



Genetisk diversitet: Den usynlige biodiversitet

Big Bang 2025

Emma Emilie Andersen

Biodiversitet i gymnasiet

www.biodiversitetigymnasiet.dk

Center for Makroøkologi, Evolution og Klima



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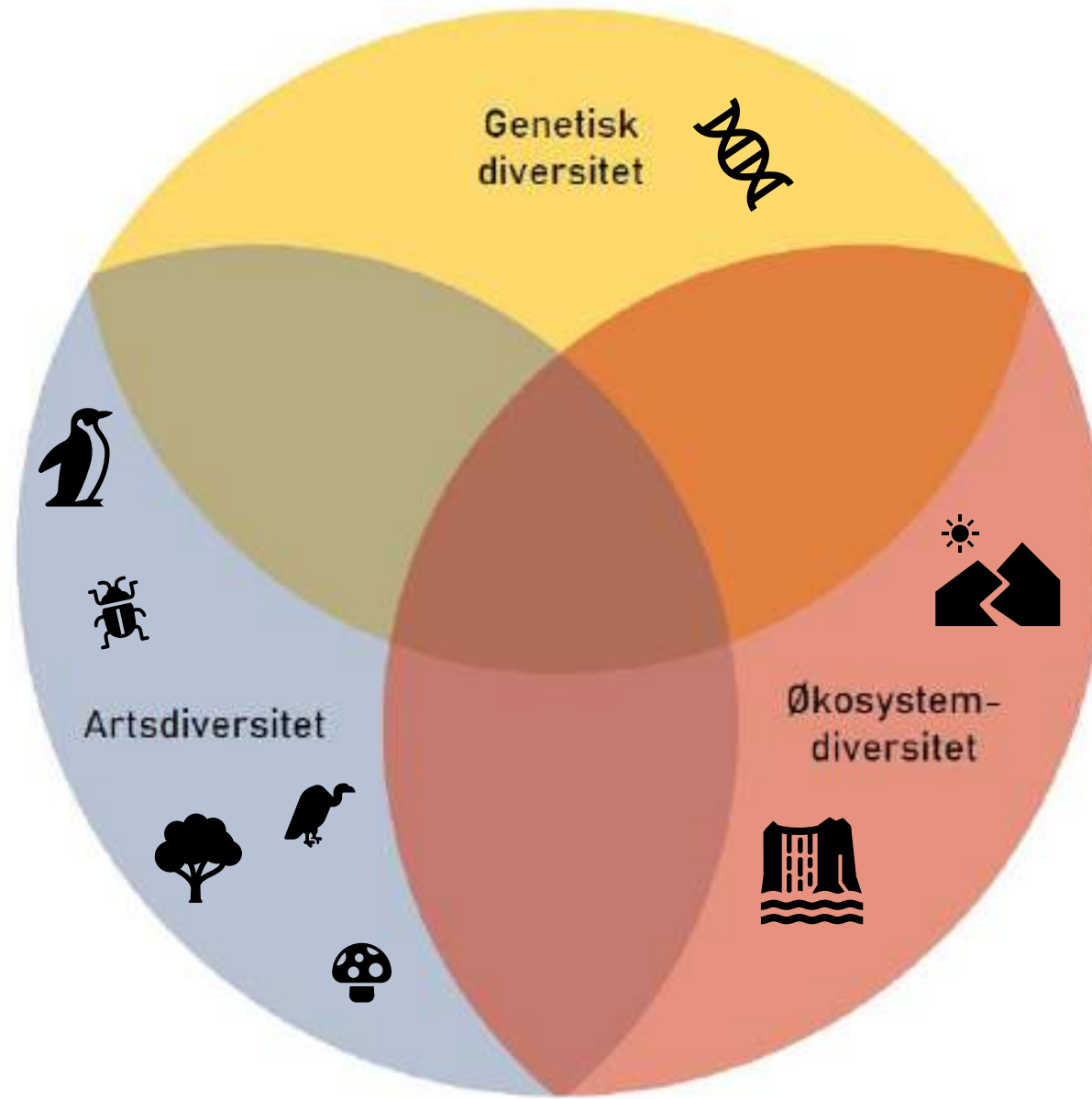
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Genetisk diversitet





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More than one in three tree species worldwide faces extinction - IUCN Red List

Cali, Colombia, 28 October 2024 (IUCN) – Thirty-eight per cent of the world's trees are at risk of extinction according to the first *Global Tree Assessment*, published in today's update of the IUCN Red List of Threatened Species™. Also in today's update, the conservation status of the Western European hedgehog has deteriorated and is now listed as Near Threatened.



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Ongoing declines for the world's amphibians in the face of emerging threats

[Jennifer A. Luedtke](#) , [Janice Chanson](#), [Kelsey Neam](#), [Louise Hobin](#), [Adriano O. Maciel](#), [Alessandro Catenazzi](#), [Amaél Borzée](#), [Amir Hamidy](#), [Anchalee Aowphol](#), [Anderson Jean](#), [Ángel Sosa-Bartuano](#), [Ansel Fong G.](#), [Anslem de Silva](#), [Antoine Fouquet](#), [Ariadne Angulo](#), [Artem A. Kidov](#), [Arturo Muñoz Saravia](#), [Arvin C. Diesmos](#), [Atsushi Tominaga](#), [Biraj Shrestha](#), [Brian Gratwicke](#), [Burhan Tjaturadi](#), [Carlos C. Martínez Rivera](#), [Carlos R. Vásquez Almazán](#), ... [Simon N. Stuart](#) [+ Show authors](#)

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Ongoing declines for thousands of species worldwide faces

[Jennifer A. Luedtke](#) , [Janice Chanson](#), [Kelsie Catenazzi](#), [Amaël Borzée](#), [Amir Hamidy](#), [Andreas Fong G.](#), [Anslem de Silva](#), [Antoine Fouquet](#), [C. Diesmos](#), [Atsushi Tominaga](#), [Bijaj Shrestha](#), [Carlos R. Vásquez Almazán](#), ... [Simon N. Stuart](#)

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KLIMA

Dyre- og plantearter er i frit dødsfald over hele kloden

Udviklingen truer menneskets eksistensgrundlag, lyder konklusionen fra 550 forskere, der har bidraget til rapporter om tab af biodiversitet i fire regioner på kloden.



