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Project Title:

Development of Polymerase Chain Reaction for Rapid Detection of Grapevine Leafroll Associated Viruses 1 through 5

Principal Investigator:

Adib Rowhani, Plant Pathology Specialist, Department of Plant Pathology/Foundation Plant Materials Service, University of California, One Shields Avenue, Davis, CA 95616
Phone: (530) 752-5401
Fax: (530) 752-2132
E-mail: akrowhani@ucdavis.edu

Cooperator:

Deborah A. Golino, Associate Cooperative Extension Specialist, Department of Plant Pathology/Foundation Plant Materials Service, University of California, One Shields Avenue, Davis, CA 95616
Phone: (530) 754-8102
Fax: (530) 752-2132
E-mail: dagolino@ucdavis.edu

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Concise General Summary of Current Years Results

In the funding cycle 2002-2003 we mostly focused on grapevine leafroll associated viruses 1 and 2 (GLRaV). In our investigation we found that 3 isolates (among 17) of GLRaV 1 which initially were tested positive by ELISA were negative when used in reverse transcriptase-polymerase chain reaction (RT-PCR) using primers adopted for the detection of this virus. In addition, the PCR primers designed to amplify the coat protein (CP) gene used for sequencing and sequence comparison among different isolates failed to amplify the CP of these 3 isolates. Also in the same population we found 3 other isolates which were tested positive by ELISA and detection primers but not by the CP-specific primers. When we investigated the primers binding sites for these isolates, we found that at least two nucleotide mis-match (nucleotides in the viral genome used for designing the primeres which were not complementary with the specific PCR primers sequences) were existed between PCR primers and viral genome.

For GLRaV-2 also the same problem existed for 2 and 2 different isolates which were tested positive by ELISA only or by ELISA and RT-PCR using detection primers, respectively. In this case only one isolate from each group showed that having sequence mis-match at the PCR primers' sites (as described for GLRaV 1). For two other isolates, we found that both were infected with GLRaV 1. The reason that we could get positive reaction in ELISA using GLRaV 2-ELISA system, because the antibody produced for GLRaV-2 also has the antibody component for GLRaV-1.

Based on the new sequence information we obtained for GLRaV 1 and 2 (see above), new sets of PCR-detection primers were designed and evaluated to detect all possible isolates of each in a single reaction and reduce the chance of getting false negative data.

All PCR-detection primers designed for GLRaVs 1 to 5 were further evaluated. The simplified sample preparation and one step RT-PCR protocols were also further evaluated using different types of tissue in different time of the year, especially for the sample preparation using the blotting methodology.

Objectives and Experiments Conducted to Accomplish Objectives:

The objective of this project is to develop fast, sensitive and reliable reverse transcriptase-polymerase chain reaction (RT-PCR) methods for the detection of grapevine leafroll associated viruses (GLRaV) 1 through 5 in grapevine. The specific objectives will include:

1. Develop RT-PCR methodologies for the detection of GLRaVs 1 through 5.

    - Sequence fragments of viral genome for viruses that do not have such sequences already available. The sequence information is necessary for designing PCR primers.

    - Design and evaluate virus-specific and universal primers for detection of single and multiple leafroll associated viruses, respectively.

2. Develop a simple and reliable sample preparation method for grapevine tissue for testing large number of samples at a time.

3. Investigate strain diversity among leafroll associated virus types. This will aid in design of primers that can detect all strains.

4. Investigate and develop protocols for colorimetric RT-PCR assay.

Experimental procedures:

Objective 1: To develop RT-PCR methodology for the detection of GLRaVs 1 through 5: Complementary DNAs (cDNA) were synthesized from viral genomes derived from total RNA extractions or double-stranded RNAs (dsRNA) and cloned. Cloned cDNAs were sequenced using the facilities available at UC Davis. Oligonucleotide primers (20-30 bases) were made from the sequences for RT-PCR use. For some of these viruses (e.g., GLRaV 2 and 3), the complete genome sequences published by other investigators were available from the GenBank. In these cases we used the available information for designing PCR primers. In addition, for GLRaVs-1 to -3, sequences obtained from the same genome segment of up to 10 different isolates of each (obtained either from the Genbank or cloned and sequenced in our laboratory) were piled up and specific primers were designed to identify all isolates of the same virus (objective 3). The specificity of each primer pair in detecting the virus was evaluated by testing them against number of different virus isolates collected from different regions. The primer pairs which specifically amplified each viral genome and its different isolates and strains were selected for virus detection application and field survey work. We also investigated the use of nested RT-PCR in detection of these viruses. This method is reported to be more sensitive than regular PCR. In this method, our general PCR primers were used to amplify a target sequence. Then part of the amplified product was diluted and an aliquot was added to a different PCR reagent containing new set of primers which were designed to internally amplify a segment from the original PCR product.

Objective 2: Develop a simple and reliable sample preparation method for grapevine tissue for testing large number of samples at a time: Grapevine tissues contain large amounts of polysaccharides, phenolic compounds and other substances that have been proven to make both nucleic acid extraction and virus detection by RT-PCR difficult and unreliable. Therefore, preparing samples from grapevine tissues for RT-PCR usually is a time consuming process and may take hours to prepare. I n this objective, different buffers, chemical additives and treatments will be tested and an optimum sample preparation method will be developed.

Objective 3: Investigate strain diversity among leafroll associated virus types. This will aid in design of primers that can detect all strains: We have gathered ELISA data from large number of different isolates on GLRaV 1 through 5. These ELISA data indicated that the OD405 reading values (reading was done by an ELISA plate reader) for different plants varied from very low and boarder line readings to very high readings. These data suggested the possibility of the occurrence of more than one strain of the virus in different plants. Therefore, we designed specific PCR primers to amplify the coat protein gene of these viruses and study their sequences. For each virus we will select at least 10 different isolates (or less for those viruses which are not reported to be widely spread and we do not have access to many), preferably from different locations or regions, and compare and study their sequences. To compare the sequences we will use a computer Pileup program. Finally, specific PCR primers will be designed from the region exhibiting perfect nucleotide match among all these isolates for each virus. These primers will be evaluated and adopted for RT-PCR detection of the above mentioned viruses.

