

Varijabilnost mitogenoma goveda

Marić, Katarina

Master's thesis / Diplomski rad

2024

Degree Grantor / Ustanova koja je dodijelila akademski / stručni stupanj: **University of Zagreb, Faculty of Agriculture / Sveučilište u Zagrebu, Agronomski fakultet**

Permanent link / Trajna poveznica: <https://um.nsk.hr/um:nbn:hr:204:022446>

Rights / Prava: [In copyright](#)/[Zaštićeno autorskim pravom.](#)

Download date / Datum preuzimanja: **2024-11-28**



Repository / Repozitorij:

[Repository Faculty of Agriculture University of Zagreb](#)



SVEUČILIŠTE U ZAGREBU
AGRONOMSKI FAKULTET

VARIJABILNOST MITOGENOMA GOVEDA

DIPLOMSKI RAD

Katarina Marić

Zagreb, srpanj, 2024.

**SVEUČILIŠTE U ZAGREBU
AGRONOMSKI FAKULTET**

Diplomski studij:

Genetika i oplemenjivanje životinja

VARIJABILNOST MITOGENOMA GOVEDA

DIPLOMSKI RAD

Katarina Marić

Mentor:

doc. dr. sc. Vladimir Brajković

Zagreb, srpanj, 2024.

SVEUČILIŠTE U ZAGREBU
AGRONOMSKI FAKULTET

**IZJAVA STUDENTA
O AKADEMSKOJ ČESTITOSTI**

Ja, **Katarina Marić**, JMBAG 0178119537, rođena 12.10.1999. u Novoj Gradiški, izjavljujem da sam samostalno izradila diplomski rad pod naslovom:

VARIJABILNOST MITOGENOMA GOVEDA

Svojim potpisom jamčim:

- da sam jedina autorica ovoga diplomskog rada;
- da su svi korišteni izvori literature, kako objavljeni tako i neobjavljeni, adekvatno citirani ili parafrazirani, te popisani u literaturi na kraju rada;
- da ovaj diplomski rad ne sadrži dijelove radova predanih na Agronomskom fakultetu ili drugim ustanovama visokog obrazovanja radi završetka sveučilišnog ili stručnog studija;
- da je elektronička verzija ovoga diplomskog rada identična tiskanoj koju je odobrio mentor;
- da sam upoznata s odredbama Etičkog kodeksa Sveučilišta u Zagrebu (Čl. 19).

U Zagrebu, dana _____

Potpis studenta / studentice

SVEUČILIŠTE U ZAGREBU
AGRONOMSKI FAKULTET

IZVJEŠĆE
O OCJENI I OBRANI DIPLOMSKOG RADA

Diplomski rad studentice **Katarine Marić**, JMBAG 0178119537, naslova

VARIJABILNOST MITOGENOMA GOVEDA

obranjen je i ocijenjen ocjenom _____, dana _____.

Povjerenstvo:

potpisi:

1. doc. dr. sc. Vladimir Brajković mentor

2. prof. dr. sc. Vlatka Čubrić Čurik član

3. prof. dr. sc. dr. h. c. Ino Čurik član

Zahvala

Zahvaljujem svom mentoru, Vladimiru Brajkoviću, na nesebičnom dijeljenju znanja, strpljenju i vođenju kroz svaki korak ovog istraživanja. Njegova stručnost i podrška bili su ključni za završetak mog diplomskog rada.

Također, želim izraziti duboku zahvalnost svojim roditeljima, čija je neprekidna ljubav, ohrabrenje i vjera u mene pružila neophodnu snagu i motivaciju. Posebnu zahvalnost dugujem i svojoj braći, čija su podrška i razumijevanje bili od neprocjenjivog značaja. Bez vaše pomoći, ovo postignuće ne bi bilo moguće. Hvala vam svima od srca.

Sadržaj

1. Uvod.....	1
2. Cilj istraživanja	3
3. Pregled literature	4
4. Materijal i metode	16
4.1. Materijal.....	16
4.2. Metode	18
4.2.1. Preuzimanje i evidencija mitogenoma	18
4.2.2. Poravnavanje sekvenci.....	18
4.2.3. Određivanje haplogrupa pomoću MitoToolPy softvera	18
4.2.4. Deskriptivna statistika.....	19
4.2.5. P-distanca.....	22
4.2.6. BEAST analiza.....	22
4.2.7. Izračun haplotipova i izrada median-joining mreže.....	23
4.2.8. Distribucija haplogrupa po državama	24
5. Rezultati	26
5.1. Varijabilna mjesta	26
5.2. P-distanca.....	26
5.3. Filogenetska analiza.....	27
5.4. Prikaz haplotipova median-joining mrežom.....	29
5.5. Distribucija haplogrupa.....	32
6. Rasprava.....	35
7. Zaključak.....	37
8. Popis literature	38
9. Prilozi	41
Životopis	82

Sažetak

Diplomskog rada studentice **Katarine Marić**, naslova

VARIJABILNOST MITOGENOMA GOVEDA

Cijeli mitogenom goveda kroz analizu haplotipova/haplogrupa pruža uvide u evoluciju, filogeografiju i genetičku raznolikost različitih pasmina. U ovom diplomskom radu analiziran je set novodostupnih mitogenoma u GenBank repozitoriju koji se sastojao od 670 sekvenci dužine 16338 parova baza zajedno s referentnim mitogenomom V00654 i 33 referenta mitogenoma kao predstavnike T₁, T₂, T₃, T₄, T₅, I, P, R, Q haplogrupa. Set je obuhvatio 77 pasmina raspoređenih kroz 22 države od čega su najzastupljenije Indija s 343, Kina s 271 i Mongolija s 27 jedinki. Identificirano je ukupno 1433 varijabilna mjesta od čega je 788 parsim informativnih i 645 singleton mjesta te je izračunat 481 haplotip uz visoku raznolikost haplotipova od 0.9966. Analiza p-distanci otkrila je veće razlike između određenih kineskih i indijskih pasmina, kao i između indijskih i europskih pasmina. Beast filogenetska analiza klasificirala je 334 mitogenoma u haplogrupu I₁, 119 u I₂ i 176 mitogenoma u T₃ haplogrupu kao najfrekventnije, a filogeografska distribucija navedenih haplogrupa je pokazala da u Kini 110 mitogenoma pripada haplogrupi I₁, 93 haplogrupi T₃ i 11 haplogrupi I₂, u Indiji 219 haplogrupi I₁, 105 haplogrupi I₂ i 17 haplogrupi T₃ te u Mongoliji 12 mitogenoma haplogrupi T₃, sedam haplogrupi T₂, šest haplogrupi T₄ i dva haplogrupi I₁. Također, analizom velikog broja mitogenoma haplogrupe I u Beast filogenetskom stablu uočena je pojava četiri subhaplogrupe koje su odvojene s posteriori vjerojatnošću 0.95 što bi moglo predstavljati osnovu za reklasifikaciju I₁ i I₂ u više subhaplogrupa. Ista podjela I haplogrupe na četiri subhaplogrupe potvrđena je median-joining mrežom uz jasno odvajanje od ostalih haplogrupa. Rezultati MJ mreže i filogenetskog stabla ukazali su na značajnu razliku između haplogrupa I i T₃, potvrđujući da su pasmine haplogrupe I potekle od *Bos indicusa*, dok su pasmine haplogrupe T₃ potekle od *Bos taurus*. Ova studija doprinos je razumijevanju genetičke raznolikosti i evolucijske povijesti goveda, posebno u kontekstu njihove filogeografske distribucije.

Ključne riječi: govedo, mitogenom, haplogrupa, genetska raznolikost

Summary

Of the master's thesis – student **Katarina Marić**, entitled

VARIABILITY OF THE BOVINE MITOGENOME

The whole mitochondrial genome of cattle provides insights into the evolution, phylogeography and genetic diversity of different breeds. In this thesis, a newly available set of mitochondrial genomes from the GenBank repository consisting of 670 sequences with a length of 16,338 base pairs, together with the mitochondrial reference genome V00654 and 33 mitochondrial reference genomes representing the haplogroups T1, T2, T3, T4, T5, I, P, R and Q were analysed. The set comprised 77 breeds from 22 countries, with India being the most represented with 343 individuals, followed by China with 271 and Mongolia with 27 individuals. A total of 1,433 variable sites were identified, of which 788 were parsimony informative and 645 were singleton sites. A total of 481 haplotypes were calculated, with a high haplotype diversity of 0.9966. Analysis of p-distances revealed major differences between certain Chinese and Indian breeds and between Indian and European breeds. The BEAST phylogenetic analysis classified 334 mitochondrial genomes in haplogroup I1, 119 in I2 and 176 in haplogroup T3, which is the most common. The phylogeographic distribution of these haplogroups showed that in China 110 mitochondrial genomes belonged to haplogroup I1, 93 to haplogroup T3 and 11 to haplogroup I2; in India 219 to haplogroup I1, 105 to haplogroup I2 and 17 to haplogroup T3; and in Mongolia 12 mitochondrial genomes belonged to haplogroup T3, seven to haplogroup T2, six to haplogroup T4 and two to haplogroup I1. In addition, analysis of a large number of mitochondrial genomes of haplogroup I in the BEAST phylogenetic tree revealed the appearance of four subhaplogroups separated from each other with a posterior probability of 0.95, which could form the basis for the reclassification of I1 and I2 into multiple subhaplogroups. This division of haplogroup I into four subhaplogroups was also confirmed by a median-joining network, which shows a clear separation from other haplogroups. The results of the MJ network and the phylogenetic tree indicated a significant difference between haplogroups I and T3 and confirmed that the breeds of haplogroup I descended from *Bos indicus*, while the breeds of haplogroup T3 descended from *Bos taurus*. This study contributes to the understanding of the genetic diversity and evolutionary history of cattle, especially in the context of their phylogeographic distribution.

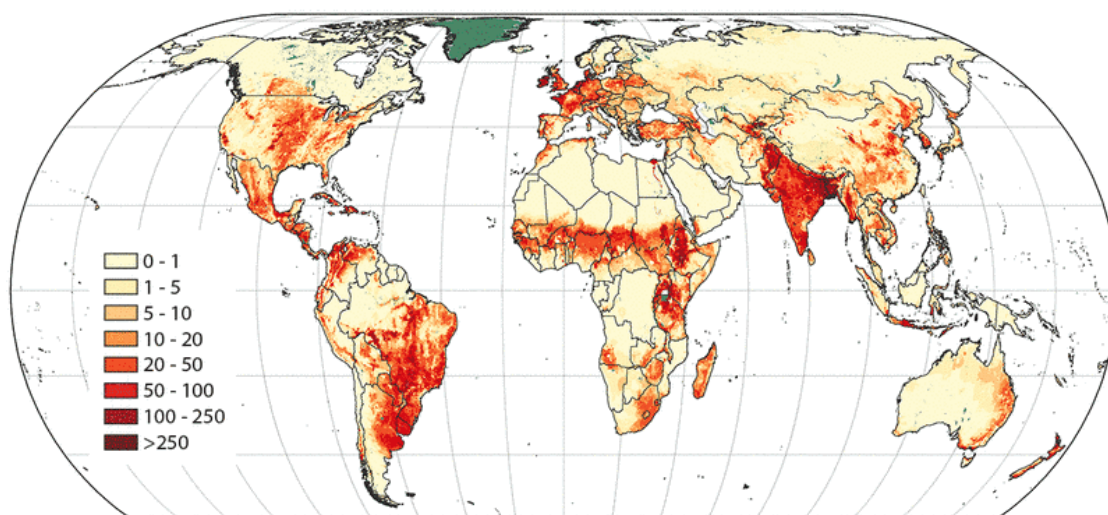
Keywords: cattle, mitogenome, haplogroup, genetic diversity

1. Uvod

Vjeruje se da je pripitomljavanje goveda počelo prije 10.000 godina, označavajući jedan od najranijih i najznačajnijih koraka u ljudskoj civilizaciji. Poznate su dvije glavne vrste goveda *Bos taurus* i *Bos indicus*. Taurin goveda (*Bos taurus*) pripitomljena su od divljeg goveda *Bos primigenius primigenius* oko 10,5 tisuća godina pr.Kr. u Plodnom polumjesecu (Helmer i sur., 2005.). Zebu (*Bos indicus*) goveda pripitomljena su od *Bos primigenius namadicusa*, 1500 godina kasnije u dolini Inda u današnjem Pakistanu (Meadow, 1993). Zebu govedo razlikuju se od taurinskih goveda (*Bos taurus*) zbog svojih jedinstvenih fizičkih karakteristika, od kojih su najistaknutije grba na ramenima i velike, spuštene uši. Ove osobine su prilagodbe koje im pomažu da prežive u vrućim i vlažnim klimama.

Moderna goveda, uključujući i taurin (*Bos taurus*) i zebu (*Bos indicus*) pasmine, imaju široku geografsku rasprostranjenost na globalnoj razini. Taurin goveda potječu iz Europe i trenutno prevladavaju, uz Europu, i u Sjevernoj Americi, Južnoj Americi, Aziji i Australiji, gdje se uzgajaju za proizvodnju mesnih i mliječnih proizvoda. Zebu goveda, poznata po svojoj otpornosti na vrućinu i prilagođenosti tropskim područjima, uglavnom se nalaze u južnoj Aziji, Africi i dijelovima jugoistočne Azije. Zemlje poput Indije, Brazila, Nigerije i Pakistana imaju značajnu populaciju zebu goveda.

Rasprostranjenost modernog goveda pod utjecajem je povijesti pripitomljavanja, ljudskih migracija, trgovine i klimatskih pogodnosti. Njihov značaj u poljoprivredi i stočarskoj proizvodnji doveo je do nastanka mnogih pasmina. Trenutno, u svijetu je poznato 1433 pasmine goveda od kojih je 174 izumrlo (CGRFA-18/21/10.2/Inf.6, 2020.).



Slika 1. Broj goveda po kilometru kvadratnom u 2015. godini
izvor: <https://www.fao.org/livestock-systems/global-distributions/cattle/en/> -
pristup 27.7.2023.

Goveda imaju vrlo važnu ulogu u današnjem društvu kao i kroz povijest. Značajan su izvor hrane, opskrbljuju visokokvalitetnim mesom i mliječnim proizvodima. Osim toga, uzgoj goveda utječe na život milijuna ljudi stvarajući prihode i mogućnosti zapošljavanja u mesnoj i mliječnoj industriji. Nutritivne prednosti goveđih proizvoda, uključujući proteine, vitamine i minerale, doprinose uravnoteženoj i hranjivoj prehrani. Goveda, također, nude vrijedne nusproizvode poput kože i raznih materijala koji se koriste u različitim industrijama. Štoviše, pravilno upravljana ispaša stoke igra ulogu u održivom upravljanju zemljištem, održavanju travnjaka i promicanju bioraznolikosti. Tijekom ljudske povijesti, goveda su postala duboko ukorijenjena u kulturne tradicije dok su služila i kao predmet istraživanja u medicinske i znanstvene svrhe. Sve u svemu, goveda imaju višestruk značaj koji se proteže na različite aspekte ljudskog života, podržavajući gospodarstvo, zdravlje i društvenu dobrobit.

Očuvanje genetske raznolikosti kod goveda usmjereno je na očuvanje raznolikosti genetskih svojstava unutar populacije. Time je omogućena prilagodba goveda na različita okruženja i uvjete, otpornost na bolesti i održavanje općeg zdravlje populacije. To uključuje očuvanje tradicionalnih pasmina goveda, krioprezervaciju genetskog materijala, kontrolirano križanje te korištenje genetskog testiranja i upravljanja podacima. Kod domaćih životinja i njihovih bliskih srodnika, mtDNA sekvence su bile prvi izvor molekularnih informacija korišten u počecima analiza drevne DNA te se i danas koristi kao jedan od glavnih molekularnih markera za proučavanje genetske raznolikosti.

Mitogenom je mala, kružna molekula DNA koja kodira 37 gena, a prepoznatljiva je po družini otprilike 16000 bp. Osim toga, mitogenome se nasljeđuje isključivo od majke, što omogućuje istraživačima da prate majčinu stranu i proučavaju protok gena. Raznolikost mitohondrijskog genoma može se opisati na tri razine: položaj nukleotida, haplotipovi (jedinostveni nizovi nukleotida) i haplogrupe (viša razina srodnih skupina među haplotipovima) (Dorji i sur. 2022.). Proučavanje mtDNA ima široku daljnju primjenu u raznim područjima npr. forenzika, proučavanje demografske dinamike, genetske povijesti ili migracija. Kroz ovaj rad bit će prikazana varijabilnost mitogenoma te klasifikacija mitogenoma na haplogrupe što je uvelike povezano sa geografskom distribucijom.

2. Cilj istraživanja

Posljednjih nekoliko godina varijabilnost i filogeografska analiza mitogenoma goveda prikazana je kroz metaanalize 802 sekvence mitogenoma rada Čubrić Čurik i sur., (2022) i 1833 sekvence mitogenoma rada Dorji i sur., (2022). Preliminarnim pregledom repozitorija GenBank (Clark i sur., 2016), utvrđena je prisutnost novih 670 mitogenoma koji nisu analizirani kroz kontekst navedenih metaanaliza.

Ciljevi ovog radu su:

- Analiza varijabilnosti novih mitogenoma pasmina goveda dostupnih u GenBank (Clark i sur., 2016) repozitoriju.
- Analiza filogenetskih odnosa haplotipova/haplogrupa novih mitogenoma usporedno s utvrđenim predstavnicima haplogrupa kod goveda.
- Prikazati filogeografsku distribuciju haplogrupa mitogenoma analiziranih uzoraka.

3. Pregled literature

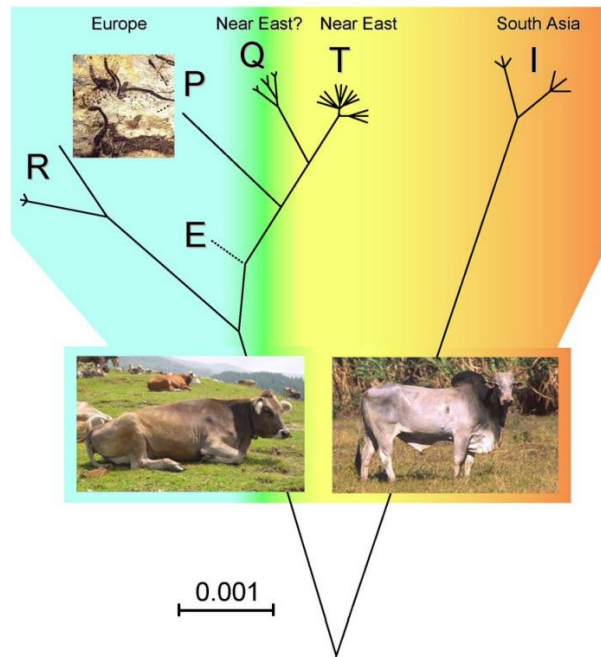
Pregledom dostupne literature odabrano je jedanaest važnijih radova koji prikazuju varijabilnost mitogenoma goveda (Tablica 1.). Radovi obuhvaćaju interval od 2009. do 2022. godine, a analizirane su cijele sekvence mitogenoma i D-loop kao molekularni markeri. Ukupno je identificirano 19 haplogrupa kod goveda analizirajući varijabilnost mitohondrijske DNA.

Tablica 1. Radovi koji prikazuju varijabilnost mitogenoma s osnovnim informacijama i rezultatima

Rad	Analizirana područja	Broj jedinki	Utvrđene haplogrupe mitogenoma
Achilli i sur. (2008.), D-loop	J Europa i Bliski Istok	106	T, T1, T1a, T2, T1'2'3, T3, T3a, T4, T5, Q, P, I, I1, I2
Achilli i sur. (2009.) mitogenom, D-loop	Italija	619	T1, T2, T3, Q, R
	Francuska	50	T1, T2, T3
	Švicarska	10	T3
Zhang (2013.) mitogenom	Kina	18	T1, T2, T3, T1'2'3, C
Olivieri i sur. (2015.) mitogenom	Delta Nila	31	T1, T2, T3, Q1
Chen i sur. (2018.) mitogenom	Kina	107	T2, T3, T4, I1a
	Afrika	12	T1
	Eurpa	11	
	Iran	7	T2
	Koreja	6	P, T2, T3
	Zebu govedo	4	
Xia i sur. (2018.) d-loop	Kina	1105	T1a, T2, T3, T4, T5, I1, I2
Xia i sur. (2019.) mitogenom	Kina	129	T, T1, T2, T3, T4, T5, I1, I2
Verdugo i sur. (2019.) mitogenom	Plodni polumjesec	67	T, T1, T2, T3, I1, I2
Xia i sur. (2021.) mitogenom	S i I Azija	170	T3
	Istočna Azija	6	T4, T3
Čubrić Ćurik i sur. (2022.) mitogenom	JI Europa	802	I, R, P, T5, T2, T3, T1, T4, T6, T7, P1, K
Dorji i sur. (2022.) mitogenom	Europa, Afrika, Azija, Australija	1883	I1, I2, T1, T2, T3, T4, T5, T6, P, Q1, Q2, I1a

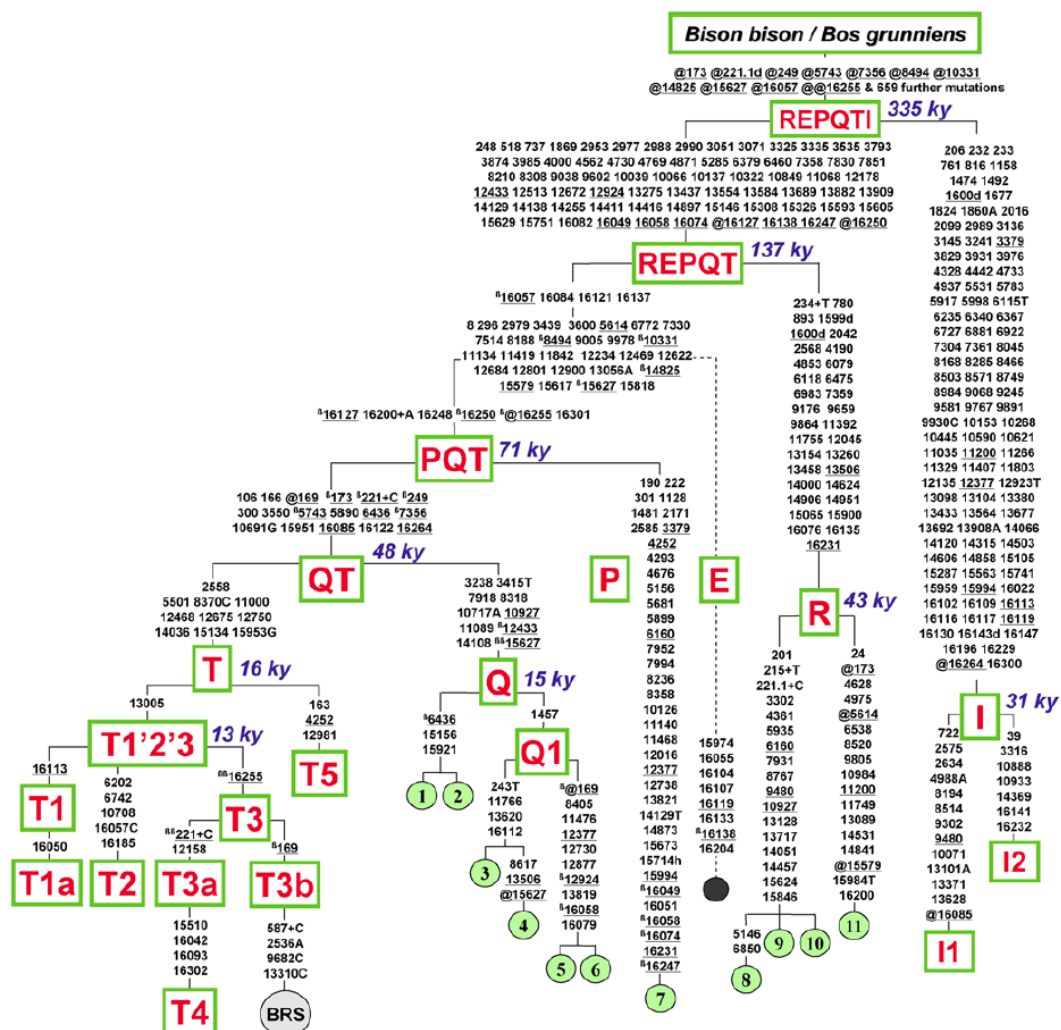
Usporedbom D-loop regije mtDNA 56 mitogenoma sa područja južne Europe i Bliskog Istoka i 50 ranije objavljenih mitogenoma, Achilli i sur. (2008.) otkrili su da većina mitogenoma pripada haplogrupama I i T koje su nastale od *Bos indicusa* i *Bos primigeniusa*. Također, filogenetskom analizom otkrili su signifikantno odvajanje haplogrupa P i Q. Studija je identificirala šest glavnih haplogrupa (T1, T2, T3, T5, I1 i I2) koje obuhvaćaju gotovo sve mitogenome opažene u modernim taurinim i zebuinim pasminama.