Alle arter af havskildpadder er truet af udryddelse. (Foto: © DAVID GRAY, iStock)

 LÆS OP  ORD OG  TEKST

af [Marie Lise Behrendt](#)

SE FLERE OPLÆG | [SE FLERE BEHANDLINGER](#)

Præcis hvor mange arter, der findes her på Jorden, får vi nok aldrig opklaret. De fleste rækker tæller på mellem 5-50 millioner, men nogle forskere mener, at der kan være op til

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... species worldwide faces

... – Thirty-eight per cent of the world's trees are at risk of extinction, according to a new Tree Assessment, published in today's update of the Red List of Threatened Species. Also in today's update, the conservation status of the ... is now listed as Near Threatened.



KLIMA

Forskere: Verdens sidste vilde natur er ved at forsvinde

Tab af levesteder er den største trussel mod biodiversitet både globalt og i Danmark, siger dansk professor.



Regnskoven ved Amazona-floden er et af de naturområder der er voldsomt truet af mindrebril, landbrug og skovhældning. (© University of Queensland)

LES OP ORDBOG TEKST

af Anders Worsø

31. OKT 2018 | MERE END 30 DAGE GAMMEL

Mennesket er Jordens altdominerende art.

Det kan også mærkes på naturen overalt på vores lille blå planet. Faktisk forsvinder verdens sidste ødemarker hastigt.

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Alle arter af hovskildpadler er truet af udryddelse. (Foto: © DAVID GRAY, ianpfo)



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Just 3% of world's ecosystems remain intact, study suggests

Pristine areas in the Amazon and Siberia may expand with animal reintroductions, scientists say

Damian Carrington
Environment editor
Thu 14 Apr 2017 06:00 CEST

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Deforestation in the Brazilian Amazon - one of the few fragments of wilderness undamaged by human activities. Photograph: Florian Plech/WWF/Getty Images

Just 3% of the world's land remains ecologically intact with healthy populations of all its original animals and undisturbed habitat, a study suggests.

These fragments of wilderness undamaged by human activities are mainly in parts of the Amazon and Congo tropical forests, east Siberian and northern Canadian forests and tundra, and the Sahara. Invasive alien species including cats, foxes, rabbits, goats and camels have had a major impact on native species in Australia, with the study finding no intact areas left.

The researchers suggest reintroducing a small number of important species to some damaged areas, such as elephants or wolves - a move that could restore up to 20% of the world's land to ecological intactness.

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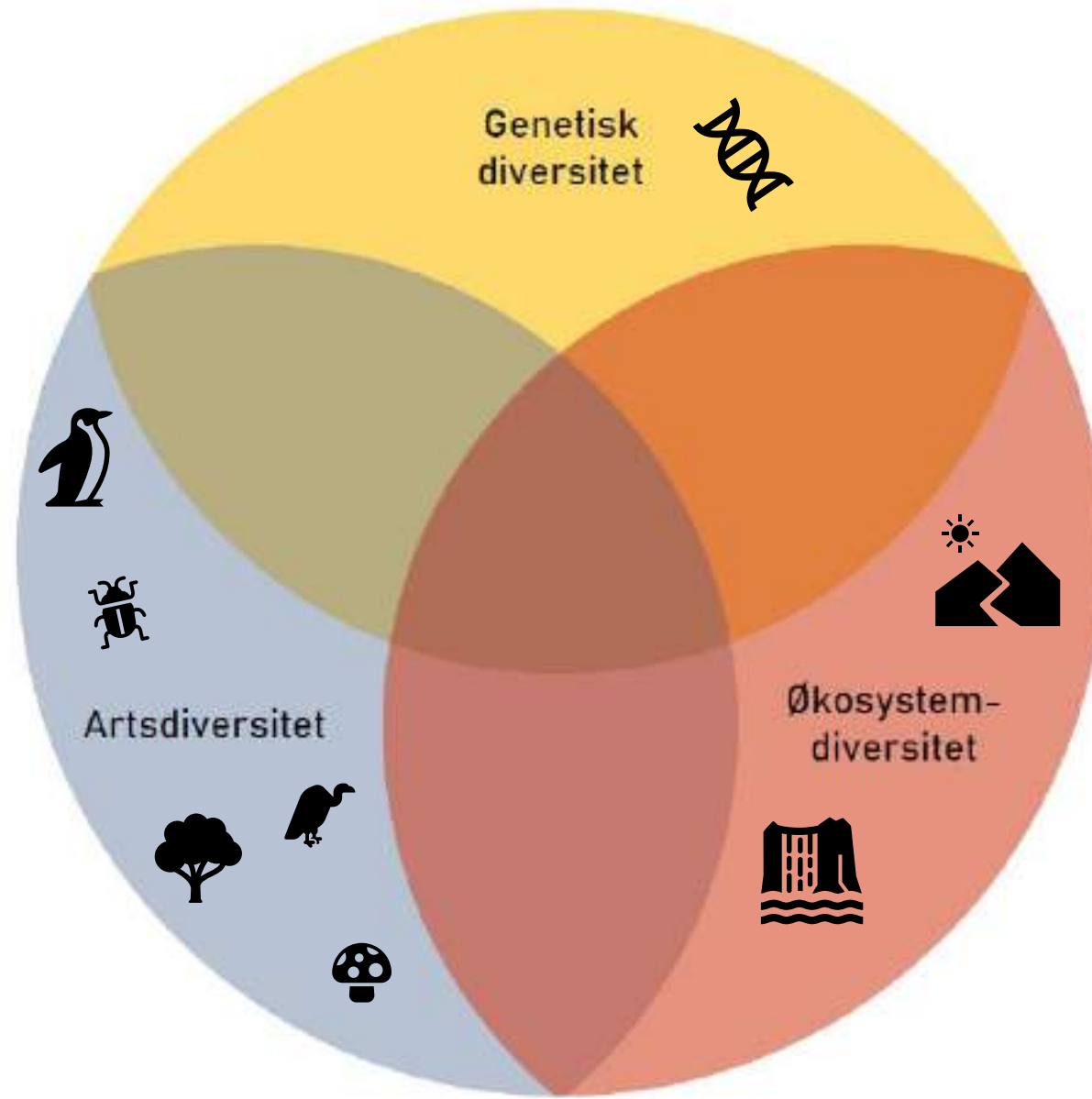
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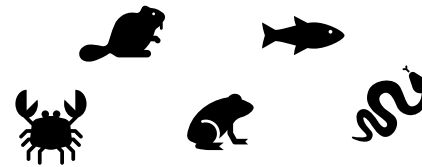
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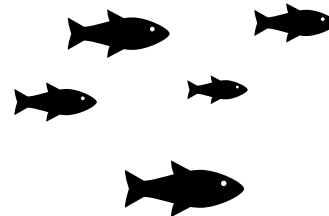
Interspecifik genetisk diversitet

