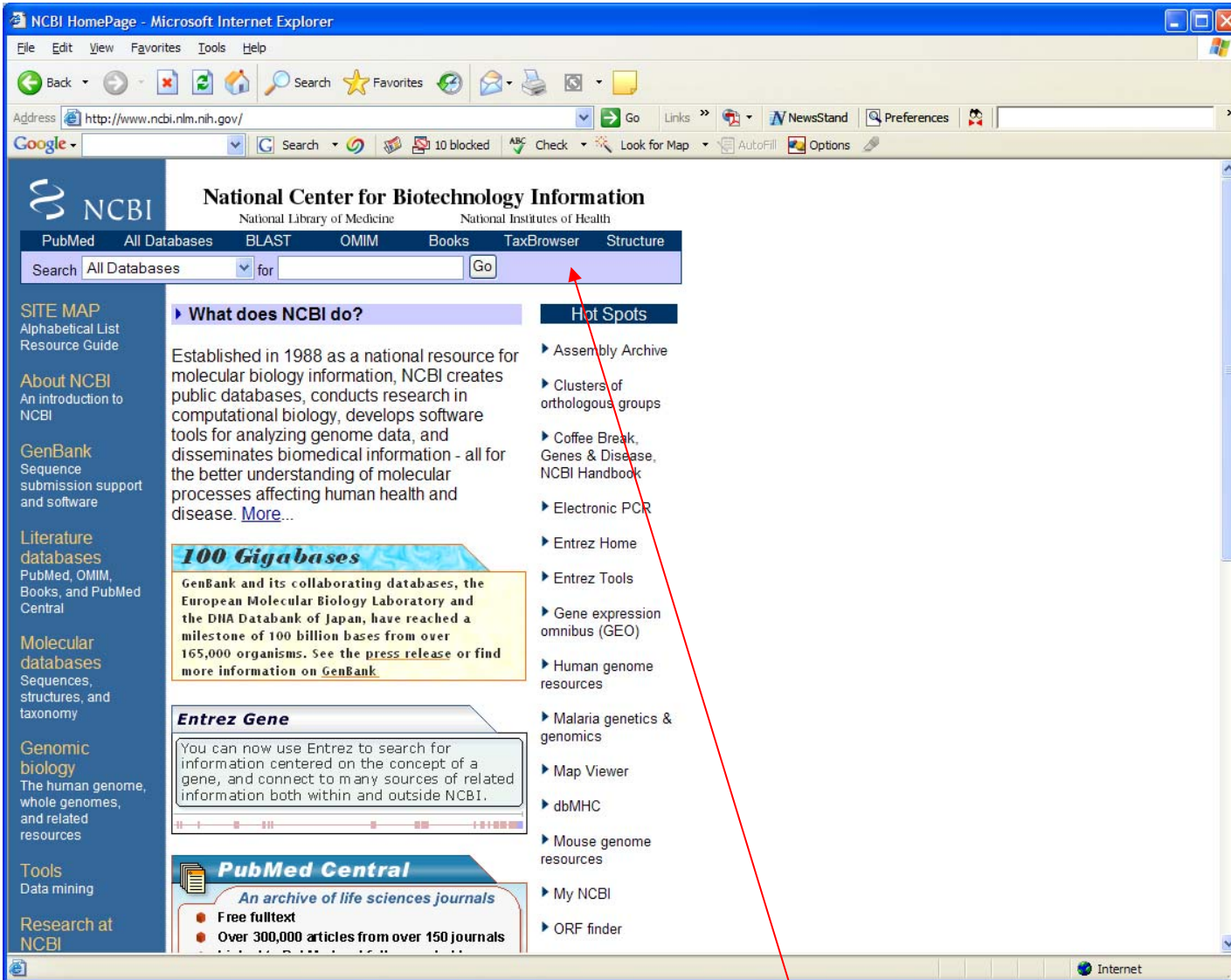


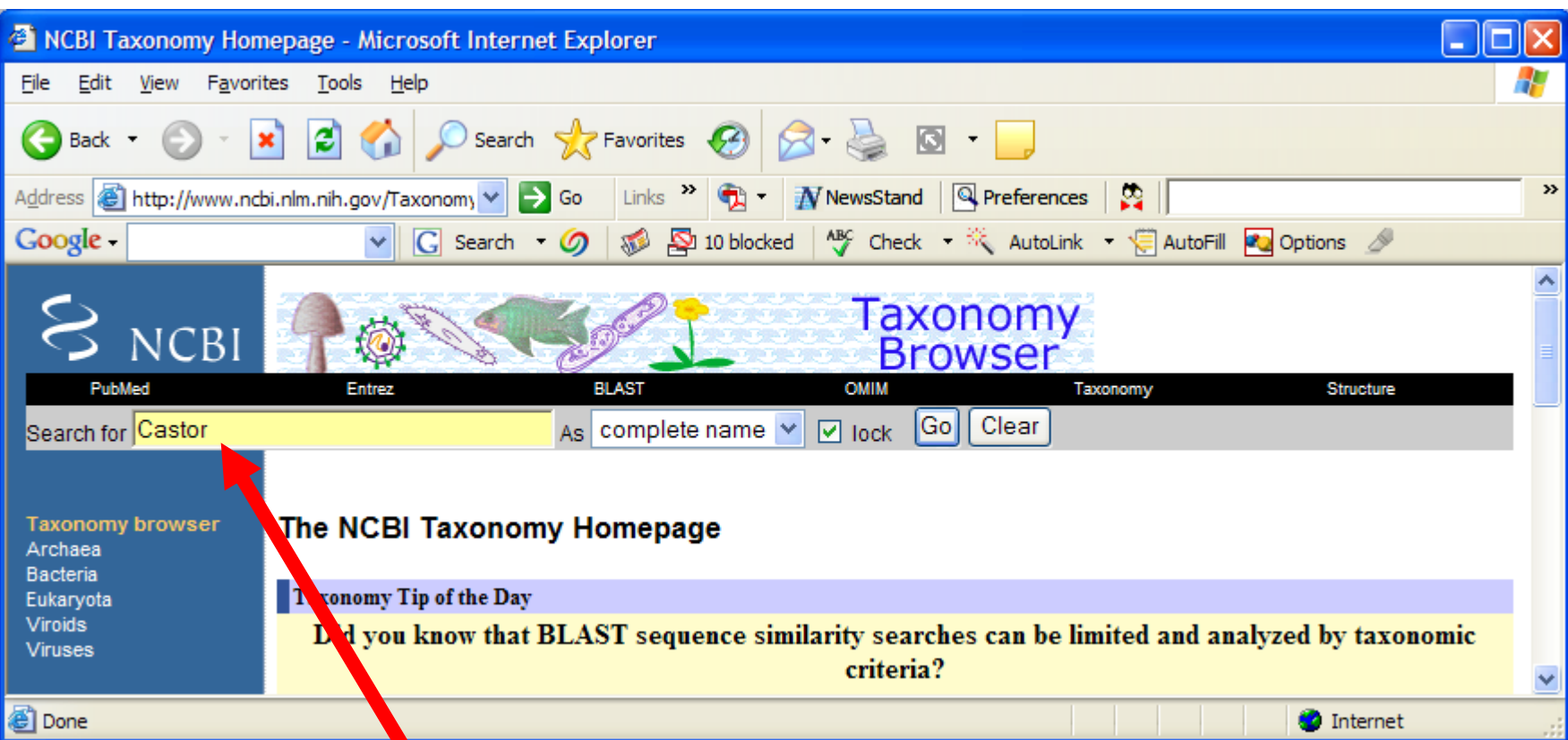
Majava-aiheinen Mega-demo

Kysymyksiä:

- Voiko euroopanmajavan ja kanadalaisen erottaa jotenkin helpommin kuin kallon luita mittaamalla?
- Onko Suomessa vielä alkuperäistä majavaa, entä Karjalassa?
- Voivatko majavalajit risteytyä?



<http://www.ncbi.nlm.nih.gov/>



Taxonomy browser (Castor) - Microsoft Internet Explorer

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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for **Castor** as complete name lock Go Clear

Display 3 levels using filter: none

☐ Nucleotide ☐ Protein ☐ Structure ☐ Genome Sequences ☐ Genome Projects ☐ Popset ☐ SNP
☐ 3D Domains ☐ Domains ☐ GEO Datasets ☐ GEO Expressions ☐ UniGene ☐ UniSTS ☐ PubMed Central
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Lineage (full): [root](#); [cellular organisms](#); [Eukaryota](#); [Fungi/Metazoa group](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Coelomata](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Euarchontoglires](#); [Glires](#); [Rodentia](#); [Sciurognathi](#); [Castoridae](#)

o [Castor](#) [LinkOut](#) Click on organism name to get more information.

- [Castor canadensis](#) (American beaver) [LinkOut](#)
- o [Castor fiber](#) (Eurasian beaver) [LinkOut](#)
 - [Castor fiber albicus](#)
 - [Castor fiber birulai](#)
 - [Castor fiber fiber](#)