U radu Achilli i sur. (2009.) provedeno je istraživanje D-loop regije mtDNA (približno 840 bp) na setu od 619 mitogenoma taurinih goveda, 26 europskih pasmina, te je utvrđeno da se grupiraju unutar T haplogrupe (T1, T2, T3) bliskoistočnog porijekla. Najzastupljenija haplogrupa bila je T3, koja je obuhvatila 89,2% svih analiziranih uzoraka. Haplogrupa T1 bila je prisutna u 5,3% uzoraka, dok je haplogrupa T2 otkrivena u 3,8% uzoraka. Također, identificirano je 8 mtDNA koje se ne uklapaju u T haplogrupu. Analizom cijelog mitogenoma utvrdili su da su četiri mitogenoma, od preostalih 8, pripadnici nedavno otkrivene haplogrupe Q, sve 4 talijanske pasmine (1 s područja Toskane, 1 s područja Friuli i 2 s područja Romanja). Druga četiri mitogenoma pripadaju novoj haplogrupi R, kako je i sugerirala analiza kontrolne regije. Haplogrupa R predstavlja najstariju poznatu podjelu u mtDNA filogeniji *Bos primigeniusa*, koji je predak modernih domaćih goveda. Ta podjela dogodila se nakon duboke razdvojenosti koja je dala podrijetlo dvjema glavnim linijama, taurinskim govedima (*Bos taurus*) i zebuinskim govedima (*Bos indicus*). Filogeografski podatci ukazuju da su R mtDNA proizašli od ženskih europskih goveda, vjerojatno s talijanskog poluotoka, dok suprotno tome dostupni podaci sugeriraju da su Q mtDNA i T potgrupe (slika 2.) bile uključene u isti neolitički događaj domestikacije na Bliskom Istoku (Achilli i sur. 2009.).



Slika 2. Filogenetski prikaz mitogenoma goveda

Izvor: Achilli A, Bonfiglio S, Olivieri A, Malusa` A, Pala M, i sur. (2009) The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome. PLoS ONE 4(6): e5753. doi:10.1371/journal.pone.0005753 -pristup: 27.7.2023.



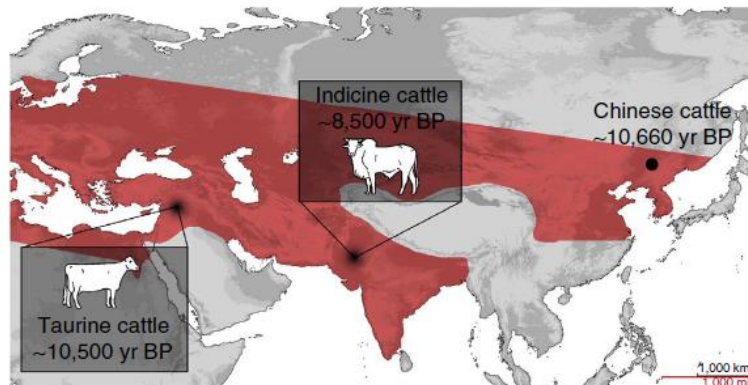
Slika 3. Stablo kompletnih sekvenci mitohondrijske DNA kod goveda

Izvor: Achilli A, Bonfiglio S, Olivieri A, Malusa^A, Pala M, et al. (2009) The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome. PLoS ONE 4(6): e5753. doi:10.1371/journal.pone.0005753 -pristup: 27.7.2023.

Slika 3. prikazuje filogenetsko stablo koje predstavlja genetske odnose između različitih haplogrupa mtDNA. Ove haplogrupe su označene različitim slovima i brojevima, a stablo prikazuje njihovu evolucijsku divergenciju i vremenske procjene (u tisućama godina, označeno s "ky" što znači tisuća godina, ili "kilo years") kada su se te grupe odvojile jedna od druge.

Rad autora Zhang (2013.) donosi morfološke i genetske dokaze o upravljanju taurin govedima u sjeveroistočnoj Kini tokom ranog holocena (slika 4). U radu su analizirani uzorci datirani metodom ugljika, određene su morfološke karakteristike, te je proučena drevna mitohondrijska DNK (mtDNA). Sekvence drevne mtDNA kineskih uzoraka uspoređene su s 26 javno

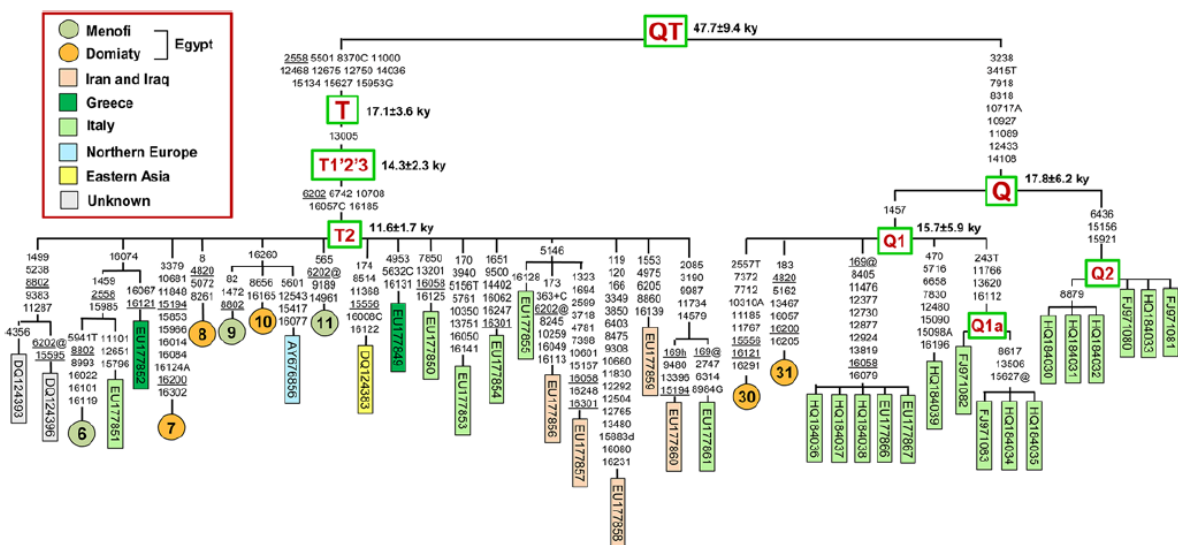
dostupnih mitogenoma modernih goveda, uključujući 14 taurina, 3 zebu goveda, 3 jaka, 3 američka bizona i 3 europska bizona. Filogenetska analiza svrstava kineske uzorke zajedno s taurin govedima, ali u nepoznatu haplogrupu. Jedna sekvenca se izdvaja od ostalih, a Zhang tu haplogrupu naziva haplogrupa C.



Slika 4. Lokacija centara domestikacije goveda u usporedbi s distribucijom aurochsa

Izvor: Zhang, H., Paijmans, J. L., Chang, F., Wu, X., Chen, G., Lei, C., ... & Hofreiter, M. (2013). Morphological and genetic evidence for early Holocene cattle management in northeastern China. *Nature communications*, 4(1), 2755. ONE 4(6): e5753. doi:10.1371/journal.pone.0005753 -pristup: 27.7.2023.

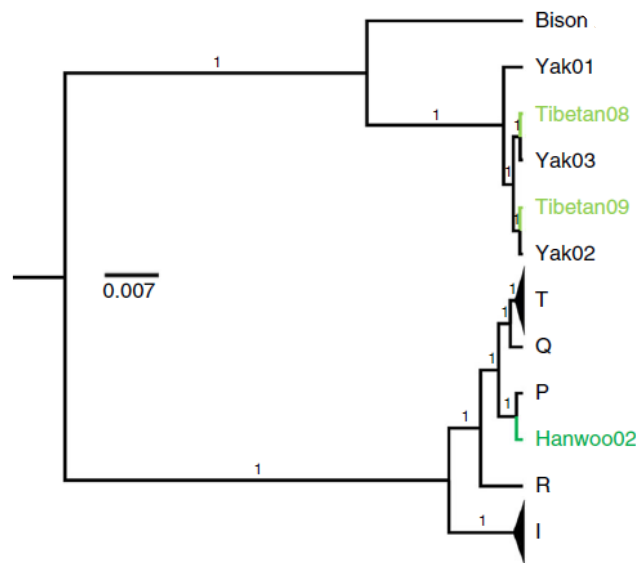
Analizom 31 mitogenoma s područja Delte Nila, Olivieri i sur. (2015.) utvrdili su prevladavanje T1 haplogrupe koja je karakteristična za afrička goveda. S nešto manjom frekvencijom pronađene su T2 i T3 haplogrupe. Navedene haplogrupe su prisutne kod obje analizirane egipatske pasmine, Menofi i Domiaty. Dva mitogenoma pripadaju rijetkoj haplogrupi Q1 koja je dotad pronađena samo kod talijanskih pasmina što doprinosi boljem poznavanju povijesti miješanja pasmina i razvoja modernih goveda. Slika 5. prikazuje filogenetsko stablo haplogrupa mitogenoma s fokusom na haplogrupe Q i T i njezine podgrupe.



Slika 5. Svjetska filogenija taurinskih haplogrupa T2 i Q

Izvor: Olivieri A, Gandini F, Achilli A, Fichera A, Rizzi E, Bonfiglio S, et al. (2015) Mitogenomes from Egyptian Cattle Breeds: New Clues on the Origin of Haplogroup Q and the Early Spread of *Bos taurus* from the Near East. PLoS ONE 10(10): e0141170. doi:10.1371/journal.pone.0141170

Rad Chen i sur. (2018.) pišu da su moderna taurinska goveda pokazala T haplogrupu i nekoliko dodatnih manjih haplogrupa (Q, P i R), dok su zebu goveda nosila samo I haplogrupu. 147 mitogenoma imalo je pokrivenost veću od 100 puta, uključujući 107 kineskih goveda, 12 afričkih goveda, 11 europskih goveda, 7 iranskih goveda, 6 korejskih goveda i 4 zebu goveda, te su usklađeni s 24 referentna mitogenoma. Filogenetske analize pokazale su da su sva istočnoazijska taurinska goveda karakterizirana T haplogrupom, osim jednog korejskog Hanwoo goveda, koje je pripadalo P haplogrupi tipičnoj za europsko pragovedo i dva tibetanska goveda, koja su nosila haplogrupe jaka, što sugerira regrutiranje materinskog roda pragoveda i jaka u istočnoazijskih goveda (slika 6.). Istočnoazijska taurinska goveda uglavnom su pripadala T3 i T2 haplogrupama, goveda s Bliskog istoka pripadala su T2 haplogrupi, afrička goveda pripadala su T1 haplogrupi, a samo jedan tibetanski pojedinac pripadao je T4 haplogrupi. Unutar linije *B. indicus*, kineska zebu goveda uglavnom su pripadala I1a, novoj podhaplogrupi unutar I1 koja se granala u obliku zvijezde, sugerirajući njen brzi populacijski rast iz jedne početne sekvence.

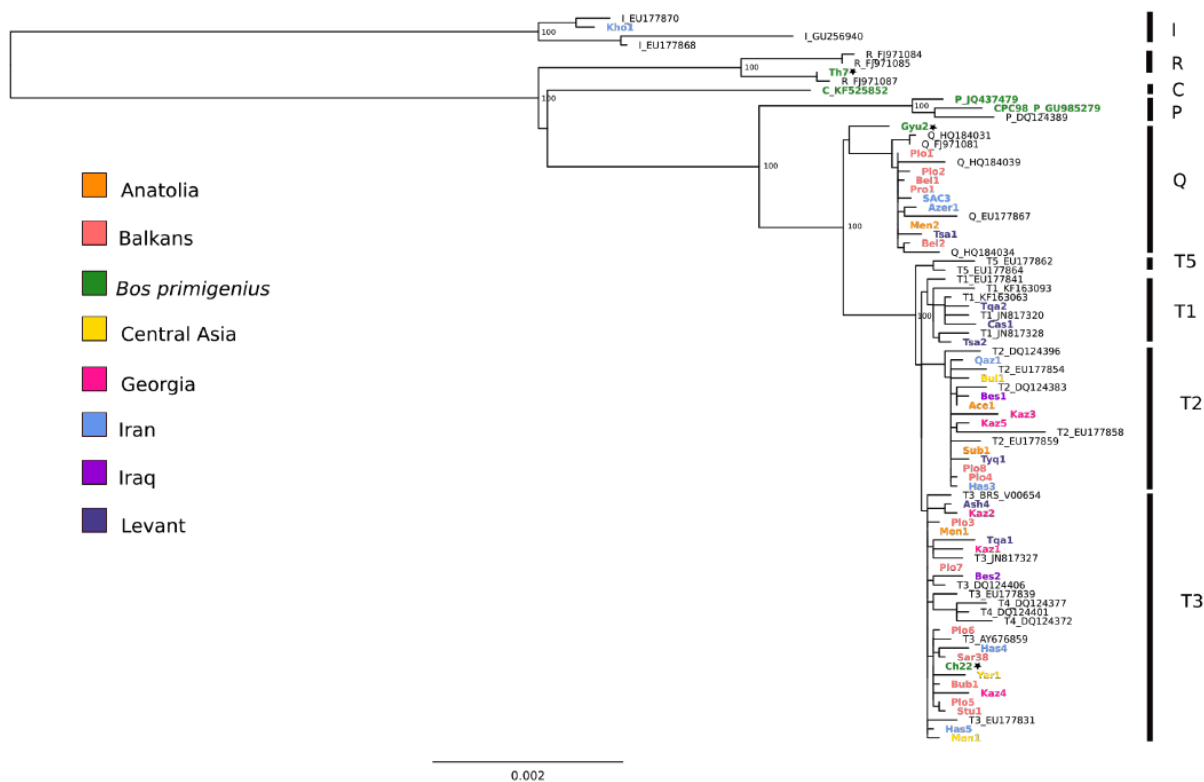


Slika 6. Ukorijenjeno filogenetsko stablo Maximum likelihood koje detaljno prikazuje odnose među svim dostupnim haplogrupama goveda I, P, Q, R i T mtDNA, američkim bizonom mtDNA i tri mitogenoma jaka.

Izvor: Chen, N., Cai, Y., Chen, Q., Li, R., Wang, K., Huang, Y., ... & Lei, C. (2018). Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. *Nature Communications*, 9(1), 2337.

U radu Xia i sur. (2019.) analizirana je genetska raznolikost Yunling goveda koja su nastala križanjem Brahman i Murray Grey goveda te lokalnim Yunnan govedima tijekom više od 30 godina. Genetska raznolikost ove pasmine ispitivana je korištenjem mitogenoma. Studija je otkrila da Yunling goveda sadrže nekoliko haplogrupa, uključujući glavne taurinske haplogrupe T, T1, T2, T3, T4, T5 i indicinske haplogrupe I1 i I2. Ova raznolikost haplogrupa ukazuje na složenu evolucijsku povijest i značajnu genetsku raznolikost pasmine.

Verdugo i sur. (2019.) analizirali su 67 drevnih genomskih uzoraka goveda kako bi rekonstruirali povijest i dinamiku populacija u Plodnom polumjesecu. Analiza haplogrupa mtDNA otkrila je prisutnost nekoliko ključnih haplogrupa, uključujući taurinske haplogrupe T, T1, T2 i T3, te indicinske haplogrupe I1 i I2. Ovi rezultati ukazuju na složenu genetsku povijest drevnih goveda u regiji Plodnog polumjeseca, uključujući miješanje i brze promjene populacija. Također, rad otkriva da je regija Plodnog polumjeseca bila mjesto intenzivne promjene genetičkog sastava goveda tijekom vremena, što ukazuje na brze promjene u stočarstvu i migracijama ljudi.



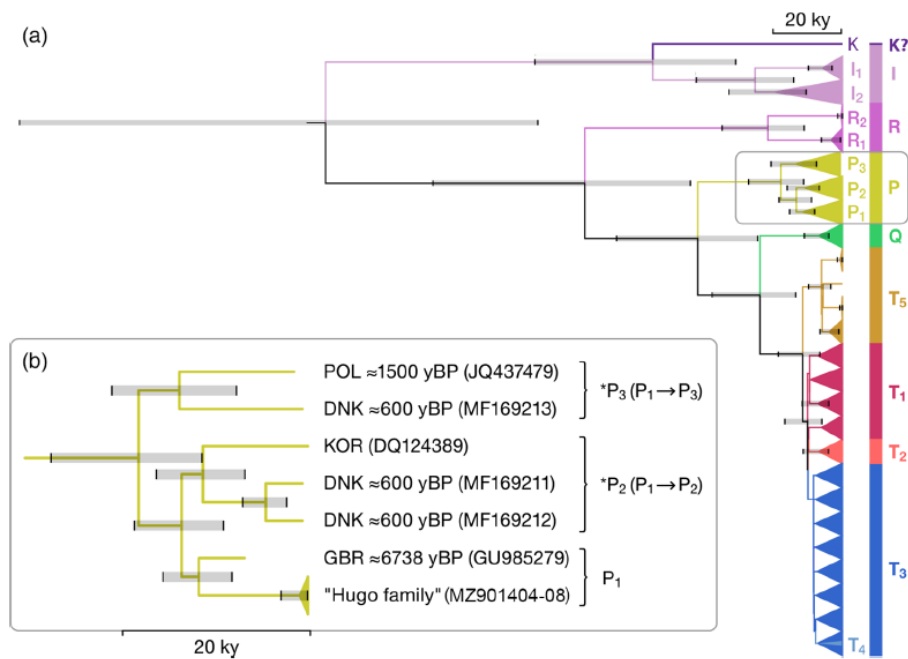
Slika 7. mtDNA Maximum Likelihood Stablo.

Izvor: Verdugo, M. P., Mullin, V. E., Scheu, A., Mattiangeli, V., Daly, K. G., Maisano Delser, P., ... & Bradley, D. G. (2019). Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. *Science*, 365(6449), 173-176.

U radu Xia i sur. (2021.) analizirano je 170 mitogenoma s područja Sjeverne i Istočne Azije. Uzorci su pripadali 10 modernih pasmina tauro-mongolskih goveda. Analiza je pokazala da svi uzorci pripadaju dvjema podgrupama unutar haplogrupe T3. Kako bi istražili odnos između modernog i drevnog istočnoazijskog goveda, usporedili su set sa šest drevnih sekvenci. Rezultati su pokazali da drevne sekvence također pripadaju, uz T4 haplogrupu, navedenim podgrupama T3.

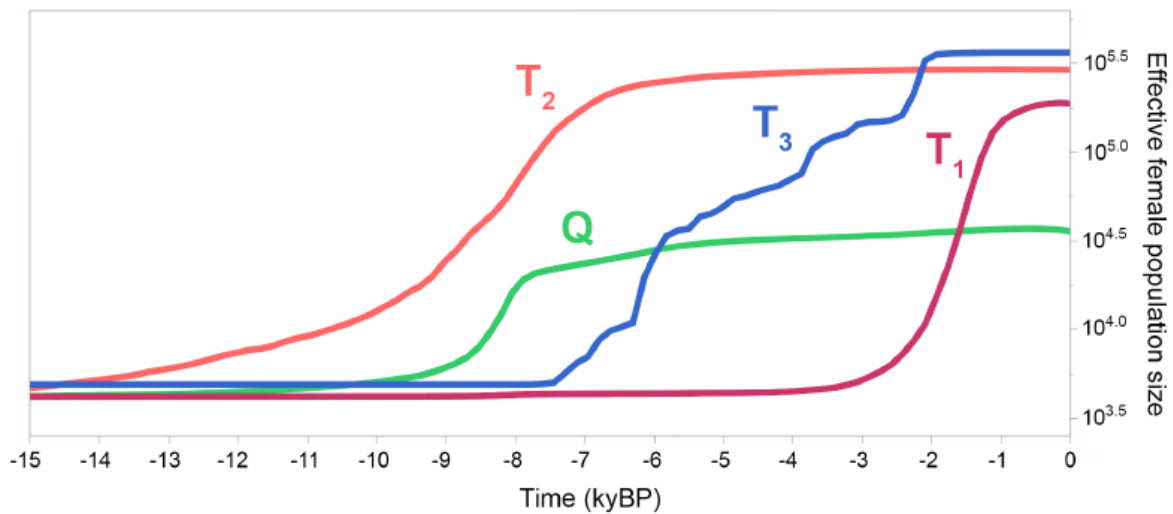
Kako bi detaljnije opisali klasifikaciju i demografske događaje koji su doveli do trenutne distribucije haplogrupa, Čubrčić i sur. (2022.) proveli su istraživanje nad 802 sekvence i time pokrili 114 pasmina goveda. Glavni cilj bio pomnije opisati filogenetiku rijetkih haplotipova, odnosno haplogrupu P. Velik broj uzoraka prikupljen je u jugoistočnoj Europi. Pronađeno je 1725 polimorfni mjesta te 701 jedinstveni haplotip. Polimorfna mjesta su uključivala 810 singleton i 853 parsinformativnih mjesta. Pronađene su sljedeće haplogrupe: I (10), R (10), P (6), Q (22), T5 (10), T2 (42), T3 (528), T1 (154), T4 (11), T6 (3) i T7 (1). Dominantna haplogrupa je T3. Slika 10. prikazuje distribuciju analiziranih mitogenoma

goveda. Po majčinskom rodu, identificirana je P1 haplogrupa, naslijeđena od divljeg goveda (*Bos primigenius*) kod jedinke austrijskog murbodnera što predstavlja dokaz da su se divlja goveda križala s modernim govedima u Europi tokom domestikacije (Slika 8.b.). Slika 8.a. prikazuje kompletno filogenetsko stablo koje je konstruirano na temelju 802 mitogenoma. Stablo ilustrira evolucijski odnos između različitih haplogrupa koje su pronađene u analiziranom setu. U prikazanom odnosu haplogrupa, jedna se značajno odvaja od haplogrupe I te potencijalno predstavlja novu haplogrupu K koja je naslijeđena od *Bos primigenius namadicusa*. Slika 9. prikazuje demografsku povijest različitih haplogrupa D-loop regija mtDNA tijekom vremena. Grafikon prikazuje promjene u efektivnoj veličini ženske populacije za haplogrupe T2, T3, T1 i Q kroz vrijeme (u tisućama godina prije sadašnjosti, označeno kao kyBP).



