



Taxonomic identification of sample by DNA

Sample ID: CGG_6_000415_M

Samples collected: 10/04/2016

Locality: Fyn

Number of samples: 1

Type of material: saliva from roe deer meat

DNA investigation: DNA was successfully isolated from the sample using Blood and Tissue kit (Qiagen) following manufacturer's recommendations. Mitochondrial DNA was amplified for two mitochondrial fragments with the primers H16498_R-L15995_F (370bp, universal primer) and WDLloopL-WDLloopH254 (250 bp, dog/wolf specific primer). The universal primer pair amplified the prey (roe deer). The WDLloop primer pair amplified DNA from a carnivore, *Canis lupus*. The consensus sequence yields a BLAST id of 100% for *Canis lupus*.

Consensus sequence for the primer pair WDLloopL-WDLloopH254 (CGG_6_000415_M):
 TTCCCTGACACCCCTACATTCATATATTGAATCACCCCTACTGTGCTATGTCAGTATC
 TCCAGGTAAACCCCTTCTTCCCTCCCCTATGTACGTCGTGCATTAATGGTTTGCCCCAT
 GCATATAAGCATGTACATAATATTACATTCTTACATAGGACATATTAECTCAATCTC
 ATAATTCAGTATCTATCAACAGTAATCAAATGCATATCACTTAGTCCAATAAGGGC
 TTAATCACCA

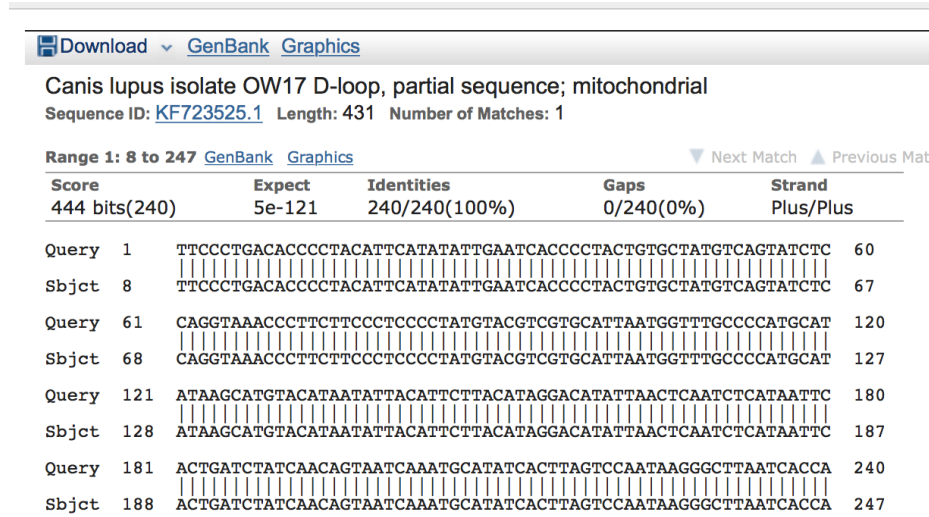


Figure 3. Screenshot for the BLAST search. Query refers to our sequences and Sbjct is the sequence in the database. The best match for our samples is the sequence ID: KF723525 belonging to a wolf.



Consensus sequence for the primer pair H16498_R- L15995_F (CGG_6_000415_M):
 GGGGGCGGGATACGCATGTTGACAAGGACAGATTTGACTTAATGCGCTATGTACGA
 TCAATAACATAATGTGCTATGTACTATTAATGACTTAATGGACTTGCTTATAAGCAT
 GGGGCATATAATATAATGTACTATTATACATATTATGTCCTAATACATTAACTTAAT
 GTACTATAAGCGCATTAAAGTTATATCGTACATACGTTGCTACATGCTTGTGTAGTTA
 ATTATATGTAGCGTATATAATTGGGTATTGAGTACAAAACCTGAATTAATTAAGTAA
 GATTTTAAAAAATTTAATACTGGTAAAGTTCTTGGTTTTTTGGAACTATATTAATAAC
 GTATCAGGGAATAGTTTAATTAGAACT

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Capreolus capreolus partial D-loop sequence
 Sequence ID: [AM279273.1](#) Length: 746 Number of Matches: 1