 - [Castor fiber galliae](#)
 - [Castor fiber pohlei](#)
 - [Castor fiber tuvinicus](#)

Disclaimer: The NCBI taxonomy database is not an authoritative source for nomenclature or classification - please consult the relevant scientific literature

Internet

Taxonomy browser (Castor fiber albicus) - Microsoft Internet Explorer

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Display 3 levels using filter: none

Castor fiber albicus

Taxonomy ID: 331605
Rank: subspecies
Genetic code: [Translation table 1 \(Standard\)](#)
Mitochondrial genetic code: [Translation table 2 \(Vertebrate Mitochondrial\)](#)

Lineage (full)
[cellular organisms](#); [Eukaryota](#); [Fungi/Metazoa group](#); [Metazoa](#); [Eumetazoa](#); [Bilateria](#); [Coelomata](#); [Deuterostomia](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Gnathostomata](#); [Teleostomi](#); [Euteleostomi](#); [Sarcopterygii](#); [Tetrapoda](#); [Amniota](#); [Mammalia](#); [Theria](#); [Eutheria](#); [Euarchontoglires](#); [Glires](#); [Rodentia](#); [Sciurognathi](#); [Castoridae](#); [Castor](#); [Castor fiber](#)

Entrez records	
Database name	Direct links
Nucleotide	4
Protein	2
Popset	3
Taxonomy	1

Disclaimer: The NCBI taxonomy database is not an authoritative source for nomenclature or classification - please consult the relevant scientific literature for the most reliable information.