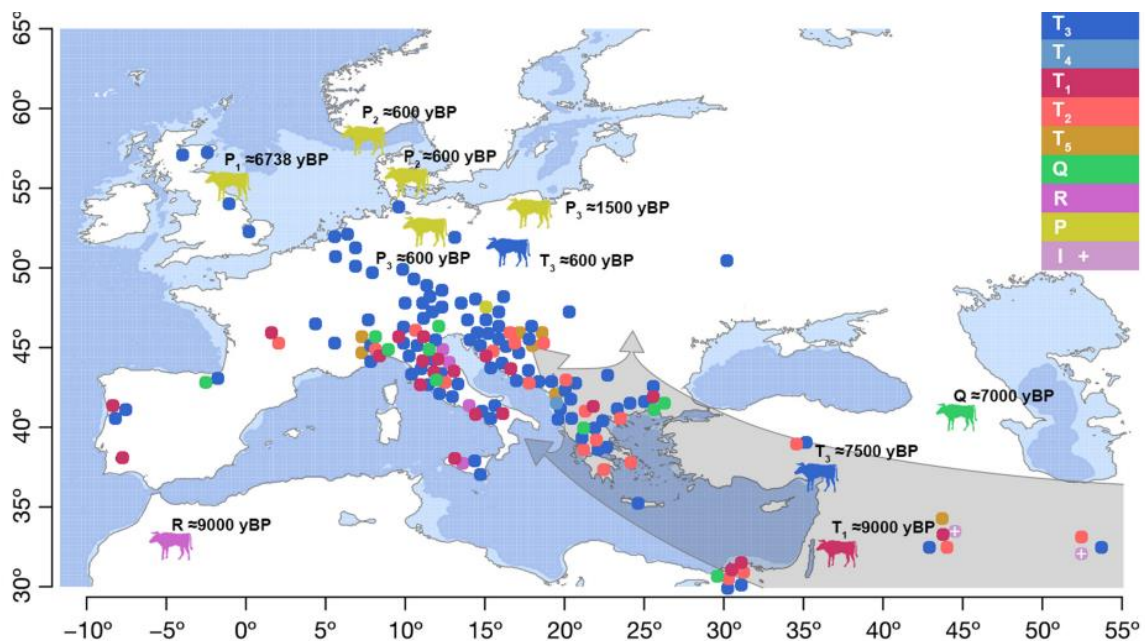
Slika 8. Bayesovski filogenetsko stablo izvedeno je na 802 potpune sekvence mitogenoma goveda. (a) Kompletno filogenetsko stablo (b) Djelomično filogenetsko stablo koje predstavlja P haplotipove (DNK, Danska; GBR, Velika Britanija; KOR, Koreja; POL, Poljska).

Izvor: Cubric-Curik, V., Novosel, D., Brajkovic, V., Rota Stabelli, O., Krebs, S., Sölkner, J., ... & Medugorac, I. (2022). Large-scale mitogenome sequencing reveals consecutive expansions of domestic taurine cattle and supports sporadic aurochs introgression. *Evolutionary applications*, 15(4), 663-678. -pristup: 28.7.2023.



Slika 9. Bayesov grafikon prikazuje trend efektivne veličine ženske populacije tijekom posljednjih 15 tisuća godina za haplogrube Q, T2, T3 i T1, izveden iz informacija o D-loop sekvenci (od np 16.042 do np 16.276).

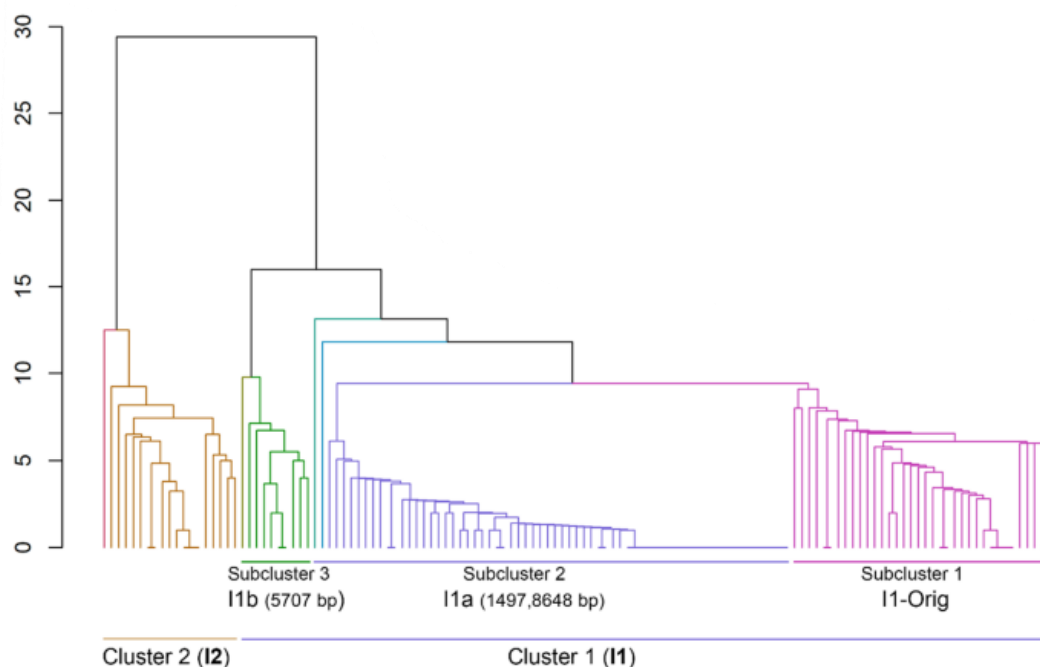
Izvor: Cubric-Curik, V., Novosel, D., Brajkovic, V., Rota Stabelli, O., Krebs, S., Sölkner, J., ... & Medugorac, I. (2022). Large-scale mitogenome sequencing reveals consecutive expansions of domestic taurine cattle and supports sporadic aurochs introgression. *Evolutionary applications*, 15(4), 663-678. -pristup: 28.7.2023.



Slika 10. Ilustracija geografske distribucije analiziranih sekvenci mitogenoma europskih pasmina modernih goveda s dodjeljenom haplogrupom prema Bayesovoj filogenetskoj analizi

Izvor: Cubric-Curik, V., Novosel, D., Brajkovic, V., Rota Stabelli, O., Krebs, S., Sölkner, J., ... & Medugorac, I. (2022). Large-scale mitogenome sequencing reveals consecutive expansions of domestic taurine cattle and supports sporadic aurochs introgression. *Evolutionary applications*, 15(4), 663-678. -pristup: 28.7.2023.

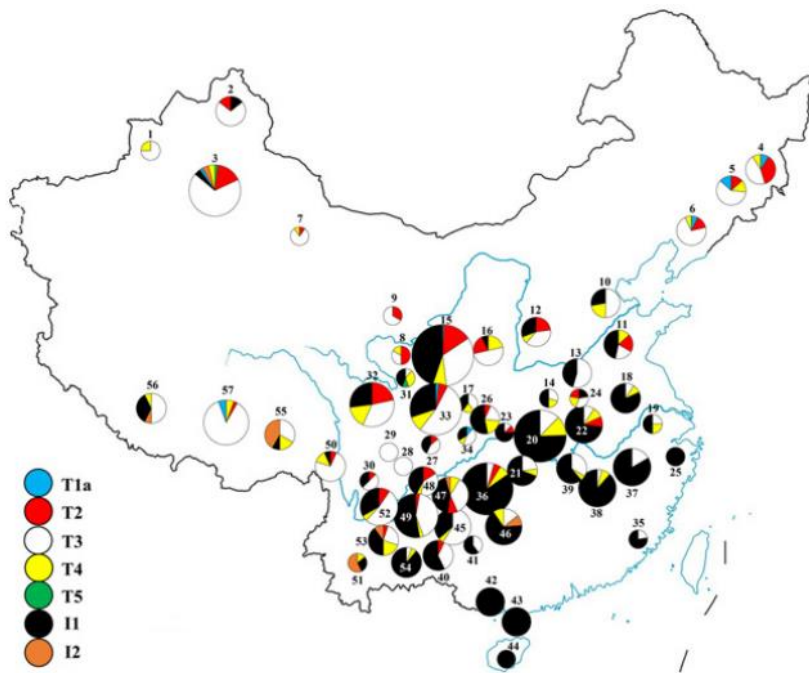
Dorji i sur. (2022.) proveli su istraživanje nad 1883 jedinke kako bi dokazali da se fenotipske razlike mogu objasniti određenom varijabilnošću na mitogenomu. Rezultati su pokazali da unutar 156 istraženih pasmina postoji 11 glavnih haplogrupa (I1, I2, T1, T2, T3, T4, T5, T6, P,Q1, Q2). T3 je dominantna haplogrupa kojoj pripadaju 1502 jedinke, a dijele se na 15 podgrupa. P2 i T4 haplogrupe se pojavljuju samo jednom (Korean Hanwoo i Wagyu goveda), dok se haplogrupa T6 pojavljuje 7 puta kod jedinki koje potječu od Angus goveda. Afričke pasmine goveda bile su uniformno klasificirane pod haplogrupu T1, koja je fiksirana u afričkim taurinskim pasminama dok su moderna taurinska goveda bila uglavnom klasificirana pod haplogrupu T. Indicinska goveda uglavnom su pripadala haplogrupi I. Unutar haplogrupe I1, identificirana je podskupna I1a (slika 11.) koja ima dvije specifične mutacije karakteristične za kineska goveda.



Slika 11. Podgrupiranje jedinki haplogrupe I na I1 i I2 te podgrupiranje unutar I1a grupe
 Izvor: Dorji, J., Vander Jagt, C.J., Chamberlain, A.J. et al. Recovery of mitogenomes from whole genome sequences to infer maternal diversity in 1883 modern taurine and indicine cattle. *Sci Rep* 12, 5582 (2022).
<https://doi.org/10.1038/s41598-022-09427-y> -pristup: 30.7.2023.

Rad autora Xia i sur. (2018.) predstavlja temeljito istraživanje genetske raznolikosti mitogenoma u različitim populacijama goveda u Kini. Tokom istraživanja provedeno je sekvenciranje cijele D-loop regije mtDNA kod 1105 pojedinaca, uključujući taurinska i zebu goveda. Identificirano je ukupno 250 taurinskih haplotipova i 88 zebu haplotipova što predstavlja pet glavnih haplogrupa kod *Bos taurus* (T1a, T2, T3, T4 i T5) i dvije haplogrupe kod *Bos indicus* (I1 i I2) što je prikazano na slici 12. Haplogrupa T1a koncentrirana je uglavnom u sjeveroistočnoj regiji Azije, a T2, T3 i T4 bile su dominantne kod kineskih goveda. Haplogrupa T5 povremeno je otkrivena kod mongolskih i Pingwu goveda.

Haplogrupa I1 bila je široko prisutna, dok je I2 pronađena samo u određenim regijama jugozapadne Kine, uključujući Yunnan-Guizhou visoravan i autonomnu regiju Tibet, te autonomnu regiju Xinjiang Uygur.



Slika 12. Geografska distribucija haplogrupa *Bos taurus* i *Bos indicus* unutar 57 kineskih pasmina goveda

Izvor: Xia, X., et al. "Comprehensive analysis of the mitochondrial DNA diversity in Chinese cattle." *Animal genetics* 50.1 (2019): 70-73. -pristup 28.7.2023.

4. Materijal i metode

4.1. Materijal

Za potrebe ovog diplomskog rada koristila sam banku gena kao osnovni izvor podataka, a okosnica mi je bio rad Čubrić-Čurik i sur. (2022.). Iz spomenutog rada preuzela sam 33 sekvence koje su mi služile kao predstavnici haplogrupa. Dodatno, iz repozitorija GenBank (Clark i sur., 2016) preuzela sam 670 sekvenci (Tablica S1.) koje su doprinijele većem setu podataka kako bih vidjela kolika je njihova raznolikost. Također, u tablici S1 evidentirane su sljedeće informacije: pasmina, vrsta, država, geografska lokacija uzorkovanja te izvor.

Kao referentnu sekvencu mitogenoma koristila sam sekvencu pod pristupnim brojem V00654 (Anderson et al., 1982). U konačnici, skup podataka obuhvatio je 704 sekvence, a unutar njih prisutno je 77 pasmina rasprostranjenih kroz 22 države. Broj jedinki svake haplogrupe po državama prikazana je u tablici 2.

Tablica 2. Broj jedinki svake haplogrupe po državi

Haplogrupa	Država	Broj jedinki	Bez predstavnika
I1	Irak	1	328
	Mongolija	2	
	Kina	110	
	Kazahstan	1	
	Indija	219	
I2	Indija	105	116
	Šri Lanka	1	
	Irak	1	
	Iran	1	
	Kina	11	
P1	Velika Britanija	1	0
	Poljska	1	
	Austrija	1	
Q1	Italija	2	3
	Kina	3	
	Grčka	1	
R1	Italija	1	
R2	Italija	2	0
T1	Etiopija	1	33
	S. Koreja	1	
	J. Afrika	1	
	Egipat	1	
	Kina	32	

	Kazahstan	1	
T2	Irak	1	21
	Kina	9	
	Kazahstan	3	
	Mongolija	7	
	Turska	1	
	Grčka	1	
	Indija	2	
T3	Indija	17	150
	Njemačka	26	
	Kina	93	
	Kazahstan	3	
	Mongolija	12	
	Austrija	2	
	Velika Britanija	1	
T4	Japan	1	17
	S. Koreja	1	
	kina	11	
	Mongolija	6	
T5	Irak	1	0
	Hrvatska	1	
	Albanija	1	
T6	Kina	2	2

4.2. Metode

4.2.1. Preuzimanje i evidencija mitogenoma

GenBank (Clark i sur., 2016) je javno dostupna baza podataka koja sadrži informacije o nukleotidnim sekvencama. Za preuzimanje sekvenci iz banke gena pomoću računalnog okruženja R (R Core Team, 2021) bilo je potrebno prvo stvoriti .txt datoteku sa popisom pristupnih brojeva sekvenci koje želimo preuzeti. Prilikom pokretanje R skripte u RStudio (RStudio Team, 2020) bilo je potrebno instalirati paket „ape“ (Paradis i Schliep, 2019), a najbitnija funkcija kojom sam preuzela sekvence je „read.Genbank“.

4.2.2. Poravnavanje sekvenci

Nakon preuzimanja sekvenci iz banke gena, iste sam poravnala pomoću softvera Clustal Omega (Chenna i sur., 2003). Clustal Omega (Chenna i sur., 2003) je popularan softver za višestruko poravnanje proteinskih ili nukleotidnih sekvenci. Razvijen je kao poboljšana verzija prethodnih Clustal alata, nudeći bržu i precizniju analizu poravnanja velikih skupova sekvenci te pruža korisnicima visokokvalitetne rezultate koji su od velikog značaja za proučavanje evolucijskih odnosa među sekvencama. Izlaznu datoteku s poravnanim setom sekvenci otvorila sam u softveru MEGA7 (Molecular Evolutionary Genetics Analysis) (Kumar i sur., 2016) radi vizualizacije i daljnje obrade. MEGA7 (Kumar i sur., 2016) je softver za molekularnu evoluciju i genetičku analizu koji se koristi u istraživanjima biologije, genetike, evolucije i srodnih disciplina. Razvijen je kao alat za analizu filogenetskih odnosa, genetičke divergencije i evolucijskih procesa. Omogućuje korisnicima da provode različite vrste analiza, uključujući izgradnju filogenetskih stabala, procjenu evolucijskih udaljenosti, analizu molekularne evolucije, rekonstrukciju filogenetskih mreža i identifikaciju genetskih markera. Osim toga, podržava različite formate ulaznih podataka, uključujući FASTA, NEXUS, PHYLIP i MEGA format. Dodatno sam ručno poravnala i složila sve sekvence prema referentnom mitogenomu V00654. Prosječna dužina sekvenci u poravnanom setu bila je 16.338 bp. Takav set sam preimenovala na način da mi je radno ime sadržavalo informaciju o pristupnom broju, državi (ISO2 kod), pasmini i haplogrupi. Preimenovanje sekvenci, prema navedenom načinu, odradila sam pomoću RStudio (RStudio Team, 2020) skripte i paketa Tidyverse (Wickham i sur., 2019) kako bih mogla lakše pratiti rezultate budućih analiza.

4.2.3. Određivanje haplogrupa pomoću MitoToolPy softvera

MitoToolPy (Peng i sur., 2017) je bioinformatički alat za analizu mitohondrijske DNA (mtDNA), dizajniran za potrebe genetičara i evolucijskih biologa. Pruža niz funkcionalnosti za filogenetsku analizu, identifikaciju haplogrupa i analizu varijabilnosti mitogenoma. Ključne značajke MitoToolPy-a uključuju sposobnost rukovanja velikim skupovima podataka,

izvođenje obrade u serijama i generiranje grafičkih prikaza visoke kvalitete za potrebe publikacija (Zhang i sur., 2019). Program omogućuje analizu mitogenoma kod 8 različitih vrsta domaćih životinja. MitoToolPy (Peng i sur., 2017) koristila sam za klasifikaciju haplogrupa na kojima se bazirala deskriptivna statistika.

4.2.4. Deskriptivna statistika

U cilju detektiranja varijabilnih mjesta unutar seta, kroz softver MEGA7 (Kumar i sur., 2016) izračunala sam osnove deskriptivne statistike. Varijabilna mjesta su iste pozicije na DNA sekvenci koje sadrže najmanje dva različita nukleotida između više različitih organizama, a dijele se na parsimonijska informativna mjesta i singleton mjesta. Parsimonijska informativna mjesta su mjesta koja sadrže najmanje dva različita tipa nukleotida ili aminokiselina, pri čemu se svaki od njih pojavljuje barem dva puta, a singleton mjesta sadrže najmanje dva različita tipa nukleotida ili aminokiselina, pri čemu se jedan od njih može pojaviti više puta. Također, napravila sam tablicu u Excelu (Microsoft Corporation, 2018) sa popisom država i brojem jedinki, te brojnošću pojedine pasmine koja je uzorkovana, a prikazano je na tablici 3.

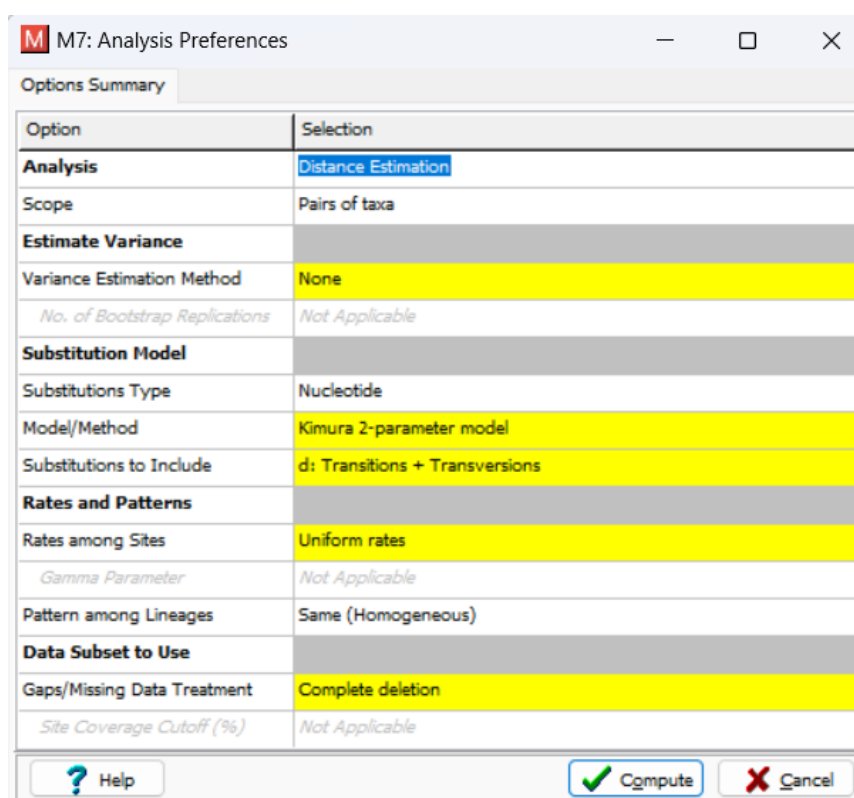
Tablica 3. Brojnost pasmina po državama

Država	Broj jedinki	Broj pasmina	Pasmine										
Albanija	1	1	Skodra buša										
Austrija	3	2	Murbodner 2	Fleckvieh									
Kina	271	8	Anxi 5	Tibetan 48	Yunlig 160	Weizhou 17	Nandan 18	Longlin 21	Diqin 1	B. tau. 1			
Hrvatska	1	1	S.s. Podolian										
Egipat	1	1	Menofi										
Etiopija	1	1	Arsi										
Njemačka	26	1	Erman holstein										
Grčka	2	2	Katerini	Gr. S. pindos									
Indija	343	46	Amrit mahal	Bachaur	Badri	Bargur	Belahi	Binjharpuri	Dangi	Deoni	Gangatiri	Gaolao	
			9	5	5	9	12	4	6	5	6	5	
			Kangayam	Kankrej	Kenkatha	Khariar	Kherigarh	Kosali	K. kapila	Khillar	Krishna valley 8	Lakhimi	
			4	20	6	6	6	6	5	4	8	12	
			Motu	Nagori	Nellore	Nimari	Ponwar	Ongole	Punganur	Pulikulam	Rathi	Sahiwal	
			6	8	2	6	6	6	6	6	7	18	
			Tharparkar	Vechur	Umblachery	Thutho							
			4	3	6	7							
Ghumusari	Gir	Hallikar	Hariana										
6	28	5	11										
Ladakhi	Mewati	Malvi	Malnad gidda 5										
11	10	8	5										
Red sindhi	Red kandhari	Siri	Shweta kapila 10										
3	3	9	10										
Iran	1	1	Iranian										

Irak	4	1	Iraqi			
Italija	5	4	Cabannina 2	Cinisara	Romagnola	Marchigiana
Japan	1	1	Japanese black			
Kazahstan	8	1	Kazakh			
Mongolija	27	1	Mongolian			
Nizozemska	1	1	Holstein			
Poljska	1		Bos primigenius			
J. Africa	1	1	Nguni			
S. Koreja	2	2	Korean native	Korean c.		
Šri lanka	1	1	Zwergzebu			
Turska	1	1	Anatolian black			
Velika Britanija	2		Bos tauru	B. prim.		

