

Name : Aman Bashar

Contact: Amanbashar96@gmail.com

Mobile: +91 9085429899

Title: Phylogenetic Tree analysis

Answer the following questions below and upload them in the google form.

1. Investigate the evolutionary relationships among bats, whales, and artiodactyls (even-toed ungulates) groups.
 - a. Choose 3 to 5 species in each group. Mention each species, i. Name, ii. GenBank Accession Number, iii. Sequence Length & iv. Sequence.
 - b. Construct a phylogenetic tree using sequence data for the chosen species.
 - c. Analyze the tree to identify key evolutionary events and relationships in about 350 words.
 - d. Compare and contrast the evolutionary histories of the groups in about 250 words.
 - e. Discuss the implications of your findings for our understanding of mammalian evolution in about 150 words.

a. Species Detail

i. Whale Species :-

a. Physeter catodon ([NC_002503](#) REGION: 7059..7742) 684 bp

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>NC_002503.2:7059-7742 Physeter catodon mitochondrion, complete genome
ATGGCATACCCCCTTCAACTAGGTTTCCAAGACGCAACCTCTCCCATTATAGAGGAACCTTTACACTTTC
ATGATCACACCCTAATAATTGTTTTCTTAATTAGCTCTCTAGTCCTCTACATTATCACCTAATACTAAC
AACCAAATAACACATATCAACACAATAGACGCCAAGAAGTAGAGACCATTGTAACCGTTCTCCCGCT
ATCATTCTAATCCTAATCGCCCTACCATCCCTACGAATCCTCTACATAATAGACGAAATCAACAGCCCCT
CTCTTACTGTAAAGACAATAGGTCACCAATGATATTGAAGCTACGAATATACCGACTACGAAGACCTGTC
CTTTGACTCTTACATAATCCCAACATCGGACTTAAAACCAGGAGACCTACGACTATTAGAAGTCGACAAC
CGAATAGTATTGCCTATAGAAATAACAATCCGAGTCTTAGTCTCCTCCGAGGATGTCCTACACTCATGAG
CTGTCCCCTCCCTAGGCCTAAAAACAGACGCAATCCCCGGGCGCCTAAACCAAACAACCTTAATATCAAC
ACGACCAGGCTTATTCTACGGACAATGTTTCAGAAATCTGCGGCTCAAACCATAGTTTCATACCAATTGTC
CTCGAACTAGTACCCCTAGAAAACCTTTGAAAAATGATCCATCTCAATACTGTAA
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b. *Orcinus orca* ([NC_064558](#) REGION: 7055..7738) 684 bp

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>NC_064558.1:7055-7738 Orcinus orca mitochondrion, complete genome
ATGGCATATCCCTTTCAACTAGGCCTACAAGACGCAGCATCACCTGTTATGGAAGAGCTTCTACAATTTT
ACGACCACGCATTAATGATCATCTTCCTGATTAGCTCCTTAGTTCTTTATATTATTACACTAATACTTAC
AACCAAATTAACCCACACTAGTACAATAAATGCTCAAGAAGTAGAACTATTTGAACTATCCTCCCAGCC
GCTATTCTAATCATAATCGCCCTACCCTCTCTACGAATCCTCTACATAATAGACGAAATTAACAATCCCT
CCCTTACCGTAAAAACAATAGGACACCAATGATACTGAAGCTATGAATATACCGACTACGAAGACCTAAA
CTTTGACTCATACATAATTCCAACCCAGATCTAAAACCAGGTGAACACGATTATTAGAGGTAGATAAT
CGAATGGTCTTACCCTTACAAATGACGATCCGAATACTAGTCTCCTCAGAAGACGTACTACACTCATGAG
CCATCCCTTCCCTAGGCCTAAAAACAGATGCAATTCCTGGCCGCTAAACCAACAACCTAACATCAAC
ACGACCTGGCCTGTTCTATGGACAATGTTTCAGAAGTTTGTGGCTCAAATCACAGCTTTATACCAATCGTT
CTCGAGCTAGTACCTTTAGAAAGCTTCGAAAAATGATCCGCATCCATATTGTAA
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c. *Megaptera novaeangliae* ([NC_006927](#) REGION: 7065..7748) 684 bp

