

Supplementary data S1. The alignment between “*KU_Sej_R21_2012* (NCBI accession: JN627495)” gene and *L. interrogans* serovar Pomona (taxid:44276), and only two genomes from *L. interrogans* serovar Bataviae strain 1489 (orange color) and serovar Canicola strain 782 (green color) showed 74.53% identity with the *KU_Sej_R21_2012* gene.

Your search is limited to records that include: *Leptospira interrogans* (taxid:173), *Leptospira interrogans* serovar Pomona (taxid:44276), *Leptospira interrogans* serovar Pomona str. UT364 (taxid:1049925), *Leptospira interrogans* serovar Pomona str. Kennewicki LC82-25 (taxid:1049924), *Leptospira interrogans* serovar Pomona str. CSL4002 (taxid:1240691), *Leptospira interrogans* serovar Pomona str. Pomona (taxid:1001587), *Leptospira interrogans* serovar Pomona str. Fox 32256 (taxid:1218574), *Leptospira interrogans* serovar Pomona str. CSL10083 (taxid:1240692), *Leptospira kirschneri* serovar Pomona (taxid:561005), *Leptospira borgpetersenii* serovar Pomona (taxid:1192865), *Leptospira borgpetersenii* serovar Pomona str. 200901868 (taxid:1192866)

RID: DTK9YZ64013
 Job Title:JN627495:Leptospira borgpetersenii serovar...
 Program: BLASTN
 Query: Leptospira borgpetersenii serovar Sejroe clone R21-2012 truncated leucine-rich repeat protein (LRR) gene, partial cds ID: JN627495.1(nucleic acid) Length: 643
 Database: nt Nucleotide collection (nt)

Sequences producing significant alignments:

					Scientific	Common	Max	
Total Query	E	Per.	Acc.		Name	Name	Taxid	Score
Description	Score	cover	Value	Ident Len Accession				
Leptospira borgpetersenii serovar Sejroe clone R21-2012...	1118	100%	0.0	100.00 643 JN627495.1	Leptospira b...	NA	338220	1118
Leptospira borgpetersenii serovar Ceylonica strain Piyasena...	1083	100%	0.0	98.60 3670231 CP026671.1	Leptospira b...	NA	508536	1083
Leptospira borgpetersenii strain FMAS_AP2 chromosome 1, comple...	1083	100%	0.0	98.60 3595436 CP072630.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_AP3 chromosome 1, comple...	1083	100%	0.0	98.60 3595898 CP072628.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_AP4 chromosome 1, comple...	1083	100%	0.0	98.60 3595848 CP072626.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_PN1 chromosome 1, comple...	1083	100%	0.0	98.60 3596207 CP072624.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_PN4 chromosome 1, comple...	1083	100%	0.0	98.60 3595796 CP072622.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_AP8 chromosome 1, comple...	1083	100%	0.0	98.60 3595870 CP072620.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain FMAS_AP9 chromosome 1, comple...	1083	100%	0.0	98.60 3595582 CP072618.1	Leptospira b...	NA	174	1083
Leptospira borgpetersenii strain R14-L chromosome 1	1028	100%	0.0	96.42 3581013 CP047516.1	Leptospira b...	NA	174	1028