Comments and questions to info@ncbi.nlm.nih.gov
Credits: Joe Bischoff, Mikhail Domrachev, Scott Federhen, Carol Hottel, Detlef Leipe, Vladimir Sousoff, Richard Sternberg, Sean Turner.

Done Internet

Entrez Nucleotide - Microsoft Internet Explorer

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Google Search 10 blocked Check AutoLink AutoFill Options

Limits Preview/Index History Clipboard Details

Display Summary Show 20 Sort by Send to

All: 4 bacteria: 0 mRNA: 0 RefSeq: 0

Items 1 - 4 of 4 One page.

☐ 1: [DQ088704](#) Reports Links
Castor fiber albicus cytochrome b (cytb) gene, complete cds; mitochondrial
gi68271293|gb|DQ088704.1|[68271293]

☐ 2: [DQ088701](#) Reports Links
Castor fiber albicus haplotype al2 control region, partial sequence; mitochondrial
gi68271290|gb|DQ088701.1|[68271290]

☐ 3: [DQ088700](#) Reports Links
Castor fiber albicus haplotype al1 control region, partial sequence; mitochondrial
gi68271289|gb|DQ088700.1|[68271289]

☐ 4: [DQ060686](#) Reports Links
Castor fiber albicus MHC class II antigen (Cafi-DRB) gene, Cafi-DRB*01 allele, exon 2 and partial cds
gi67037885|gb|DQ060686.1|[67037885]

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NCBI Sequence Viewer v2.0 - Microsoft Internet Explorer

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Range: from begin to end Reverse complemented strand Features: ☐ SNP ☐ CDD ☒ MGC ☒ HPRD ☒ STS ☒ tRNA Refresh

☐ 1: [DQ088701](#). Reports Castor fiber albi...[gi:68271290]

LOCUS DQ088701 490 bp DNA linear ROD 05-OCT-2005

DEFINITION Castor fiber albicus haplotype al2 control region, partial sequence; mitochondrial.

ACCESSION DQ088701

VERSION DQ088701.1 GI:68271290

KEYWORDS .

SOURCE mitochondrion Castor fiber albicus

ORGANISM [Castor fiber albicus](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Castoridae; Castor.

REFERENCE 1 (bases 1 to 490)

AUTHORS Durka,W., Babik,W., Ducroz,J.F., Heidecke,D., Rosell,F., Samjaa,R.,
P Saveljev,A., Stubbe,A., Ulevicius,A. and Stubbe,M.