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>NC_006927.1:7065-7748 Megaptera novaeangliae mitochondrion, complete genome
ATGGCATATCCATTCCAAGTGGTTTCCAAGATGCAGCATCACCCATTATAGAAGAACTCCTACATTTCC
ATGATCATACACTAATAATCGTTTTTCTAATTAGCTCCTTAGTCCTCTACATTATTACCCTGATACTTAC
AACCAAATAACACATACTAGTACAATAGATGCCCAAGAAGTAGAACTGTCTGAACCATCCTTCCAGCC
ATCATCTTAATTTTAATTGCCTTACCTTCCTTACGAATCCTTTACATGATAGACGAAGTCAATAACCCCT
CCCTCACTGTAAAAACAATAGGCCACCAATGATACTGAAGCTATGAATATACTGACTACGAAGACCTAAG
TTTCGACTCCTACATAATCCCAACACCCAGACCTAAAACCAGGAGAGCTGCGATTATTAGAAGTAGATAAC
CGAGTTGTTTTTACCCATAGAAATAACAATCCGAATATTAGTCTCATCAGAAGACGTACTCCACTCATGAG
CCGTACCCTCCTTAGGCCTAAAAACGGATGCAATCCCAGGACGCCTAAACCAACAACCTTAATATCAAC
ACGACCAGGCCTATTCTACGGACAATGCTCAGAAATCTGCGGCTCAAACCATAGTTTTTATACCAATTGTC
CTAGAATTAGTACCCTAGAAACCTTTGAAAAATGATCTGTATCAATATTGTAA
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ii. Bats :-

a. *Noctilio Leporinus*([NC_037137](#) REGION: 7033..7717) 685 bp

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>NC_037137.1:7033-7717 Noctilio leporinus voucher Institut des Sciences de
l'Evolution de Montpellier, ISEM-V-1890, ISEM-T-4573 mitochondrion, complete
genome
ATGGCATATCCCTTTCCAAGTGGCTTCCAAGATGCAACCTCACCTATCATAGAAGAGCTCCTACACTTTC
ACGATCACGCACTAATAATTGTATTTCTAATTAGCTCACTAGTACTTTATATTATCTCTCTAATACTAAC
TACAAGTCTTACCCATACAAGCACTATAGATGCTCAAGAGGTAGAGACAATTTGAACAATCCTTCCAGCT
ATTATCTTGATTACAATTGCCCTACCCTCACTACGAATCCTATATATAATAGATGAGATTAATAACCCCC
TCATAACAGTAAAAACAATAGGGCACCAATGATACTGAAGCTATGAATACACCGACTATGAATGTCTCAC
CTTCGACTCCTATATAGTCCCTACATCTGATTTAAAACCAGGAGAACTGCGCCTACTAGAAGTAGATAAC
CGAGTAGTACTACCAATAGAAACAACAATTCGAATATTAATTTCTCTGAAGATGTCTTACACTCATGAG
CCGTACCTTCATTAGGACTAAAAACAGATGCCATCCCCGGACGACTTAACCAACAACCTCTACTATCTAC
TCGTCCAGGTCTTTATTATGGACAGTGCTCTGAAATTTGTGGCTCAAACCACAGCTTTATACCAATCGTA
CTTGAAATAGTACCCTACAATATTTTCGAGAAGTGATCCGCCTCAATACTAAATT
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b. *Rhinolophus monoceros* ([NC_005433](#) REGION: 7032..7715) 684 bp

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>NC_005433.1:7032-7715 Rhinolophus monoceros mitochondrion, complete genome
ATGGCGTACCCCTTTCCAAGTGGCTTCCAAGATGCCACATCACCCATTATAGAAGAACTTCTACACTTCC
ACGACCACACCCTAATGATCGTCTTCCTGATCAGTCCCTAGTACTGTACATTATTTCACTCATATTAAC
AACCAGCCTAACCCTATACCAGCACAATAGACGCACAAGAAGTAGAGACGATTTGAACCATCCTACCGGCC
ATTATCCTTATCATAATTGCCCTCCCTTCCCTACGAATCCTGTACATGATGGATGAAATTAACAACCCAT
CCCTGACCGTTAAAACCATAGGACATCAATGATACTGAAGCTATGAATATACAGACTACGAAGACCTCAG
CTTCGACTCATATATAATCCCCACATCCGATCTAAAACCGGGTGAACCTCCGCTTACTAGAAGTAGACAAT
CGAGTCGTATTACCTATAGAAATAACTATCCGTATGCTAATCTCATCTGAAGATGTCTGCACTCATGAG
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CCGTGCCCTCTCTCGGCCTAAAAACAGATGCCATCCCAGGACGCCTGAACCAAACAACCCTCCTGTCCAC
TCGACCTGGCCTCTATTACGGCCAATGCTCAGAAATTTGTGGATCAAACCACAGCTTCATGCCAATCGTC
CTTGAAGTAGTCCCCTAAACACTTTGAAAAATGATCATCATCAATAGTATAA