Leptospira borgpetersenii strain R6L chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3580531 CP047520.1					
Leptospira borgpetersenii strain R14 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3601002 CP047504.1					
Leptospira borgpetersenii strain R6 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3513910 CP047372.1					
Leptospira borgpetersenii strain Mo4 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3581767 CP047334.1					
Leptospira borgpetersenii strain R28 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3580481 CP047332.1					
Leptospira borgpetersenii strain R23 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3579904 CP047370.1					
Leptospira borgpetersenii strain R29 chromosome 1	Leptospira b...	NA	174	1028	
1028 100% 0.0 96.42 3580756 CP047330.1					
Leptospira borgpetersenii str. 4E chromosome 1	Leptospira b...	NA	1141102	1028	
1028 100% 0.0 96.42 3550837 CP015814.2					
Leptospira borgpetersenii serovar Ballum strain 56604 chromoso...	Leptospira b...	NA	280505	1028	
1028 100% 0.0 96.42 3550837 CP012029.1					
Leptospira borgpetersenii strain 34-PK chromosome 1, complete...	Leptospira b...	NA	174	1017	
1017 100% 0.0 95.96 3603305 CP097464.1					
Leptospira borgpetersenii serovar Hardjo-bovis strain L49...	Leptospira b...	NA	338217	892	977
100% 0.0 91.60 3620710 CP033440.1					
Leptospira borgpetersenii serovar Hardjo-bovis strain 203...	Leptospira b...	NA	338217	892	977
100% 0.0 91.60 3589981 CP021412.1					
Leptospira borgpetersenii serovar Hardjo strain NVSL S 818...	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3584464 CP015052.1					
Leptospira borgpetersenii serovar Hardjo strain NVSL S 1343...	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3613654 CP015050.1					
Leptospira borgpetersenii serovar Hardjo strain BK-30 chromoso...	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3629289 CP015048.1					
Leptospira borgpetersenii serovar Hardjo strain BK-9 chromosome 1	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3631634 CP015046.1					
Leptospira borgpetersenii serovar Hardjo strain BK-6 chromosome 1	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3649879 CP015044.1					
Leptospira borgpetersenii strain KR39 chromosome 1, complete...	Leptospira b...	NA	174	892	977
100% 0.0 91.60 3603773 CP096127.1					
Leptospira borgpetersenii serovar Hardjo strain TC129 chromoso...	Leptospira b...	NA	328971	892	977
100% 0.0 91.60 3585597 CP084038.1					
Leptospira borgpetersenii strain TC147 chromosome I, complete...	Leptospira b...	NA	174	892	977
100% 0.0 91.60 3585599 CP084040.1					
Leptospira borgpetersenii strain TC273 chromosome I, complete...	Leptospira b...	NA	174	892	977
100% 0.0 91.60 3585577 CP084042.1					
Leptospira borgpetersenii strain TC112 chromosome I, complete...	Leptospira b...	NA	174	892	977
100% 0.0 91.60 3585599 CP084036.1					
Leptospira borgpetersenii serovar Hardjo-bovis JB197 chromosom...	Leptospira b...	NA	355277	892	977
100% 0.0 91.60 3576473 CP000350.1					

Leptospira borgpetersenii serovar Hardjo-bovis L550 chromosome...	Leptospira b...	NA	355276	892	977
100% 0.0 91.60 3614446 CP000348.1					
Leptospira mayottensis strain MDI272 chromosome I, complete...	Leptospira m...	NA	1137606	757	757
100% 0.0 87.42 3861885 CP030147.1					
Leptospira mayottensis 200901116 chromosome I, complete sequence	Leptospira m...	NA	1192864	757	757
100% 0.0 87.42 3815263 CP024871.1					
Leptospira weilii strain CUD13 chromosome I, complete sequence	Leptospira w...	NA	28184	679	
1121 100% 0.0 83.18 3978120 CP040843.1					
Leptospira weilii strain CUDO6 chromosome I, complete sequence	Leptospira w...	NA	28184	679	
1121 100% 0.0 83.18 3965053 CP040840.1					
Leptospira weilii strain FMAS_PD2 chromosome 1, complete sequence	Leptospira w...	NA	28184	679	
1121 100% 0.0 83.18 4222777 CP092203.1					
Leptospira mayottensis strain MDI222 chromosome I	Leptospira m...	NA	1137606	606	606
100% 1e-168 82.58 3934431 CP030144.1					
Leptospira mayottensis strain VS2413 chromosome I, complete...	Leptospira m...	NA	1137606	602	602
100% 2e-167 82.43 3803942 CP030142.1					
Leptospira borgpetersenii serovar Sejroe clone R21-N2012...	Leptospira b...	NA	338220	601	601
53% 6e-167 100.00 350 JN627491.1					
Leptospira borgpetersenii serovar Ballum clone R3-N2012...	Leptospira b...	NA	280505	585	585
53% 3e-162 98.84 350 JN627493.1					
Leptospira borgpetersenii serovar Javanica clone R12-N2012...	Leptospira b...	NA	280504	561	561
53% 3e-155 97.10 350 JN627494.1					
Leptospira borgpetersenii serovar Sejroe clone R21-C2012...	Leptospira b...	NA	338220	517	517
46% 7e-142 100.00 297 JN627492.1					
Leptospira interrogans serovar Bataviae strain 1489 chromosome...	Leptospira i...	NA	312175	454	454
99% 6e-123 74.53 4431091 CP043893.1					
Leptospira interrogans serovar Canicola strain 782 chromosome ...	Leptospira i...	NA	211880	454	454
99% 6e-123 74.53 4556406 CP043884.1					
Leptospira weilii strain FMAS_RT1 chromosome 1, complete sequence	Leptospira w...	NA	28184	442	442
100% 3e-119 73.99 4275568 CP092206.2					
Leptospira borgpetersenii serovar Mini clone R15-N2012 truncat...	Leptospira b...	NA	280507	434	434
53% 9e-117 88.12 349 JN627496.1					
Leptospira santarosai strain U233 chromosome I	Leptospira s...	NA	28183	171	171
21% 1e-37 87.50 3605957 CP028377.1					
Leptospira santarosai strain U164 chromosome I	Leptospira s...	NA	28183	171	171
21% 1e-37 87.50 3730310 CP028370.1					
Leptospira santarosai strain ah2 chromosome I sequence	Leptospira s...	NA	28183	171	171
21% 1e-37 87.50 3545388 CP022887.1					
Leptospira santarosai strain U160 chromosome I	Leptospira s...	NA	28183	151	151
21% 9e-32 83.82 3768600 CP027843.1					
Leptospira santarosai serovar Shermani str. LT 821 chromosome ...	Leptospira s...	NA	758847	151	151
21% 9e-32 83.82 3659905 CP006694.199% 2e-126 74.53 4556406 CP043884.1					