4.2.5. P-distanca

P-distanca je proporcija nukleotidnih mjesta na kojima se dvije uspoređene sekvence razlikuju, a dobiva se dijeljenjem broja razlika u nukleotidima s ukupnim brojem uspoređenih nukleotida. Koristi se kao mjerilo genetičke udaljenosti između jedinki, populacija ili skupina jedinki. Računanjem p-distance u MEGA7 (Kumar i sur ., 2016) dobijemo matricu udaljenosti svih parova jedinki ili svih grupa. Da bismo dobili matricu udaljenosti, potrebno je pravilno namjestiti parametre za izračun. Parametri koje sam ja koristila za izračun p-distance prikazani su na slici 13. Raspon udaljenosti (p) se kreće od 0 do 1. Ukoliko je udaljenost (p) jednaka nuli to znači da su sekvence iste uzimajući sve nukleotide u obzir, a rezultat jednak 1 znači suprotno, da su sekvence različite prema svim nukleotidima. Dobivenu matricu p-distanci sam pomoću koda u RStudiu (RStudio Team, 2020) pretvorila u tablicu s tri kolone radi preglednosti i jednostavnijeg opisa rezultata.



Slika 13. Parametri za izračun p-distance

4.2.6. BEAST analiza

Programski paket Bayesian Evolutionary Analysis by Sampling Trees (BEAST), koji sadrži programe Beast, Beauti, Loganalyser, Logcombiner, Treeannotator i Treestat, čvrsto se afirmirao u raznolikim biološkim područjima, uključujući filogenetiku, paleontologiju, dinamiku populacija, drevnu DNA, te filodinamiku i molekularnu epidemiologiju zaraznih bolesti (Drummond et al., 2012). BEAST analiza je metoda koja se koristi u molekularnoj

evoluciji za procjenu evolucijskih parametara, poput vremena podrijetla, stopa evolucije i filogenetskih odnosa između organizama, koristeći molekularne podatke, poput DNA sekvenci ili aminokiselina. Specifičan fokus BEAST analize temelji se na vremenski skalirana stabla i evolucijskim analizama koje su ovisne o njima (Suchard et al., 2018). BEAST (Drummond et al., 2012) koristi Bayesovsku statistiku za procjenu parametara i stvaranje filogenetskih stabala. Ova analiza omogućuje modeliranje različitih aspekata evolucijskih procesa, uključujući vrijeme podrijetla vrsta, brzinu evolucije genetskog materijala i sl., koristeći vremenske informacije. Također, BEAST (Drummond et al., 2012) pruža fleksibilnost u korištenju različitih modela evolucije i metoda procjene parametara, što omogućuje prilagodbu analize specifičnim značajkama podataka i potrebama istraživanja.

BEAUTi program (Bayesian Evolutionary Analysis Utility) (Suchard i sur., 2018), koji ima grafičko korisničko sučelje, korisniku omogućuje uvoz podataka (sekvenci), odabir modela, odabir prethodne distribucije, određivanje postavki za Bayesov zaključak i procjenu granične vjerojatnosti te definirane parametre pohranjuje u .xml datoteku (Suchard et al., 2018). Pomoću Beast programa se vrši analiza pokretanjem prethodno kreirane .xml datoteke, a po završetku Beast analize (izlazne datoteke su .log i .trees), programom Tracer verzije 1.7.2 (Rambaut i sur., 2018) se otvara .log datoteka i provjeravaju vrijednosti efektivne veličine uzorka (ESS) koja daje uvid u statistiku odabranih parametara te potencijalnih problema s konvergencijom parametara. Pomoću programa TreeAnnotator iz .trees datoteke, koja sadrži izračunata filogenetska stabla, sažima se jedno stablo s izračunom posteriori vrijednosti te se uklanja određeni postotak stabala („burn in“) ovisno o konvergenciji i stabilizaciji parametara što se je prethodno provjerilo pomoću programa Tracer verzije 1.7.2 (Rambaut i sur., 2018). Završno stablo s posteriori vrijednostima, koje označavaju vjerojatnost razdvajanja klastera na filogenetskom stablu, vizualizira i uređuje se pomoću FigTree (Rambaut i sur., 2016) programa.

Za potrebe analiza koristila sam BEAST programski paket (Bayesian Evolutionary Analysis Sampling trees) verzije 1.10.5 (pre-release of ThorneyclockLikelihood v0.1.2). Na setu od 704 mitogenoma korišten je GTR (General Time-Reversible) supstitucijski model, strogi model sata (engl. strict clock model), prior stabla Coalescent Bayesian Skyline Trees i MCMC dužina lanca 100 000 000 s prikazom stanja i parametara svakih 10 000 iteracija. Kod sažimanje stabla uklonilo se („burn-in“) 20% stabala koji su prvi u nizu konvergencije.

Pomoću FigTree (Rambaut i sur., 2016) vizualizirala sam i uredila filogenetsko stablo te pod opcijom „node labels“ aktivirala posterior vjerojatnosti kako bih vidjela koji klasteri/haplogrupe se značajno odvajaju. Haplogrupe koje se značajno odvajaju prema posteriori vrijednosti obojala sam paletom boja kakva se koristi i u ostalim analizama diplomskog rada kako bi se rezultati analiza mogli lakše pratiti i uspoređivati. U rezultatima ću detaljnije opisati kakav odnos prikazuje filogenetsko stablo između organizama i haplogrupa na analiziranom setu te kolika je evolucijska udaljenost između njih.

4.2.7. Izračun haplotipova i izrada median-joining mreže

DnaSP (DNA Sequence Polymorphism) je softver za analizu DNA polimorfizama (Librado i Rozas, 2009). Koristila sam ga za računanje haplotipova i njihove raznolikosti za svaku

pasminu. Haplotip je specifična kombinacija nukleotidnih varijacija na jednom kromosomu/mitogenomu koji se nasljeđuje zajedno. Raznolikost haplotipova je mjera genetičke varijabilnosti unutar određene populacije ili skupine jedinki. Ova mjera se odnosi na broj različitih haplotipova prisutnih u toj populaciji. Visoka raznolikost haplotipova ukazuje na veću genetsku varijabilnost unutar populacije što može implicirati različite genetske pozadine ili evolucijske putove. Analiza raznolikosti haplotipova omogućuje dublji uvid u genetsku strukturu populacije. Može pružiti informacije o migracijama, udaljenostima između populacija, selekciji te drugim evolucijskim procesima koji su oblikovali genetsku raznolikost unutar populacije. Također, raznolikost haplotipova može biti korisna u istraživanjima populacijske dinamike, evolucijskih trendova te genetskih bolesti. Za izračun haplotipa, prvo sam pripremila .meg file u MEGI 7 (Kumar i sur., 2016), potom sam ga otvorila u DnaSP-u (Librado i Rozas, 2009). Pošto su bili prisutni nepoznati oblici nukleotida, pojavilo se upozorenje „error“ te je bilo potrebno ručno fazirati sekvence odnosno nepoznate nukleotide zamijeniti s poznatim i frekventnijima. Također, spremila sam podatke o broju i brojnosti haplotipova kao .nex format datoteku.

Za izradu legende, koja služi za prikaz Median Joining mreže (Bandelt i sur., 1999) potrebno je bilo izraditi matricu frekvencija haplotipova po definiranim grupama. Za izradu matrice, koristila sam program Arlequin verzije 3.5 (An Integrated Software for Population Genetics Data Analysis) (Excoffier i sur., 2010), a generiranu izlaznu datoteku otvorila sam u TexPad-u. Nakon što sam prilagodila matricu kako bi odgovarala formatu kodiranja .nex datoteke, integrirala sam je na kraj već postojeće koja je generirana iz programa DnaSP (Librado i Rozas, 2009). Takva datoteka je bila potrebna za izradu Median Joining mreže (Bandelt i sur., 1999) u PopART programu (Population Analysis with Reticulate Trees) (Leigh i Bryant, 2015), a matrica je omogućila bojanje haplotipova u skladu s legendom.

```
Input Data File: C:\...\set_704_popart_haplotipovi.nex
Number of sequences: 704   Number of sequences used: 704
Selected region: 1-1340   Number of sites: 1340
Total number of sites (excluding sites with gaps / missing data): 1340

Sites with alignment gaps: not considered
Number of variable sites: 1340

===== Haplotype Distribution =====
Number of haplotypes, h: 481
Haplotype diversity, Hd: 0.9966
```

Slika 14. haplotip datoteka u .nex formatu generirana u DnaSP-u

4.2.8. Distribucija haplogrupa po državama

Sljedeća analiza koju sam provela uključuje izračun frekvencije haplogrupa mitogenoma, određenih putem BEAST analize (Drummond et al., 2012), po državama koristeći R (R Core

Team, 2021), RStudio (RStudio Team, 2020) i paket „ggplot2“ (Wickham, 2016). Kako bih dobila usporedive podatke, prikazala sam i distribuciju haplogrupa iz rada Čubrić Čurik i sur. (2022), što mi je omogućilo analizu doprinosa novih mitogenoma u kontekstu geografske distribucije haplogrupa (Tablica 4.). Izradu karte svijeta s označenim jedinkama također sam napravila u RStudiu (RStudio Team, 2020). Excel tablicu sam učitala u RStudio (RStudio Team, 2020), a pomoću funkcije „ggplot“ (Wickham, 2016) izradila sam mapu. Varijable Longitude_X i Latitude_Y sadržavale su potrebne koordinate za pojedine jedinke, koje su prikazane na kartama, dok je varijabla beast_haplogrupa sadržavala informacije o haplogrupi kojoj pripada svaka jedinka prema BEAST analizi (Drummond et al., 2012). Uz to, frekvenciju haplogrupa na karti prikazala sam pomoću kružnog grafa, čime sam dodatno ilustrirala geografsku distribuciju haplogrupa.

Tablica 4. Brojnost pojedine haplogrupe mitogenoma analiziranih u radu Čubrić Čurik i sur. (2022) te doprinos novih mitogenoma

Haplogrupa	Broj jedinki	Doprinos novih mitogenoma
I	9	1
P	10	3
Q	27	6
R	11	3
T1	155	35
T2	42	24
T3	549	176
I1	-	334
I2	-	119
T5	-	3

5. Rezultati

5.1. Varijabilna mjesta

U analizi varijabilnih mjesta 704 mitogenoma, ustanovljeno je ukupno 1433 varijabilnih mjesta. Od tog broja, identificirano je 788 parsimonijskih informativnih mjesta i 645 singleton mjesta korisnih za rekonstrukciju filogenetskog stabla. U radu Čubrić Čurik i sur. (2022) obuhvaćeno je 804 mitogenoma, na kojim je ustanovljeno 1725 varijabilnih mjesta ili 853 parsimonijskih informativnih mjesta i 810 singleton mjesta, što prikazuje tablica 5. Ovi rezultati pružaju uvid u genetičku varijabilnost unutar ovog seta mitogenoma te su od važnosti za daljnje filogenetske i populacijske analize.

Tablica 5. Varijabilna mjesta 704 mitogenoma u usporedbi sa setom iz rada Čubrić Čurik i sur. (2022)

	C	V	Pi	S
Moj set	14905	1433	788	645
Čubrić Čurik i sur. (2022)	14551	1725	853	810

5.2. P-distanca

Rezultati prikazani u tablici P2. daju nam uvid u sličnost odnosno razliku između pojedinih pasmina analiziranih tokom ovog istraživanja. Prema rezultatima, identični mitogenom imaju talijanske pasmine romagnola i marchigiana. P distanca jednaka im je 0.00 što ukazuje na vrlo blisku geografsku i genetsku povezanost ili mogući nedavni zajednički predak. Također, međusobno indijske pasmine imaju p distance 0.00 kao što su nellore i gir, belahi i nagori što su sve indicina goveda. Ako uspoređujemo indijske pasmine s europskim, p distance su veće zato što su europske pasmine taurin goveda. Na primjer, p distanca između indijskog goveda vechur i austrijskog goveda murbodner iznosi 0.02. Isti iznos p distance izračunat je i između nekoliko azijskih taurin goveda i indijskih, a to su korejsko domaće govedo i thutho. Nešto manju p distancu imaju egipatski menofi i indijski malvi, a ona iznosi 0.1. Najveće p distance zabilježene su između kineske pasmine diqin i nekoliko pasmina iz različitih regija Europe i Azije, te između indijskih pasmina.

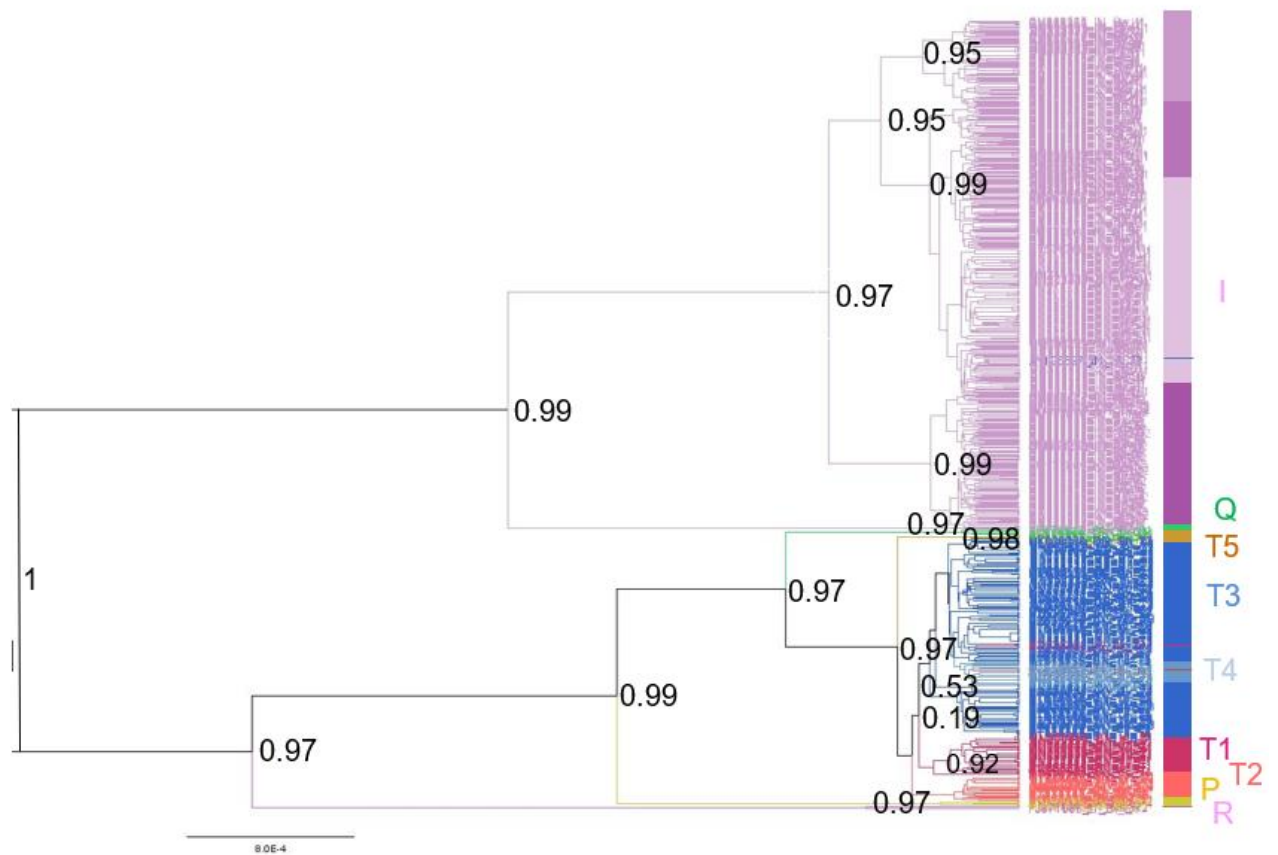
5.3. Filogenetska analiza

U filogenetskoj analizi, korištenjem programa BEAST (Drummond et al., 2012), analizirani su mitogenomi kako bi se dobila dublja spoznaja o njihovoj evolucijskoj povijesti i međusobnim genetičkim odnosima. Rezultati ove analize pokazali su poneke razlike u određivanju haplogrupa između prethodno dobivene klasifikacije pomoću MitoToolPy-a (Peng i sur., 2017) i onih dobivenih kroz BEAST analizu (Drummond et al., 2012). Od 704 analiziranih mitogenoma, njih 24 je preklasificirano u drugu haplogrupu. Tablica 6. prikazuje popis mitogenoma i njihovu haplogrupu određenu MitoToolPy-em te haplogrupu dodijeljenu BEAST analizom (Drummond et al., 2012). Ova razlika u klasifikaciji haplogrupa sugerira moguću potrebu za ažuriranjem prethodnih taksonomskih klasifikacija ili možda ukazuje na specifičnosti evolucijskih putova ovih mitogenoma koje BEAST metoda (Drummond et al., 2012) može bolje detektirati. Primjerice, mitogenom s radnim nazivom AY126697_IN_NI_T3, koji je prethodno bio klasificiran u haplogrupu T3, nakon BEAST analize (Drummond et al., 2012) je klasificiran u haplogrupu I1. Svi ostali navedeni mitogenomi preklasificirani u T3 haplogrupu, a pripadaju japanskim (apanese black), sjeverno korejskim (Korean native i Korean cattle), kineskim (Yunglin, Longlin i Tibetan), kazahstanskim (Kazakh) i mongolskim pasminama (Mongolian). Slika 15. prikazuje filogenetsko stablo izrađeno u programu Fig Tree (Rambaut i sur., 2016). Grane stabla obojane su prema posterior vrijednostima prateći podjelu na haplogrupe. gdje se vrijednosti veće od 0.95 smatraju značajnima i time potvrđuju podjelu između haplogrupa. Haplogrupe I i T3 jasno se izdvajaju, dok unutar haplogrupe I postoji dodatna podjela na četiri podgrupe što je naznačeno četirima nijansama ljubičaste boje (Slika 15.).

Tablica 6. Mitogenomi s različitim haplogrupama nakon BEAST analize

RADNI NAZIV	HAPLOGRUPA MitoToolPy	BEAST HAPLOGRUPA
AB074964_JP_Jb_T4	T4	T3
AY126697_IN_NI_T3	T3	I1
AY526085_KR_Nk_T1	T1	T3
DQ124375_KR_Kc_T4	T4	T3
MN200795_CN_Yu_T4	T4	T3
MN200841_CN_Yu_T4	T4	T3
MN200842_CN_Yu_T4	T4	T3
MN200846_CN_Yu_T6	T6	T3
MN200848_CN_Yu_T4	T4	T3
MN200860_CN_Yu_T4	T4	T3
MN200876_CN_Yu_T4	T4	T3
MN200896_CN_Yu_T6	T6	T3
MN200937_CN_Yu_T4	T4	T3
MN714182_CN_Lg_T4	T4	T3
MN714183_CN_Lg_T4	T4	T3

MT576741_CN_Tb_T4	T4	T3
MT576752_CN_Tb_T4	T4	T3
MT576761_KZ_Kz_T1	T1	T3
MT576769_MN_Mn_T4	T4	T3
MT576774_MN_Mn_T4	T4	T3
MT576820_MN_Mn_T4	T4	T3
MT576821_MN_Mn_T4	T4	T3
MT576822_MN_Mn_T4	T4	T3
MT576828_MN_Mn_T4	T4	T3



Slika 15. Filogenetsko stablo analiziranog seta

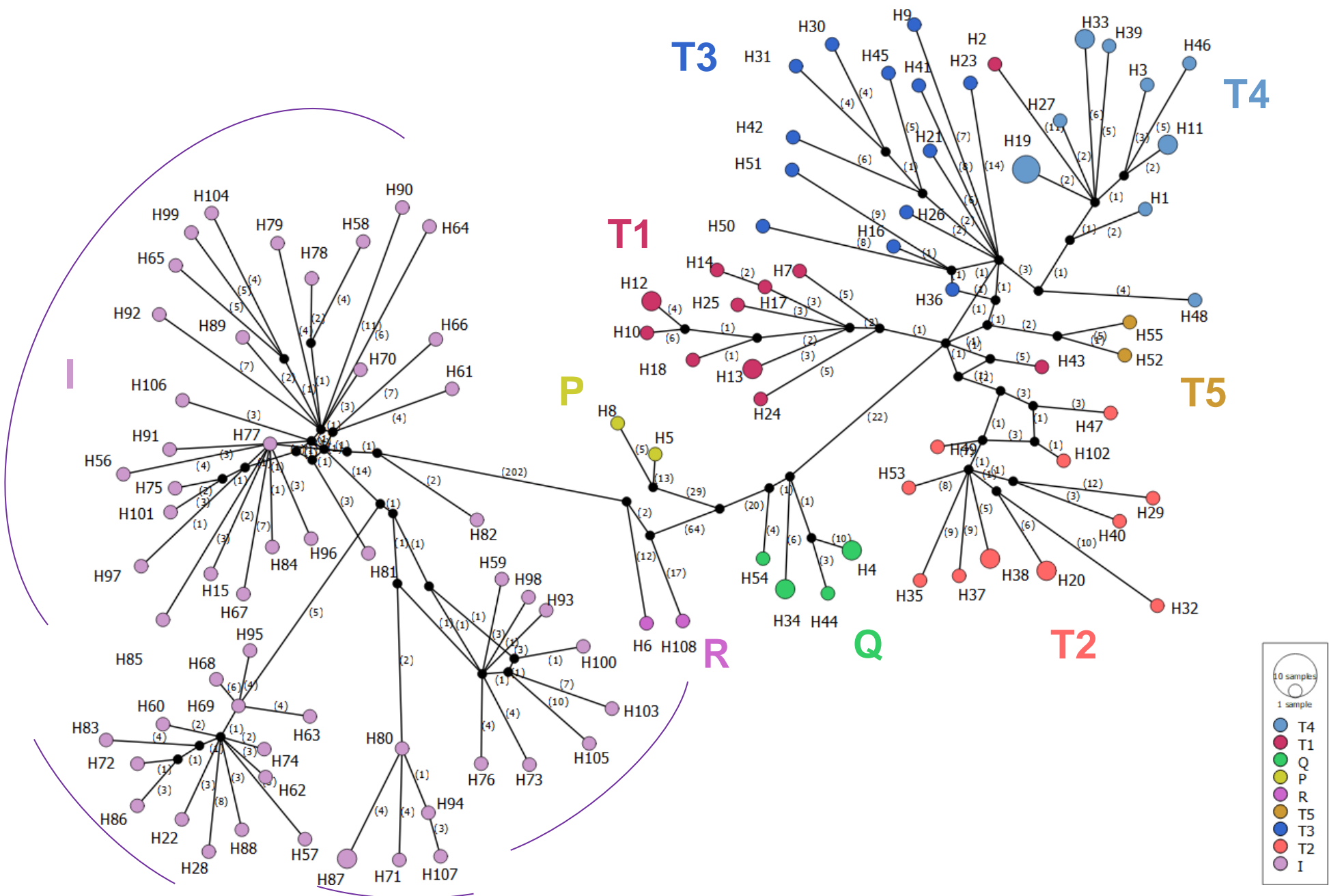
5.4. Prikaz haplotipova median-joining mrežom

U analizi 704 mitogenoma, ukupno je identificirano 481 haplotip unutar analiziranog seta podataka. Raznolikost haplotipova, izražena kao 0.9966, ukazuje na visok stupanj genetičke varijabilnosti između haplotipova, što sugerira širok spektar genetičkih profila unutar analiziranog seta. Takvi rezultati naglašavaju bogatstvo genetičkih informacija koje se mogu dobiti analizom haplotipova. Najfrekventniji je haplotip 39 u kojeg je svrstan 31 mitogenom kineskih pasmina (yunling, longlin, nandan, weizhou), a svi su pripadnici I1 haplogrupe. Haplotip 41 broji 12 mitogenoma kineske pasmine yunling (T3) te haplotip 281 s 8 mitogenoma indijskih pasmina, također I1. Tablica 7. prikazuje navedeni rezultat. Svim ostalim haplotipovima su pripadali između jednog i pet mitogenoma.