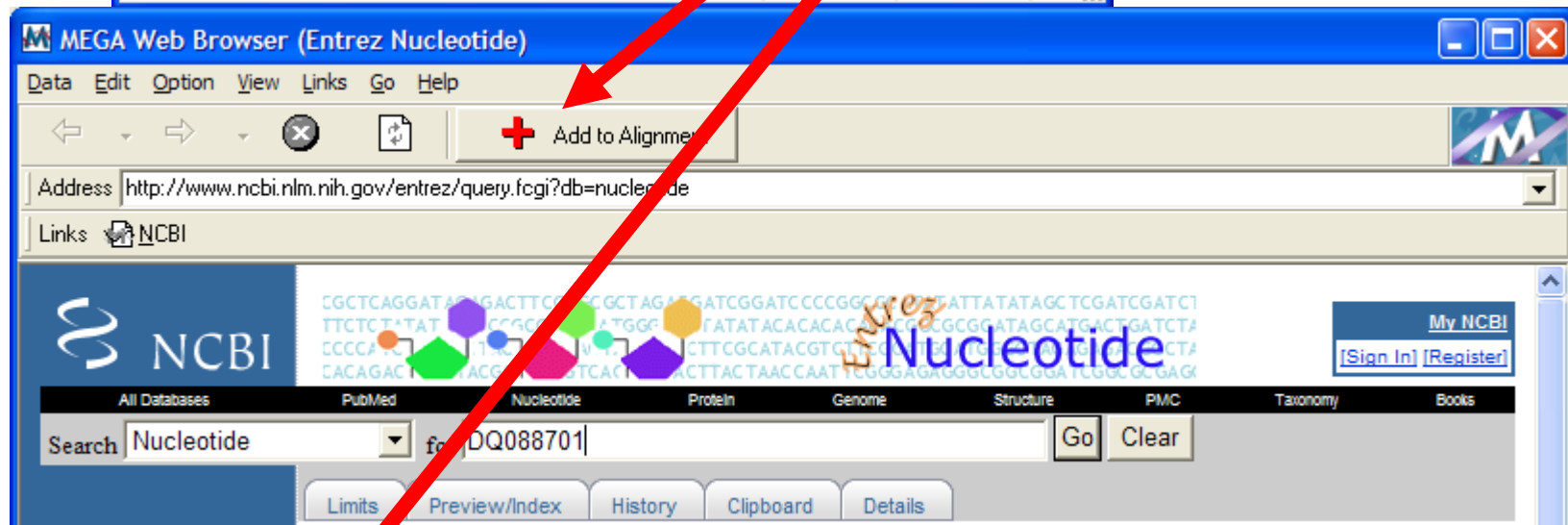
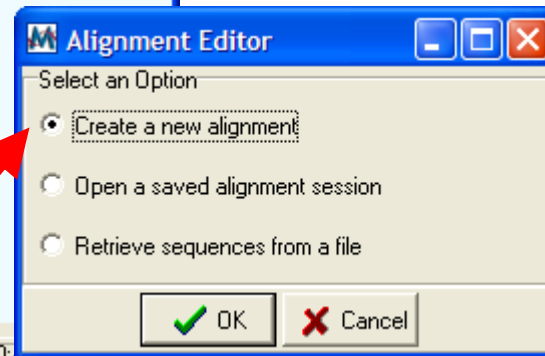
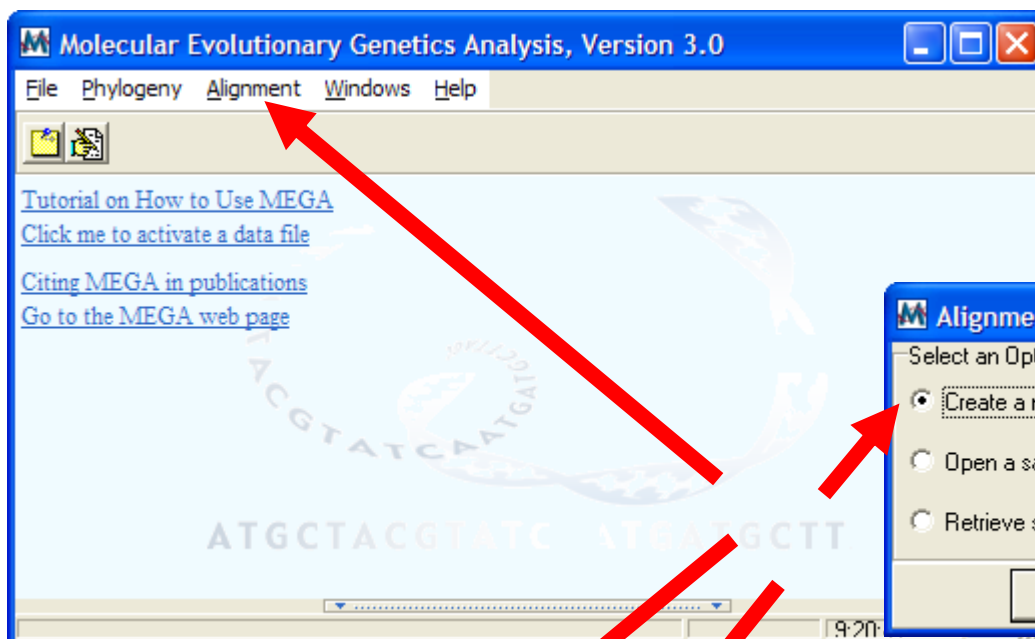
TITLE Mitochondrial phylogeography of the Eurasian beaver Castor fiber L

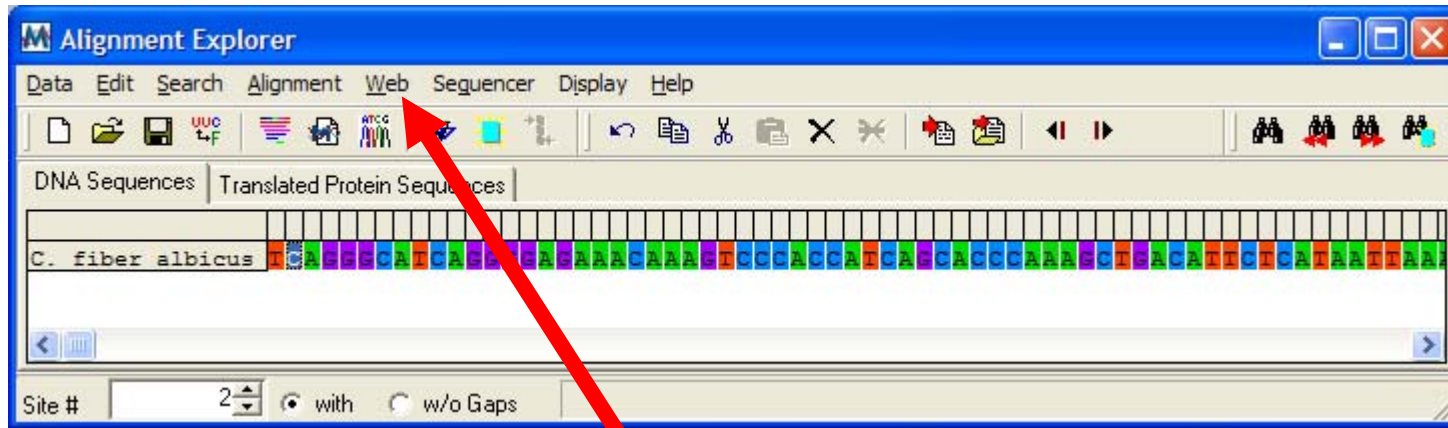
JOURNAL Mol. Ecol. 14 (12). 3843-3856 (2005)

Done Internet

Ahaa, vihko
ei ole vielä
ilmestynyt,
mutta tulee
tänään!