Objective 4: Investigate and develop protocols for colorimetric RT-PCR assay: We have developed a much simplified colorimetric assay for the detection of some of the viruses attacking fruit and nut trees (7). In this protocol the RT-PCR products were analyzed in an ELISA plate and the resulting color development (for virus-positive samples) were evaluated and quantified by an ELISA reader. In colorimetric PCR, the microtiter plates were coated with streptavidine. After 1 hour incubation at 37C, the plates were washed and then incubated with virus-specific biotin-labeled detection probes (an oligonucleotide complementary to an internal site of PCR product for a given virus) and incubated for 30 min at 37C. After washing, the denatured PCR product labeled with Digoxygenin (PCR product was labeled by adding Digoxygenin-labeled dUTP in the PCR reaction) was added and incubated for 1.5 hr at 46C. Plates were washed and incubated with alkaline phosphatase-conjugated antibody prepared to Digoxygenin and incubated for 1 hr at 37C. Finally, the plates were washed and incubated at room temperature with colorimetric substrate for 1-2 hours. Color development was then analyzed by measuring absorbance at 405 nm with an ELISA plate reader.

Summary of Research by Objectives:

Objective 1: We have designed and evaluated specific detection PCR primers for GLRaVs-1 to 5 (Fig. 1). These primers were designed based on the information we have gathered on sequence pileup experiments (objective 3) to ascertain that the primers sequences have almost 100% match with the sequences of all the isolates for each virus used in this investigation. Nested PCR primers were also designed for all these five different GLRaVs and are being used for their detection in

samples which regular PCR test results are inconsistent or weak (due to low virus concentration or uneven distribution in the plant) and they worked quite well (Fig. 2). For example, the detection limit using regular PCR primer for LR-1 was at 1:1 dilution of the sample while with nested PCR this dilution increased to 1:100 (Fig. 2A). The same was true for GLRaV-3 in which its limit of detection with the regular PCR primer was at 1:10 while when using nested PCR a strong band (representing the PCR product) was visible at 1:100 dilution (Fig. 2B).

Objective 2: A simple sample preparation method for RT-PCR detection of grapevine viruses in grape tissue was developed. This simplified method is not any more complex or labor intensive compared to the method used in ELISA. In this method grape tissues were homogenized in ELISA extraction buffer (a carbonate-based buffer containing PVP40, BSA, and Tween 20) at a ratio of 1:20 to 1:40 of sample:buffer, and two microliters from this homogenate were added to 25 microliters of GES buffer (glycine buffer containing EDTA, 2-mercaptoethanol, and NaCl) and boiled at 95C for 5-10 min. Finally, 2 microliters from this preparation was added to PCR cocktail and amplified. We also have developed a sample blotting method for collecting samples in the field. In this method, a cross section was made on leaf petioles or young shoots and the cut area blotted on special type of nitrocellulose or nylon membrane and air dried. Later in the laboratory each blot (representative of a sample) was cut and processed in GES buffer, then an aliquot from this processed sample was added to PCR reaction for amplification and detection. This is a very simple method for sample collection, it does not require any technical training to collect and blot the samples on the membrane. The blotted membranes could simply be shipped in an envelop to the laboratory for processing and testing. If necessary samples prepared by this method could be stored for a long time at room temperature before processing for PCR detection.

RT-PCR is a two step reaction procedure. In the first step, reaction cocktails are prepared to synthesize the first cDNA strand from the viral RNA genome (most plant viruses including all known grapevine viruses contain RNA as their genome) to be used by an enzyme called Taq DNA polymerase (which make copies only from DNA templates) and in the second step, a different cocktail containing Taq DNA polymerase enzyme is added to use the first cDNA strand as a template and amplify the desired segment from the viral genome. We have modified this two step RT-PCR and developed a one step reaction in which all the reagents necessary for the first cDNA synthesis and for amplification were mixed together including the dye and other reagent needed for gel electrophoresis and proceeded with the reactions in a thermocycler. This one-tube (or one step) method requires less sample manipulation, therefore, significantly reduces chance of cross contamination. Also it reduces the time required for set up of the PCR reaction and preparation of the product for gel electrophoresis and analysis.

Objective 3: In order to develop a reliable PCR detection methodology, it is very important to identify variations among different isolates (or strains) of each one of these GLRaVs and accordingly design PCR primers that could detect all diverse isolates. We maintain a collection of GLRaVs here in Davis and have evaluated the reactivity of number of these isolates selected from different types of GLRaVs by ELISA. In this study we have selected 17, 17, 10, and 5 different isolates respectively, for GLRaVs-1, -2, -3, and -5. For GLRaV-4 only one isolate was available.

These selected isolates were all tested positive by ELISA with different degrees of reaction. The coat protein gene from these isolates was amplified by RT-PCR (using specific primers designed for amplification of the coat protein gene) and sequenced. For GLRaV-1, 680 nt sequences of the coat protein from 17 different isolates were compared with each other and with the one published in the GeneBank (GB). An example of sequence pile up and nucleotide comparison is represented in Fig. 3. The complete sequence matches in this figure are designated by asterisks. These isolates also included 3 which were tested positive by ELISA and PCR (using the primers used for the detection of the virus) but did not amplify the coat protein gene and 3 other isolates which were positive by ELISA but negative by detection and coat protein primers. Data showed that these 6 isolates had at least 2 nucleotide mis-match at the primers site, therefore, the PCR primers could not attach to the target sequences and failed the amplification. Overall, we found that all these isolate had 91-94% homology with the sequence of the isolate published in the GB and 88-99% sequence homology among themselves at the coat protein gene segment compared. For GLRaV-2 also about 654 nt sequences covering the coat protein gene of 17 different isolates were compared with each other and with the one published in the GB. From this sequence, one pair of primers, LR2CP1 and LR2CP2, which flank the coat protein region, was designed. At the beginning we had problem amplifying the coat protein gene by this pair of primers. Repeated efforts using different types of tissue or use of dsRNA as template did not produce any product. Finally, we developed a nested RT-PCR method (which showed to be 10-100 times more sensitive than regular RT-PCR) and designed another pair of primers, LR2CP3 and LR2CP4, and used them in combination with previously designed primers LR2CP1 and LR2CP2. Initial RT-PCR was carried out with primers LR2CP3 and LR2CP4. This reaction resulted in a PCR product of 715 nt in size (because of low amount it was non detectable on gel). This PCR product was then diluted 15 times and used in a second round of nested PCR using primers LR2CP3 and LR2CP2 resulted in a product of 654 nt in size. Fifteen isolates of this virus were eventually analyzed by using nested-RT-PCR. The PCR products were cloned, sequenced, and the sequences were analyzed. Thirteen of these isolates were very similar in their coat protein sequences, ranging from 99% to 100% in nucleotide sequence homology. These 13 isolates had 89% homology to the published GLRaV 2 virus sequence. four of these isolates were more divergent and they had 89% and 92% sequence homology to the rest of the isolates. Among all the isolates included in this investigation, 2 isolates were tested positive by ELISA and negative by detection and coat protein primers, also another 2 which were positive by ELISA and detection primers but negative by the coat protein primers. By modifying the sample preparation methodology and using the total RNA extract we could amplify the coat protein gene of one of the isolates from each of the first and second groups and study their sequences. We were not able to amplify any product from the other 2 isolates in these groups even from the one in the second group which was tested positive once by detection primers indicating that we had a false positive or contamination in our first experiment. The same two isolates were ELISA positive indicating that the antibody we use for the detection of GLRaV-2 also contains antibody for other leafroll viruses, hence can detect viruses other than GLRaV-2 (the source of antibody used in this experiment also contains antibody to GLRaV-1). For GLRaV-3 10 isolates were compared and found that 9 of them had about 98-99% sequence homology (they were almost identical) among each other. Only one of these isolates was showing some differences (about 92% homology with other 9 isolates). . For GLRaV-4, the coat protein sequence is not available yet. We attempted several times using different strategies to clone and sequence part or the genome of this virus including the coat protein