- Genetisk diversitet mellem arter

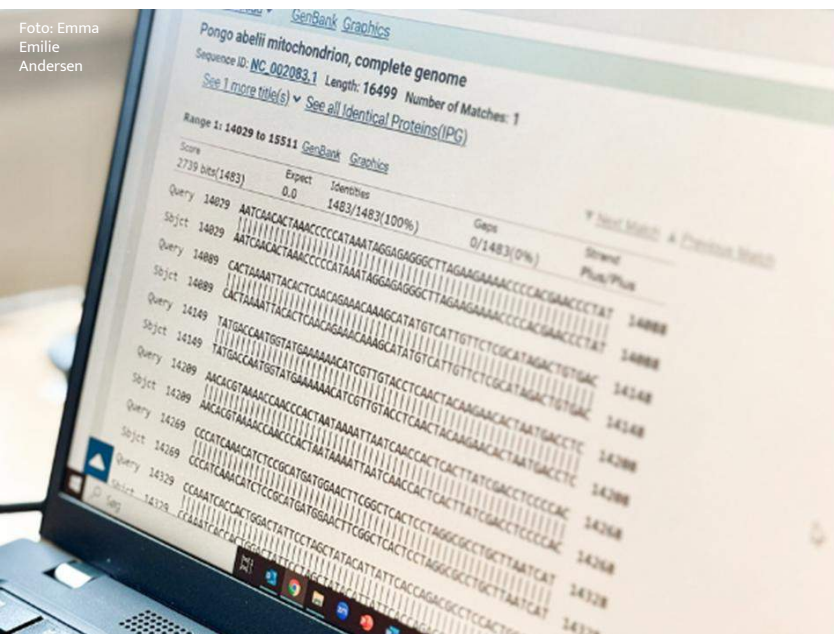


Intraspecifik genetisk diversitet

- Genetisk diversitet mellem individer af samme art
- Godt, hvis den er høj
- Skidt, hvis den er lav



Hvordan indsamler man data om genetisk diversitet?



Genetiske databaser



Feltarbejde



Videnskabelige samlinger

Foto: Emma Emilie Andersen

Foto: Jesper Sonne

Foto: Birgitte Rubæk

Hvordan beregner man genetisk diversitet?

