ɪ ' ' ɪ

Pararetroviruses (*C m* and *H*) hav
double-stranded DNA genome and resemble retroviruses in
they employ reverse transcription for genome replication, but
the processes and molecular machinery for integration into the l
genome (Temin, 1985). However, with the increasing decryp
of plant genomes, a growing number of endogenous pararetrov
(EPRV) sequences have been discovered as ancient integrated ana
of most members of the *C m* family,. is incide
integration of pararetroviruses was thought to involve illegitim
recombination or double-strand break repair via non-homolog
end joining between the pararetrovirus and host genomes.Rice tur
disease is a signi cant constraint on rice (L.) yields in Sc
and South-East Asia. e disease is caused primarily by infection v
rice tungro bacilliform virus (*C m* , ; RTBV),
known extant rice pararetrovirus e evolutionary history of rice
been studied deeply and described. Cultivated rice, which includes
subspecies and , was domesticated from the wild
species . . . is thought to have diverged int
least two ecotypes, perennial and annual (the annual type is also ca
.), 0.16 million years ago (Mya), as estimated by the molec
clock.Here, we compared the eRTBVL sequences from the three
genome databases by comprehensive analyses and scree
orthologous sequences in diverse cultivated and wild rice accession
understand the evolutionary route of the eRTBVL sequences.

To investigate the origin of the endogenous pararetrovirus eleme
in the rice genome, we performed a strict
viruses during rice speciation, and inferred the geographical c

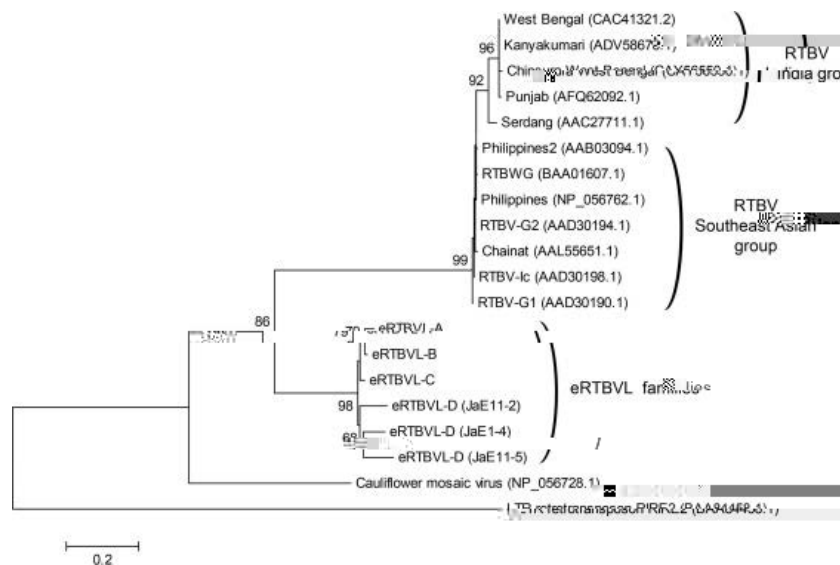blue, W1943). Sequences sorted into the same family are indicated by

Figure 1: Distribution of eRTBAL in Aisa.

the eRTBVL families and RTBV strains was based on the amino acid sequences of the RT/RH region using the WAG+G model, which was chosen a er model testing. Support for the ML trees was evaluated by 1000 bootstrap replicates. All the sequence alignments

C

Total DNAs were extracted from the leaf samples of the cultivated and wild rice accessions by Plant DNAzol (Invitrogen, Carlsbad, CA, USA). e DNA concentration in each sample was measured by NanoDrop 2000 (ermo Fisher Scienti c, Wilmington, DE, USA) and all were adjusted to a similar level. Primer pairs were generally designed and used as follows: for ampli cation 1, a forward primer for the le ank (P1) and a reverse primer for the interior of the eRTBVL locus (P2) were used; for ampli cation 2, a forward primer for the interior of the eRTBVL locus (P3) and a reverse primer for the right ank (P4) were used; for ampli cation 3, a primer pair for le and right anks (P1, P4) were used to amplify the whole length of the eRTBVL locus or the empty donor site. Polymerase chain reactions (PCR) were performed using Ex Taq or LA Taq polymerase (Takara, Shiga, Japan) in a PTC-200 thermal cycling system (GMI, Ramsey, MN, USA). When the whole length of some long eRTBVLs failed to amplify, the reaction was adjusted to amplify the possible empty donor sites in the corresponding rice accessions. e PCR products were resolved on a 1–2% agarose gel and analyzed with a Typhoon 8600 PhosphorImager (GE Healthcare, Little Chalfont, U.K.).Consensus sequences of the eRTBVL-A1, -A2, -B, -C and -X families were acquired by aligning the nucleotide sequences from the de ned regions for each family (the chimeric sequences that possibly resulted from intra-recombination a er integration were excluded). e eRTBVL sequences that spanned at least 80% of the length of each region in the three rice genomes were used in the alignments. e consensus sequences of each region were combined, and ambiguous regions at the terminals were trimmed to produce the nal whole length consensus sequences. ese consensus sequences were then aligned by ClustalW and manually edited for use in the recombination analysis. We employed the RDP,

GENECONV and BOOTSCAN methods in the RDP3 package. eRTBVL sequences from the Nipponbare genome DDBJ accession numbers: BR000029-BR000031as queries. e following BLAST parameters were used: word size, 11; gap open, 5; gap extend, 2; penalty, –3; and reward, 2. e contigs spanning high-identity matches (e-values<1e−10, alignment length>100 bp) were extracted, and ltered so that only the contigs with>50 bp anking at least one end of the eRTBVL loci.

References

1. Zhou Z, Robards K (2002) Composition and functional properties of rice. Int J

2. Yoshida H, Tomiyama Y, Mizushina Y(2010) Lipid components, fatty acids and triacylglycerol molecular species of black and red rices. Food Chem 123: 210-215.

3. Kim NH, Kwak J, Baik JY, Yoon MR, Lee JS, et al. (2015) Changes in lipid substances in rice during grain development.

4. Heinemann RJB, Fagundes PDL (2005) Comparative study of nutrient composition of commercial brown, parboiled and milled rice from Brazil. J Food

5. Chen HH, Hung CL (2015)
storage characteristics of brown rice. Food Bioprocess Technol 8: 471–477.

Stout MJ, Riggio MR, Zou L, Roberts R(2002)
and feeding behaviour of the rice water weevil, Lissorhoptrus oryzophilus (Coleoptera: Curculionidae). J Econ Entomol 95: 715-721.

7. Zou L, Stou MJ (2004) Degree-day models to predict the emergence and development of rice water weevil (Coleoptera: Curculionidae) in southwest Louisiana. Environ Entomol 33: 1541-1548.

8. Zou L, Stout MJ (2004)
Lissorhoptrus oryzophilus Kuschel on the growth and yield components of rice, Oryza Sativa

9. Stout MJ, Hamm JC(2011)
dermacorX-100 against the rice water weevil at three planting dates. Annu Res Report 103: 331-332.

10. Blackman B, Autin T (2014) Management practices of Louisiana and Texas rice growers. La Agric Mag 57: 14-15.