gene but all our efforts failed. We used isolate LR106 in our investigation. The vine infected with this virus seemed to be singly infected with GLRaV-4. However, we tried to extract virus-specific dsRNA and use in our cloning and sequencing, but we could not obtain enough dsRNA for our experiment due to the low titer of virus in the host. We increased the amount of tissue used for this purpose, but again the efforts failed. Some preliminary data indicated that this virus is closely related to GLRaV-5, therefore, we tried to use the coat protein sequence information available for GLRaV-5 and design degenerate PCR primers and use them for amplification of the coat protein of GLRaV-4. In this effort we obtained a PCR product from GLRaV-4 infected vine with expected size revealed in gel electrophoresis, but when we sequenced the product and compared it with other GLRaVs, it did not show any homology with any of these viruses.
For GLRaV-5 we had access to only 5 isolates. We designed a pair of PCR primer that could amplify the coat protein gene of this virus. We used this pair of primer, amplified the coat protein gene and sequenced. This sequence consisted of 786 nt. Sequence comparison among these 5 isolates showed 95-99% homology indicating that these tested viruses were quite homogeneous.

Objective 4: For this objective, we designed specific probes for each of the viruses used in this investigation for trapping the PCR products in ELISA plates. Our many attempts failed to detect these viruses by the colorimetric PCR. Finally we concluded that one of the necessary components used in this reaction, Dig-11-dUTP labeled reagent, was not stable enough to maintain through the PCR reaction. In the control reactions for each virus, when dTTP (substitute for dUTP in regular PCR) was used and the products were analyzed by get electrophoresis, the related PCR products were observed on the gel, while the results with Dig-11-dUTP on the gel were not consistent and usually a smeared bands (instead of sharp intense bands) were observed. Our experiments indicated that the problem is related to the quality of the product. Boehringer Mannheim Chemical Co. had the monopoly on the product and their labeling product was working very well in our PCR system. About 2 years ago the company was merged with Roche Chemical Co. and since then their product has not been working well. We also repeatedly contacted the Roche Co. and consulted with their technical personnel about the product but unable to fix the problem

Reliability and sensitivity of RT-PCR for the detection of GLRaVs-1 to -5 was compared with ELISA and with symptom expression of leafroll disease on its biological indicator. From 137 vines tested in this experiment, 26, 16, and 29, respectively tested positive on biological indicator, ELISA, and RT-PCR. The results indicate that the RT-PCR is more sensitive than either indexing on biological indicator host or ELISA. For GLRaV-5 in this experiment only PCR test was compared, because we did not have access to a reliable ELISA reagent for this virus. We have established confidence on our PCR procedure for GLRaVs and have started using the procedure routinely for testing all quarantine and newly introduced grape selections (brought to FPMS for disease testing and elimination). Also we have provided the RT-PCR detection services to grapevine nurseries and growers for testing their valuable and propagative source plants for different viruses.

Publications or Reports:

1. Golino, D.A., Sim, S., Gill, R., and Rowhani, A. 2002. California mealybugs can spread grapevine leafroll disease. Cal. Agri. 56:196-201.
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3. Routh, G., Zhang, Y.P., Saldarelli, P., and Rowhani, A. 1998. Use of degenerate primers for partial sequencing and RT-PCR-based assay of grapevine leafroll-associated viruses 4 and 5. Phytopathology 88: 1238-1243.
4. Rowhani, A., Biardi, L., Johnson, R., Saldarelli, P., Zhang, Y.P., Chin, J., and Green, M. 2000. Simplified sample preparation method and one-tube RT-PCR for grapevine viruses. Abstract and presentation in the "13th Meeting of the International Council for the Study of Viruses and Virus-Like Diseases of the Grapevine". 12-17 March 2000. Adelaide, South Australia.
5. Rowhani, A., Chin, J., Zhang, Y.P., Biardi, L., and Golino, D.A. 1999. Simplified extraction method for sample preparation for PCR and development of a colorimetric detection technique for analysis of PCR products of virus-infected grapevine. Am. J. Enol. Vitic. 50: 374.
6. Weber, E., Golino, D.A., and Rowhani, A. 2002. Laboratory testing for grapevine diseases. PWV, January/February:13-26.
7. Zhang, Y.P., and Rowhani, A. 2000. A strategy for rapid cDNA cloning from double-stranded RNA templates isolated from plants infected with RNA viruses by using Taq DNA polymarase. J. Virol. Methods 80: 59-63.

Research Success Statements:

Reverse transcriptase-polymerase chain reaction (RT-PCR) is a very sensitive and reliable molecular methodology which have been developed and used for the detection of many plant RNA viruses (viruses which contain RNA as their genome constituent, which include all known viruses in grapevine). In this project we developed RT-PCR detection methodology for the detection of grapevine leafroll associated viruses 1 to 5 (GLRaV) and a working protocol was developed.