Tablica 7. Haplotipovi s najviše pripadajućih mitogenoma

Hap_39	Hap_41	Hap_281
MN200780_CN_Yu_I1	MN200782_CN_Yu_T3	OM868367_IN_Hl_I1
MN200797_CN_Yu_I1	MN200787_CN_Yu_T3	OM868433_IN_Ko_I1
MN200801_CN_Yu_I1	MN200847_CN_Yu_T3	OM868450_IN_Ld_I1
MN200802_CN_Yu_I1	MN200852_CN_Yu_T3	OM868489_IN_Mw_I1
MN200805_CN_Yu_I1	MN200859_CN_Yu_T3	OM868541_IN_Rt_I1
MN200807_CN_Yu_I1	MN200864_CN_Yu_T3	OM868558_IN_Sw_I1
MN200844_CN_Yu_I1	MN200873_CN_Yu_T3	OM868598_IN_Um_I1
MN200849_CN_Yu_I1	MN200880_CN_Yu_T3	OM868600_IN_Um_I1
MN200853_CN_Yu_I1	MN200915_CN_Yu_T3	
MN200861_CN_Yu_I1	MN200917_CN_Yu_T3	
MN200871_CN_Yu_I1	MN200927_CN_Yu_T3	
MN200902_CN_Yu_I1	MN200934_CN_Yu_T3	
MN200908_CN_Yu_I1		
MN200920_CN_Yu_I1		
MN200926_CN_Yu_I1		
MN200933_CN_Yu_I1		
MN200935_CN_Yu_I1		
MN714167_CN_Lg_I1		
MN714171_CN_Lg_I1		
MN714172_CN_Lg_I1		
MN714175_CN_Lg_I1		
MN714176_CN_Lg_I1		
MN714181_CN_Lg_I1		
MN714186_CN_Nd_I1		
MN714187_CN_Nd_I1		
MN714188_CN_Nd_I1		
MN714198_CN_Nd_I1		
MN714200_CN_Nd_I1		

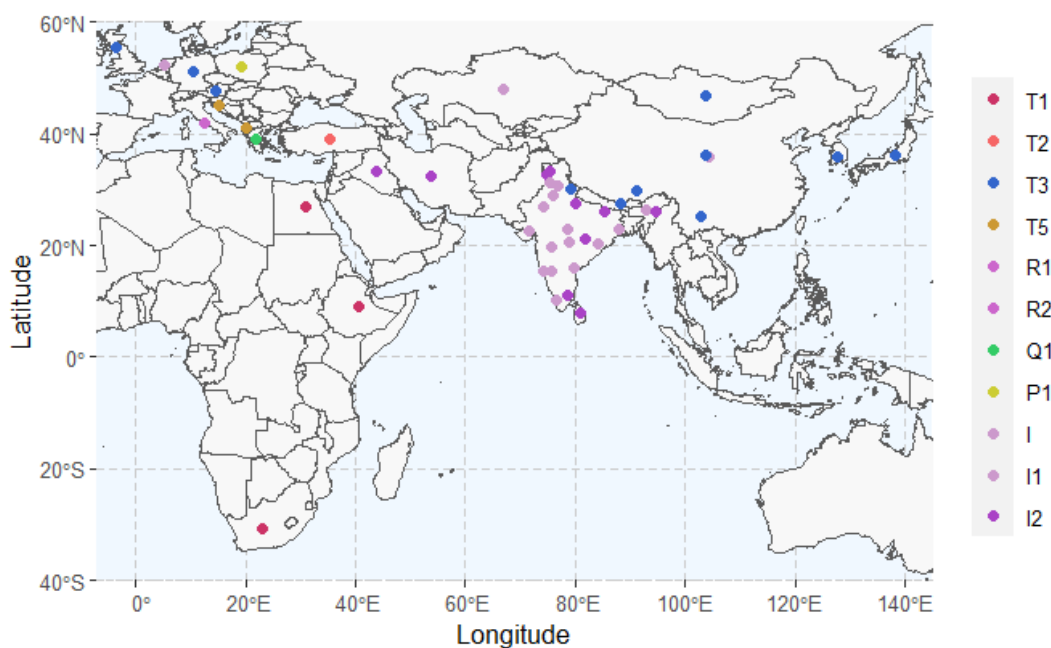
Zbog nemogućnosti prikaza 481 haplotipa dobivenih na setu 704 sekvence na median-joining mreži, smanjila sam set na 120 sekvenci tako što sam za svaku haplogrupu iz BEAST analize (Drummond et al., 2012), koja je odvojena s posteriori vrijednosti 0.95, nasumično odabrala 13 ili 14 sekvenci te po dvije sekvence kao referentni predstavnici za svaku haplogrupu iz rada Čubrić Čurik i sur. (2022.). Također, za četiri podskupa haplogrupe I koji se značajno odvajaju (posterior vrijednost veća od 0.95) samisto sam nasumično odabrala po 14 sekvenci kao predstavnike. Analizom 120 sekvenci dobiveno je 108 haplotipova, podijeljenih u 9 haplogrupa čiji je filogenetski odnos prikazan median joining mrežom na slici 16.. Boja kružića je u skladu s legendom, a označava haplogrupu kojoj pripadaju. Brojevi na granama prikazuju broj varijabilnih mjesta koja se nalaze između pojedinih haplotipova. Zbog toga je jasno vidljivo da se najviše odvaja haplogrupa I koja je od najbližije jedinice haplogrupe R udaljena 216 varijabilna mjesta. Također, haplogrupa I je podijeljena u četiri manje skupine koje se jasno odvajaju na slici 16. Na drugi kraj median-joining mreže, grupirale su se T1, T2, T3, T4 i T5 haplogrupe čiji su haplotipovi međusobno udaljeni svega nekoliko varijabilnih. Haplotipovi pripadnici T haplogrupa su u prosjeku udaljeni 300 varijabilnih mjesta od haplotipova I haplogrupe.



Slika 16. Medina Joining mreža.

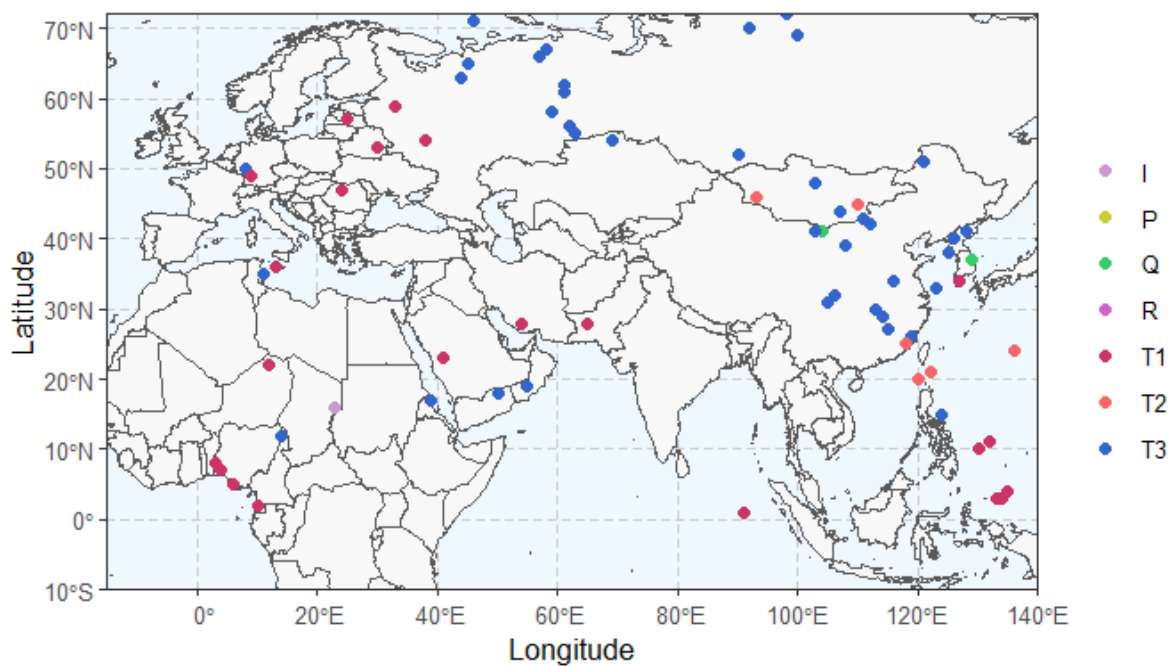
5.5. Distribucija haplogrupa

Rezultati analize distribucije haplogrupa na karti svijeta ukazuju na geografski specifične koncentracije određenih haplogrupa u različitim regijama. Primjerice, u istočnoj Africi prevladava haplogrupa T1, dok se u Europi može primijetiti prisutnost različitih haplogrupa, uključujući T3, T5, R2, Q1, P1 i I1. Haplogrupe I1 i I2 pokazuju visoku koncentraciju u Indiji i Kini. Nadalje, haplogrupa T3 identificirana je kao dominantna u regijama Kine i Mongolije, naglašavajući geografski specifične genetičke obrasce koji odražavaju povijesne migracije ili lokalne populacijske dinamike. Slika 17. prikazuje distribuciju haplogrupa na karti Euroazije.

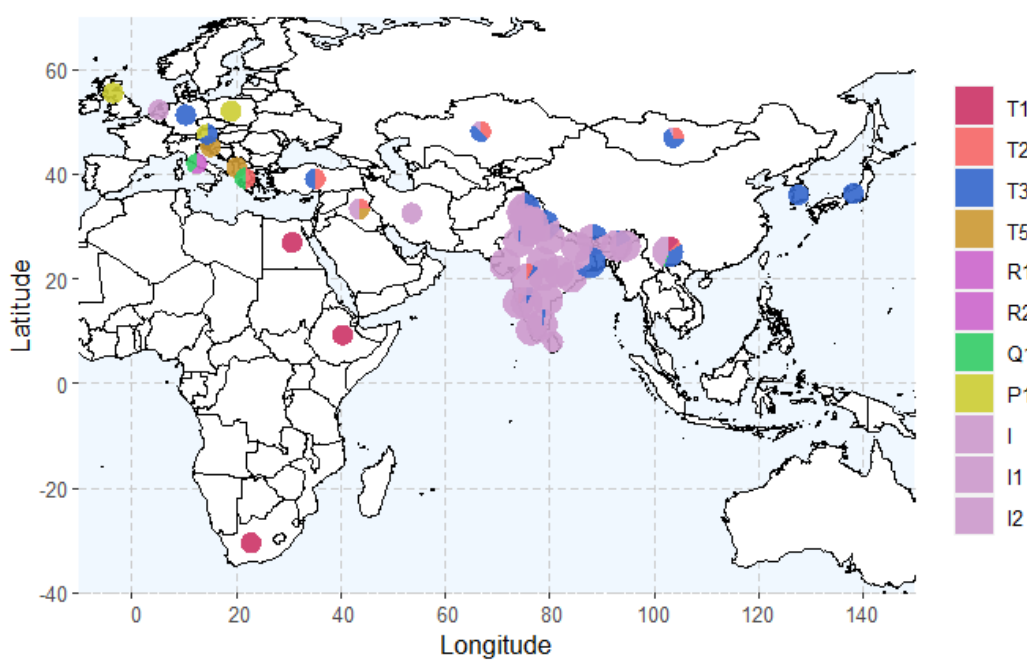


Slika 17. Distribucija haplogrupa.

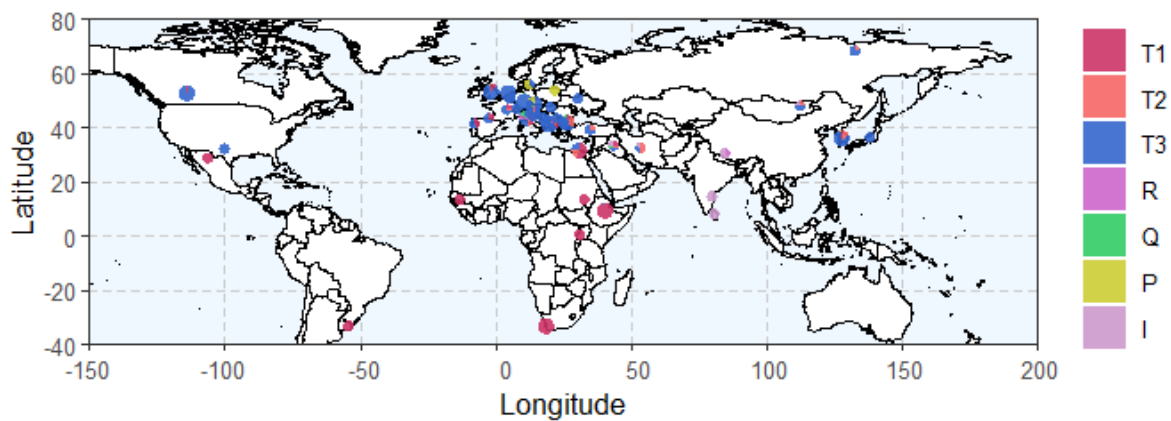
Na slici 18. prikazana je distribucija haplogrupa iz rada Čubrić Čurik i sur. (2022). Sa slike je vidljivo da je u radu analizirana znatna količina haplogrupe T3 koja je široko rasprostranjena. Ponajviše je koncentrirana u Rusiji, Mongoliji i istočnoj Kini. T1 haplogrupa, osim u Africi, prisutna je i u Europi, na Bliskom Istoku i u južnoj Aziji, a T2 haplogrupa samo u Aziji. Haplogrupa I nije znatno analizirana, prisutan je samo jedan predstavnik u središnjoj Africi. Usporedba slike 17. i 18. pokazuje kako se rezultati iz oba rada mogu međusobno nadopunjavati. Dok slika 17. naglašava prisutnost haplogrupe I u Indiji, rad prikazan na slici 18. pruža širi kontekst i ukazuje na genetske raznolikosti u drugim regijama te potencijalne migracijske obrasce. Kombiniranjem ovih podataka možemo dobiti cjelovitiji uvid u genetsku povijest i dinamiku populacija. Isti rezultati prikazani su i pomoću kružnog grafa na slikama 19. i 20. predstavljajući usporedbu distribucije haplogrupa 704 sekvence po državama ovog rada i rada Čubrić Čurik i sur. (2022.).



Slika 18. Distribucija haplogrupa iz rada Čubrić Čurik i sur. (2022).



Slika 19. Distribucija haplogrupa prikazana kružnim grafom.



Slika 20. Distribucija haplogrupa prikazana kružnim grafom iz rada Čubrić Čurik i sur. (2022).

6. Rasprava

U ovom istraživanju analizirala sam set od 704 sekvence mitogenoma goveda što je omogućilo detaljnu analizu genetske raznolikosti i divergencije među različitim pasminama i haplogrupama. Analizom je otkriveno 1433 varijabilna mjesta što ukazuje na značajnu genetsku raznolikost unutar proučavanih uzoraka. Identificirano je 11 različitih haplogrupa: I1, I2, P1, Q1, R1, R2, T1, T2, T3, T4 i T5. Najviše analiziranih mitogenoma pripada indijskim pasminama koje su isključivo klasificirane kao haplogrupe I1 i I2. Osim indijskih pasmina, I haplogrupe prisutne su i u Kini, no među kineskim pasminama dominira haplogrupa T3. Ova distribucija haplogrupa pokazuje geografske i povijesne obrasce širenja i miješanja goveda, posebno u Aziji.

Izračunom p distance među različitim pasminama dobili smo važne uvide u njihove genetske odnose. Najmanje vrijednosti p distance pronađene su između talijanskih pasmina romagnola i marchigian (0.00) što znači da nema genetskih razlika između sekvenci mitogenoma ovih dviju pasmina, ukazujući na izuzetno blisku genetičku sličnost, vjerojatno zbog zajedničkog pretka ili intenzivnog križanja. Također, niske vrijednosti p distance zabilježene su između indijskih pasmina što je u skladu s domestikacijom *Bos indicusa* na području doline Inda. Malu p distancu imaju Iransko govedo i Zwergzebu. Iako su geografski udaljeni, vjerojatno je tokom povijesti došlo do miješanja tih dviju pasmina. Mala vrijednost p distance, vjerojatno zbog geografske blizine, dobivena je između slavonsko-srijemskog podolca i skodre buše. S druge strane, najveće genetske udaljenosti izračunate su između taurin i indicinih goveda. Na primjer, indijsko govedo vechur i austrijsko govedo murbodner imaju p distancu 0.02. Ovi rezultati ukazuju na složenu evolucijsku povijest i raznolikost među govedima iz različitih regija. Rezultati p distance pružaju dubok uvid u genetičku sličnost i divergenciju među različitim pasminama goveda.

Koristeći DnaSP analizu, identificirano je 481 haplotipova u setu od 704 sekvenci, koji su podijeljeni u 9 haplogrupa. Haplogrupa I se najviše izdvaja, s 216 varijabilnih mjesta udaljenosti od najbližije jedinice haplogrupe R. Također, haplogrupa I se dijeli na četiri manje skupine koje su odvojene po posterior vrijednosti (veća od 0,95) u filogenetskoj analizi. S druge strane, haplogrupe T1, T2, T3, T4 i T5 su međusobno vrlo slične. Haplotipovi haplogrupa T su u prosjeku udaljeni 300 varijabilnih mjesta od haplotipova haplogrupe I, što ukazuje na njihovu značajnu genetsku razliku te potkrjepljuje činjenicu da su domestikacije taurin i indicinih goveda dva zasebna događaja, geografski udaljena.

U ovom istraživanju provedena je filogenetska analiza koristeći BEAST softver, koja je obuhvatila ukupno 704 mitogenoma. Rezultati analize pokazali su da je 24 od tih mitogenoma preklasificirano u drugu haplogrupu. Ova preklasifikacija ukazuje na dinamičnu prirodu genetske varijacije među govedima. Preklasifikacija mitogenoma može biti rezultat nekoliko faktora. Jedan od ključnih razloga može biti povijesne migracije. Preklasifikacija haplogrupa ukazuje na potrebu za daljnjim istraživanjima kako bi se bolje razumjela evolucijska povijest goveda. Analize poput ove mogu pružiti vrijedne uvide u migracijske puteve i genetske

adaptacije, što je od ključne važnosti za očuvanje genetske raznolikosti i za buduće uzgojne programe.

Tijekom povijesti, goveda su migrirala iz jednog područja u drugo, što je dovelo do miješanja različitih genetskih linija. Ove migracije su mogle biti uzrokovane promjenama u okolišu, potrebom za novim pašnjacima ili ljudskim aktivnostima kao što su trgovina i uzgoj. Genetska varijacija među govedima također može biti rezultat prirodne selekcije i genetskog drifta. Različite populacije goveda su bile izložene različitim selekcijskim pritiscima, što je moglo dovesti do adaptacija koje su zabilježene u mitogenomima. Genetski drift, kao nasumični proces promjene učestalosti alela u populaciji, također je mogao doprinijeti ovoj dinamici.

7. Zaključak

Na temelju pregleda literature te rezultata analiza provedenih na uzorku od 670 novodostupnih mitogenoma u Genbank repozitoriju, zaključuje se sljedeće:

- Na uzorku dužine 16338 parova baza identificirano je ukupno 1433 varijabilna mjesta od čega je 788 parsim informativnih i 645 singleton mjesta te je izračunat 481 haplotip uz visoku raznolikost haplotipova od 0.9966.
- Beast filogenetska analiza klasificirala je 334 mitogenoma u haplogrupu I₁, 119 u I₂ i 176 mitogenoma u T₃ haplogrupu kao najfrekventnije.
- Beast filogenetskim stablom s posteriori vjerojatnošću između 0.95 i 1 uočilo se razdvajanje četiri subhaplogrupe unutar haplogrupe I što bi moglo predstavljati osnovu za reklasifikaciju subhaplogrupa I₁ i I₂ u više subhaplogrupa.
- Beast filogenetskom analizom korigirana je klasifikacija 24 mitogenoma u haplogrupe prethodno provedene MitoToolpy programom što naglašava važnost korištenja naprednih filogenetskih alata za detaljno razumijevanje genetske strukture populacija. 19 mitogenoma T₄ haplogrupe preklasificirano je u T₃, jedna haplogrupa T₃ u I₁, dvije haplogrupe T₁ u T₃ i dvije haplogrupe T₆ u T₃.
- Analiza p-distanci otkrila je veće razlike između određenih kineskih i indijskih pasmina, kao i između indijskih i europskih pasmina. Niske vrijednosti p distance ukazuju na blisku genetičku povezanost, moguće zbog zajedničkog porijekla, povijesnih migracija ili uzgojnih praksi. S druge strane, veće vrijednosti p distance ukazuju na veću genetičku razliku, što može biti rezultat dugotrajne geografske izolacije ili različitih evolucijskih puteva.
- Filogeografska distribucija navedenih haplogrupa pokazala je da su uzorci porijeklom iz Indije, njih 219 pripada haplogrupi I₁, 105 haplogrupi I₂ i 17 haplogrupi T₃, a uzorci porijeklom iz Kine, njih 110 pripada haplogrupi I₁, 93 haplogrupi T₃ i 11 haplogrupi I₂.
- Ovi rezultati pružaju vrijedan uvid i doprinos u filogeografsku strukturu mitogenoma goveda, naglašavajući važnost daljnjih istraživanja kako bi se bolje očuvala genetička raznolikost te razumjela evolucijska povijest goveda, migracijski putevi i adaptacije.