DNA-sekvenser i en population

Individ A: **A** **C** **T** **G** **C** **G** **T** **A** **A**

Individ B: **A** **T** **T** **G** **C** **A** **C** **A** **A**

Individ C: **A** **G** **G** **T** **C** **C** **A** **G** **T**

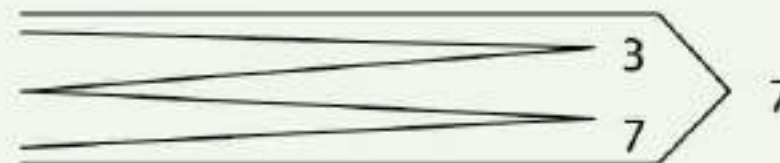
Gennemsnitlige nukleotidforskelle

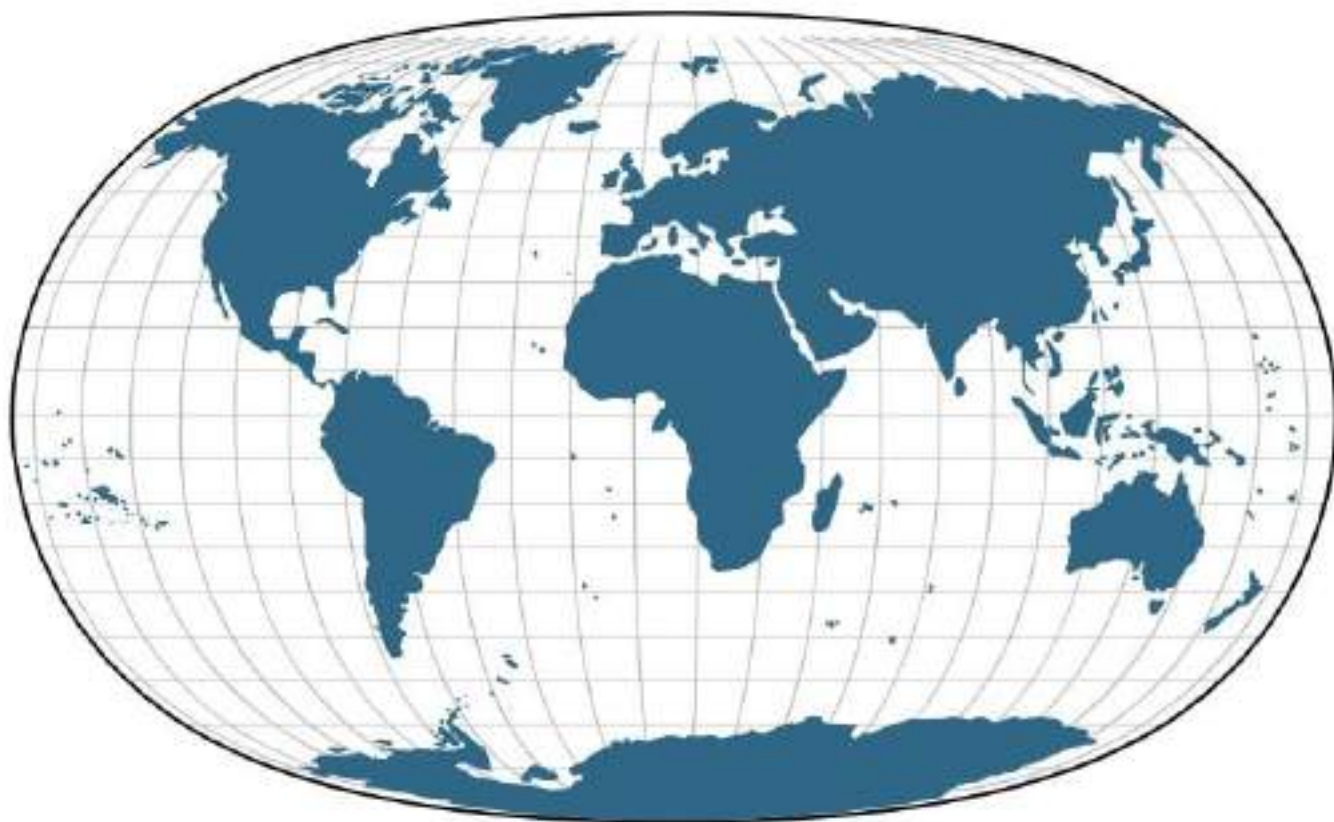
$$(3+7+7)/3 = 5,66$$

Gennemsnitlig genetisk diversitet

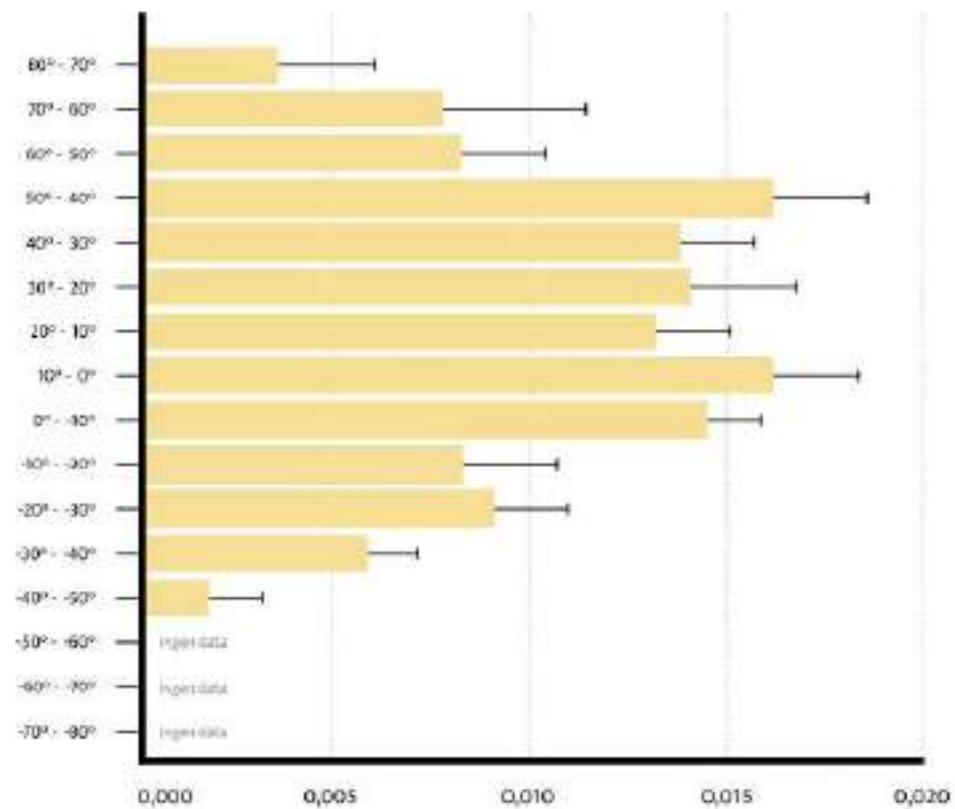
$$5,66/9 = 0,629$$

Nukleotidforskelle





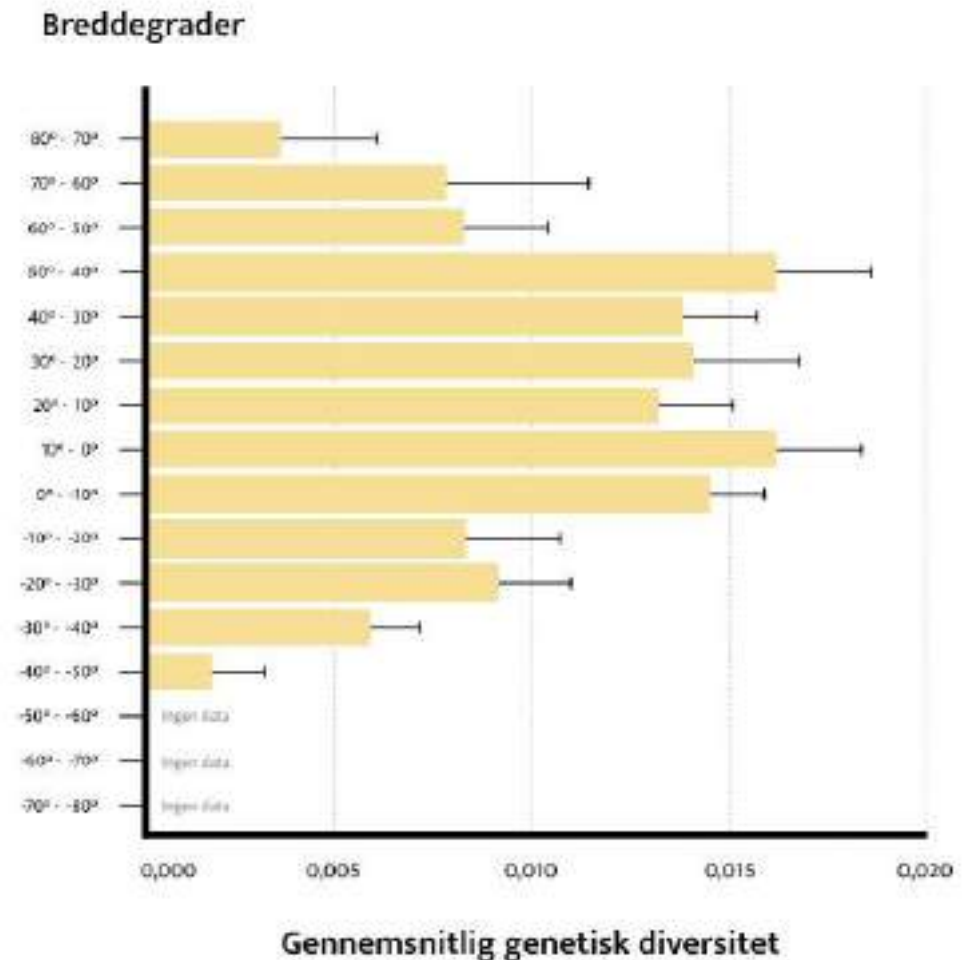
Breddegrader



Gennemsnitlig genetisk diversitet

Hvorfor er genetisk diversitet højest i tropenerne?