In order to develop a reliable RT-PCR detection method, it is very important to identify variations among different isolates (or strains) of each one of these GLRaVs and accordingly design PCR primers that could detect all diverse isolates. In this experiment, we cloned and sequenced the coat protein gene from 5-17 different isolates of each one of these isolates, sequences were compared among isolates selected for each virus, and PCR primers were designed in order to detect all variants.

In general, sample preparation for PCR test is a tedious and time consuming process, especially when grapevine tissues are involved. These tissues contain large amounts of polysaccharides and phenolic compounds that are detrimental to different enzymes used in PCR procedure, therefore, they should be eliminated. A simple sample preparation methodology was developed and refined to use for testing grapevine plants for grapevine leafroll associated viruses 1 to 5 by RT-PCR. In addition, a simple blotting methodology for sample collection in the field was developed. In this method, leaf petioles or young shoots are cut and blotted on specific nylon or nitrocellulose

membrane and then these membranes are brought to the laboratory for processing and virus detection. The advantages of this method are: no technical training is required, and if necessary, the samples can be stored for a long time before they are processed for testing.

Reliability and sensitivity of RT-PCR for the detection of GLRaVs-1 to -5 was compared with ELISA and with symptom expression of leafroll disease on its biological indicator, Cabernet Franc. The results indicated that RT-PCR was more sensitive than either indexing on biological indicator host or ELISA.

The methodologies developed in this investigation were shared with other private laboratories in the State to improve their sampling and testing methods, and with other scientists in the nation and worldwide.

FIGURE 1

Gel Analysis of RT-PCR Products. Petiole samples from infected and healthy grapevines were prepared and used in PCR detection of GLRaVs 1-5.

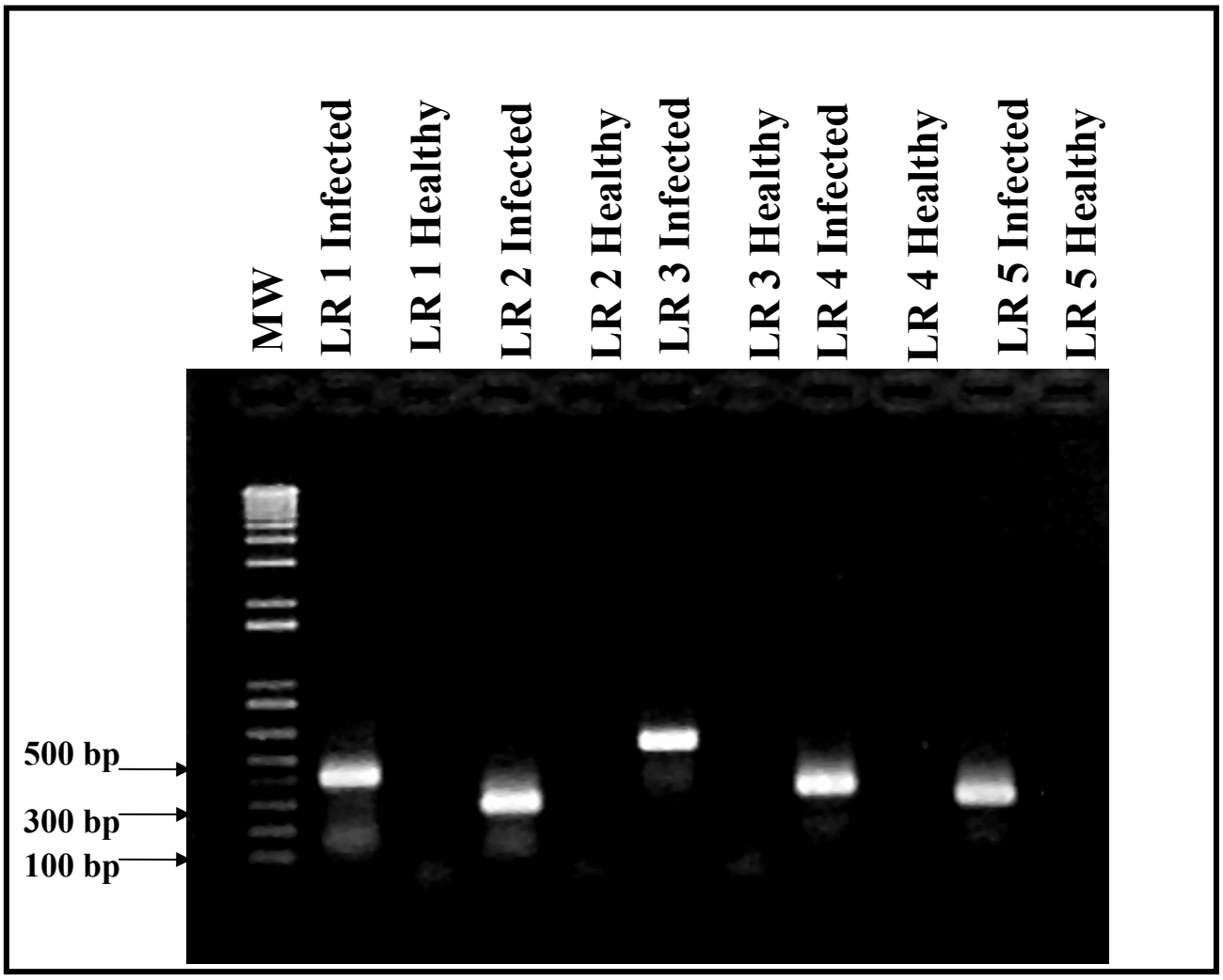
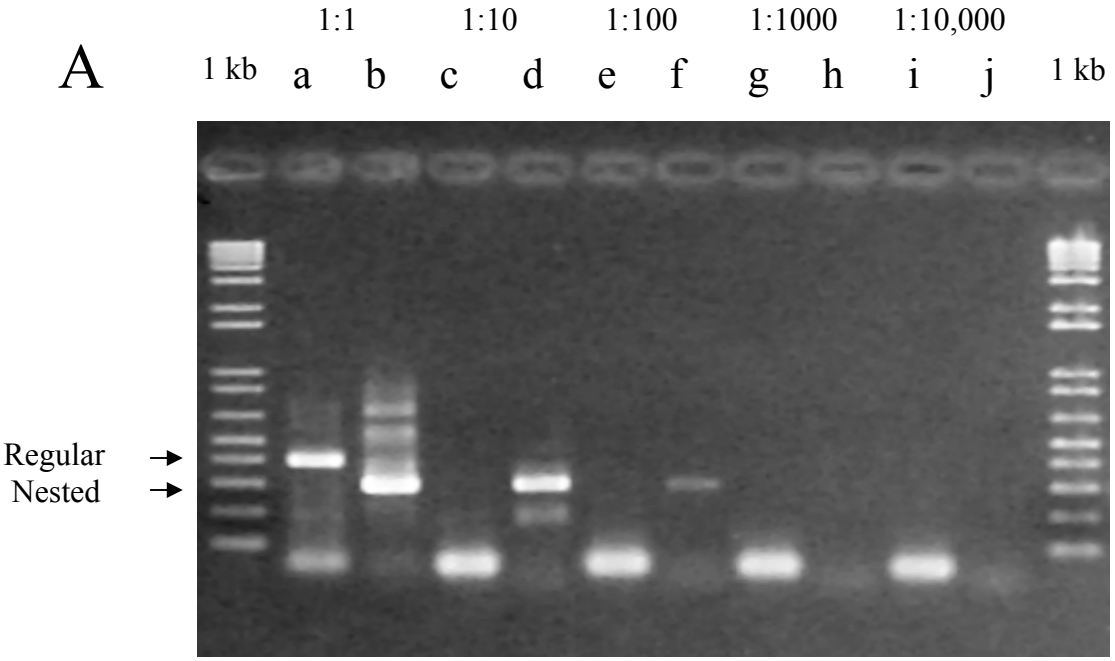