c. Pteropus Alecto([NC_023122](#) REGION: 7034..7717) 684 bp

>NC_023122.1:7034-7717 Pteropus alecto mitochondrion, complete genome
ATGGCATACCCCTTTCCAAGTGGTTTCCAAGACGCAACATCCCCTATTATAGAAGAACTTCTGCACTTCC
ACGACCACGCACTAATAATCGTCTTCTTAATCAGCTCTCTCGTACTATATCTAATTTTCAGTAATGTTAAC
AACTAGCCTAACCCACACTAGCACCATGGACGCACAGGAGGTAGAAACCATCTGAACATTCTGCCAGCT
ATCATCCTAATTATAATTGCACTCCCCTCCCTTCGAATCCTATATATAATGGACGAAATTAATAATCCCT
ATTTAACTGTAAAAACCATAGGTACCAATGATATTGAAGTTATGAGTACACAGATTACGAAGACTTAAC
CTTCGACTCCTATATGGTCCCAACACAAGACTTAAAACCTGGAGAGCTGCGACTTCTAGAAGTTGACAAC
CGAGTAGTACTACCCATGGAAGTACCATTTCGAATGCTAATTTTCATCTGAAGACGTATTACACTCATGAG
CCGTCCCCTCCCTGGGCCTAAAAACAGATGCAATCCCAGGACGCCTAAATCAGACAACGCTACTATCTAC
ACGGCCAGGCCTATATTACGGCCAATGCTCCGAAATTTGCGGATCAAATCACAGCTTCATACCAATTGTC
CTTGAAGTAGTCCCCTAAAGTATTTTGAAAAATGATCCTCGTCCATACTGTAA

iii. Artiodactyls

a. Antilocapra americana([NC_020679](#) REGION: 7017..7700) 684 bp

>NC_020679.1:7017-7700 Antilocapra americana isolate UAM mitochondrion, complete genome
ATGGCATACCCCAATACTAGGCTTCCAGGACGCAACATCACCAATTATAGAAGAACTCCTACACTTTTC
ATGACCACACACTCATAATTGTATTCTTAATTAGCTCATTAGTACTTTATATTATCACCTTTATATTAAC
AACGAACTAACCCACACTAGTACAATGGACGCACAAGAAGTGGAGACAGTTTGAACGATCCTACCAGCC
ATTATTTTAAATTTTAAATTGCCCTACCTTCTCTGCAATCTTGTACATGATAGACGAAATCAATAATCCAT
CTCTTACAGTAAAAACCATAGGACACCAAGTACTGAAGCTATGAATACACAGACTATGAAGACTTAAG
CTTCGACTCCTACATAATCCCAACATCAGAATAAAACCAGGCGAACTACGACTGCTAGAAGTAGATAAC
CGAGTAGTTCTACCAATAGAAATGACAGTTTGAATACTAGTTTCTTCAGAAGACGTATTACACTCATGAG
CTGTACCATCTCTAGGACTAAAAACAGACGCAATCCCAGGCCGCTTAAATCAAACAACCCTAATATCAAC
CCGACCCGGCCTATACTACGGACAATGTTTCAGAAATCTGCGGGTCAAACCACAGCTTTTATACCTATTGTC
CTTGAAGTAGTTCCACTAAACACTTTCGAAGAATGATCAGCATCAATGTCATAA

b. Giraffa giraffa ([NC_012100](#) REGION: 7015..7698) 684 bp

>NC_012100.1:7015-7698 Giraffa camelopardalis angolensis mitochondrion, complete genome
ATGGCGTACCCCATGCAGCTAGGATTTCAAGATGCAACATCACCCATTATAGAAGAATTACTACATTTTC
ATGACCACACACTAATAATTGTTTTCTTATTAGCTCACTAGTGCTCTATATTATTTCACTAATACTAAC
AACAAAATAACCCATACAAGCACAATAGATGCACAGGAAGTAGAGACAATCTGAACCATTCTACCAGCT
ATTATCCTAATTATAATTGCCCTCCCCTCTCTGCAATTTTATATATAATAGATGAGATTAATAACCCAT
CTCTTACAGTAAAAACTATAGGACACCAATGATACTGAAGCTATGAATATACAGACTATGAAGACCTAAC
CTTCGACTCTTATATAATTCCCACATCGGAATAAAGCCAGGAGAACTGCGACTGTTAGAAGTAGATAAT
CGAGTAGTATTACCAATAGAAATAACAATCCGAATGCTAGTTTCATCAGAAGACGTATTACATTCATGAG
CCGTACCCTCTCTAGGATTAAAAACGGATGCAATCCCAGGCCGCTTAAACCAAACAACCCTTATGTCAAC
CCGACCAGGCCTATATTACGGACAATGCTCAGAGATCTGCGGATCAAACCATAGTTTTTATACCCATTGTC
CTTGAATTAGTTCCACTAGAGTATTTTGAAAAATGATCTGCATCAATACTGTAA