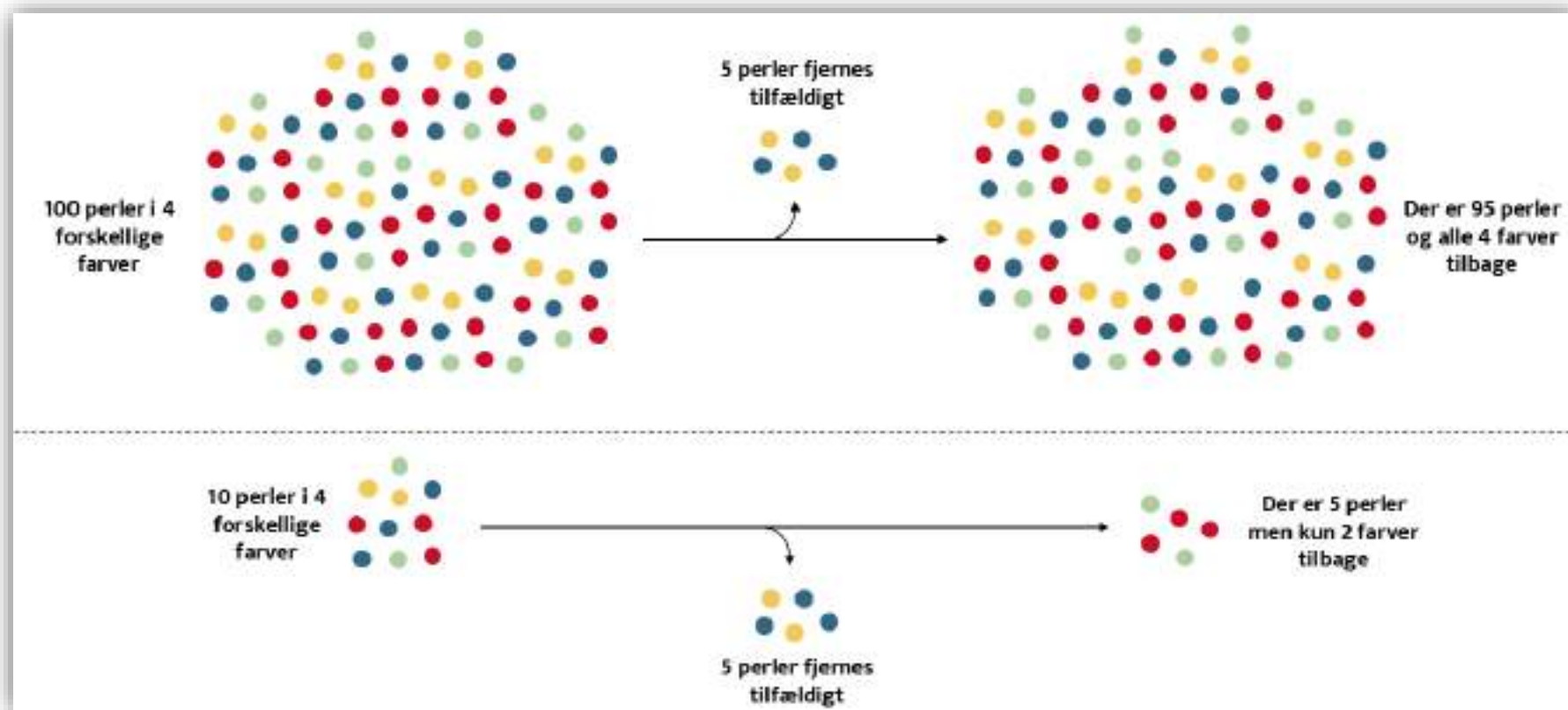
- Flere hypoteser:
 - Geologisk ældre områder
 - Klimatisk stabilitet
 - Temperatur
 - Og andre...
- Svaret er nok en kombination



De evolutionære kræfter former den genetiske diversitet på Jorden

1. Genflow
2. Genetisk drift
3. Mutationer
4. Naturlig selektion

De evolutionære kræfter former den genetiske diversitet på Jorden



Genetisk drift





Makrogenetik: Et nyt forskningsområde



Baseret på 92.801 mitokondrielle sekvenser fra >4.500 arter af pattedyr og padder.

“In science, it’s rare that a new idea comes along that stops people in their tracks. For ecologists, this has just happened...”

Bill Laurence, 11. oktober 2016

Genetisk diversitet

UNDERVISNINGSFORLØB

Helt nyt undervisningsforløb på
www.biodiversitetigymnasiet.dk/genetisk-diversitet/





A-niveau

Læs og gennemgå fagtekst

Fokuser særligt på beregning af genetisk diversitet (figur 2) og afsnit 4 om, hvordan den genetiske diversitet fordeler sig på Jorden.

Lav øvelsen 'Beregn den genetiske diversitet'

Her lærer eleverne, hvordan genetisk diversitet beregnes. Øvelsen er relativt lukket, og eleverne følger blot øvelsesvejledningen.

Lav aktiviteten 'Global genetisk diversitet'

Her undersøger eleverne et stort interaktivt datasæt, som viser den genetiske diversitet for pattedyr på Jorden, og skriver en rapport om emnet. I rapportskabelonen bliver eleverne guidet gennem hele undersøgelses- og skriveprocessen.

Valgfrit:

Brug www.globalgenetik.dk som værktøj til videre undersøgelser, faglige diskussioner i klassen eller i større skriftlige opgaver.



Genetisk diversitet

FAGTEKST

Fag
Biologi og
bioteknologi

Antal
normalsider
6,5

Skrivet af
Center for Makroøkologi,
Evolution og Klima



ARTICLE

BIODIVERSITY

An Anthropocene map of genetic diversity

Andrea Miraldo,^{1*} Sen Li,² Michael K. Borregaard,³ Alexander Pirro-Rodrigues,⁴ Stryer Gopalakrishnan,⁵ Mirnesa Ritzmann,⁶ Zhibang Wang,^{4,7} Carsten Rahbek,^{1,8} Katharine A. Martin,⁹ David Nogues-Bravo¹⁰

The Anthropocene is witnessing a loss of biodiversity, with well-documented declines in the diversity of ecosystems and species. For intraspecific genetic diversity, however, we lack even basic knowledge on its global distribution. We generated 52,501 mitochondrial sequences for >4500 species of terrestrial mammals and amphibians, and found that genetic diversity is 2.7% higher in the tropics than in nontropical regions. Overall, habitats that are more affected by humans hold less genetic diversity than wilder regions, although results for mammals are sensitive to choice of genetic locus. Our study associates geographic coordinates with publicly available genetic sequences at a massive scale, yielding an opportunity to investigate both the drivers of this component of biodiversity and the genetic consequences of the anthropogenic modification of nature.