MEGA3 pitää
asentaa, avata





Etsitään MEGA3 linjausohjelmaan yksi sekvenssi malliksi, sitten mennään Web-palveluihin ja tehdään BLAST-haku



NCBI

nucleotide-nucleotide **BLAST**

Nucleotide

Protein

Translations

Retrieve results for an RID

[Search](#)

```
TCAGGGCATCAGGGGAGAAACAAAGTCCCACCATCAGCACCCAAAGCTGACATTCTCATA
ATTAAACTATCCCCTGTAACATATACATGTACATAATACAACAGTCTATGTATATCGTGC
ATTATGTTATATTCCACATTAAATAATGCTTGAGTACTTCAAATGCTAATCGTACATAGTA
CATAACTGTATAATCGTACATATTAAGTTCCCCGAGCAGGAATAACAAGCACGTATAGTA
ATGACAAGGTAGACTATAACACATAGCAGTATTGATCAACATAACACCAATTCAACATGG
```

[Set subsequence](#)

From:

To:

[Choose database](#)

nr

Now:

BLAST!

or

[Reset query](#)[Reset all](#)**Options** for advanced blasting[Limit by entrez query](#)

or select from:

All organisms

[Choose filter](#)☒

Low complexity

☐

Human repeats

☐

Mask for lookup table only

☐

Mask lower case

[Expect](#)

10

[Word Size](#)

11

[Other advanced](#)

BLAST-tuloksia

Sequences producing significant alignments:		Score (Bits)	E Value
gi 68271290 gb DQ088701.1 	Castor fiber albicus haplotype al2...	971	0.0
gi 68271289 gb DQ088700.1 	Castor fiber albicus haplotype al1...	963	0.0
gi 68271292 gb DQ088703.1 	Castor fiber galliae haplotype ga1...	924	0.0
gi 68271291 gb DQ088702.1 	Castor fiber fiber haplotype fil c...	852	0.0
gi 54303867 gb AY623642.1 	Castor fiber haplotype in2 control...	805	0.0
gi 54303866 gb AY623641.1 	Castor fiber haplotype in1 control...	797	0.0
gi 54303859 gb AY623634.1 	Castor fiber birulai haplotype bi3...	797	0.0
gi 54303858 gb AY623633.1 	Castor fiber birulai haplotype bi2...	791	0.0
gi 54303868 gb AY623643.1 	Castor fiber haplotype in3 control...	789	0.0
gi 54303857 gb AY623632.1 	Castor fiber birulai haplotype bi1...	777	0.0
gi 54303864 gb AY623639.1 	Castor fiber tuvinicus haplotype t...	775	0.0
gi 54303860 gb AY623635.1 	Castor fiber pohlei haplotype po1 ...	775	0.0
gi 54303863 gb AY623638.1 	Castor fiber tuvinicus haplotype t...	767	0.0
gi 54303861 gb AY623636.1 	Castor fiber pohlei haplotype po2 ...	767	0.0
gi 54303862 gb AY623637.1 	Castor fiber tuvinicus haplotype t...	759	0.0
gi 54303865 gb AY623640.1 	Castor fiber tuvinicus haplotype t...	751	0.0
gi 55583671 gb AY787826.1 	Castor canadensis haplotype F D-1a...	137	3e-28