8. Popis literature

1. Achilli A., Bonfiglio S., Olivieri A., Malusa` A., Pala M., et al. (2009). The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome. *PLoS*
2. Achilli A., Olivieri A., Pellecchia M., Ubaldi C., Colli L., Al-Zahery N., et al. (2008). Mitochondrial genomes of extinct aurochs survive in domestic cattle. *Current Biology*, 18(4), R157-R158
3. Anderson S. M. H. L., De Bruijn M. H. L., Coulson A. R., Eperon I. C., Sanger F., & Young I. G. (1982). Complete sequence of bovine mitochondrial DNA conserved features of the mammalian mitochondrial genome. *Journal of molecular biology*, 156(4), 683-717
4. Bandelt H, Forster P, Röhl A. (1999). Median-joining networks for inferring intraspecific phylogenies. *Mol Biol Evol* 16(1):37–48
5. Bonfiglio S., Achilli A., Olivieri A., Negrini R., Colli L., Liotta L., et al. (2010). The enigmatic origin of bovine mtDNA haplogroup R: sporadic interbreeding or an independent event of *Bos primigenius* domestication in Italy?. *PLoS One*, 5(12), e15760
6. Chen N., Cai Y., Chen Q., Li R., Wang K., Huang Y., ... & Lei, C. (2018). Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. *Nature Communications*, 9(1), 2337
7. Chenna R., Sugawara H., Koike T., Lopez R., Gibson T.J., Higgins D., Thompson J.D. (2003). Multiple sequence alignment with the Clustal series of programs. *Nucleic Acid Research*, 31(13), 3497-3500
8. Chung H.Y. and Ha J.M. Neobjavljen rad. Haplotype analysis of mitochondrial DNA in Korean native cattle. <https://www.ncbi.nlm.nih.gov>
9. Clark K., Karsch-Mizrachi I., Lipman D. J., Ostell J., Sayers, E. W. (2016). GenBank. *Nucleic acids research*, 44(D1), D67-D72
10. Cubric-Curik Vlatka, et al. "Large-scale mitogenome sequencing reveals consecutive expansions of domestic taurine cattle and supports sporadic aurochs introgression." *Evolutionary Applications* 15.4 (2022): 663-678
11. Dorji, Jigme, et al. "Recovery of mitogenomes from whole genome sequences to infer maternal diversity in 1883 modern taurine and indicine cattle." *Scientific Reports* 12.1 (2022): 5582
12. Drummond Alexei J., et al. "Bayesian phylogenetics with BEAUti and the BEAST 1.7." *Molecular biology and evolution* 29.8 (2012): 1969-1973
13. Edwards C. J., Magee D. A., Park S. D., McGettigan P. A., Lohan A. J., Murphy A., et al. (2010). A complete mitochondrial genome sequence from a mesolithic wild aurochs (*Bos primigenius*). *PLoS One*, 5(2), e9255
14. Excoffier, Laurent, and Heidi EL Lischer. "Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows." *Molecular ecology resources* 10.3 (2010): 564-567
15. Helmer D., Gourichon L., Monchot H., Peters J., Segui M. S. (2005). Identifying early domestic cattle from Pre-Pottery Neolithic sites on the Middle Euphrates using sexual

- dimorphism. In J. D. Vigne, J. Peters, & D. Helmer (Eds.), *The first steps of animal domestication: New archaeozoological approaches* (pp. 86–95). Oxbow Books.
16. Hiendleder S., Lewalski H., Janke A. (2008). Complete mitochondrial genomes of *Bos taurus* and *Bos indicus* provide new insights into intra-species variation, taxonomy and domestication. *Cytogenetic and genome research*, 120(1-2), 150-156
 17. Horsburgh K. A., Prost S., Gosling A., Stanton J. A., Rand C., Matisoo-Smith E. A. (2013). The genetic diversity of the Nguni breed of African Cattle (*Bos* spp.): complete mitochondrial genomes of haplogroup T1. *PloS one*, 8(8), e71956
 18. Kinoshita A., Kenez A., Hasselmann M., Daenicke S., Huber K. Neobjavljen rad. Inter-individual variation in adaptive capacity at onset of lactation: Linking metabolic phenotype with mitochondrial DNA haplotype in Holstein dairy cows. <https://www.ncbi.nlm.nih.gov>
 19. Kumar S., Stecher G., Tamura K. (2016). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 33: 1870-1874. DOI:10.1093/molbev/msw054
 20. Leigh JW., Bryant D. (2015). PopART: Full-feature software for haplotype network construction. *Methods Ecol Evol* 6(9):1110–1116
 21. Librado P., Rozas J. (2009). DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. *Bioinformatics*, 25(11), 1451-1452
 22. Liu D.H., Wei Y.F. Neobjavljen rad. Complete mitochondrial genome of the hybrid of Simmental and Chinese local cattle. <https://www.ncbi.nlm.nih.gov>
 23. Manisha S., Rahul S., Vijh R.K. Neobjavljen rad. <https://www.ncbi.nlm.nih.gov>
 24. Mannen H., Morimoto M., Tsuji S., Neobjavljen rad. Identification of mitochondrial DNA substitutions related to meat quality in Japanese Black cattle. <https://www.ncbi.nlm.nih.gov>
 25. Meadow R. H. (1993). Animal domestication in the Middle East: a revised view from the eastern margin. *Harappar Civilization. ONE* 4(6): e5753. doi:10.1371/journal.pone.0005753
 26. Microsoft Corporation. (2018). Microsoft Excel. Retrieved from <https://office.microsoft.com/excel>
 27. Miretti M.M., Pereira H.A. Jr., Greggio C., Suzuki J. Jr., Ferro J.A., Ferro M.I., Meirelles F., Garcia J.M., Smith L.C. Neobjavljen rad. The complete mitochondrial genome nucleotide sequence of *Bos indicus*. <https://www.ncbi.nlm.nih.gov>
 28. National Center for Biotechnology Information (NCBI)[Internet]. Bethesda (MD): National Library of Medicine (US), National Center for Biotechnology Information; [1988] – [citirano 2024 Lip 25]. Available from: <https://www.ncbi.nlm.nih.gov/>
 29. Olivieri A., Gandini F., Achilli A., Fichera A., Rizzi E., Bonfiglio S., ... & Torroni A. (2015). Mitogenomes from Egyptian cattle breeds: new clues on the origin of haplogroup Q and the early spread of *Bos taurus* from the Near East. *PLoS One*, 10(10), e0141170
 30. Paradis E, Schliep K. (2019). “ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R.” *Bioinformatics*, 35, 526-528. doi:10.1093/bioinformatics/bty633.

31. R Core Team. (2021). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.project.org/>.
32. Rambaut A, Drummond AJ, Xie D, Baele G and Suchard MA. (2018) Posterior summarisation in Bayesian phylogenetics using Tracer 1.7. *Systematic Biology*. syy032. doi:10.1093/sysbio/syy032.
33. Rambaut A. (2016). FigTree v1.4.3. <http://tree.bio.ed.ac.uk/software/figtree/>
34. RStudio Team. (2020). RStudio: Integrated Development for R. RStudio, PBC, Boston, MA URL <http://www.rstudio.com/>.
35. Shin H.D., Kim L.H. Neobjavljen rad. Bos taurus mitochondrion, complete genome sequence of Korean cattle, beef cattle and Holstein-Friesian. <https://www.ncbi.nlm.nih.gov>
36. Suchard MA, Lemey P, Baele G, Ayres DL, Drummond AJ & Rambaut A. (2018) Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10 *Virus Evolution* 4, vey016. DOI:10.1093/ve/vey016
37. Suchard M. A., Lemey P., Baele G., Ayres D. L., Drummond A. J., Rambaut A. (2018). BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. *PLoS Computational Biology*, 10(4), e1003537. doi:10.1371/journal.pcbi.1003537.
38. Verdugo Marta Pereira, et al. "Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent." *Science* 365.6449. (2019): 173-176.
39. Wang Z., Shen X., Liu B., Su J., Yonezawa T., Yu Y., Guo S., Ho S.Y.W., Vila C., Hasegawa M., Liu J. Neobjavljen rad. Deep genetic divergences within domesticated yak are the result of quaternary climatic oscillations and orogeny on the Qinghai-Tibetan Plateau. <https://www.ncbi.nlm.nih.gov>
40. Wickham H. (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, <https://ggplot2.tidyverse.org>.
41. Wickham H, Averick M, Bryan J, Chang W, McGowan LD, François R, Golemund G, Hayes A, Henry L, Hester J, Kuhn M, Pedersen TL, Miller E, Bache SM, Müller K, Ooms J, Robinson D, Seidel DP, Spinu V, Takahashi K, Vaughan D, Wilke C, Woo K, Yutani H. (2019). "Welcome to the tidyverse." *Journal of Open Source Software*, 4(43), 1686. doi:10.21105/joss.01686
42. Xia X. T., Achilli A., Lenstra J. A., Tong B., Ma Y., Huang Y. Z., ... & Chen N. B. (2021). Mitochondrial genomes from modern and ancient Turano-Mongolian cattle reveal an ancient diversity of taurine maternal lineages in East Asia. *Heredity*, 126(6), 1000-1008
43. Xia X., et al. "Comprehensive analysis of the mitochondrial DNA diversity in Chinese cattle." *Animal genetics* 50.1 (2019): 70-73
44. Xia X., Qu K., Zhang G., Jia Y., Ma Z., Zhao X., ... & Lei, C. (2019). Comprehensive analysis of the mitochondrial DNA diversity in Chinese cattle. *Animal genetics*, 50(1), 70-73
45. Zhang H., Paijmans J. L., Chang F., Wu X., Chen G., Lei C., ... & Hofreiter M. (2013). Morphological and genetic evidence for early Holocene cattle management in northeastern China. *Nature communications*, 4(1), 2755

9. Prilozi

Tablica P1. Popis analiziranih mitogenoma

Fasta_name	Beast haplogrupa	pasmina	vrsta	država	lokacija	Latitude_Y	Longitude_X	autor	godina
AB074964_JP_Jb_T4	T3	Japanese Black	BT	Japan	/	36.20482	138.25292	Mannen,H.	/
AF492350_LK_Zw_I2	I2	Zwergzebu	BT	Sri Lanka	/	7.87305	80.77179	Hiendleder,S.	2008
AY126697_IN_Nl_T3	I1	Nellore	BT	India	/	20.59368	78.96288	Miretti,M.M.	/
AY526085_KR_Nk_T1	T3	Korean native	BT	South Korea	/	35.90775	127.76692	Chung,H.Y.	/
DQ124375_KR_Kc_T4	T3	Korean cattle	BT	South Korea	/	35.90775	127.76692	Shin,H.D.	/
DQ124403_NL_Ho_I	I	Holstein	BT	Netherlands	/	52.13263	5.29126	Shin,H.D.	/
EU177856_IQ_Iq_T2	T2	Iraqi	BT	Iraq	/	33.22319	43.67929	Achilli,A.	2008
EU177864_IQ_Iq_T5	T5	Iraqi	BT	Iraq	/	33.22319	43.67929	Achilli,A.	2008
EU177866_IT_Cb_Q1	Q1	Cabannina	BT	Italia	/	41.87194	12.56738	Achilli,A.	2008
EU177868_IQ_Iq_I1	I1	Iraqi	BT	Iraq	/	33.22319	43.67929	Achilli,A.	2008
EU177869_IQ_Iq_I2	I2	Iraqi	BT	Iraq	/	33.22319	43.67929	Achilli,A.	2008
EU177870_IR_In_I2	I2	Iranian	BT	Iran	/	32.4279	53.68804	Achilli,A.	2008
FJ971085_IT_Ci_R1	R1	Cinisara	BT	Italia	/	41.87194	12.56738	Achilli,A.	2008
FJ971087_IT_Rm_R2	R2	Romagnola	BT	Italia	/	41.87194	12.56738	Achilli,A.	2008
FJ971088_MN_Mn_I1	I1	Mongolian	BT	Mongolia	/	46.86249	103.84665	Achilli,A.	2008
GU256940_CN_Dq_I1	I1	Diqin	BT	China	/	35.86166	104.19539	Wang,Z.	/
GU985279_GB_Bp_P1	P1		BP	United Kingdom	/	55.37805	-3.43597	Edwards,C.J.	2010
HQ184038_IT_Cb_Q1	Q1	Cabannina	BT	Italia	/	41.87194	12.56738	Bonfiglio,S.	2010
HQ184045_IT_Mc_R2	R2	Marchigiana	BT	Italia	/	41.87194	12.56738	Bonfiglio,S.	2010
JN817304_ET_As_T1	T1	Arsi	BT	Ethiopia	/	9.145	40.48967	Bonfiglio,S.	2010
JQ437479_PL_Bp_P1	P1		BP	Poland	/	51.91943	19.14513	Lipinski,D.	2012
KF163083_ZA_Ng_T1	T1	Nguni	BT	South Africa	/	-30.55948	22.9375	Horsburgh,K.A.	2013
KP143771_CN_Bt_I1	I1		BT	China	/	35.86166	104.19539	Liu,D.H.	/
KT184464_EG_Mf_T1	T1	Menofi	BT	Egypt	/	26.82055	30.80249	Olivieri,A.	2015
MK028725_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028726_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028727_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028728_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/

MK028729_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028730_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028731_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028732_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028733_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028734_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028735_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028736_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028737_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028738_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028739_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028740_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028741_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028742_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028743_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028744_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028745_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028746_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028747_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028748_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028749_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MK028750_DE_Gh_T3	T3	German Holstein	BT	Germany	/	51.16569	10.45152	Kinoshita,A.	/
MN200779_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200780_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200781_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200782_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200783_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200784_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200785_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200786_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200787_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019

MN200788_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200789_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200790_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200791_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200792_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200793_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200794_CN_Yu_T2	T2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200795_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200796_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200797_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200798_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200799_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200800_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200801_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200802_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200803_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200804_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200805_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200806_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200807_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200808_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200809_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200810_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200811_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200812_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200813_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200814_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200815_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200816_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200817_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200818_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019

MN200819_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200820_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200821_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200822_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200823_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200824_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200825_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200826_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200827_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200828_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200829_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200830_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200831_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200832_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200833_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200834_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200835_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200836_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200837_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200838_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200839_CN_Yu_T2	T2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200840_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200841_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200842_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200843_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200844_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200845_CN_Yu_T2	T2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200846_CN_Yu_T6	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200847_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200848_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200849_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019

MN200850_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200851_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200852_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200853_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200854_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200855_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200856_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200857_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200858_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200859_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200860_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200861_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200862_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200863_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200864_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200865_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200866_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200867_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200868_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200869_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200870_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200871_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200872_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200873_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200874_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200875_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200876_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200877_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200878_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200879_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200880_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019

MN200881_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200882_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200883_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200884_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200885_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200886_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200887_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200888_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200889_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200890_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200891_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200892_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200893_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200894_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200895_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200896_CN_Yu_T6	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200897_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200898_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200899_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200900_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200901_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200902_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200903_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200904_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200905_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200906_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200907_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200908_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200909_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200910_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200911_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019

MN200912_CN_Yu_T2	T2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200913_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200914_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200915_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200916_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200917_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200918_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200919_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200920_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200921_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200922_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200923_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200924_CN_Yu_I2	I2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200925_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200926_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200927_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200928_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200929_CN_Yu_T1	T1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200930_CN_Yu_T2	T2	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200931_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200932_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200933_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200934_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200935_CN_Yu_I1	I1	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200936_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200937_CN_Yu_T4	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN200938_CN_Yu_T3	T3	Yunling	BT	China	Yunnan	25.04529	102.70972	Xia,X	2019
MN714163_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714164_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714165_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714166_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019

MN714167_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714168_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714169_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714170_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714171_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714172_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714173_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714174_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714175_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714176_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714177_CN_Lg_T3	T3	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714178_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714179_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714180_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714181_CN_Lg_I1	I1	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714182_CN_Lg_T4	T3	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714183_CN_Lg_T4	T3	Longlin	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714184_CN_Nd_T3	T3	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714185_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714186_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714187_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714188_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714189_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714190_CN_Nd_T3	T3	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714191_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714192_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714193_CN_Nd_T3	T3	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714194_CN_Nd_T3	T3	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714195_CN_Nd_T3	T3	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714196_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714197_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019

MN714198_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714199_CN_Nd_I2	I2	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714200_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714201_CN_Nd_I1	I1	Nandan	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714202_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714203_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714204_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714205_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714206_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714207_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714208_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714209_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714210_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714211_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714212_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714213_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714214_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714215_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714216_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714217_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MN714218_CN_We_I1	I1	Weizhou	BT	China	/	35.86166	104.19539	Xia,X.	2019
MT576712_CN_Ax_T2	T2	Anxi	BT	China	Gansu province	36.05941	103.82634	Xia,X.T.,	2021
MT576713_CN_Ax_T2	T2	Anxi	BT	China	Gansu province	36.05941	103.82634	Xia,X.T.,	2021
MT576714_CN_Ax_T2	T2	Anxi	BT	China	Gansu province	36.05941	103.82634	Xia,X.T.,	2021
MT576715_CN_Ax_T3	T3	Anxi	BT	China	Gansu province	36.05941	103.82634	Xia,X.T.,	2021
MT576716_CN_Ax_T3	T3	Anxi	BT	China	Gansu province	36.05941	103.82634	Xia,X.T.,	2021
MT576726_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576727_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576728_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576729_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576730_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021

MT576731_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576732_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576733_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576734_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576735_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576736_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576737_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576738_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576739_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576740_CN_Tb_T2	T2	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576741_CN_Tb_T4	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576742_CN_Tb_Q1	Q1	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576743_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576744_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576745_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576746_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576747_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576748_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576749_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576750_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576751_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576752_CN_Tb_T4	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576753_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576754_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576755_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576761_KZ_Kz_T1	T3	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576762_KZ_Kz_T2	T2	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576763_KZ_Kz_T2	T2	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576764_KZ_Kz_T3	T3	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576765_KZ_Kz_T3	T3	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576766_KZ_Kz_T3	T3	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021

MT576767_KZ_Kz_T2	T2	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576768_KZ_Kz_I1	I1	Kazakh	BT	Kazakhstan	/	48.01957	66.92368	Xia,X.T.,	2021
MT576769_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576770_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576771_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576772_MN_Mn_I1	I1	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576773_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576774_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576775_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576776_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576777_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576778_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576779_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576780_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576781_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576790_CN_Tb_Q1	Q1	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576791_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576792_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576793_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576794_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576795_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576796_CN_Tb_T1	T1	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576797_CN_Tb_T1	T1	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576798_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576811_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576812_CN_Tb_Q1	Q1	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576813_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576814_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576815_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576816_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576817_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021

MT576818_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576819_CN_Tb_T3	T3	Tibetan	BT	China	Tibet	29.64723	91.11745	Xia,X.T.,	2021
MT576820_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576821_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576822_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576823_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576824_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576825_MN_Mn_T2	T2	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576826_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576827_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576828_MN_Mn_T4	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576829_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576830_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576831_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MT576832_MN_Mn_T3	T3	Mongolian	BT	Mongolia	/	46.86249	103.84665	Xia,X.T.,	2021
MZ901377_TR_Ab_T2	T2	Anatolian Black	BT	Turkey	/	38.96374	35.24332	Cubric-Curik,V.	2022
MZ901408_AT_Mu_P1	P1	Murbodner	BT	Austria	/	47.51623	14.55007	Cubric-Curik,V.	2022
MZ901409_AT_Mu_T3	T3	Murbodner	BT	Austria	/	47.51623	14.55007	Cubric-Curik,V.	2022
MZ901420_AT_Fl_T3	T3	Fleckvieh	BT	Austria	/	47.51623	14.55007	Cubric-Curik,V.	2022
MZ901623_HR_Ss_T5	T5	Slavonian Syrmian Podolian	BT	Croatia	/	45.1	15.2	Cubric-Curik,V.	2022
MZ901640_GR_Kt_T2	T2	Katerini	BT	Greece	/	39.0742	21.82431	Cubric-Curik,V.	2022
MZ901648_GR_Gs_Q1	Q1	Greece Shorthorn Pindos	BT	Greece	/	39.0742	21.82431	Cubric-Curik,V.	2022
MZ901743_AL_Sb_T5	T5	Skodra Buša	BT	Albania	/	41.15333	20.16833	Cubric-Curik,V.	2022
NC_005971_IN_Nl_I1	I1	Nellore	BT	India	/	20.59368	78.96288	Miretti,M.M.	2004
OM868266_IN_Am_I2	I2	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868267_IN_Am_I2	I2	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868268_IN_Am_I2	I2	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868269_IN_Am_T3	T3	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868270_IN_Am_T3	T3	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868271_IN_Am_I1	I1	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868272_IN_Am_I1	I1	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/

OM868273_IN_Am_I2	I2	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868274_IN_Am_I1	I1	Amrit_Mahal	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868275_IN_Bh_I1	I1	Bachaur	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868276_IN_Bh_I1	I1	Bachaur	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868277_IN_Bh_I2	I2	Bachaur	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868278_IN_Bh_I1	I1	Bachaur	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868279_IN_Bh_I1	I1	Bachaur	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868280_IN_Ba_I1	I1	Badri	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868281_IN_Ba_I1	I1	Badri	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868282_IN_Ba_I1	I1	Badri	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868283_IN_Ba_I1	I1	Badri	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868284_IN_Ba_T3	T3	Badri	BI	India	Uttarakhand	30.06675	79.01929	Manisha,S.	/
OM868285_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868286_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868287_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868288_IN_Br_I2	I2	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868289_IN_Br_I2	I2	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868290_IN_Br_I2	I2	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868291_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868292_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868293_IN_Br_I1	I1	Bargur	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868294_IN_B1_I1	I1	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868295_IN_B1_I2	I2	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868296_IN_B1_I1	I1	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868297_IN_B1_I2	I2	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868298_IN_B1_I2	I2	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868299_IN_B1_I1	I1	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868300_IN_B1_I2	I2	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868301_IN_B1_I1	I1	Belahi	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868302_IN_B1_I1	I1	Belahi	BI	India	Chandigarh	30.73331	76.77941	Manisha,S.	/
OM868303_IN_B1_I2	I2	Belahi	BI	India	Chandigarh	30.73331	76.77941	Manisha,S.	/

OM868304_IN_BI_I1	I1	Belahi	BI	India	Chandigarh	30.73331	76.77941	Manisha,S.	/
OM868305_IN_BI_I1	I1	Belahi	BI	India	Chandigarh	30.73331	76.77941	Manisha,S.	/
OM868306_IN_Bn_I2	I2	Binjharपुरi	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868307_IN_Bn_I1	I1	Binjharपुरi	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868308_IN_Bn_I1	I1	Binjharपुरi	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868309_IN_Bn_I1	I1	Binjharपुरi	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868310_IN_Dn_I1	I1	Dangi	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868311_IN_Dn_I1	I1	Dangi	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868312_IN_Dn_I2	I2	Dangi	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868313_IN_Dn_I1	I1	Dangi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868314_IN_Dn_I2	I2	Dangi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868315_IN_Dn_I2	I2	Dangi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868316_IN_De_T2	T2	Deoni	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868317_IN_De_I1	I1	Deoni	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868318_IN_De_I1	I1	Deoni	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868319_IN_De_I1	I1	Deoni	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868320_IN_De_I1	I1	Deoni	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868321_IN_Gg_I2	I2	Gangatiri	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868322_IN_Gg_I1	I1	Gangatiri	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868323_IN_Gg_I2	I2	Gangatiri	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868324_IN_Gg_I1	I1	Gangatiri	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868325_IN_Gg_I1	I1	Gangatiri	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868326_IN_Gg_I2	I2	Gangatiri	BI	India	Bihar	25.96444	85.27224	Manisha,S.	/
OM868327_IN_Gl_I1	I1	Gaolao	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868328_IN_Gl_I2	I2	Gaolao	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868329_IN_Gl_T3	T3	Gaolao	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868330_IN_Gl_I2	I2	Gaolao	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868331_IN_Gl_I2	I2	Gaolao	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868332_IN_Gu_I1	I1	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868333_IN_Gu_I1	I1	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868334_IN_Gu_I1	I1	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/

OM868335_IN_Gu_I1	I1	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868336_IN_Gu_I2	I2	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868337_IN_Gu_I2	I2	Ghumusari	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868338_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868339_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868340_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868341_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868342_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868343_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868344_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868345_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868346_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868347_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868348_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868349_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868350_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868351_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868352_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868353_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868354_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868355_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868356_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868357_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868358_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868359_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868360_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868361_IN_Gr_I2	I2	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868362_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868363_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868364_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868365_IN_Gr_I1	I1	Gir	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/