Intraspecific genetic diversity, as the amount of genetic variation among individuals within a species, provides the critical basis for evolutionary change (1, 2), such as adaptation to new environmental conditions. Because it both reflects and influences processes at the population (3, 4), species (5, 6), community (7), and ecosystem levels (8, 9), genetic diversity is often considered the most fundamental dimension of biodiversity (10). Although the global distribution of species and ecosystems and their responses to global change have been intensively investigated in recent decades (11–14), the global distribution of intraspecific genetic diversity is still largely unknown (15). Genetic diversity has already diminished for many species as a result of abrupt climate fluctuations and human activity since the Late Quaternary (16), and this trend may be accelerating today. Knowledge of the global distribution of genetic diversity is therefore of critical importance if we want to fully understand the long-term impacts of human-induced global changes on diverse and least well-known genetic diversity, evaluate the potential of species to adjust to global change in the Anthropocene, and ultimately to succeed in halting biodiversity loss. Indeed, genetic diversity has recently been identified as an essential biodiversity variable (17) required to monitor biosphere integrity, one of the nine environmental planetary boundaries within which humanity can safely operate (18).

Most of the current knowledge about the spatial distribution of intraspecific genetic diversity comes from the results of phylogeographic studies accumulated over the past 50 years. Although these studies have reported some emergent spatial patterns of genetic diversity at regional scales (19, 20), few regions have been studied as intensively as temperate Europe and North America (21), and truly global patterns thus remain to be identified. However, millions of genetic sequences from a diverse array of studies have been deposited in public repositories during the same period (>100 million in GenBank alone), constituting an exceptional source of primary genetic data that could be used to explore global geographical patterns. While impossible in nature, the majority of these sequences are not accompanied by geographic coordinates (>80% of sequences in GenBank), and their integration with other biodiversity information would require manually reviewing the thousands of individual papers in which they are published.

Here, we took advantage of sequence data available in the GenBank and NCBI E-utilities and derived biogeographic tools to reveal the global distribution of genetic diversity (22). We linked geospatial coordinates to a total of 52,501 mitochondrial sequences (21,039 for amphibians and 31,462 for terrestrial mammals), representing 38% and 23% of available sequences for amphibians and mammals, respectively. Using both cytochrome *b* (*cytb*) sequences, we performed species-specific sequence alignments for all species and calculated nucleotide diversity π sites for each species through pairwise comparison of mitochondrial aligned sequences (23), with sequences from 3000 species. The mean coverage number of genetic mutations globally (Fig. 1), we calculated the genetic diversity each equal area grid cell (1–100,000 km²) by averaging nucleotide diversity per site across all species (24).

The global map of genetic diversity for mammals and amphibians together (Fig. 1) shows that the tropical Andes and Amazonia harbor some of the highest levels of genetic diversity (40th percentile: ~6000; 5g, 200). Other regions with high genetic diversity include the subtropical parts of South Africa for mammals (90th percentile: ~0.016) and eastern parts of the Sino-Japanese region for amphibians (80th percentile: ~0.022; 5g, 100). Within the temperate regions of the planet, western North America also contains high levels of genetic diversity, coinciding with the high mammalian species richness there (25), whereas eastern South America harbors high levels of genetic diversity to a significant extent in the global center of speciation and species richness for mammals (26). These patterns are robust to alternative tests to sampling intensity, as demonstrated by simulation analysis (27), but the high variability of genetic diversity across grid cells with low sample size requires a cautious interpretation of local patterns. The same analysis based on an alternative gene for mammals, cytochrome oxidase subunit 1 (*cytb*), sequence across 3400 species, shows that although genetic diversity values between land are not correlated for individual grid cells ($r = 0.094$, $P = 0.04$; Fig. 1), they are highly congruent across latitudinal bands ($r = 0.70$, $P = 0.004$; Fig. 2b).

Sequence availability and geographic coverage vary greatly across the globe. The maps of ignorance (Fig. 2 and Fig. S3) illustrate the spatial distribution of key gaps in both types of coverage. Unsurprisingly, the majority of knowledge comes from western Europe, North America, and for East Asia, plus individual regions that have recently been the focus of much biogeographic and phylogeographic research, such as Madagascar.

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ARTICLE

<https://doi.org/10.1038/s41467-020-16444-3> **OPEN**

Evolutionary history and past climate change shape the distribution of genetic diversity in terrestrial mammals

Spyros Theodoridis^{1,2}, Damien A. Fordham^{1,2}, Stuart C. Brown^{1,2}, Sen Li^{1,3}, Carsten Rahbek¹ & David Nogues-Bravo^{1,2,4}

Knowledge of global patterns of biodiversity, ranging from intraspecific genetic diversity (GD) to taxonomic and phylogenetic diversity, is essential for identifying and conserving the processes that shape the distribution of life. Yet, global patterns of GD and its drivers remain elusive. Here we assess existing biodiversity theories to explain and predict the global distribution of GD in terrestrial mammal assemblages. We find a strong positive covariation between GD and interspecific diversity, with evolutionary time, reflected in phylogenetic diversity, being the best predictor of GD. Moreover, we reveal the negative effect of past rapid climate change and the positive effect of inter-annual precipitation variability in shaping GD. Our models, explaining almost half of the variation in GD globally, uncover the importance of deep evolutionary history and past climate stability in accumulating and maintaining intraspecific diversity, and constitute a crucial step towards reducing the Wallacean shortfall for an important dimension of biodiversity.

Science

GENETIC GEOGRAPHY

Global map of genetic diversity

An Anthropocene map of genetic diversity

Miraldo, A., Li, S., Borregaard, M., Pirro-Rodrigues, A., Gopalakrishnan, S., Ritzmann, M., Wang, Z., Rahbek, C., Martin, K., and Nogues-Bravo, D.