Fig. 2. Nested RT-PCR method used for amplifying GLRaV 1 (panel A) and 3 (panel B)in comparison to regular RT-PCR. Samples were prepared and serially diluted from 1:1 to 1:10,000 and tested by regular RT-PCR (Lanes a, c, e, g, and i). Then an aliquot from regular RT-PCR product was added to nested PCR reagent and amplified again using nested primers (Lanes b, d, f, h, and j). Regular, represents the regular RT-PCR product and Nested, represents nested RT-PCR product.



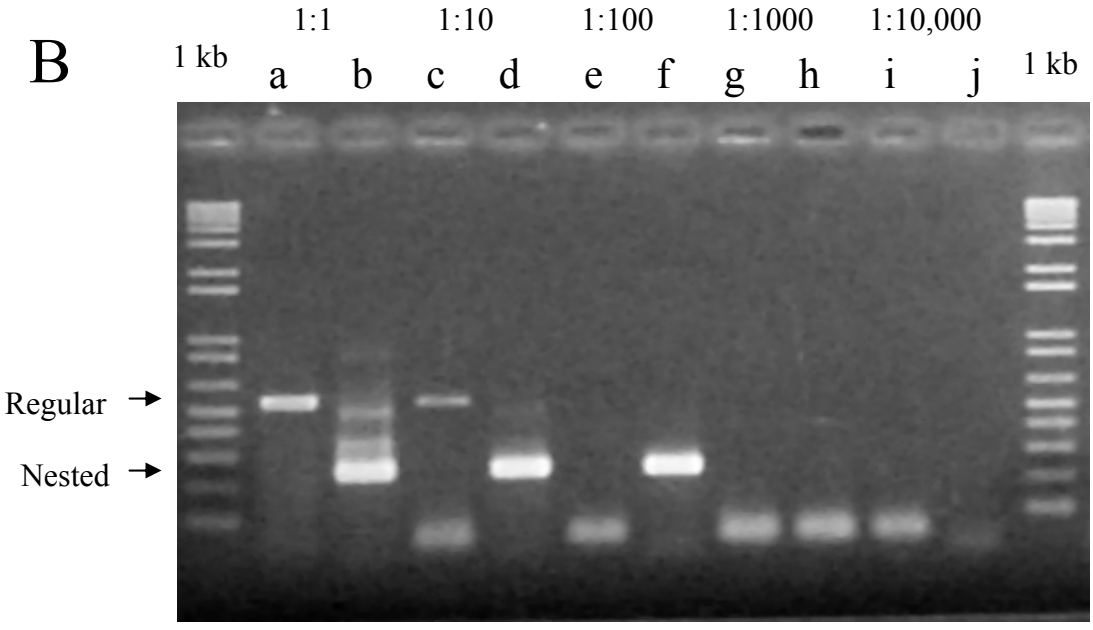


Fig. 3. Sequence alignment among 17 different isolate of GLRaV-1 and the sequence published in the GeneBank (LR1-GB-CP). Asterisks indicate complete match among the sequences. Total of 680 nucleotide (nt) from each isolate has been compared.