OM868366_IN_HI_I1	I1	Hallikar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868367_IN_HI_I1	I1	Hallikar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868368_IN_HI_I1	I1	Hallikar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868369_IN_HI_I2	I2	Hallikar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868370_IN_HI_I1	I1	Hallikar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868371_IN_Ha_I1	I1	Haryana	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868372_IN_Ha_I1	I1	Haryana	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868373_IN_Ha_I1	I1	Haryana	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868374_IN_Ha_I2	I2	Haryana	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868375_IN_Ha_I1	I1	Haryana	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868376_IN_Ha_I1	I1	Haryana	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868377_IN_Ha_I1	I1	Haryana	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868378_IN_Ha_I1	I1	Haryana	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868379_IN_Ha_I1	I1	Haryana	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868380_IN_Ha_I2	I2	Haryana	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868381_IN_Ha_I2	I2	Haryana	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868382_IN_Ky_I1	I1	Kangayam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868383_IN_Ky_I2	I2	Kangayam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868384_IN_Ky_I1	I1	Kangayam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868385_IN_Ky_T3	T3	Kangayam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868386_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868387_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868388_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868389_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868390_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868391_IN_Kj_I2	I2	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868392_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868393_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868394_IN_Kj_I1	I1	Kankrej	BI	India	Gujarat	22.67083	71.57239	Manisha,S.	/
OM868395_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868396_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/

OM868397_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868398_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868399_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868400_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868401_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868402_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868403_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868404_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868405_IN_Kj_I1	I1	Kankrej	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868406_IN_Kn_I2	I2	Kenkatha	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868407_IN_Kn_I1	I1	Kenkatha	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868408_IN_Kn_I2	I2	Kenkatha	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868409_IN_Kn_I1	I1	Kenkatha	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868410_IN_Kn_I1	I1	Kenkatha	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868411_IN_Kn_I1	I1	Kenkatha	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868412_IN_Ka_I1	I1	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868413_IN_Ka_I2	I2	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868414_IN_Ka_I2	I2	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868415_IN_Ka_I2	I2	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868416_IN_Ka_I1	I1	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868417_IN_Ka_I1	I1	Khariar	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868418_IN_Kr_I1	I1	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868419_IN_Kr_I2	I2	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868420_IN_Kr_T3	T3	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868421_IN_Kr_I1	I1	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868422_IN_Kr_I1	I1	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868423_IN_Kr_T3	T3	Kherigarh	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868424_IN_Kl_I1	I1	Khillar	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868425_IN_Kl_I1	I1	Khillar	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868426_IN_Kl_I2	I2	Khillar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868427_IN_Kl_I2	I2	Khillar	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/

OM868428_IN_Kk_I2	I2	Konkan_Kapila	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868429_IN_Kk_I1	I1	Konkan_Kapila	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868430_IN_Kk_I2	I2	Konkan_Kapila	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868431_IN_Kk_I1	I1	Konkan_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868432_IN_Kk_I2	I2	Konkan_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868433_IN_Ko_I1	I1	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868434_IN_Ko_I1	I1	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868435_IN_Ko_I2	I2	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868436_IN_Ko_I1	I1	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868437_IN_Ko_I1	I1	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868438_IN_Ko_I2	I2	Kosali	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868439_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868440_IN_Kv_I2	I2	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868441_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868442_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868443_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868444_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868445_IN_Kv_I1	I1	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868446_IN_Kv_I2	I2	Krishna_Valley	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868447_IN_Ld_I1	I1	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868448_IN_Ld_I1	I1	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868449_IN_Ld_I1	I1	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868450_IN_Ld_I1	I1	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868451_IN_Ld_I1	I1	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868452_IN_Ld_I2	I2	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868453_IN_Ld_I2	I2	Ladakhi	BI	India	Jammu	32.7266	74.85702	Manisha,S.	/
OM868454_IN_Ld_I2	I2	Ladakhi	BI	India	Kashmir	33.27783	75.34121	Manisha,S.	/
OM868455_IN_Ld_T3	T3	Ladakhi	BI	India	Kashmir	33.27783	75.34121	Manisha,S.	/
OM868456_IN_Ld_I2	I2	Ladakhi	BI	India	Kashmir	33.27783	75.34121	Manisha,S.	/
OM868457_IN_Ld_I2	I2	Ladakhi	BI	India	Kashmir	33.27783	75.34121	Manisha,S.	/
OM868458_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/

OM868459_IN_Lk_I2	I2	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868460_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868461_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868462_IN_Lk_T3	T3	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868463_IN_Lk_T3	T3	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868464_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868465_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868466_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868467_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868468_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868469_IN_Lk_I1	I1	Lakhimi	BI	India	Assam	26.2006	92.93757	Manisha,S.	/
OM868470_IN_Mg_I1	I1	Malnad_Gidda	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868471_IN_Mg_I2	I2	Malnad_Gidda	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868472_IN_Mg_I1	I1	Malnad_Gidda	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868473_IN_Mg_I1	I1	Malnad_Gidda	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868474_IN_Mg_I1	I1	Malnad_Gidda	BI	India	Karnataka	15.31727	75.71388	Manisha,S.	/
OM868475_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868476_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868477_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868478_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868479_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868480_IN_MI_I2	I2	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868481_IN_MI_I1	I1	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868482_IN_MI_I2	I2	Malvi	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868483_IN_Mw_I2	I2	Mewati	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868484_IN_Mw_I2	I2	Mewati	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868485_IN_Mw_I1	I1	Mewati	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868486_IN_Mw_I2	I2	Mewati	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868487_IN_Mw_I2	I2	Mewati	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868488_IN_Mw_I1	I1	Mewati	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/
OM868489_IN_Mw_I1	I1	Mewati	BI	India	Haryana	29.05877	76.0856	Manisha,S.	/

OM868490_IN_Mw_I2	I2	Mewati	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868491_IN_Mw_I2	I2	Mewati	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868492_IN_Mw_I1	I1	Mewati	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868493_IN_Mo_I1	I1	Motu	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868494_IN_Mo_I1	I1	Motu	BI	India	Orissa	20.23755	84.27001	Manisha,S.	/
OM868495_IN_Mo_I2	I2	Motu	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868496_IN_Mo_I2	I2	Motu	BI	India	Chhattisgarh	21.27865	81.86614	Manisha,S.	/
OM868497_IN_Mo_I1	I1	Motu	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868498_IN_Mo_I2	I2	Motu	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868499_IN_Na_I1	I1	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868500_IN_Na_I1	I1	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868501_IN_Na_I2	I2	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868502_IN_Na_I2	I2	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868503_IN_Na_I2	I2	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868504_IN_Na_I2	I2	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868505_IN_Na_I1	I1	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868506_IN_Na_I2	I2	Nagori	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868507_IN_Ni_I2	I2	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868508_IN_Ni_I2	I2	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868509_IN_Ni_I1	I1	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868510_IN_Ni_I2	I2	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868511_IN_Ni_I2	I2	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868512_IN_Ni_I1	I1	Nimari	BI	India	Madhya_Pradesh	22.97342	78.65689	Manisha,S.	/
OM868513_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868514_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868515_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868516_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868517_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868518_IN_On_I1	I1	Ongole	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868519_IN_Pw_I1	I1	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868520_IN_Pw_I1	I1	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/

OM868521_IN_Pw_I2	I2	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868522_IN_Pw_I2	I2	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868523_IN_Pw_T3	T3	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868524_IN_Pw_I2	I2	Ponwar	BI	India	Uttar_Pradesh	27.57058	80.09818	Manisha,S.	/
OM868525_IN_Pl_I2	I2	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868526_IN_Pl_I2	I2	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868527_IN_Pl_I1	I1	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868528_IN_Pl_I2	I2	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868529_IN_Pl_I1	I1	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868530_IN_Pl_I1	I1	Pulikulam	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868531_IN_Pn_I1	I1	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868532_IN_Pn_I1	I1	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868533_IN_Pn_I1	I1	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868534_IN_Pn_I2	I2	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868535_IN_Pn_I1	I1	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868536_IN_Pn_I1	I1	Punganur	BI	India	Andhra_Pradesh	15.91289	79.73998	Manisha,S.	/
OM868537_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868538_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868539_IN_Rt_I2	I2	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868540_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868541_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868542_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868543_IN_Rt_I1	I1	Rathi	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868544_IN_Rk_I2	I2	Red_Kandhari	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868545_IN_Rk_I2	I2	Red_Kandhari	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868546_IN_Rk_I1	I1	Red_Kandhari	BI	India	Maharashtra	19.75147	75.71388	Manisha,S.	/
OM868547_IN_Rs_I1	I1	Red_Sindhi	BI	India	/	20.59368	78.96288	Manisha,S.	/
OM868548_IN_Rs_I2	I2	Red_Sindhi	BI	India	/	20.59368	78.96288	Manisha,S.	/
OM868549_IN_Rs_I1	I1	Red_Sindhi	BI	India	/	20.59368	78.96288	Manisha,S.	/
OM868550_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868551_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/

OM868552_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868553_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868554_IN_Sw_I2	I2	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868555_IN_Sw_I2	I2	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868556_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868557_IN_Sw_I2	I2	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868558_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868559_IN_Sw_I1	I1	Sahiwal	BI	India	Punjab	31.14713	75.34121	Manisha,S.	/
OM868560_IN_Sw_I1	I1	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868561_IN_Sw_T3	T3	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868562_IN_Sw_I1	I1	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868563_IN_Sw_I2	I2	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868564_IN_Sw_I2	I2	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868565_IN_Sw_I1	I1	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868566_IN_Sw_I2	I2	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868567_IN_Sw_I1	I1	Sahiwal	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868568_IN_Sk_T3	T3	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868569_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868570_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868571_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868572_IN_Sk_I2	I2	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868573_IN_Sk_I2	I2	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868574_IN_Sk_T2	T2	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868575_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868576_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868577_IN_Sk_I1	I1	Shweta_Kapila	BI	India	Goa	15.29932	74.12399	Manisha,S.	/
OM868578_IN_Si_I1	I1	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/
OM868579_IN_Si_I2	I2	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/
OM868580_IN_Si_I1	I1	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/
OM868581_IN_Si_I1	I1	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/
OM868582_IN_Si_I2	I2	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/

OM868583_IN_Si_T3	T3	Siri	BI	India	Sikkim	27.35164	88.32393	Manisha,S.	/
OM868584_IN_Si_T3	T3	Siri	BI	India	Bengal	22.98675	87.85497	Manisha,S.	/
OM868585_IN_Si_T3	T3	Siri	BI	India	Bengal	22.98675	87.85497	Manisha,S.	/
OM868586_IN_Si_I1	I1	Siri	BI	India	Bengal	22.98675	87.85497	Manisha,S.	/
OM868587_IN_Tr_I2	I2	Tharparkar	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868588_IN_Tr_I1	I1	Tharparkar	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868589_IN_Tr_I1	I1	Tharparkar	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868590_IN_Tr_I1	I1	Tharparkar	BI	India	Rajasthan	27.0238	74.21793	Manisha,S.	/
OM868591_IN_Tt_I1	I1	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868592_IN_Tt_I1	I1	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868593_IN_Tt_I1	I1	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868594_IN_Tt_I1	I1	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868595_IN_Tt_I2	I2	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868596_IN_Tt_I1	I1	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868597_IN_Tt_I2	I2	Thutho	BI	India	Nagaland	26.15843	94.56244	Manisha,S.	/
OM868598_IN_Um_I1	I1	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868599_IN_Um_I1	I1	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868600_IN_Um_I1	I1	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868601_IN_Um_I1	I1	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868602_IN_Um_I2	I2	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868603_IN_Um_I2	I2	Umblachery	BI	India	Tamil_Nadu	11.12712	78.65689	Manisha,S.	/
OM868604_IN_Ve_I1	I1	Vechur	BI	India	Kerala	10.16315	76.64127	Manisha,S.	/
OM868605_IN_Ve_I1	I1	Vechur	BI	India	Kerala	10.16315	76.64127	Manisha,S.	/
OM868606_IN_Ve_I1	I1	Vechur	BI	India	Kerala	10.16315	76.64127	Manisha,S.	/
V00654_GB_Bt_T3	T3		BT	United Kingdom	/	55.37805	-3.43597	Anderson,S.	1982

- Fasta_ime = GenBank pristupni broj_država_pasmina_haplogrupa
- BI = *Bos indicus*
- BP = *Bos primigenius*
- BT = *Bos taurus*

Tablica P2. P-distance između svih pasmina unutar analiziranog seta

pair_1	pair_2	distanc e	pair_1	pair_2	distanc e	pair_1	pair_2	distanc e
Hariana	Nellore	0.00	Siri	Belahi	0.01	Shweta_Kapila	Pulikulam	0.00
Hallikar	Nellore	0.00	Shweta_Kapila	Belahi	0.00	Lakhimi	Pulikulam	0.00
Kangayam	Nellore	0.00	Lakhimi	Belahi	0.00	Ladakhi	Pulikulam	0.00
Kankrej	Nellore	0.00	Ladakhi	Belahi	0.00	Malnad_Gidda	Pulikulam	0.00
Gir	Nellore	0.00	Malnad_Gidda	Belahi	0.00	Malvi	Pulikulam	0.00
Khariar	Nellore	0.00	Malvi	Belahi	0.00	Krishna_Valley	Pulikulam	0.00
Kherigarh	Nellore	0.01	Krishna_Valley	Belahi	0.00	Yunglin	Pulikulam	0.01
Kenkatha	Nellore	0.00	Yunglin	Belahi	0.01	Kosali	Pulikulam	0.00
Konkan_Kapila	Nellore	0.00	Kosali	Belahi	0.00	Nagori	Pulikulam	0.00
Khillar	Nellore	0.00	Nagori	Belahi	0.00	Nimari	Pulikulam	0.00
Bargur	Nellore	0.00	Nimari	Belahi	0.00	Ongole	Pulikulam	0.00
Badri	Nellore	0.00	Ongole	Belahi	0.00	Motu	Pulikulam	0.00
Bachaur	Nellore	0.00	Motu	Belahi	0.00	Mewati	Pulikulam	0.00
Belahi	Nellore	0.00	Mewati	Belahi	0.00	Mongolian	Pulikulam	0.01
Greece_S_Pindos	Nellore	0.01	Mongolian	Belahi	0.01	G_Holstein	Pulikulam	0.01
Katerini	Nellore	0.02	G_Holstein	Belahi	0.01	Menofi	Pulikulam	0.01
Skodra_Bu~a	Nellore	0.01	Menofi	Belahi	0.01	Iraqi	Pulikulam	0.01
Amritmahal	Nellore	0.00	Iraqi	Belahi	0.01	Cabannina	Pulikulam	0.01
Murbodner	Nellore	0.02	Cabannina	Belahi	0.01	Zwergzebu	Pulikulam	0.00
Anatolian_Black	Nellore	0.01	Zwergzebu	Belahi	0.00	Japanese_black	Pulikulam	0.01
Slavonian_S_Podoliana	Nellore	0.01	Japanese_black	Belahi	0.01	Korean_native	Pulikulam	0.01
Fleckvvieh	Nellore	0.01	Korean_native	Belahi	0.02	Holstein	Pulikulam	0.00
Gaolao	Nellore	0.00	Holstein	Belahi	0.00	Korean_cattle	Pulikulam	0.01
Ghhumusari	Nellore	0.00	Korean_cattle	Belahi	0.01	Iranian	Pulikulam	0.00
Gangatiri	Nellore	0.00	Iranian	Belahi	0.00	Marhigiana	Pulikulam	0.01
Binjharपुरi	Nellore	0.00	Marhigiana	Belahi	0.01	Arsi	Pulikulam	0.01
Dangi	Nellore	0.00	Arsi	Belahi	0.01	Nguni	Pulikulam	0.01
Deoni	Nellore	0.00	Nguni	Belahi	0.01	bos_primigenius	Pulikulam	0.01
Red_Sindhi	Nellore	0.00	bos_primigenius	Belahi	0.01	Romagnola	Pulikulam	0.01
Sahiwal	Nellore	0.00	Romagnola	Belahi	0.01	Cinisara	Pulikulam	0.01
Red_Kandhari	Nellore	0.00	Cinisara	Belahi	0.01	Diqin	Pulikulam	0.00
Rathi	Nellore	0.00	Diqin	Belahi	0.00	Tibetan	Pulikulam	0.01
Pulikulam	Nellore	0.00	Tibetan	Belahi	0.01	Kazakh	Pulikulam	0.01
Ponwar	Nellore	0.00	Kazakh	Belahi	0.01	Anxi	Pulikulam	0.01
Punganur	Nellore	0.00	Anxi	Belahi	0.01	Weizhou	Pulikulam	0.00
Thutho	Nellore	0.00	Weizhou	Belahi	0.00	Longlin	Pulikulam	0.00
Tharparkar	Nellore	0.00	Longlin	Belahi	0.00	Nandan	Pulikulam	0.00
Vechur	Nellore	0.00	Nandan	Belahi	0.01	Punganur	Ponwar	0.00
Umblachery	Nellore	0.00	Katerini	Greece_S_Pindos	0.00	Thutho	Ponwar	0.00
bos_taurus	Nellore	0.01	Skodra_Bu~a	Greece_S_Pindos	0.00	Tharparkar	Ponwar	0.00
Siri	Nellore	0.01	Amritmahal	Greece_S_Pindos	0.01	Vechur	Ponwar	0.00
Shweta_Kapila	Nellore	0.00	Murbodner	Greece_S_Pindos	0.00	Umblachery	Ponwar	0.00
Lakhimi	Nellore	0.00	Anatolian_Black	Greece_S_Pindos	0.00	bos_taurus	Ponwar	0.01
Ladakhi	Nellore	0.00	Slavonian_S_Podoliana	Greece_S_Pindos	0.00	Siri	Ponwar	0.01
Malnad_Gidda	Nellore	0.00	n	Greece_S_Pindos	0.00	Shweta_Kapila	Ponwar	0.01
Malvi	Nellore	0.00	Fleckvvieh	Greece_S_Pindos	0.01	Lakhimi	Ponwar	0.00
Krishna_Valley	Nellore	0.00	Gaolao	Greece_S_Pindos	0.01	Ladakhi	Ponwar	0.00
Yunglin	Nellore	0.01	Ghhumusari	Greece_S_Pindos	0.01	Malnad_Gidda	Ponwar	0.00
Kosali	Nellore	0.00	Gangatiri	Greece_S_Pindos	0.01	Malvi	Ponwar	0.00
Nagori	Nellore	0.00	Binjharपुरi	Greece_S_Pindos	0.01	Krishna_Valley	Ponwar	0.00
Nimari	Nellore	0.00	Dangi	Greece_S_Pindos	0.01	Yunglin	Ponwar	0.01
Ongole	Nellore	0.00	Deoni	Greece_S_Pindos	0.01	Kosali	Ponwar	0.00
Motu	Nellore	0.00	Red_Sindhi	Greece_S_Pindos	0.01	Nagori	Ponwar	0.00
Mewati	Nellore	0.00	Sahiwal	Greece_S_Pindos	0.01	Nimari	Ponwar	0.00
Mongolian	Nellore	0.01	Red_Kandhari	Greece_S_Pindos	0.01	Ongole	Ponwar	0.00
G_Holstein	Nellore	0.01	Rathi	Greece_S_Pindos	0.01	Motu	Ponwar	0.00
Menofi	Nellore	0.01	Pulikulam	Greece_S_Pindos	0.01	Mewati	Ponwar	0.00
Iraqi	Nellore	0.01	Ponwar	Greece_S_Pindos	0.01	Mongolian	Ponwar	0.01
Cabannina	Nellore	0.01	Punganur	Greece_S_Pindos	0.01	G_Holstein	Ponwar	0.01
Zwergzebu	Nellore	0.00	Thutho	Greece_S_Pindos	0.01	Menofi	Ponwar	0.01
Japanese_black	Nellore	0.01	Tharparkar	Greece_S_Pindos	0.01	Iraqi	Ponwar	0.01
Korean_native	Nellore	0.02	Vechur	Greece_S_Pindos	0.01	Cabannina	Ponwar	0.01
Holstein	Nellore	0.00	Umblachery	Greece_S_Pindos	0.01	Zwergzebu	Ponwar	0.00
Korean_cattle	Nellore	0.01	bos_taurus	Greece_S_Pindos	0.01	Japanese_black	Ponwar	0.01
Iranian	Nellore	0.00	Siri	Greece_S_Pindos	0.01	Korean_native	Ponwar	0.01
			Shweta_Kapila	Greece_S_Pindos	0.01			