Kaapataan kaikki ja
lisätään linjaukseen,
yksi kerrallaan

Analysis Preferences

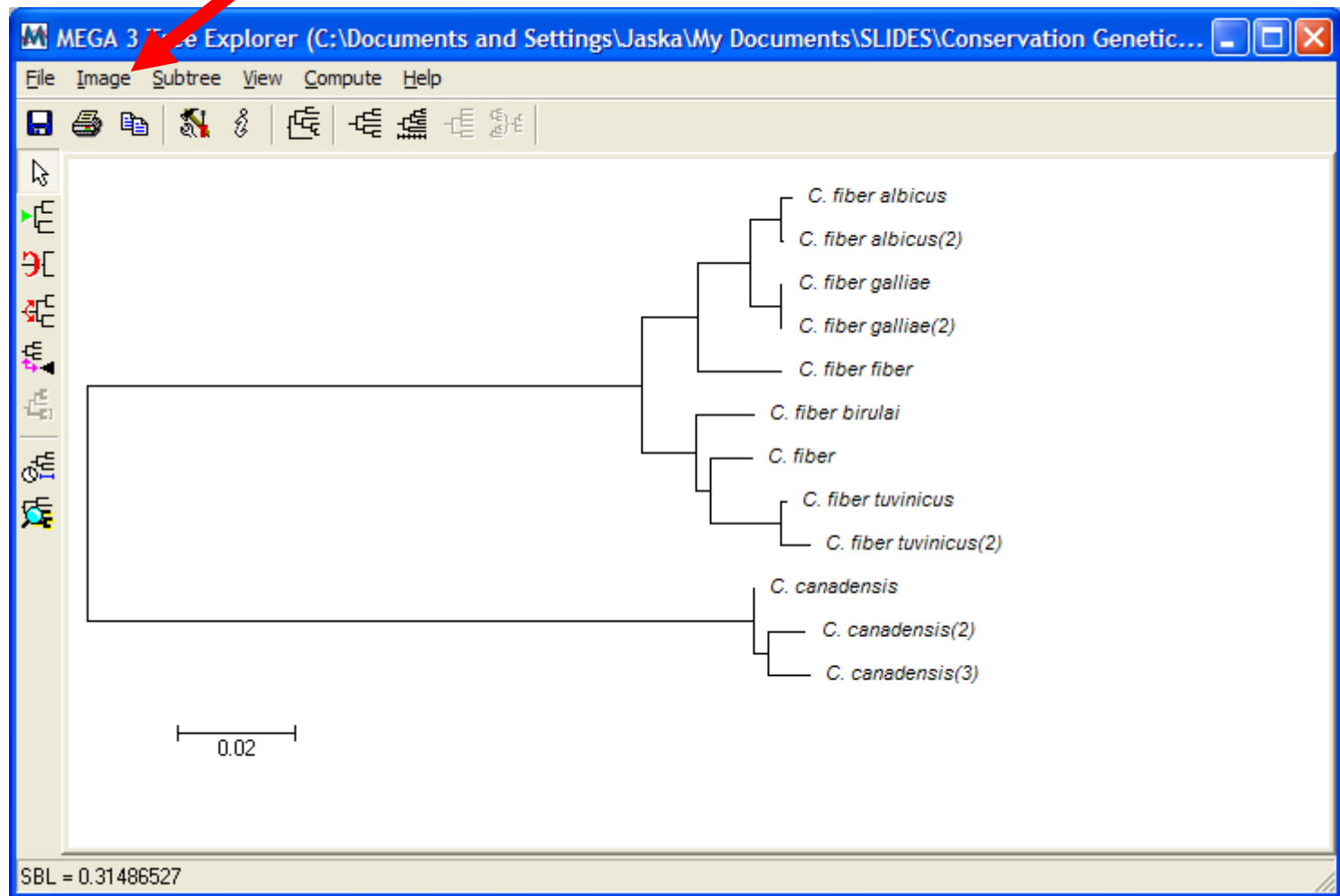
Options Summary | Test of Phylogeny

Option	Selection
Data Type	Nucleotide
Analysis	Phylogeny reconstruction
Tree Inference	
Method	Neighbor-Joining
Phylogeny Test and options	None ☒
Include Sites	
Gaps/Missing Data	Complete Deletion ☒
Substitution Model	
Model	Nucleotide: Kimura 2-parameter ☒
Substitutions to Include	d: Transitions + Transversions ☒
Pattern among Lineages	Same (Homogeneous)

