

Supplementary materials

A subunit

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1          11          21          31          41
NGDKLYRADS RPPDEIKRSG GLMPRGHNEY FDRGTQMNIN LYDHARGTQT
51         61         71         81         91
GFVRYDDGYV STSLSLRSAH LAGQSILSGY STYIIVIAT APNMFNVNDV
101        111        121        131        141
LGVYSPHPYE QEVSALGGIP YSQIYGWYRV NFGVIDERLH RNREYRDRYY
151        161        171        181        191
RNLNIAPAED CYRLAGFPPD HQAWREEPWI HHAPQGCGNS SRTITGDTCN
201        211        221        231
EETQNLSTIY LRKYQSKVKR QIFSDYQSEV DIYNRIRDEL
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B subunit

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1          11          21          31          41
APQSITELCS EYRNTQIYTI NDKILSYTES MAGKREMVII TFKSGATFQV
51         61         71         81         91
EVPGSQHIDS QKKAIERMKD TLRITYLTET KIDKLCVWNN KTPNSIAAIS
101
MEN
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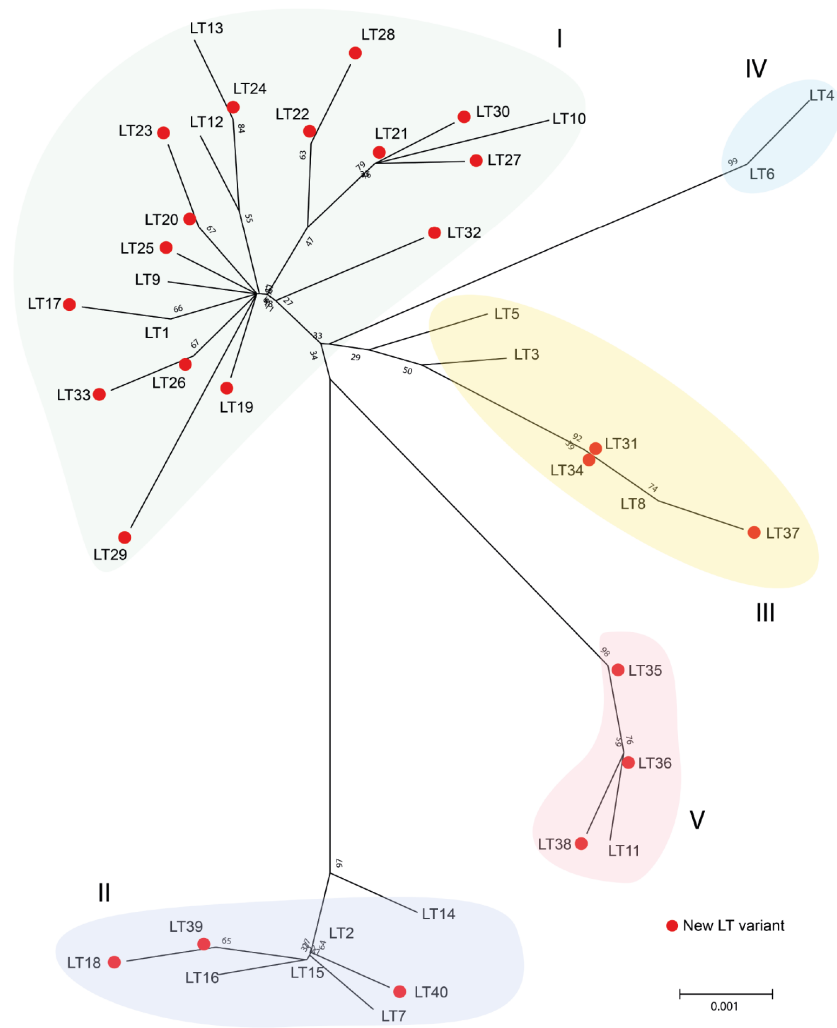
Legend:

The selection scale:

1 2 3 4 5 6 7

Positive selection Purifying selection

Supplementary figure 1. Results of the selection analysis onto the primary sequence of the A and B subunit of LT toxin using MEC model. The analysis of positive selection indicative of variation, and purifying selection that indicate conserved residues were colored in shades of yellow and magenta, respectively. Twenty DNA sequences of the representative LT variants were included in the analysis using a web-based Selecton version 2,2 (<http://selecton.bioinfo.tau.ac.il>).



Supplementary figure 2. SNP phylogenetic analysis of the LT variants. The phylogenetic relatedness was determined using an unrooted phylogenetic tree based on single nucleotide polymorphism (SNPs) of the LT variant nucleotide sequence reported (15) (*LT1-LT16*) and the new LT variants founded in this study (*LT17-LT40*). The tree was constructed by neighbour-joining method using MEGA5.2.