c. Capreolus capreolus ([NC_020684](#) REGION: 7014..7697) 684 bp

>NC_020684.1:7014-7697 Capreolus capreolus isolate CYTO mitochondrion, complete genome
ATGGCTTACCCCTATACAATTAGGTTTCCAAGATGCAACATCACCTATTATAGAAGAATTATTACACTTCC
ATGACCACACATTAATAATTGTTTTCTTAATCAGCTCATTAGTACTTTACATTATCTCATTAACTAAC
AACAAAATTAACCCACACCAGTACAATAGACGCCAAGAAGTAGAAACAGTCTGAACATTCTACCAGCA
ATTATCCTAATCTTAATTGCCCTTCCATCTTTACGAATTTCTGTATATGATGGATGAGATTAATAATCCAT
CACTCACAGTAAAAACTATAGGACATCAATGATATTGAAGTTATGAATATACAGATTACGAAGACTTGAG
TTTTGACTCTTATATAATCCCAACATCAGAATTAAAACCAGGAGAACTACGACTGCTAGAAGTAGATAAC

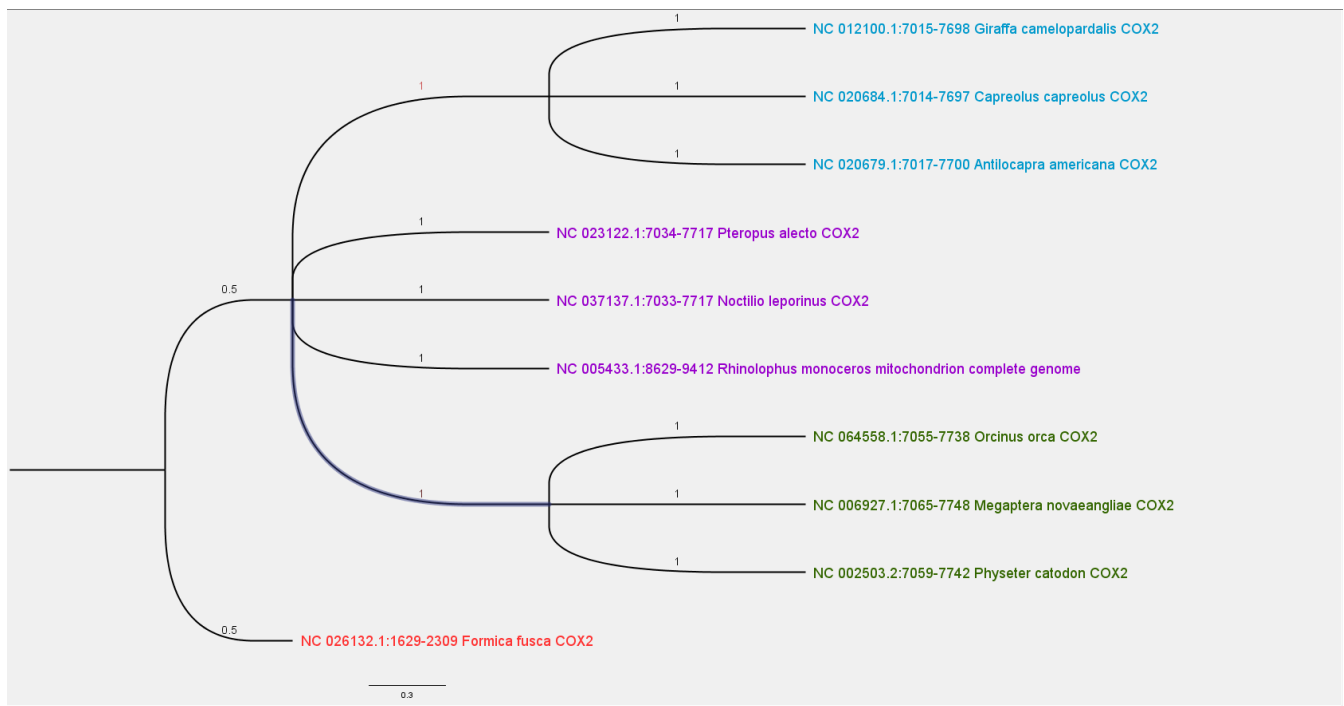
CGAGTCGTTCTACCAATGGAAATAACAATCCGAGTCTTAGTTTCTTCTGAAGATGTGTTACACTCCTGAG
CCGTGCCTTCTTTAGGACTAAAAACAGACGCAATTCCAGGTCGCCTCAACCAAACAACCCTCATGTCAAC
TCGACCCGGTCTATACTACGGACAATGCTCTGAAATCTGCGGATCAAACCACAGCTTTATACCTATTGTC
CTAGAACTAGTTCCACTAAAGTTTTTCGAAAAATGATCTGCATCAATGTTATAA

