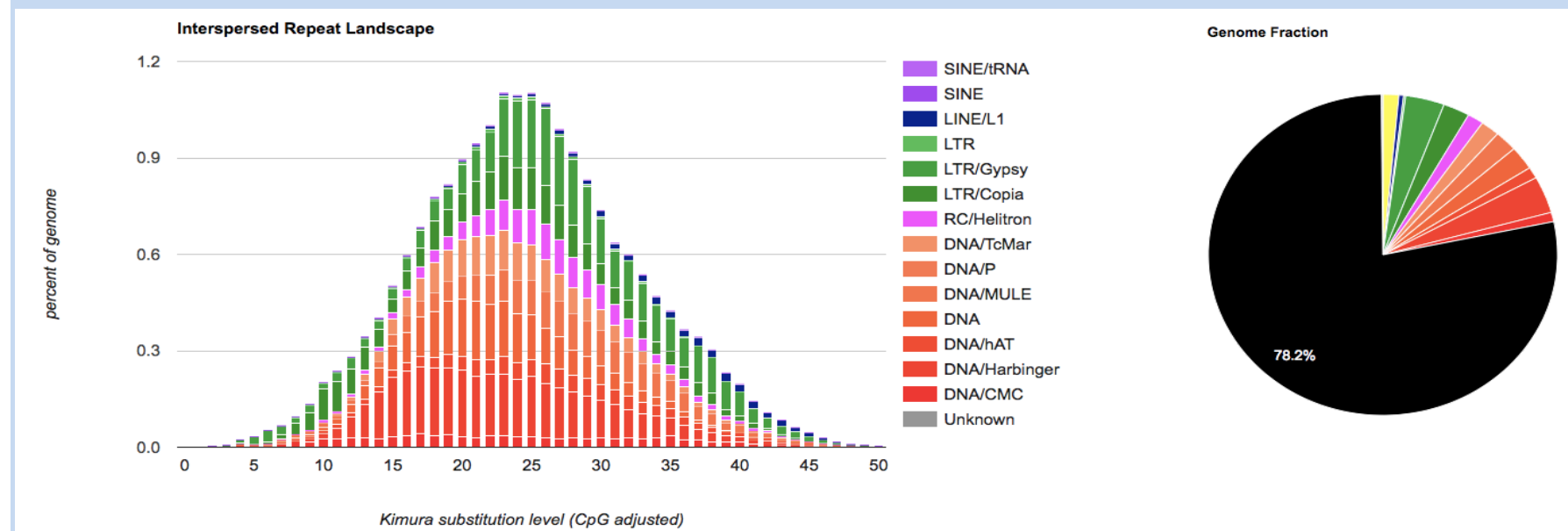


Figure 2c. TE fraction in *O. punctata* (48.55%)



Figure 7. Phylogeny analysis of Plant disease resistance (R) gene loci of *Oryza sativa* Nipponbare

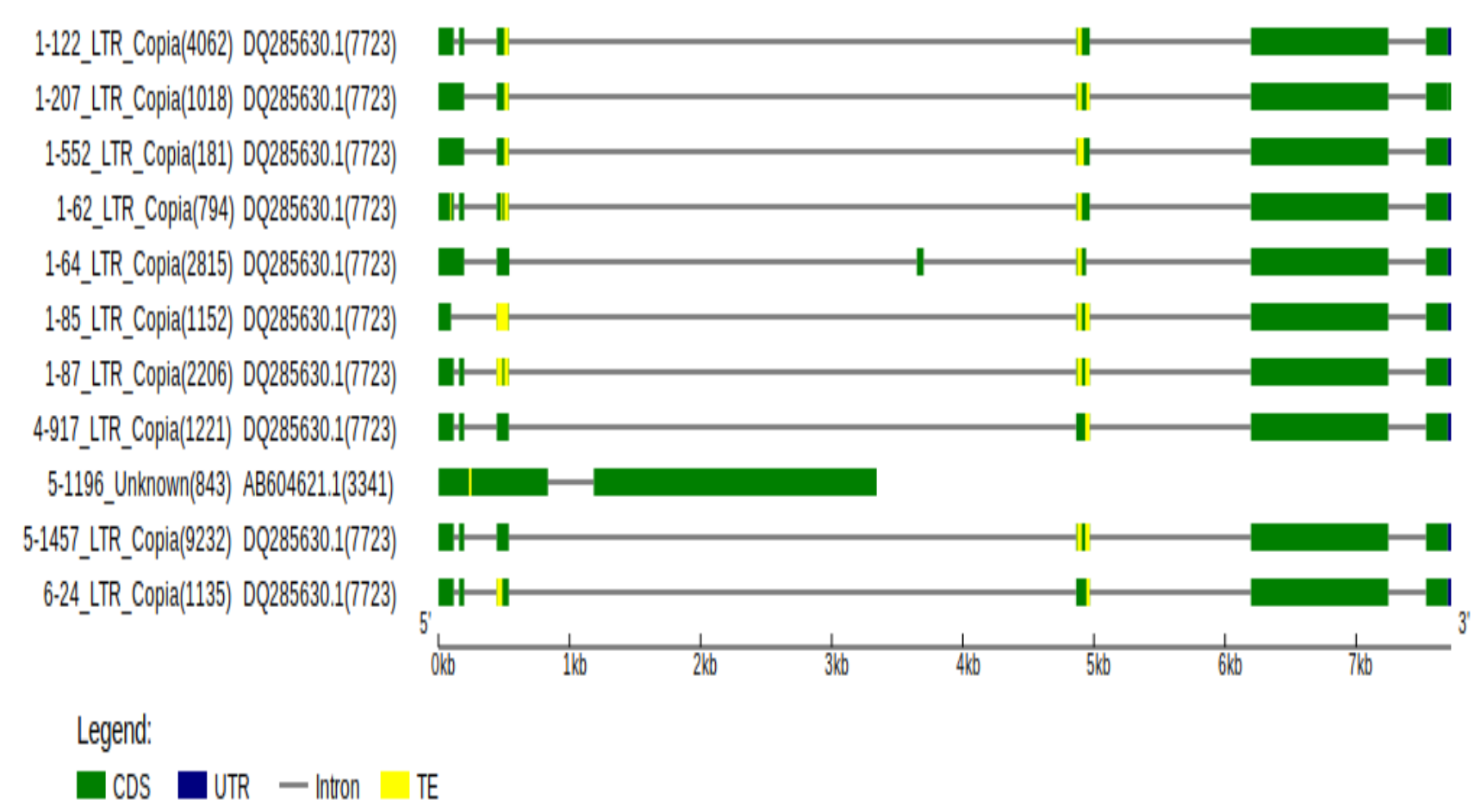


Figure 8. The two R-genes (Pi9\_Nbs6) which have 10 TEs footprints in rice species *Oryza sativa* Indica 75-1-127 and Pia\_Os11gRGA4 which have one TE footprint in rice *Oryza sativa* Nipponbare.

## REFERENCES

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