Alignments:

>Leptospira interrogans serovar Bataviae strain 1489 chromosome 1, complete sequence
Sequence ID: CP043893.1 Length: 4431091
Range 1: 1058849 to 1059488

Score:454 bits(1043), Expect:2e-126,
Identities:480/644(75%), Gaps:7/644(1%), Strand: Plus/Plus

Query	1	CAGGGAAAAAATGAATGGTGGAAATATCTATTCTGGATTTTGGACGAAAAAGATTCTGCA	60
Sbjct	1058849	CAAGAAAAGCAAGAATGGTGGAAATATCTAGTCTGGCTTTTGAACGAAAAGCATTCTTCG	1058908
Query	61	ACTGAATCCAACA---TAGATTCTCTTTTCGGAAGACGGAGTTTGTCCGCTCCGCCTTCC	117
Sbjct	1058909	ACTCAACCTAGGAATTTATATTATCTTCCGAGCGACGGGATTCTGGCGGCTCCGCCTTCC	1058968
Query	118	GATAAAAAGTTGAGCCAAGGTACCGAAGTAAGATTTCGATTGGTTAACTTCCTTAATAGAG	177
Sbjct	1058969	GATGAACAATTGAGCCAAGCTACCGAGGTAAGATTTCGATGGGTTGACTTCTTTGGCGGAG	1059028
Query	178	GTTCCGTTGGGTAAAATGCCGACTTTGGATACTTTGGATCTATATCCTCGAGAAGGAAAA	237
Sbjct	1059029	GTTACGTTAGGCAAAATGTCTGACTCTCGATAAATTGACGGTGCTCCCCGGCAAAGAAAAG	1059088
Query	238	AATGCTTCTAAACTTTCTTCTTTGGACGGAATTGAACGAGCGTCCGGATTAATTAAATTG	297
Sbjct	1059089	AAAGCTCCTAAACTTTCTTCTTTGGATGGAATCGAACGAGCGCCTTGGTTAGCCAGATTG	1059148
Query	298	AATGTGGAGAGAAATCAAGGCATATCGGATCTCGGTCTTTTGTCAAAAACCTTCCTAATTT	357
Sbjct	1059149	GACATG---AGCATGCAAGACGTCTCGAATATAGACCTTTTATCGAAA-CTTCCGAATTT	1059204
Query	358	GAAAACCTTTTAGCGGATCGAATAACTCGATTAAGGATTTGTCTCCACTTTCTCAGTGCAA	417
Sbjct	1059205	AAAAGTTCTTCACGGATCGTATAACTCGATCAAAGATCTATCTCCGCTTTCTCAGTGCCG	1059264
Query	418	AAATTTAAATGCGCTTTATCTCAATAAAAAATAAAATCTCCGATGTTTCCCCGCTTTCTTC	477
Sbjct	1059265	AAACTTAGAAATACTTTATCTCGACAAAAATAAAATTTCCGACGTCTCTCCCCTTTCTTC	1059324
Query	478	ACTTTCAAAAATAGAACTCTTTGCTTAGCCGACAATCCGATCCAGGATATTCTTCCTTT	537
Sbjct	1059325	GCTTTTGGAAATAGAAACGCTTTGGATATCCGACAATCCGATCAAGGATATTCTTCCTTT	1059384
Query	538	GGCCGGTTTaaaaaaaTTAAAGAATTGAAAGTGCCGTCGAAACTCCCCGAAGAAAATTT	597
Sbjct	1059385	AACGGGTTTGAAGAACTGAAAGAAGTGAAGCTTTTCGAAAGAGAATTT	1059444
Query	598	AGCGAAGTTTAAAGAAATTACGCCCGATGTGAAAATCTCATTTT	641
Sbjct	1059445	AGAACAGTTCAAAAAACTACGTCCCGATGTGAAGATTTCTTTTT	1059488