Outgroup

Formica fusca([NC_026132](#) REGION: 1629..2309) 681 bp

>NC_026132.1:1629-2309 Formica fusca mitochondrion, complete genome
ATTAATACATGATTATTAACATTACAAAATTCAAATTCACCTACATATGATATAATAATTTTTTTCATG
ATTTTACTATAATAATTTTAACTTTTATTACTTTTATTAATTCTTTTTATTTTATCTAGTCTAATTAATAA
TAAATTTATTAATCGATTTCTTCTCCAAGGCCATACAATTGAATTAATCTGAACAATTACTCCTATATTA
ATTCTAATTTTTATTGCCATTCCATCAATTAAGATTTTATATTTAACAGATGAGATATTTAATAATAAAA
TTACTATTAAATCAATTGGTCACCAATGATACTGAAGTTACGAATATTCTGATTTTTTAAATATTGATTT
TAATTCATTTATAATTCCTCTCAATGAACCTAATATCAATGAATTTTCATCTACTTGACGTAGATAATCGA
TGTATTTTACCTTTCAATTACCCTATTTCGAATGTTAACAACCTCTATAGACGTAATCCACTCATGAACCG
TTCCTTCTTTAGGTATCAAAATAGACTCAACCCCTGGACGTCTTAATCAATCATTATTACTTATAAATCG
TCCTGGATTATTCTTTGGACAATGTTTCAGAAATTTGTGGAATAAATCATAGATTTATACCTATTGTAATT
GAATCAACTAATTTTCTCAACTTTAAAAATTGATTAAAAATCATTCTATTAA

b. Phylogenetic Tree



c. Evolutionary events and relationships

Artiodactyl split: The tree clearly divides early on, separating "Giraffa camelopardalis, Capreolus capreolus, Antilocapra americana" (artiodactyls) from the remaining groups. This confirms their distinct evolutionary path within mammals.

Cetacean divergence: Within artiodactyls, "Orcinus orca, Megaptera novaeangliae, Physeter catodon" (whales) branch off as a monophyletic group, indicating their shared ancestry within artiodactyls and separate evolution from other members.

Bat diversity: Interestingly, the bat species ("Pteropus alecto, Noctilio leporinus, Rhinolophus monoceros") form a separate clade, highlighting their independent evolution and adaptation for flight despite belonging to Laurasiatheria, a different mammalian superorder compared to artiodactyls.

d. Evolutionary History

Artiodactyls: This group underwent significant diversification, adapting to diverse herbivorous niches. Notably, within artiodactyls, ruminants like giraffes, deer, and antelopes form a distinct lineage showcasing shared digestive adaptations.

Cetaceans: Whales emerged from artiodactyls, undergoing remarkable transformations for aquatic life. They lost limbs, developed flukes for propulsion, and refined echolocation for underwater communication and hunting. Their closest artiodactyl relative, not shown in the tree, is the hippopotamus, hinting at possible aquatic tendencies in their shared ancestry.

Bats: While bats share Laurasiatherian ancestry with carnivores and insectivores, they independently developed echolocation and powered flight, showcasing convergent evolution. Their diverse wing structures further emphasize independent adaptations within the bat lineage.

e. Mammalian Evolution

This analysis reinforces the dynamic nature of mammalian evolution:

Convergence: Traits like echolocation can evolve independently in distantly related groups like bats and whales.

Adaptation: Terrestrial mammals can adapt to diverse environments, even becoming fully aquatic like whales.

Shared ancestry: Close relationships can exist between seemingly disparate groups, like whales and artiodactyls.