1220 | 9 SEPTEMBER 2019 | VOL. 353 | DOI:10.1126/science.1252001

Andrea Miraldo *et al.*, An Anthropocene map of genetic diversity. *Science* **353**, 1532-1535 (2016).

nature COMMUNICATIONS

ARTICLE

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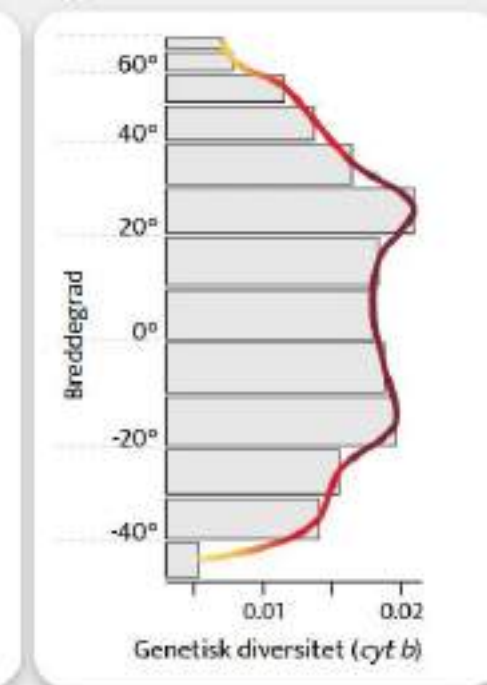
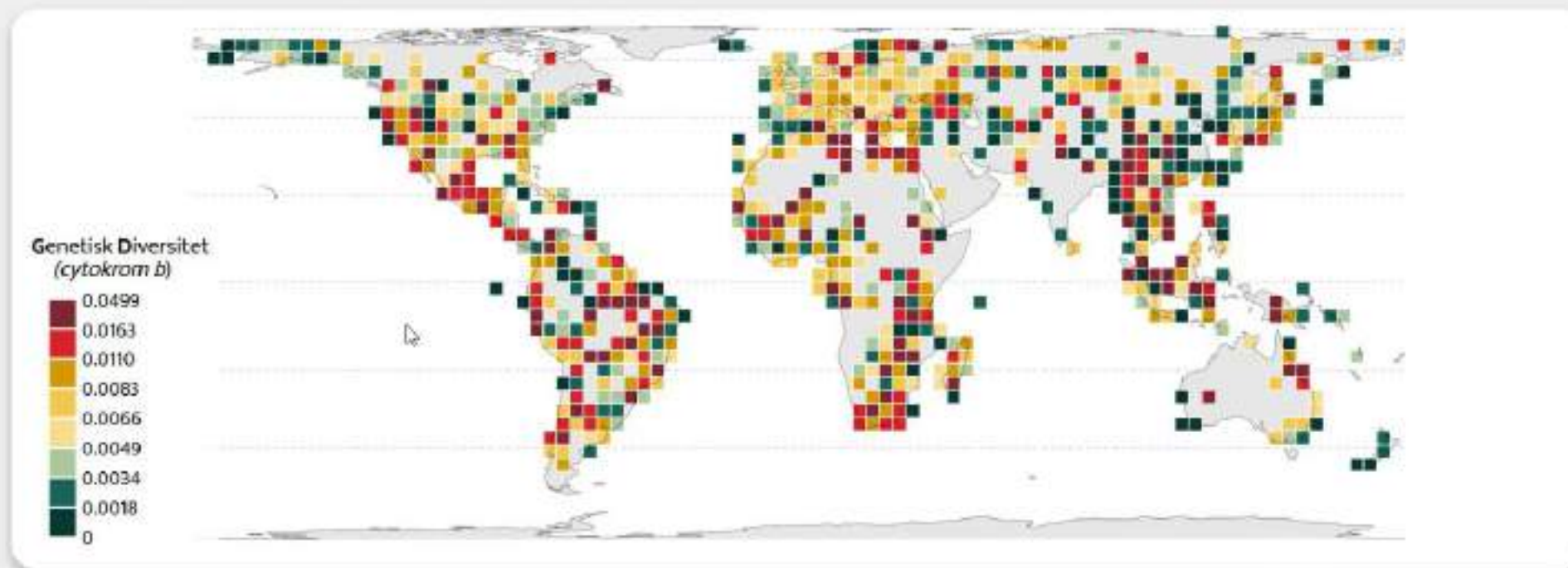
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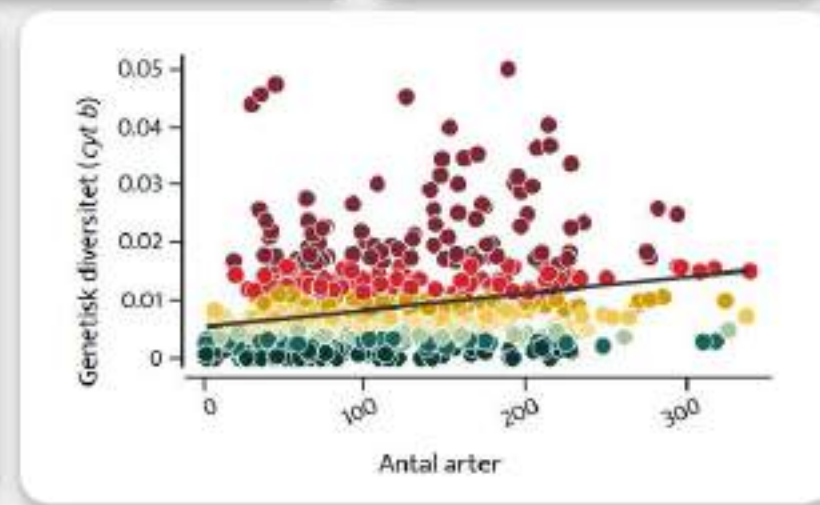
Genetisk diversitet

Undersøg den genetiske diversitet for pattedyr på global skala

[Om siden](#)



Geografisk skala	Datafilter	Variable
<input type="checkbox"/> Kvadrater	<input type="checkbox"/> Alle data	<input type="checkbox"/> Artsrigdom
<input type="checkbox"/> Regioner	<input type="checkbox"/> Filtrede data	<input type="checkbox"/> Årligt temperaturgennemsnit
		<input type="checkbox"/> Primærproduktion





DNA-sekvenser i en population

Individ A: A C T T C C G T A A
 Individ B: A T T T C C A C A A
 Individ C: A G G T C C G A A T

Nukleotidforskelle

Gennemsnitlige nukleotidforskelle
 $(3+7+7)/3 = 5,66$
 Gennemsnitlig genetisk diversitet
 $5,66/9 = 0,629$