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A2V49-CP        CTCTCCGTCCTTCTCGACCATCTACGGGTCAGCGTTCGGGGGATTCTGAGGTGGCCAGAC 60
A1V49-CP        CTCTCCGTCCTTCTCGACCGTCTACGGGTCAGCGTTCGGGGGATTCTGAGGTGGCCAGAC 60
A2V35-CP        CACTTCGCCAATCTCGACCCTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
A1V1-CP         CACTTCGCCAATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
A1V79-CP        CACTTCGCCAATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
A2V43-CP        CACTTCGCCAATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
LR1-9-CP        CACAACGCCTATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAAAC 60
LR1-13-CP       CACAACGCCTATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
LR1-02-CP       CACAACGCCTATCTCGACCTTCAACGGGTCAGCGTTTAGGGGATTCTGAGGTAGCCAGAC 60
LR1-16-CP       CACAACGCCTATCTCGACCTTCTACGGGTCAGCGTTCGGCGGATTCCGAGGTGGCCAGAC 60
LR1-20-CP       CACAACGCCTATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCTAGAC 60
LR1-4-CP        CACAACGCCTATCTCGACCTTCTACGGGCCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
LR1-7-CP        CACAACGCCTATCTCGACCTTCTACGGGTCAGCGTTCAGGGGATTCTGAAGTGGCCAGAC 60
LR1-22-CP       CACAACGCCTATCTCGACCTTCAACGGGTCAGCGTTCAGGGGATTCTGAGGTGGCCAGAC 60
LR1-23-CP       CACTCCGCCCATCTCGACCTTCGACGGGTCAGCGTTCGGGGGATTCAGAGGTGGCTAGAC 60
A3V87-CP        CACTCCGCTTGTCTCGACCTTCGACGGGTCAGCGTTCGGGGGATTCTGAGGTGGCCAGAC 60
LR1-18-CP       CACAACGCCTATCTCGACCTTCGACGGGTCAGCGTCGCGGGGATTCTGAGGTGACCAGAC 60
LR1-GB-CP       CACAACGCCTATCTCGACCTTCTACAGGTCAGCGATTTGGGGATTCAGAGGTGGTCAGAC 60
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A2V49-CP        GTGAAATGGGTGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATTTTTACTAATCCCG 120
A1V49-CP        GTGAAATGGGTGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATTTTTACTAATCCCG 120
A2V35-CP        GTGAAATGGGTGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATTTTTACTAATCCCG 120
A1V1-CP         GTGAAATGGGTGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATTTTTACTAATCCCG 120
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LR1-13-CP       GTGAAATGGGTGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATTTTTACTAATCCCG 120
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LR1-16-CP       GTGAAATGGGTGGCAAGCTTAAAAGAACTTTCAATATCGCAGAAATCTTTTCTAATCCCG 120
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LR1-7-CP        GTGAAATGGGTGACAAGCTTAAGAGAACTTTTAATATCGCAGAGATCTTTACTAATCCCG 120
LR1-22-CP       GTGATATGGGCGACAAGCTTAAAAGAACTTTTAATATCGCAGAAATCTTCACTAATCCCG 120
LR1-23-CP       GTGAAATGGGCGATAAGCTTAAACGAACTTTTAATATTGCCGAAATCTTTACCAACCCCG 120
A3V87-CP        GTGAAATGGGGGACAAGCTTAAACGTACTTTTAATATTGCGGAAATCTTCACTAATCCTG 120
LR1-18-CP       GTGAAATGGGTGACAAGCTTAAACGAACTTTTAATATTGCAGAAATCTTTACAAACCCCG 120
LR1-GB-CP       GTGAAATGGGCGACAAGCTTAAAAGAACTTTTAATATAGCAGAAATCTTTACCAACCCCG 120
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A2V49-CP        AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
A1V49-CP        AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
A2V35-CP        AGATGAATATTATCCTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
A1V1-CP         AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
A1V79-CP        AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
A2V43-CP        AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
LR1-9-CP        AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
LR1-13-CP       AGATGAATATTATCTTTGAACCACCAAAGGAAATGGAGGTTTCTGTAGTTGTACCAACCG 180
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LR1-02-CP       AGATGAATATTATTTTTGAACCACCAAAGGACATGGAGGTTTCGGTAGTAGTACCAACTG 180
LR1-16-CP       AGATGAACATCATCTTTGAACCACCGAAGGAAATGGAGGTTTCGGTGGTAGTACCAACAG 180
LR1-20-CP       AGATGAACATTATCTTCGAACCACCAAAGGAAATGGAGGTTTCGGTAGTGGTACCAACCG 180
LR1-4-CP        AGATGAACATCATCTTTGAACCACCAAAGGACATGGAGGTTTCGGTAGCAATACCAACCG 180
LR1-7-CP        AGATGAATATCATCTTTGAACCACCAAAGGACATGGAGGTTTCGGTAATAGTACCAACCG 180
LR1-22-CP       AGATGAATATCATCTTTGAACCACCAAAGGATATGGAGGTTTCGGTAATAGTACCAACCG 180
LR1-23-CP       AGATGAATGTTATCTTTGAACCACCAAAGGACATGGAGGTTTCGGTAGTAGTACCAACCG 180
A3V87-CP        AGATGAATATTATCTTTGAACCACCAAAGGACATGGAGGTTTCGGTAGTAGTACCAACCG 180
LR1-18-CP       AGATGAATATCATTTTTGAACCACCAAAGGATATGGAGGTTTCGGTAATAGTGCCAACCG 180
LR1-GB-CP       AGATGAATATCATCTTTGAACCACCAAAGGATATGGAGGTTTCGGTAGTATTACCAACCG 180
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A2V49-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACGGAATTAAAAAATTTGT 240
A1V49-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACGGAATTAAAAAATTTGT 240
A2V35-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACGGAATTAAAAAATTTGT 240
A1V1-CP         GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACGGAATTAAAAAATTTGT 240
A1V79-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACGGAATTAAAAAATTTGT 240
A2V43-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACAGAATTAAAAAATTTGT 240
LR1-9-CP        GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACAGAATTAAAAAATTTGT 240
LR1-13-CP       GGCCCGGCTTGGTTACGCCAGCGGTGGCAACAGCTATTTCAACAGAATTAAAAAATTTGT 240
LR1-02-CP       GACCCGGCTTGGTTACACCAGCGGTGGCGACAGCTATTTCAACAGAATTAAAAAATTTAT 240
LR1-16-CP       GGCCCGGCTTAGTTACACCAGCGGTGGCGACAGCAATATCAACAGAATTAAAAAATTTAT 240
LR1-20-CP       GACCCGGCTTGGTTACACCAGCGGTGGCAACGGCTATATCAACAGAATTAAAAAATTTAT 240
LR1-4-CP        GACCCGGCTTGGTTACACCAGTGGTGGCAACAGCTATTTCGTCAGAATTGAAAAATTTAT 240
LR1-7-CP        GGCCTGGCTTGGTTACACCAGCGGTGGCGACCGCTATTTCGACAGAACTAAAAAATTTAT 240
LR1-22-CP       GACCCGGCTTGGTTACGCCAGCGGTGGCGACGGCCATTTCTACAGAATTAAAAAATTTAT 240
LR1-23-CP       GACCCGGCTTGGTCACGCCGGCGGTGGCAACTGCAATTTCCACAGAATTAAAAAATTTAT 240
A3V87-CP        GACCCGGCTTGGTCACACCAGCGGTGGCAACTGCAATTTCCACAGAATTAAAAAATTTAT 240
