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LIST OF ABBREVIATIONS

AU	Australia
bp	Basepair+
C	Capsid
CA	Canada
cDNA	Complementary deoxyribonucleic acid
CN	China
DE	Germany
DNA	Deoxyribonucleic acid
dNTPs	Deoxynucleoside triphosphates
dsRNA	Double-stranded ribonucleic acid
EM	Electron microscope
FR	France
g	Gram
G	Genogroup
GB	Great Britain
GR	Greece
HBGAs	Histo-blood group antigens
HK	Hong Kong
hr	Hour
HU	Hungary
IN	India
IR	Iran
IT	Italy
JP	Japan
Kb	Kilobasepair

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kDa	Kilodalton
KR	Korea (South)
min	Minute
ml	Milliliter
mM	Millimolar
NL	Netherlands
nm	Nanometer
NS	Nonstructural
NSPs	Nonstructural proteins
NTPase	Nucleoside triphosphatase
NoV	Norovirus
nt	Nucleotide
NZ	New Zealand
ORFs	Open reading frames
P	Polymerase
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
Pro	Proteinase
PT	Portugal
RdRp	RNA dependent RNA polymerase
RNA	Ribonucleic acid
RNase	Ribonuclease
rpm	Revolution per minute
RT	Reverse transcription
RT-PCR	Reverse transcription-polymerase chain reaction
RU	Russia
SA	Saudi Arabia
SaV	Sapovirus
SE	Sweden
sec	Second
ssRNA	Single-stranded ribonucleic acid
TAE	Tris-acetate EDTA

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TH	Thailand
TW	Taiwan
UK	United Kingdom
US	United States of America
UV	Ultraviolet
VLPs	Virus-like particles
VN	Vietnam
VPs	Viral proteins

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LIST OF SYMBOLS

%	Percent
^{o}C	Degree Celsius
µl	Microliter
µg	Microgram
µM	Micromolar

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GLOSSARY

BLAST	The Basic Local Alignment Search Tool: The program finds the similarity between biological sequences. This program compares nucleotide or protein sequences to sequence databased and calculates the statistical significance of matches. In addition, this program can be used to infer functional and evolutionary relationships between sequences as well as help identifying the members of gene families.
MEGA	Molecular Evolutionary Genetics Analysis: The program provides tools for conducting sequence alignment, inferring phylogenetic trees, estimating divergence times, mining online databases, estimating rates of molecular evolution, inferring ancestral sequences, and testing evolutionary hypotheses.
NCBI	The National Center for Biotechnology Information: A national resource for the molecular biology information was established in 1988 which is part of the United States National Library of Medicine (NLM), a branch of the National Institutes of Health (NIH). NCBI provides public databases, develops software tools for analyzing biological data, and performing research in computational biology.
NoroNet	The Norovirus typing tool. An online tool conducted by a network of virologists and epidemiologists in European countries since 1999, who share databases of molecular and epidemiological data of norovirus.
RDP4	Recombination Detection Program version 4. The program detects and analyses recombination and/or genomic reassortment signals in a set of aligned sequences.

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ข้อความแห่งการริเริ่ม

1) การศึกษานี้แสดงให้เห็นว่าเชื้อไวรัสโนโรเป็นสาเหตุที่สำคัญที่พบได้บ่อยในการทำให้เกิดโรคกระเพาะอาหารและลำไส้อักเสบเฉียบพลันในเด็กที่เข้ารับการรักษาในโรงพยาบาลในจังหวัดเชียงใหม่

2) การศึกษานี้ได้รายงานการเกิดไวรัสโนโรสายพันธุ์ใหม่ ๆ ขึ้นโดยผ่านทางกระบวนการ genetic recombination โดยที่การศึกษานี้ได้รายงานไวรัสโนโรสายพันธุ์ลูกผสม (recombinant strains) จำนวน 9 สายพันธุ์ ในจำนวนนี้ 8 สายพันธุ์เป็นสายพันธุ์ใหม่ที่ไม่เคยมีผู้รายงานมาก่อนในประเทศไทย

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STATEMENTS OF ORIGINALITY

1) This study demonstrated an important role of norovirus (NoV) as a common cause of acute gastroenteritis in hospitalized children in Chiang Mai.

2) This study reported the emerging of novel NoV strains through the mechanism of genetic recombination. Nine different NoV recombinant strains were detected. Of these, 8 strains were reported for the first time in Thailand.

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