Range 1: 88 to 456 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous

Score	Expect	Identities	Gaps	Strand
671 bits(363)	0.0	367/369(99%)	0/369(0%)	Plus/Minus
Query 1	GGGGGCGGGATACGCATGTTGACAAGGACAGATTTGACTTAATGCGCTATGTACGATCAA	60		
Sbjct 456	GGGGGCGGGATACGCATGTTGACAAGGACAGATTTGACTTAATGCGCTATGTACGATCAA	397		
Query 61	TAACATAATGTGCTATGTACTATTAATGACTTAATGGACTTGCTTATAAGCATGGGGCAT	120		
Sbjct 396	TAACATAATGTACTATGTACTATTAATGACTTCATGGACTTGCTTATAAGCATGGGGCAT	337		
Query 121	ATAATATAATGTACTATTATACATATTATGTCCTAATACATTAACTTAATGTACTATAAG	180		
Sbjct 336	ATAATATAATGTACTATTATACATATTATGTCCTAATACATTAACTTAATGTACTATAAG	277		
Query 181	CGCATTAAAGTTATATCGTACATACGTTGCTACATGCTTGTGTAGTTAATTATATGTAGCG	240		
Sbjct 276	CGCATTAAAGTTATATCGTACATACGTTGCTACATGCTTGTGTAGTTAATTATATGTAGCG	217		
Query 241	TATATAATTGGGTATTGAGTACAAAACCTGAATTAATTAATTAAGATTTTAAAAAATTTA	300		
Sbjct 216	TATATAATTGGGTATTGAGTACAAAACCTGAATTAATTAATTAAGATTTTAAAAAATTTA	157		
Query 301	ATACTGGTAAAGTTCTTGGTTTTTTGGAACTATATTAATAACGTATCAGGGAATAGTTTA	360		
Sbjct 156	ATACTGGTAAAGTTCTTGGTTTTTTGGAACTATATTAATAACGTATCAGGGAATAGTTTA	97		
Query 361	ATTAGAACT 369			
Sbjct 96	ATTAGAACT 88			

Figure 4. Screenshot for the BLAST search. Query refers to our sequences and Sbjct is the sequence in the database. The best match for our samples is the sequence ID: AM279273 belonging to a roe deer.



Taxonomic identification of sample by DNA

Sample ID: CGG_6_000415_S

Samples collected: 10/04/2016

Locality: Fyn

Number of samples: 9

Type of material: swabs

DNA investigation: DNA was successfully isolated from the sample using DNA Blood and Tissue kit (Qiagen) with some modifications from manufacturer's recommendations (protocol can be shared on request). Mitochondrial DNA was amplified for two mitochondrial fragments with the primers H16498_R-L15995_F (370bp, universal primer) and WDLLoopL-WDLLoopH254 (254 bp, dog/wolf specific primer). The universal primer pair amplified the prey (roe deer). The WDLLoop primer pair amplified DNA from a carnivore, *Canis lupus familiaris*. The consensus sequence yields a BLAST id of 100% for *Canis lupus familiaris*. These results are consistent for the 9 analyzed swabs. We are able to identify two different haplotypes in our sequences. Sequences from swabs 1,4,6 and 8 present the same haplotype (haplotype A). While sequences from swabs 2,3,5,7 and 9 can be grouped together on a different haplotype (haplotype B).

Consensus sequence for the primer pair H16498_R- L15995_F (CGG_6_000415_S):
 CCAATTATATACGCTACATATAATTAACACACAAGCATGTAGCAACGTATGTACGA
 TATAACTTAATGCGCTTATAGTACATTAAGTTAATGTATTAGGACATAATATGTATA
 ATAGTACATTATATTATATGCCCCATGCTTATAAGCAAGTCCATTAAGTCATTAATA
 GTACATAGCACATTATGTTATTGATCGTACATAGCGCATTAAAGTCAAATCTGTCCTT
 GTCAACATGCGTATCCCGCCCCCTAGATCACGAGCTTAATCACCATGCCGCGTGAAA
 CCAGCAACCCGCTTGGCAGGGATCCCTCTTCTCGCTCCGGGCCATAAATCGTGGGG
 GTAGCTATTTAATGAACTTTATCAGACA

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Capreolus capreolus haplotype Cc22 D-loop, complete sequence; mitochondrial
 Sequence ID: [KF724423.1](#) Length: 924 Number of Matches: 1

Range 1: 91 to 460 GenBank Graphics Next Match Previous

Score	Expect	Identities	Gaps	Strand
684 bits(370)	0.0	370/370(100%)	0/370(0%)	Plus/Plus
Query 1	CCAATTATATACGCTACATATAATTAACACACAAGCATGTAGCAACGTATGTACGATAT	60		
Sbjct 91	CCAATTATATACGCTACATATAATTAACACACAAGCATGTAGCAACGTATGTACGATAT	150		
Query 61	AACCTAATGCGCTTATAGTACATTAAGTTAATGTATTAGGACATAATATGTATAATAGTA	120		
Sbjct 151	AACCTAATGCGCTTATAGTACATTAAGTTAATGTATTAGGACATAATATGTATAATAGTA	210		
Query 121	CATTATATTATATGCCCCATGCTTATAAGCAAGTCCATTAAGTCATTAATAGTACATAGC	180		
Sbjct 211	CATTATATTATATGCCCCATGCTTATAAGCAAGTCCATTAAGTCATTAATAGTACATAGC	270		
Query 181	ACATTATGTTATTGATCGTACATAGCGCATTAAAGTCAAATCTGTCCTTGCAACATGCGT	240		
Sbjct 271	ACATTATGTTATTGATCGTACATAGCGCATTAAAGTCAAATCTGTCCTTGCAACATGCGT	330		
Query 241	ATCCCGCCCCCTAGATCACGAGCTTAATCACCATGCCGCGTGAACCAGCAACCCGCTTG	300		
Sbjct 331	ATCCCGCCCCCTAGATCACGAGCTTAATCACCATGCCGCGTGAACCAGCAACCCGCTTG	390		
Query 301	GCAGGGATCCCTCTTCTCGCTCCGGGCCATAAATCGTGGGGTAGCTATTTAATGAACT	360		
Sbjct 391	GCAGGGATCCCTCTTCTCGCTCCGGGCCATAAATCGTGGGGTAGCTATTTAATGAACT	450		
Query 361	TTATCAGACA 370			
Sbjct 451	TTATCAGACA 460			