LR1-18-CP       GACCCGGCTTGGTGACACCGGCGGTAGCAACTGCGATTTCTACAGAATTAAAAAATTTAT 240
LR1-GB-CP       GACCCGGCTTGGTGACGCCGGCGGTGGCAACTGCAATTTCCACAGAATTAAAGAATTTAT 240
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A2V49-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
A1V49-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
A2V35-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
A1V1-CP         GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
A1V79-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
A2V43-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
LR1-9-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
LR1-13-CP       GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACTGACTTCTTCTTGGCAATGT 300
LR1-02-CP       GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTTACGGACTTCTTCTTGGCGATGC 300
LR1-16-CP       GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTTACAGACTTCTTCTTGGCAATGT 300
LR1-20-CP       GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTTACGGACTTCTTCTTAGCAATGT 300
LR1-4-CP        GTGCTGAAGTGATGGGTAACACGGATCAGAAAAGTCTTACAGACTTCTTCTTGGCAATGT 300
LR1-7-CP        GTGCTGAAGTGATGGGTAATACGGATCAGAAGAGTCTCACAGACTTCTTCTTGGCGATGT 300
LR1-22-CP       GTGCTGAAGTGATGGGTAATACGGATCAGAAAAGTCTCACAGACTTCTTCTTGGCGATGT 300
LR1-23-CP       GTGCTGAAGTGATGGGTAATACAGATCAGAAAAGTCTTACGGACTTCTTCTTGGCGATGT 300
A3V87-CP        GTGCTGAAGTGATGGGTAATACAGATCAGAAAAGTCTTACGGACTTCTTCTTGGCGATGT 300
LR1-18-CP       GTGCTGAAGTAATGGGTAATACAGATCAGAAAAGTCTTACGGACTTCTTCTTGGCGATGT 300
LR1-GB-CP       GTGCTGAAGTGATGGGTAATACGGATCAAAAAAGTCTTACAGACTTCTTCTTGGCAATGT 300
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A2V49-CP        TGCAACTGATGTTGACATTTAGCACACCACCAGACGCAGAGAGCAAAGAAGAGTATTTTG 360
A1V49-CP        TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
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A2V35-CP        TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
A1V1-CP         TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
A1V79-CP        TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
A2V43-CP        TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-9-CP        TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-13-CP       TGCAACTGATGTTGACATTTAGCACATCACCAGACACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-02-CP       TGCAACTGATGTTGACATTTAGTACGTCGCCAGATACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-16-CP       TACAATTGATGCTGACATTTAGCACGTCACCAGATACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-20-CP       TACAATTGATGCTGACATTTAGCACGTCACCAGATACAGAGAGCAAAGAAGAGTATTTTG 360
LR1-4-CP        TACAATTGATGTTGACATTTAGCACGTCACCAGATACGGAGAGCAAAGAAGAGTACTTTG 360
LR1-7-CP        TGCAATTGATGTTGACATTTAGCACGTCACCAGATACAGAAAGCAAGGAAGAGTACTTCG 360
LR1-22-CP       TGCAATTGATGTTGACTTTTAGCACGTCGCCAGATACAGAGAGCAAAGAAGAGTACTTTG 360
LR1-23-CP       TGCAATTGATGTTGACGTTTAGCACGTCACCAGATACAGAGAGCAAAGAAGAGTATTTCG 360
A3V87-CP        TGCAATTGATGTTGACGTTTAGCACGTCACCAGATACAGAGAGCAAAGAAGAGTATTTCG 360
LR1-18-CP       TGCAATTGATGTTGACGTTCAGCACGTCACCAGATACGGAGAGCAAAGAAGAGTATTTTG 360
LR1-GB-CP       TGCAATTGATGTTGACGTTTAGCACGTCACCAGACACGGAGAGCAAAGAAGAGTATTTTG 360
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A2V49-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
A1V49-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
A2V35-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
A1V1-CP         TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
A1V79-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
A2V43-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
LR1-9-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
LR1-13-CP       TGAATTTATATAGTAACGGCGAGCGGAAATTAACTTATGAGAAGGTTAAAGGGGCCATTG 420
LR1-02-CP       TGAATTTATATAGTAACGGCGAGCGGAAATTGACTTATGAGAAGGTTAAAGGGGCTATCG 420
LR1-16-CP       TGAATTTATATAGTAACGGAGAGCGGAAATTGACCTATGAGAAGGTTAAAGGGGCCATTG 420
LR1-20-CP       TGAATTTATATAGTAACGGAGAGCGGAGATTGACTTATGAGAAGGTTAAAGGGGCGATCG 420
LR1-4-CP        TGAATTTATATAGTAACGGCGAGCGGAAATTGACCTATGAGAAGGTTAAAGGGGCCATTG 420
LR1-7-CP        TGAATTTATACAGTAACGGCGAGCGGAAATTGACCTATGAGAAGGTTAAAGGGGCTATTG 420
LR1-22-CP       TGAATTTATATAGTAACGGCGAGCGGAAACTGACTTATGAGAAGGTTAAAGGGGCCGTTG 420
LR1-23-CP       TGAATCTATATAGCAATGGCGAGCGGAAATTGACTTATGAGAAGGTTAAGGGGGCCGTTG 420
A3V87-CP        TGAATCTATATAGTAATGGCGAGCGGAAGTTGACTTATGAGAAGGTTAAGGGGGCCGTTG 420
LR1-18-CP       TGAATCTATATAGTAACGGCGAGCGGAAATTGACTTATGAGAAGGTTAAAGCGGCCGTTG 420
LR1-GB-CP       TGAATTTGTATTGTAACGGCGAGCGGAAATTGACCTATGAGAAAGTTAAAGGGGCCGTTG 420
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A2V49-CP        TCAAGGGAGCCGAGGGCTCAACGTTTGAAAATTCCATGCGTCAGTATGCTAGATTATTCT 480
A1V49-CP        TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
A2V35-CP        TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
A1V1-CP         TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
A1V79-CP        TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
A2V43-CP        CCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
LR1-9-CP        TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
LR1-13-CP       TCAAAGGAGCCGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
LR1-02-CP       TCAAGGGAGCGGAAGGTTCAACGTTTGAAAATCCTATGCGTCAGTATGCTAGACTATTCT 480
LR1-16-CP       TCAAGGGAGCTGAAGGCTCAACGTTTGAAAATCCCATGCGTCAGTATGCTAGATTATTCT 480
LR1-20-CP       TCAAGGGAGCTGAAGGCTCGACGTTTGAAAACCCTATGCGTCAGTATGCTAGATTATTTT 480
LR1-4-CP        TCAAGGGAGCCGAAGGCTCAACGTTTGAAAATCCTATGCGTCAATATGCTAGATTGTTCT 480
LR1-7-CP        TCAAGGGAGCGGAAGGTTCAACGTTTGAAAATCCTATGCGTCAGTACGCTAGATTATTCT 480
LR1-22-CP       TCAAGGGGGCTGAAGGCTCAACGTTTGAAAATCCTATGCGTCAATATGCTAGATTATTCT 480