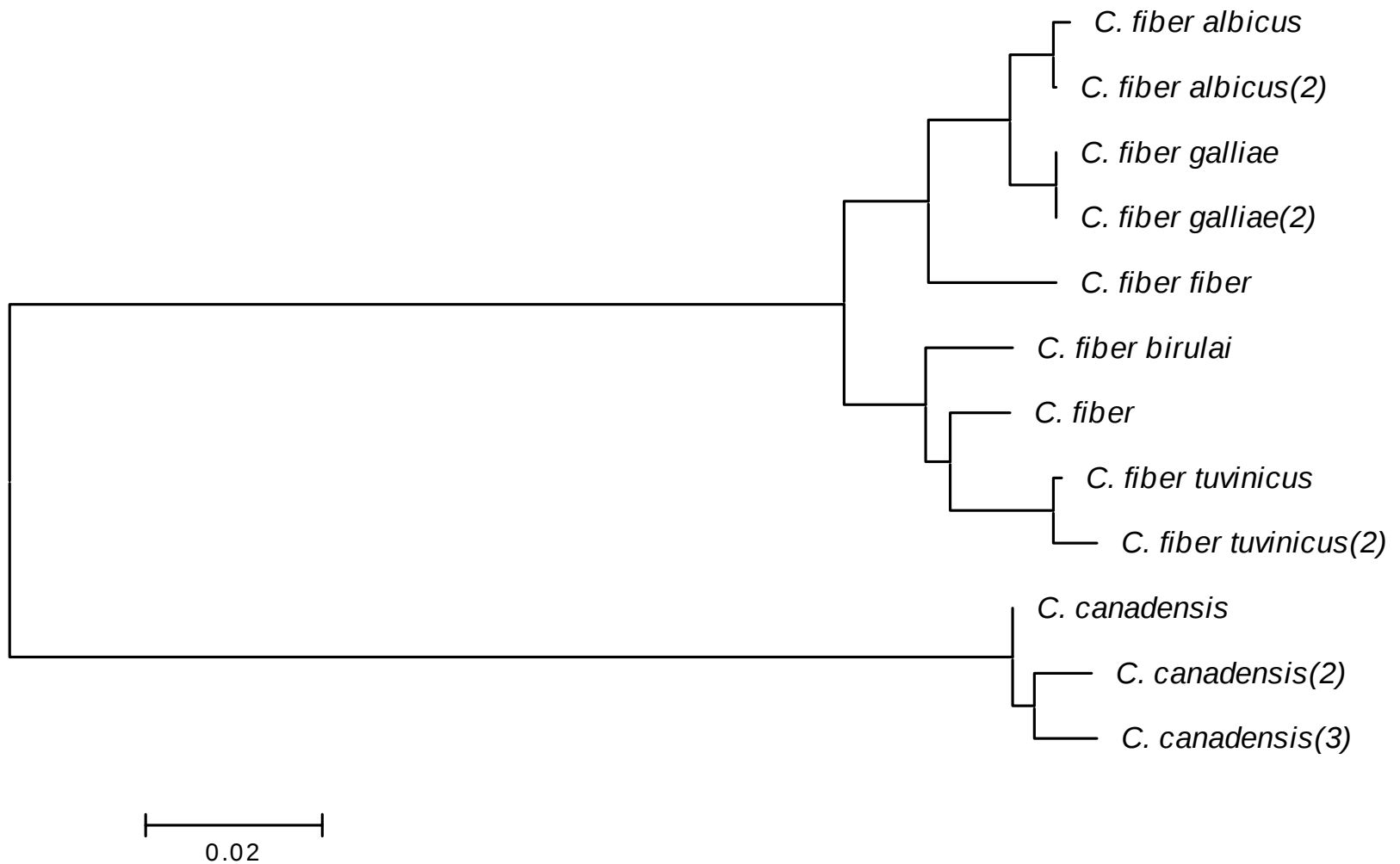
☒ Compute ☒ Cancel ☒ Help

Fylogenia-valikko

Nappaa image leikkopöydälle



Fylogeniahypoteesi: Neighbor Joining, K2P, pairwise deletion



Ahaa. No mitä sitten? No senkun vaan lotraamaan. Luetaan ensin jotain. Tästä nähdään, että majavalajit erottuvat selvästi vaikkapa tällä mitokondrion kontrollialueen sekvenssillä. Alalajejakin näyttää eurooppalaisella olevan, joten jotain kiinnostavaa voi löytyä.

Kun olin laatinut edelliset slidet 11.10.2005 aamupäivällä, menin postilaatikolleni ja poimin uuden *Molecular Ecology* –lehden numeron, jonka kansikuvassa oli majava. Siinä oli kaikki tästä aiheesta, ja olin iloinen, etten ole aloittanut mitään työlästä hommaa, tai aloituttanut sitä viattomalla opiskelijaparalla, joka nyt joutuisi toteamaan tehneensä turhaa työtä.

Jotain vielä varmaan voi tehdä, tarkempien suunnitelmien perusteella.

VOLUME 14
NUMBER 12
OCTOBER
2005

MOLECULAR ECOLOGY



Published by
Blackwell Publishing

October 2005

Mitochondrial phylogeography of the Eurasian beaver *Castor fiber* L.

WALTER DURKA,* WIESLAW BABIK,* JEAN-FRANCOIS DUCROZ,* DIETRICH HEIDECKE,†
FRANK ROSELL,‡ RAVČIGIJN SAMJAA,§ ALEXANDER P. SAVELJEV,¶ ANNEGRET STUBBE,†
ALIUS ULEVIČIUS** and MICHAEL STUBBE†

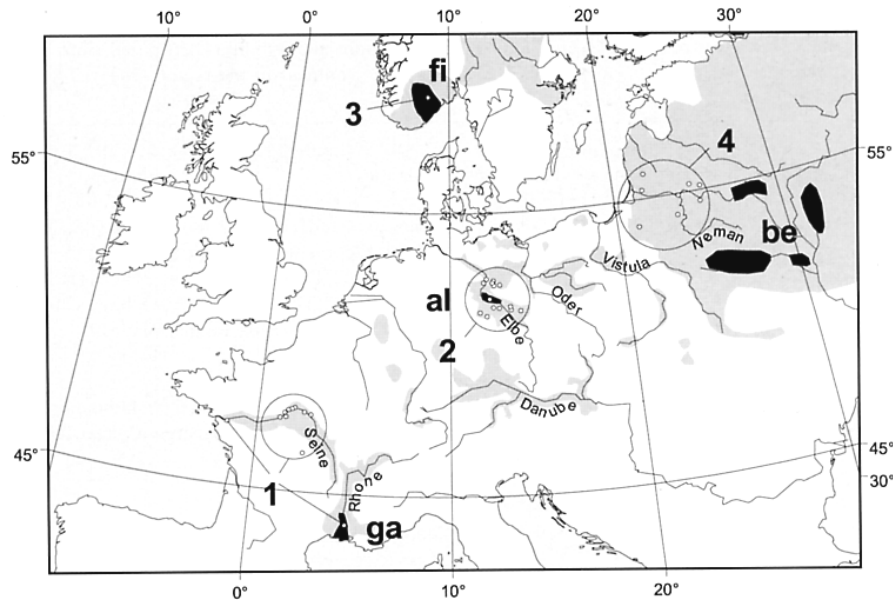
*UFZ Center for Environmental Research Leipzig-Halle GmbH, Department of Community Ecology (BZF), Theodor-Lieser-Strasse 4, 06120 Halle (Saale), Germany, †Institute of Zoology, Martin-Luther University Halle-Wittenberg, Domplatz 4, 06108 Halle (Saale), Germany, ‡Telemark University College, Department of Environmental and Health Studies, Hallvard Eikas plass, 3800 Bø in Telemark, Norway, §National University of Mongolia, Ulaan-Baatar, Mongolia, ¶Zhirkov Russian Research Institute of Game Management and Fur Farming, ul. Engel'sa 79, 610000 Kirov, Russia, **Institute of Ecology of the Vilnius University, Akademijos 2, 08412 Vilnius, Lithuania