Figure 5. Screenshot for the BLAST search. Query refers to our sequences and Sbjct is the sequence in the database. The best match for our samples is the sequence ID: KF724423 belonging to a roe deer.

Consensus sequence for haplotype A for the primer pair WDLLoopL-WDLLoopH254

(CGG_6_000415_S):

ATTCCCTGACACCCCTACATTCATATATTGAATCACCCCTACTGTGCTATGTCAGTAT
CTCCAGGTAAACCCTTCTCCCTCCCTATGTACGTCGTGCATTAATGGTTTGCCCCA
TGCATATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCT
CATAATTCAGTATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGG
CTTAATCACCATGCCTCGAGAAAC

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Canis lupus familiaris control region, partial sequence; mitochondrial
Sequence ID: [KT946984.1](#) Length: 404 Number of Matches: 1

Range 1: 51 to 304 GenBank Graphics Next Match Previous Match

Score	Expect	Identities	Gaps	Strand
470 bits(254)	9e-129	254/254(100%)	0/254(0%)	Plus/Minus
Query 1	ATTCCTGACACCCCTACATTCATATATTGAATCACCCCTACTGTGCTATGTCAGTATCT	60		
Sbjct 304	ATTCCTGACACCCCTACATTCATATATTGAATCACCCCTACTGTGCTATGTCAGTATCT	245		
Query 61	CCAGGTAAACCCTTCTCCCTCCCTATGTACGTCGTGCATTAATGGTTTGCCCCATGCA	120		
Sbjct 244	CCAGGTAAACCCTTCTCCCTCCCTATGTACGTCGTGCATTAATGGTTTGCCCCATGCA	185		
Query 121	TATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCTCATAATT	180		
Sbjct 184	TATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCTCATAATT	125		
Query 181	CACTGATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGGCTTAATCACC	240		
Sbjct 124	CACTGATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGGCTTAATCACC	65		
Query 241	ATGCCTCGAGAAAC	254		
Sbjct 64	ATGCCTCGAGAAAC	51		

Figure 6. Screenshot for the BLAST search. Query refers to our sequences and Sbjct is the sequence in the database. The best match for our samples is the sequence ID: KT946984 belonging to a dog.

Consensus sequence for haplotype B (CGG_6_000415_S):

TTCCCTGACACCCCTACATTCATATATTGAATTACCCCTACTGTGCTATGTCAGTATC
TCCAGGTAAACCCCTTCTCCCCTCCCCTATGTACGTCGTGCATTAATGGTTTGCCCCAT
GCATATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCTC
ATAGTTCAGTATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGGC
TTAATCACCATGCC

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Canis lupus familiaris isolate Cf_ws9 mitochondrion, complete genome
Sequence ID: [KM061594.1](#) Length: 16730 Number of Matches: 1

Range 1: 15454 to 15697 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
451 bits(244)	3e-123	244/244(100%)	0/244(0%)	Plus/Plus
Query 1	TTCCCTGACACCCCTACATTCATATATTGAATTACCCCTACTGTGCTATGTCAGTATCTC	60		
Sbjct 15454	TTCCCTGACACCCCTACATTCATATATTGAATTACCCCTACTGTGCTATGTCAGTATCTC	15513		
Query 61	CAGGTAAACCCCTTCTCCCCTCCCCTATGTACGTCGTGCATTAATGGTTTGCCCCATGCAT	120		
Sbjct 15514	CAGGTAAACCCCTTCTCCCCTCCCCTATGTACGTCGTGCATTAATGGTTTGCCCCATGCAT	15573		
Query 121	ATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCTCAGTTC	180		
Sbjct 15574	ATAAGCATGTACATAATATTATATCCTTACATAGGACATATTAECTCAATCTCAGTTC	15633		
Query 181	ACTGATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGGCTTAATCACCA	240		
Sbjct 15634	ACTGATCTATCAACAGTAATCGAATGCATATCACTTAGTCCAATAAGGGCTTAATCACCA	15693		
Query 241	TGCC 244			
Sbjct 15694	TGCC 15697			

Figure 7. Screenshot for the BLAST search. Query refers to our sequences and Sbjct is the sequence in the database. The best match for our samples is the sequence ID: KM061594 belonging to a dog.