>Leptospira interrogans serovar Canicola strain 782 chromosome 1, complete sequence
Sequence ID: CP043884.1 Length: 4556406
Range 1: 3551479 to 3552118

Score:454 bits(1043), Expect:2e-126,
Identities:480/644(75%), Gaps:7/644(1%), Strand: Plus/Minus

Query	1	CAGGGAAAAAATGAATGGTGGAAATATCTATTCTGGATTTTGGACGAAAAAGATTCTGCA	60
Sbjct	3552118	CAAGAAAAGCAAGAATGGTGGAAATATCTAGTCTGGCTTTTGAACGAAAAGCATTCTTCG	3552059
Query	61	ACTGAATCCAACA---TAGATTCTCTTTTCGGAAGACGGAGTTTGTCCGCTCCGCCTTCC	117
Sbjct	3552058	ACTCAACCTAGGAATTTATATTATCTTCCGAGCGACGGGATTCTGGCGGCTCCGCCTTCCG	3551999
Query	118	GATAAAAAGTTGAGCCAAGGTACCGAAGTAAGATTTCGATTGGTTAACTTCCTTAATAGAG	177
Sbjct	3551998	GATGAACAATTGAGCCAAGCTACCGAGGTAAGATTTCGATGGGTTGACTTCTTTGGCGGAG	3551939
Query	178	GTTCCGTTGGGTAAAATGCCGACTTTGGATACTTTGGATCTATATCCTCGAGAAGGAAAA	237
Sbjct	3551938	GTTACGTTAGGCAAAATGTCGACTCTCGATAAATTGACGGTGCTCCCCGGCAAAGAAAAG	3551879
Query	238	AATGCTTCTAAACTTTCTTCTTTGGACGGAATTGAACGAGCGTCCGGATTAATTAAATTG	297
Sbjct	3551878	AAAGCTCCTAAACTTTCTTCTTTGGATGGAATCGAACGAGCGCCTTGGTTAGCCAGATTG	3551819
Query	298	AATGTGGAGAGAAATCAAGGCATATCGGATCTCGGTCTTTTGTCAAAAACCTCCTAATTT	357
Sbjct	3551818	GACATG---AGCATGCAAGACGTCTCGAATATAGACCTTTTATCGAAA-CTTCCGAATTT	3551763
Query	358	GAAAACCTTTTAGCGGATCGAATAACTCGATTAAGGATTTGTCTCCACTTTCTCAGTGCAA	417
Sbjct	3551762	AAAAGTTCTTCACGGATCGTATAACTCGATCAAAGATCTATCTCCGCTTTCTCAGTGCCG	3551703
Query	418	AAATTTAAATGCGCTTTATCTCAATAAAAAATAAAATCTCCGATGTTTCCCCGCTTTCTTC	477
Sbjct	3551702	AACTTAGAAATACTTTATCTCGACAAAAATAAAATTTCCGACGTCTCTCCCCTTTCTTC	3551643
Query	478	ACTTTCAAAAATAGAAACTCTTTGCTTAGCCGACAATCCGATCCAGGATATTCTTCCTTT	537
Sbjct	3551642	GCTTTTGGAAATAGAAACGCTTTGGATATCCGACAATCCGATCAAGGATATTCTTCCTTT	3551583
Query	538	GGCCGGTTTtaaaaaaaTTAAAGAATTGAAAGTGCCGTCGAAACTCCCCGAAGAAAATTT	597
Sbjct	3551582	AACGGGTTTGAAGAACTGAAAGAAGTAAAATACCGGTGAAGCTTTCGAAAGAGAATTT	3551523
Query	598	AGCGAAGTTTAAAGAAATTACGCCCCGATGTGAAAATCTCATTTT	641
Sbjct	3551522	AGAACAGTTCAAAAACACTACGTCCCGATGTGAAGATTTCTTTTT	3551479