Abstract

Nucleotide variation in an approximately 490 bp fragment of the mitochondrial DNA control region (mtDNA CR) was used to describe the genetic variation and phylogeographical pattern in the Eurasian beaver (*Castor fiber*) over its entire range. The sampling effort was focused on the relict populations that survived a drastic population bottleneck, caused by overhunting, at the end of the 19th century. A total of 152 individuals grouped into eight populations representing all currently recognized subspecies were studied. Sixteen haplotypes were detected, none of them shared among populations. Intrapopulation sequence variation was very low, most likely a result of the severe bottleneck. Extreme genetic structure could result from human-mediated extinction of intermediate populations, but it could also be an effect of prior substantial structuring of the beaver populations with watersheds of major Eurasian rivers acting as barriers to gene flow. Phylogenetic analysis revealed the presence of two mtDNA lineages: eastern (Poland, Lithuania, Russia and Mongolia) and western (Germany, Norway and France), the former comprising more divergent haplotypes. The low level of sequence divergence of the entire cytochrome *b* gene among six individuals representing six subspecies suggests differentiation during the last glacial period and existence of multiple glacial refugia. At least two evolutionary significant units (ESU) can be identified, the western and the eastern haplogroup. The individual relict populations should be regarded as management units, the eastern subspecies possibly also as ESUs. Guidelines for future translocations and reintroductions are proposed.

Keywords: bottleneck, *Castor fiber*, conservation, control region, mitochondrial DNA, phylogeography

Received 14 April 2005; revision accepted 18 July 2005



Joo, kyllä tästä vielä jotain voisi keksiä. Tuolla Pohjois-Suomessa on euroopanmajavan täplä?

Tietävätkö nuo enemmän kuin minun suomalaiset informantit? Taitavat tietää!

[majava2.pdf](#)
[majava3.pdf](#)

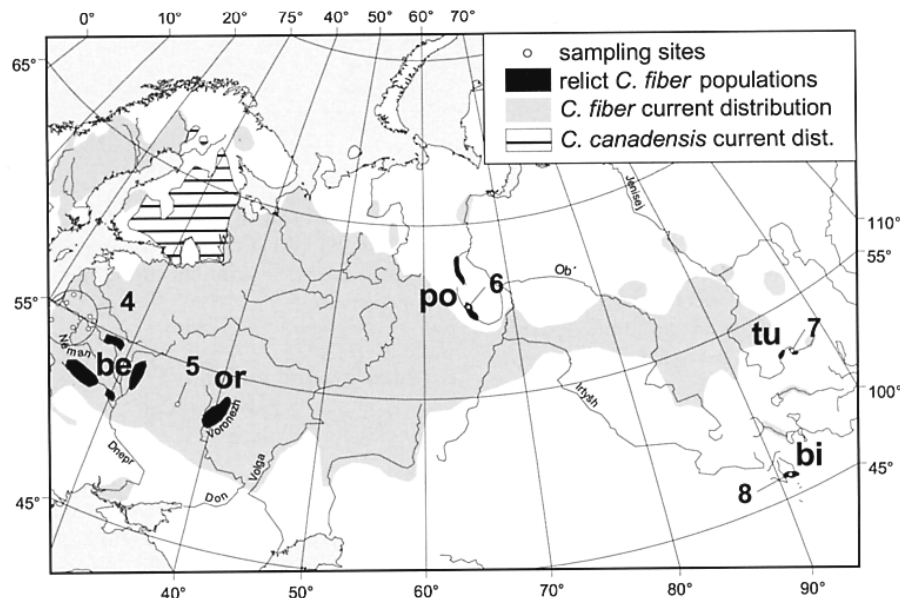


Fig. 1 Location of the sampling sites for *Castor fiber*. Current range of *C. fiber* and *Castor canadensis* according to Halley & Rosell (2002) and Saveljev (2003), except Russian far east. Relict populations remaining at the end of the 19th century: *C. f. albicus* (al), *C. f. belorussicus* (be), *C. f. birulai* (bi), *C. f. fiber* (fi), *C. f. galliae* (ga), *C. f. orientoeuropaeus* (or), *C. f. pohlei* (po) and *C. f. tuviniensis* (tu).