Læsevejledning

> *Mustela_nivalis* AB564130
 Navnet på datafilen

Nukleotidets position → 822

Nukleotid uden ændring → TTT

Nukleotid med ændring → TTT

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> *Mustela_nivalis* AM258885

ATGACCAACATTCGTAAACTCACCCTGACCAAAATCATCAACAACTCATTGACCTCCC⁶⁶CGCTCCATCAAACATCTCAGCATGATGAACTTCGGCTCCC

TTCTCGGAATCTGCCTTATTATTAGATTCTTACAGGTTATTTTTAGCCATACACTATACATCAGATACAGCCACAGCCTTTTCATCAGTCACCCACATCTGTCCG

AGACGTCAACTACGGCTGAATTATCCGATACATACATGCAAACGG²⁵⁸AGCTTCCATGTTCTTTATTGCTTATTCTACACGTTAGGACGAGGCTTATATTAGGTTCT

TATATATTCTCCGAAACATGAAACATCGGCATTATCTTATTATTCGCAGTCATAGCAACTGCATTATAGGTTACGTTTACCATGAGGACAAATATCATTTTGAG

GAGCAACCGTAATTACCAACTTACTATCCGCTATTCGGTATATTGGAACCAACCTGTAGAATGAATCTGAGGGGATTTTCAGTAGACAAAGCCACCT⁵²³TAACGGC

ATTCTTCGCTTTCATTTCATCCTACCCTTTCATCTCAGCACTAGCAGCAGTCCACCT⁴⁶⁸CTATTCTCCACGAAACAGGGTCTAACAACCTTCAGGAATCCCA

TCCGACTCTGACAAAATCCCATTCACCCTTATTATACCATCAAAGACATCCCTAGGTGCCCTATTCTCATTCTAACA⁵⁹²CTAATACTATTAGTACTATTCTCACCTG

ACTTACTAGGAGACCCAGACAACACTACATCCCGCCAACCCCTCAAT⁷⁸⁹TACACCTCCACACATTAAGCCCGAG⁷¹⁴GTGATACTTCTTATTTCGCATACGCTATCTTACGATC

CATCCCAACAAATTAGG⁸⁶⁷AGGAGTACTAGCCTTAGTCTTCTCCATCTAGTCTTAGCCATATCCCCCTACTCCATACCTCAAACAACGAAGCATGATATCCCGC

CCACTAAGTCAATG⁹⁶⁹TTATTCTGATTATTGGTAGCCGACCTCCTCACTTTAACTGAATTGGCGCCAACCGGTAGAACACCCATTGTCT⁸¹³ACTATCGGCCAACTAG

CCTCAATCCTCTACTTCATGATTCTCCTGGTCTCATACTATCACCAGCATTATCGAAAATAACATATTAATAATGAAGA¹⁰⁴⁵

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Klasse/hold: _____

Navn: _____

Rapport om
Genetisk diversitet og temperaturhypotesen
 Denne rapport tager udgangspunkt i et forskningsstudie, som undersøger fordelingen af genetisk diversitet på hele Jorden.

A Skriv en kort introduktion, hvor du med dine egne ord forklarer emnet og teorien bag forskningsstudiet.
 Du kan fx komme ind på: Genetisk diversitet, pattedyr, typer af data, cytotrom b, metoder, dataindsamling, geograf, måleusikkerheder.


Introduktion (udfyld)

B Beskriv histogrammet øverst til højre på www.globalgenetik.dk. Hvad viser det?
 Beskrivelse (udfyld)

Biodiversitetsforskere har flere hypoteser om, hvorfor mønstret for genetisk diversitet ser ud, som det gør. En af hypoteserne handler om, at den genetiske diversitet er højest dér på Jorden, hvor temperaturen er højest. Det kan hænge sammen med, at nogle biologiske processer kan foregå hurtigere, når der er varmt, fx mutationer i DNA.

Udnyt denne hypotese ud fra histogrammet.
 Du kan fx komme ind på: Temperatur, breddegrader, klimazoner, biologisk variation, måleusikkerheder, fejlkilder.

Side 1

Biodiversitet i gymnasiet 

Eksempel på udfyldt rapport med bud på korrekte svar - Til læreren

Ekstraopgave
Andre faktorer end temperatur?
 I biologiens verden er det sjældent kun én faktor, fx temperatur, som kan forklare det hele. Hvilke andre faktorer end temperatur kan have betydning for den genetiske diversitet? Det skal du undersøge nu.


f Vælg 'Regioner' og 'Årligt temperaturgennemsnit' og klik på den region i verden, hvor Sahara-ørkenen befinder sig. Den hedder 'Saharo-Arabian' i datasættet. Find datapunktet for regionen i punktdiagrammet nederst til højre. Beskriv punktdiagrammet og hvad det viser. Hvad kan være mulige forklaringer på regionens placering i diagrammet?

Punktdiagrammet viser sammenhængen mellem det årlige temperaturgennemsnit i de 11 regioner (x-aksen) og deres gennemsnitlige genetiske diversitet (y-aksen). Ligesom på den forrige figur, findes her en positiv sammenhæng mellem temperatur og genetisk diversitet. Det punkt, som vi nu skal undersøge, har dog en meget lavere genetisk diversitet (0.0113), end vi ville forvente.

Mulige forklaringer kan være:

- Sahara-Arabian-regionen er meget tør. Vand er nødvendigt for at planter kan vokse (primærproduktion), og mangel på vand betyder derfor mindre føde til dyr længere oppe i fødekæden. Det betyder, at der ikke er optimale forhold for liv i denne region, hvilket kan forklare den lave genetiske biodiversitet.
- Genetisk drift fører altid til tab af genetisk diversitet over tid, og tabet vil være større, jo mindre populationen er. Måske har populationerne været små i denne region?
- Der er få forskellige typer habitat, hvilket giver en lille biodiversitet.
- En stor ørken kan være besværlig for visse dyr at bevæge sig rundt i, hvilket resulterer i meget lidt genflow. Det kan forårsage lav genetisk biodiversitet. Er en bestemt art fx afhængig af oaser med vand i ørkenen, så kan den være bundet til små områder og vil ikke sprede sig særlig meget.
- Måske har mennesker jaget eller på en anden måde påvirket dyrene, så deres populationer blev små, og det har påvirket den genetiske diversitet.

Side 4

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I GYMNASIET



Og mød os
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