LR1-23-CP       TCAAGGGAGCCGAAGGCTCGACTTTTGAAAATCCAATGCGTCAGTATGCTAGATTGTTCT 480
A3V87-CP        TCAAGGGAGCCGAAGGCTCGACGTTTGAAAATCCTATGCGTCAGTATGCTAGATTGTTCT 480
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LR1-18-CP       TCAAGGGAGCCGAAGGCTCGACGTTTGAAAATCCTATGCGTCAGTATGCTAGATTGTTCT 480
LR1-GB-CP       TCAAGGGGGCTGAAGGCTCAACGTTTGAAAATCCTATGCGTCAGTATGCTAGATTATTCT 480
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A2V49-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
A1V49-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCAAACGAGAAAGTTGCTA 540
A2V35-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
A1V1-CP         CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
A1V79-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
A2V43-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-9-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-13-CP       CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-02-CP       CAGCGACAGCAGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTCGCTA 540
LR1-16-CP       CGGCGACAGCAGTTCATTTAATACTGAACGGAAAATTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-20-CP       CGGCGACAGCAGTTCATTTAATACTGAACGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-4-CP        CAGCGACAGCAGTTCACTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTCGCTA 540
LR1-7-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAACCGAACGAGAAAGTTGCTA 540
LR1-22-CP       CAGCGACAGCCGTCCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-23-CP       CAGCGACAGCCGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
A3V87-CP        CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-18-CP       CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCTA 540
LR1-GB-CP       CAGCGACAGCTGTTCATTTAATACTGAATGGAAAGTTGAAGCCGAACGAGAAAGTTGCAA 540
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A2V49-CP        TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
A1V49-CP        TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
A2V35-CP        TGCAGCACGAAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
A1V1-CP         TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
A1V79-CP        TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
A2V43-CP        TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
LR1-9-CP        TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
LR1-13-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
LR1-02-CP       TGCAGCACGGGGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCGTCTT 600
LR1-16-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCTTCTT 600
LR1-20-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCTTCTT 600
LR1-4-CP        TGCAGCACGGAGTACCTAAGAGGTTTCTTCCGTATACCTTCGATTTCTGCAGACCATCTT 600
LR1-7-CP        TGCAGCACGGCGTACCTAAGAGGTTCCTACCGTATACTTTTGATTTCTGCAGACCATCTT 600
LR1-22-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACTTTTGATTTCTGCAGACCATCCT 600
LR1-23-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTCCCGTATACTTTTGATTTCTGCAGACCATCTT 600
A3V87-CP        TGCAGCACGGAGTACCCAAGAGGTTCCTCCCGTATACTTTTGATTTCTGCAGACCATCTT 600
LR1-18-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTCCCGTACACTTTTGATTTTTGCAGACCATCTT 600
LR1-GB-CP       TGCAGCACGGAGTACCTAAGAGGTTCCTTCCGTATACCTTTGATTTCTGCAGACCATCTT 600
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A2V49-CP        ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
A1V49-CP        ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGNCGGCAGAATCAGCGTTCG 660
A2V35-CP        ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
A1V1-CP         ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
A1V79-CP        ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
A2V43-CP        ACTCTCAATTTAGTAACGATGCCATTANGGCATGGCAGTTGTCGGCAGAATCAGCGTTCG 660
LR1-9-CP        ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGTCGGCAGAATCAGCGTTCG 660
LR1-13-CP       ACTCTCAATTTAGTAACGATGCCATTAGGGCATGGCAGTTGTCGGCAGAATCAGCGTTCG 660
LR1-02-CP       ACTCTCAATTTAGCAACGATGCCATTAGGGCGTGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-16-CP       ACTCTCAATTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCGGAATCAGCGTTCG 660
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LR1-20-CP       TCTCTCAATTTAGCAACGATGCCATTAGAGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-4-CP        ACTCTCAATTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-7-CP        ACTCTCAATTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-22-CP       ACTCTCAATTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-23-CP       ACTCTCAGTTTAGCAACGACGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
A3V87-CP        ACTCTCAGTTTAGCAACGATGCCATTAGGGCGTGGCAGTTGTCGGCAGAATCAGCGTTCG 660
LR1-18-CP       ACTCTCAGTTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
LR1-GB-CP       ACTCTCAATTTAGCAACGATGCCATTAGGGCATGGCAGTTGGCGGCAGAATCAGCGTTCG 660
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A2V49-CP        GGCGGAAAAGTAATGTGA-CA 680
A1V49-CP        GGCGGAAAAGTAATGTGAACA 681
A2V35-CP        GGCGGGAAAGTAATGGGA-CA 680
A1V1-CP         GGCGGAAAAGTAATGTGA-CA 680
A1V79-CP        GGCGGAAAAGTAATGTGA-CA 680
A2V43-CP        GGCGGAAAAGTAATGTGA-CA 680
LR1-9-CP        GGCGGAAAAGTAATGTGA-CA 680
LR1-13-CP       GGCGGAAAAGTAATGTGA-CA 680
LR1-02-CP       GGCGGAAAAGTAATGTGA-CA 680
LR1-16-CP       GGCGGAAAAGTAATGTGA-CA 680
LR1-20-CP       GGCGGAAAAGTAATGTGA-AA 680
LR1-4-CP        GGCGGAAAAGTAATGTGA-CA 680
LR1-7-CP        GGCGGAAAAGTAATGTGA-CA 680
LR1-22-CP       GGCGGAAAAGTAATGTGA-CA 680
LR1-23-CP       GGCGGAAAAGTAATGTGA-CA 680
A3V87-CP        GGCGGAAAAGTAATGTGA-CA 680
LR1-18-CP       GGCGGAAAAGTAATGTGA-CA 680
LR1-GB-CP       GGCGGAAAAGTAATGTGA-CA 680
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