Marhigiana	Nellore	0.01	Lakhimi	Greece_S_Pindos	0.01	Holstein	Ponwar	0.01
Arsi	Nellore	0.01	Ladakhi	Greece_S_Pindos	0.01	Korean_cattle	Ponwar	0.01
Nguni	Nellore	0.02	Malnad_Gidda	Greece_S_Pindos	0.01	Iranian	Ponwar	0.00
bos_primigenius	Nellore	0.01	Malvi	Greece_S_Pindos	0.01	Marhigiana	Ponwar	0.01
Romagnola	Nellore	0.01	Krishna_Valley	Greece_S_Pindos	0.01	Arsi	Ponwar	0.01
Cinisara	Nellore	0.01	Yunglin	Greece_S_Pindos	0.01	Nguni	Ponwar	0.01
						bos_primigeniu		
Diqin	Nellore	0.00	Kosali	Greece_S_Pindos	0.01	s	Ponwar	0.01
Tibetan	Nellore	0.01	Nagori	Greece_S_Pindos	0.01	Romagnola	Ponwar	0.01
Kazakh	Nellore	0.01	Nimari	Greece_S_Pindos	0.01	Cinisara	Ponwar	0.01
Anxi	Nellore	0.01	Ongole	Greece_S_Pindos	0.01	Diqin	Ponwar	0.00
Weizhou	Nellore	0.00	Motu	Greece_S_Pindos	0.01	Tibetan	Ponwar	0.01
Longlin	Nellore	0.00	Mewati	Greece_S_Pindos	0.01	Kazakh	Ponwar	0.01
Nandan	Nellore	0.00	Mongolian	Greece_S_Pindos	0.00	Anxi	Ponwar	0.01
Hallikar	Hariana	0.00	G_Holstein	Greece_S_Pindos	0.00	Weizhou	Ponwar	0.00
Kangayam	Hariana	0.00	Menofi	Greece_S_Pindos	0.00	Longlin	Ponwar	0.00
Kankrej	Hariana	0.00	Iraqi	Greece_S_Pindos	0.01	Nandan	Ponwar	0.01
Gir	Hariana	0.00	Cabannina	Greece_S_Pindos	0.00	Thutho	Punganur	0.00
Khariar	Hariana	0.00	Zwergzebu	Greece_S_Pindos	0.01	Tharparkar	Punganur	0.00
Kherigarh	Hariana	0.01	Japanese_black	Greece_S_Pindos	0.00	Vechur	Punganur	0.00
Kenkatha	Hariana	0.00	Korean_native	Greece_S_Pindos	0.00	Umblachery	Punganur	0.00
Konkan_Kapila	Hariana	0.00	Holstein	Greece_S_Pindos	0.01	bos_taurus	Punganur	0.01
Khillar	Hariana	0.00	Korean_cattle	Greece_S_Pindos	0.00	Siri	Punganur	0.01
Bargur	Hariana	0.00	Iranian	Greece_S_Pindos	0.01	Shweta_Kapila	Punganur	0.00
Badri	Hariana	0.00	Marhigiana	Greece_S_Pindos	0.01	Lakhimi	Punganur	0.00
Bachaur	Hariana	0.00	Arsi	Greece_S_Pindos	0.00	Ladakhi	Punganur	0.00
Belahi	Hariana	0.00	Nguni	Greece_S_Pindos	0.00	Malnad_Gidda	Punganur	0.00
Greece_S_Pindos	Hariana	0.01	bos_primigenius	Greece_S_Pindos	0.00	Malvi	Punganur	0.00
Katerini	Hariana	0.01	Romagnola	Greece_S_Pindos	0.01	Krishna_Valley	Punganur	0.00
Skodra_Bu~a	Hariana	0.01	Cinisara	Greece_S_Pindos	0.01	Yunglin	Punganur	0.01
Amritmahal	Hariana	0.00	Diqin	Greece_S_Pindos	0.02	Kosali	Punganur	0.00
Murbodner	Hariana	0.01	Tibetan	Greece_S_Pindos	0.00	Nagori	Punganur	0.00
Anatolian_Black	Hariana	0.01	Kazakh	Greece_S_Pindos	0.00	Nimari	Punganur	0.00
Slavonian_S_Podolia								
n	Hariana	0.01	Anxi	Greece_S_Pindos	0.00	Ongole	Punganur	0.00
Fleckvvieh	Hariana	0.01	Weizhou	Greece_S_Pindos	0.01	Motu	Punganur	0.00
Gaolao	Hariana	0.00	Longlin	Greece_S_Pindos	0.01	Mewati	Punganur	0.00
Ghumusari	Hariana	0.00	Nandan	Greece_S_Pindos	0.01	Mongolian	Punganur	0.01
Gangatiri	Hariana	0.00	Skodra_Bu~a	Katerini	0.00	G_Holstein	Punganur	0.01
Binjharपुरi	Hariana	0.00	Amritmahal	Katerini	0.01	Menofi	Punganur	0.01
Dangi	Hariana	0.00	Murbodner	Katerini	0.00	Iraqi	Punganur	0.01
Deoni	Hariana	0.00	Anatolian_Black	Katerini	0.00	Cabannina	Punganur	0.01
			Slavonian_S_Podolia					
Red_Sindh	Hariana	0.00	n	Katerini	0.00	Zwergzebu	Punganur	0.00
Sahiwal	Hariana	0.00	Fleckvvieh	Katerini	0.00	Japanese_black	Punganur	0.01
Red_Kandhari	Hariana	0.00	Gaolao	Katerini	0.01	Korean_native	Punganur	0.02
Rathi	Hariana	0.00	Ghumusari	Katerini	0.01	Holstein	Punganur	0.00
Pulikulam	Hariana	0.00	Gangatiri	Katerini	0.01	Korean_cattle	Punganur	0.01
Ponwar	Hariana	0.00	Binjharपुरi	Katerini	0.01	Iranian	Punganur	0.00
Punganur	Hariana	0.00	Dangi	Katerini	0.01	Marhigiana	Punganur	0.01
Thutho	Hariana	0.00	Deoni	Katerini	0.01	Arsi	Punganur	0.01
Tharparkar	Hariana	0.00	Red_Sindh	Katerini	0.01	Nguni	Punganur	0.01
						bos_primigeniu		
Vechur	Hariana	0.00	Sahiwal	Katerini	0.01	s	Punganur	0.01
Umblachery	Hariana	0.00	Red_Kandhari	Katerini	0.01	Romagnola	Punganur	0.01
bos_taurus	Hariana	0.01	Rathi	Katerini	0.01	Cinisara	Punganur	0.01
Siri	Hariana	0.01	Pulikulam	Katerini	0.01	Diqin	Punganur	0.00
Shweta_Kapila	Hariana	0.00	Ponwar	Katerini	0.01	Tibetan	Punganur	0.01
Lakhimi	Hariana	0.00	Punganur	Katerini	0.01	Kazakh	Punganur	0.01
Ladakhi	Hariana	0.00	Thutho	Katerini	0.01	Anxi	Punganur	0.01
Malnad_Gidda	Hariana	0.00	Tharparkar	Katerini	0.01	Weizhou	Punganur	0.00
Malvi	Hariana	0.00	Vechur	Katerini	0.02	Longlin	Punganur	0.00
Krishna_Valley	Hariana	0.00	Umblachery	Katerini	0.01	Nandan	Punganur	0.00
Yunglin	Hariana	0.01	bos_taurus	Katerini	0.01	Tharparkar	Thutho	0.00
Kosali	Hariana	0.00	Siri	Katerini	0.01	Vechur	Thutho	0.00
Nagori	Hariana	0.00	Shweta_Kapila	Katerini	0.01	Umblachery	Thutho	0.00
Nimari	Hariana	0.00	Lakhimi	Katerini	0.01	bos_taurus	Thutho	0.01
Ongole	Hariana	0.00	Ladakhi	Katerini	0.01	Siri	Thutho	0.01
Motu	Hariana	0.00	Malnad_Gidda	Katerini	0.01	Shweta_Kapila	Thutho	0.00
Mewati	Hariana	0.00	Malvi	Katerini	0.01	Lakhimi	Thutho	0.00
Mongolian	Hariana	0.01	Krishna_Valley	Katerini	0.01	Ladakhi	Thutho	0.00
G_Holstein	Hariana	0.01	Yunglin	Katerini	0.01	Malnad_Gidda	Thutho	0.00
Menofi	Hariana	0.01	Kosali	Katerini	0.01	Malvi	Thutho	0.00
Iraqi	Hariana	0.01	Nagori	Katerini	0.01	Krishna_Valley	Thutho	0.00

Cabannina	Hariana	0.01	Nimari	Katerini	0.01	Yunglin	Thutho	0.01
Zwergzebu	Hariana	0.00	Ongole	Katerini	0.01	Kosali	Thutho	0.00
Japanese_black	Hariana	0.01	Motu	Katerini	0.01	Nagori	Thutho	0.00
Korean_native	Hariana	0.02	Mewati	Katerini	0.01	Nimari	Thutho	0.00
Holstein	Hariana	0.00	Mongolian	Katerini	0.00	Ongole	Thutho	0.00
Korean_cattle	Hariana	0.01	G_Holstein	Katerini	0.00	Motu	Thutho	0.00
Iranian	Hariana	0.00	Menofi	Katerini	0.00	Mewati	Thutho	0.00
Marhigiana	Hariana	0.01	Iraqi	Katerini	0.01	Mongolian	Thutho	0.01
Arsi	Hariana	0.01	Cabannina	Katerini	0.00	G_Holstein	Thutho	0.01
Nguni	Hariana	0.01	Zwergzebu	Katerini	0.01	Menofi	Thutho	0.01
bos_primigenius	Hariana	0.01	Japanese_black	Katerini	0.00	Iraqi	Thutho	0.01
Romagnola	Hariana	0.01	Korean_native	Katerini	0.00	Cabannina	Thutho	0.01
Cinisara	Hariana	0.01	Holstein	Katerini	0.01	Zwergzebu	Thutho	0.00
Diqin	Hariana	0.00	Korean_cattle	Katerini	0.00	Japanese_black	Thutho	0.01
Tibetan	Hariana	0.01	Iranian	Katerini	0.01	Korean_native	Thutho	0.02
Kazakh	Hariana	0.01	Marhigiana	Katerini	0.01	Holstein	Thutho	0.00
Anxi	Hariana	0.01	Arsi	Katerini	0.00	Korean_cattle	Thutho	0.01
Weizhou	Hariana	0.00	Nguni	Katerini	0.00	Iranian	Thutho	0.00
Longlin	Hariana	0.00	bos_primigenius	Katerini	0.00	Marhigiana	Thutho	0.01
Nandan	Hariana	0.00	Romagnola	Katerini	0.01	Arsi	Thutho	0.01
Kangayam	Hallikar	0.00	Cinisara	Katerini	0.01	Nguni	Thutho	0.01
						bos_primigeniu		
Kankrej	Hallikar	0.00	Diqin	Katerini	0.02	s	Thutho	0.01
Gir	Hallikar	0.00	Tibetan	Katerini	0.00	Romagnola	Thutho	0.01
Khariar	Hallikar	0.00	Kazakh	Katerini	0.00	Cinisara	Thutho	0.01
Kherigarh	Hallikar	0.01	Anxi	Katerini	0.00	Diqin	Thutho	0.00
Kenkatha	Hallikar	0.00	Weizhou	Katerini	0.01	Tibetan	Thutho	0.01
Konkan_Kapila	Hallikar	0.00	Longlin	Katerini	0.01	Kazakh	Thutho	0.01
Khillar	Hallikar	0.00	Nandan	Katerini	0.01	Anxi	Thutho	0.01
Bargur	Hallikar	0.00	Amritmahal	Skodra_Bu~a	0.01	Weizhou	Thutho	0.00
Badri	Hallikar	0.00	Murbodner	Skodra_Bu~a	0.00	Longlin	Thutho	0.00
Bachaur	Hallikar	0.00	Anatolian_Black	Skodra_Bu~a	0.00	Nandan	Thutho	0.00
			Slavonian_S_Podolia					
Belahi	Hallikar	0.00	n	Skodra_Bu~a	0.00	Vechur	Tharparkar	0.00
Greece_S_Pindos	Hallikar	0.01	Fleckvvieh	Skodra_Bu~a	0.00	Umblachery	Tharparkar	0.00
Katerini	Hallikar	0.01	Gaolao	Skodra_Bu~a	0.01	bos_taurus	Tharparkar	0.01
Skodra_Bu~a	Hallikar	0.01	Ghhumusari	Skodra_Bu~a	0.01	Siri	Tharparkar	0.01
Amritmahal	Hallikar	0.00	Gangatiri	Skodra_Bu~a	0.01	Shweta_Kapila	Tharparkar	0.00
Murbodner	Hallikar	0.01	Binjharpuri	Skodra_Bu~a	0.01	Lakhimi	Tharparkar	0.00
Anatolian_Black	Hallikar	0.01	Dangi	Skodra_Bu~a	0.01	Ladakhi	Tharparkar	0.00
Slavonian_S_Podolia								
n	Hallikar	0.01	Deoni	Skodra_Bu~a	0.01	Malnad_Gidda	Tharparkar	0.00
Fleckvvieh	Hallikar	0.01	Red_Sindhi	Skodra_Bu~a	0.01	Malvi	Tharparkar	0.00
Gaolao	Hallikar	0.00	Sahiwal	Skodra_Bu~a	0.01	Krishna_Valley	Tharparkar	0.00
Ghhumusari	Hallikar	0.00	Red_Kandhari	Skodra_Bu~a	0.01	Yunglin	Tharparkar	0.01
Gangatiri	Hallikar	0.00	Rathi	Skodra_Bu~a	0.01	Kosali	Tharparkar	0.00
Binjharpuri	Hallikar	0.00	Pulikulam	Skodra_Bu~a	0.01	Nagori	Tharparkar	0.00
Dangi	Hallikar	0.00	Ponwar	Skodra_Bu~a	0.01	Nimari	Tharparkar	0.00
Deoni	Hallikar	0.00	Punganur	Skodra_Bu~a	0.01	Ongole	Tharparkar	0.00
Red_Sindhi	Hallikar	0.00	Thutho	Skodra_Bu~a	0.01	Motu	Tharparkar	0.00
Sahiwal	Hallikar	0.00	Tharparkar	Skodra_Bu~a	0.01	Mewati	Tharparkar	0.00
Red_Kandhari	Hallikar	0.00	Vechur	Skodra_Bu~a	0.01	Mongolian	Tharparkar	0.01
Rathi	Hallikar	0.00	Umblachery	Skodra_Bu~a	0.01	G_Holstein	Tharparkar	0.01
Pulikulam	Hallikar	0.00	bos_taurus	Skodra_Bu~a	0.01	Menofi	Tharparkar	0.01
Ponwar	Hallikar	0.00	Siri	Skodra_Bu~a	0.01	Iraqi	Tharparkar	0.01
Punganur	Hallikar	0.00	Shweta_Kapila	Skodra_Bu~a	0.01	Cabannina	Tharparkar	0.01
Thutho	Hallikar	0.00	Lakhimi	Skodra_Bu~a	0.01	Zwergzebu	Tharparkar	0.00
Tharparkar	Hallikar	0.00	Ladakhi	Skodra_Bu~a	0.01	Japanese_black	Tharparkar	0.01
Vechur	Hallikar	0.00	Malnad_Gidda	Skodra_Bu~a	0.01	Korean_native	Tharparkar	0.02
Umblachery	Hallikar	0.00	Malvi	Skodra_Bu~a	0.01	Holstein	Tharparkar	0.00
bos_taurus	Hallikar	0.01	Krishna_Valley	Skodra_Bu~a	0.01	Korean_cattle	Tharparkar	0.02
Siri	Hallikar	0.01	Yunglin	Skodra_Bu~a	0.01	Iranian	Tharparkar	0.00
Shweta_Kapila	Hallikar	0.00	Kosali	Skodra_Bu~a	0.01	Marhigiana	Tharparkar	0.01
Lakhimi	Hallikar	0.00	Nagori	Skodra_Bu~a	0.01	Arsi	Tharparkar	0.01
Ladakhi	Hallikar	0.00	Nimari	Skodra_Bu~a	0.01	Nguni	Tharparkar	0.02
						bos_primigeniu		
Malnad_Gidda	Hallikar	0.00	Ongole	Skodra_Bu~a	0.01	s	Tharparkar	0.01
Malvi	Hallikar	0.00	Motu	Skodra_Bu~a	0.01	Romagnola	Tharparkar	0.01
Krishna_Valley	Hallikar	0.00	Mewati	Skodra_Bu~a	0.01	Cinisara	Tharparkar	0.01
Yunglin	Hallikar	0.01	Mongolian	Skodra_Bu~a	0.00	Diqin	Tharparkar	0.00
Kosali	Hallikar	0.00	G_Holstein	Skodra_Bu~a	0.00	Tibetan	Tharparkar	0.01
Nagori	Hallikar	0.00	Menofi	Skodra_Bu~a	0.00	Kazakh	Tharparkar	0.01
Nimari	Hallikar	0.00	Iraqi	Skodra_Bu~a	0.01	Anxi	Tharparkar	0.01
Ongole	Hallikar	0.00	Cabannina	Skodra_Bu~a	0.00	Weizhou	Tharparkar	0.00

Motu	Hallikar	0.00	Zwergzebu	Skodra_Bu~ ^o a	0.01	Longlin	Tharparkar	0.00
Mewati	Hallikar	0.00	Japanese_black	Skodra_Bu~ ^o a	0.00	Nandan	Tharparkar	0.01
Mongolian	Hallikar	0.01	Korean_native	Skodra_Bu~ ^o a	0.00	Umblachery	Vechur	0.00
G_Holstein	Hallikar	0.01	Holstein	Skodra_Bu~ ^o a	0.01	bos_taurus	Vechur	0.01
Menofi	Hallikar	0.01	Korean_cattle	Skodra_Bu~ ^o a	0.00	Siri	Vechur	0.01
Iraqi	Hallikar	0.01	Iranian	Skodra_Bu~ ^o a	0.01	Shweta_Kapila	Vechur	0.00
Cabannina	Hallikar	0.01	Marhigiana	Skodra_Bu~ ^o a	0.01	Lakhimi	Vechur	0.00
Zwergzebu	Hallikar	0.00	Arsi	Skodra_Bu~ ^o a	0.00	Ladakhi	Vechur	0.00
Japanese_black	Hallikar	0.01	Nguni	Skodra_Bu~ ^o a	0.00	Malnad_Gidda	Vechur	0.00
Korean_native	Hallikar	0.02	bos_primigenius	Skodra_Bu~ ^o a	0.00	Malvi	Vechur	0.00
Holstein	Hallikar	0.00	Romagnola	Skodra_Bu~ ^o a	0.01	Krishna_Valley	Vechur	0.00
Korean_cattle	Hallikar	0.01	Cinisara	Skodra_Bu~ ^o a	0.01	Yunglin	Vechur	0.01
Iranian	Hallikar	0.00	Diqin	Skodra_Bu~ ^o a	0.02	Kosali	Vechur	0.00
Marhigiana	Hallikar	0.01	Tibetan	Skodra_Bu~ ^o a	0.00	Nagori	Vechur	0.00
Arsi	Hallikar	0.01	Kazakh	Skodra_Bu~ ^o a	0.00	Nimari	Vechur	0.00
Nguni	Hallikar	0.01	Anxi	Skodra_Bu~ ^o a	0.00	Ongole	Vechur	0.00
bos_primigenius	Hallikar	0.01	Weizhou	Skodra_Bu~ ^o a	0.01	Motu	Vechur	0.00
Romagnola	Hallikar	0.01	Longlin	Skodra_Bu~ ^o a	0.01	Mewati	Vechur	0.00
Cinisara	Hallikar	0.01	Nandan	Skodra_Bu~ ^o a	0.01	Mongolian	Vechur	0.01
Diqin	Hallikar	0.00	Murbodner	Amritmahal	0.01	G_Holstein	Vechur	0.01
Tibetan	Hallikar	0.01	Anatolian_Black	Amritmahal	0.01	Menofi	Vechur	0.01
			Slavonian_S_Podolia					
Kazakh	Hallikar	0.01	n	Amritmahal	0.01	Iraqi	Vechur	0.01
Anxi	Hallikar	0.01	Fleckvvieh	Amritmahal	0.01	Cabannina	Vechur	0.01
Weizhou	Hallikar	0.00	Gaolao	Amritmahal	0.01	Zwergzebu	Vechur	0.00
Longlin	Hallikar	0.00	Ghhumusari	Amritmahal	0.00	Japanese_black	Vechur	0.01
Nandan	Hallikar	0.00	Gangatiri	Amritmahal	0.00	Korean_native	Vechur	0.02
Kankrej	Kangayam	0.00	Binjharपुरi	Amritmahal	0.00	Holstein	Vechur	0.00
Gir	Kangayam	0.00	Dangi	Amritmahal	0.00	Korean_cattle	Vechur	0.01
Khariar	Kangayam	0.00	Deoni	Amritmahal	0.01	Iranian	Vechur	0.00
Kherigarh	Kangayam	0.01	Red_Sindhi	Amritmahal	0.00	Marhigiana	Vechur	0.01
Kenkatha	Kangayam	0.00	Sahiwal	Amritmahal	0.00	Arsi	Vechur	0.01
Konkan_Kapila	Kangayam	0.00	Red_Kandhari	Amritmahal	0.00	Nguni	Vechur	0.02
						bos_primigeniu		
Khillar	Kangayam	0.00	Rathi	Amritmahal	0.00	s	Vechur	0.01
Bargur	Kangayam	0.00	Pulikulam	Amritmahal	0.00	Romagnola	Vechur	0.01
Badri	Kangayam	0.01	Ponwar	Amritmahal	0.01	Cinisara	Vechur	0.01
Bachaur	Kangayam	0.00	Punganur	Amritmahal	0.00	Diqin	Vechur	0.00
Belahi	Kangayam	0.00	Thutho	Amritmahal	0.00	Tibetan	Vechur	0.01
Greece_S_Pindos	Kangayam	0.01	Tharparkar	Amritmahal	0.00	Kazakh	Vechur	0.01
Katerini	Kangayam	0.01	Vechur	Amritmahal	0.00	Anxi	Vechur	0.01
Skodra_Bu~ ^o a	Kangayam	0.01	Umblachery	Amritmahal	0.00	Weizhou	Vechur	0.00
Amritmahal	Kangayam	0.01	bos_taurus	Amritmahal	0.01	Longlin	Vechur	0.00
Murbodner	Kangayam	0.01	Siri	Amritmahal	0.01	Nandan	Vechur	0.00
Anatolian_Black	Kangayam	0.01	Shweta_Kapila	Amritmahal	0.01	bos_taurus	Umblachery	0.01
Slavonian_S_Podolia								
n	Kangayam	0.01	Lakhimi	Amritmahal	0.01	Siri	Umblachery	0.01
Fleckvvieh	Kangayam	0.01	Ladakhi	Amritmahal	0.00	Shweta_Kapila	Umblachery	0.00
Gaolao	Kangayam	0.01	Malnad_Gidda	Amritmahal	0.00	Lakhimi	Umblachery	0.00
Ghhumusari	Kangayam	0.00	Malvi	Amritmahal	0.00	Ladakhi	Umblachery	0.00
Gangatiri	Kangayam	0.00	Krishna_Valley	Amritmahal	0.00	Malnad_Gidda	Umblachery	0.00
Binjharपुरi	Kangayam	0.00	Yunglin	Amritmahal	0.01	Malvi	Umblachery	0.00
Dangi	Kangayam	0.00	Kosali	Amritmahal	0.00	Krishna_Valley	Umblachery	0.00
Deoni	Kangayam	0.01	Nagori	Amritmahal	0.00	Yunglin	Umblachery	0.01
Red_Sindhi	Kangayam	0.00	Nimari	Amritmahal	0.00	Kosali	Umblachery	0.00
Sahiwal	Kangayam	0.00	Ongole	Amritmahal	0.00	Nagori	Umblachery	0.00
Red_Kandhari	Kangayam	0.00	Motu	Amritmahal	0.00	Nimari	Umblachery	0.00
Rathi	Kangayam	0.00	Mewati	Amritmahal	0.00	Ongole	Umblachery	0.00
Pulikulam	Kangayam	0.00	Mongolian	Amritmahal	0.01	Motu	Umblachery	0.00
Ponwar	Kangayam	0.01	G_Holstein	Amritmahal	0.01	Mewati	Umblachery	0.00
Punganur	Kangayam	0.00	Menofi	Amritmahal	0.01	Mongolian	Umblachery	0.01
Thutho	Kangayam	0.00	Iraqi	Amritmahal	0.01	G_Holstein	Umblachery	0.01
Tharparkar	Kangayam	0.00	Cabannina	Amritmahal	0.01	Menofi	Umblachery	0.01
Vechur	Kangayam	0.00	Zwergzebu	Amritmahal	0.00	Iraqi	Umblachery	0.01
Umblachery	Kangayam	0.00	Japanese_black	Amritmahal	0.01	Cabannina	Umblachery	0.01
bos_taurus	Kangayam	0.01	Korean_native	Amritmahal	0.01	Zwergzebu	Umblachery	0.00
Siri	Kangayam	0.01	Holstein	Amritmahal	0.01	Japanese_black	Umblachery	0.01
Shweta_Kapila	Kangayam	0.01	Korean_cattle	Amritmahal	0.01	Korean_native	Umblachery	0.01
Lakhimi	Kangayam	0.01	Iranian	Amritmahal	0.00	Holstein	Umblachery	0.00
Ladakhi	Kangayam	0.01	Marhigiana	Amritmahal	0.01	Korean_cattle	Umblachery	0.01
Malnad_Gidda	Kangayam	0.00	Arsi	Amritmahal	0.01	Iranian	Umblachery	0.00
Malvi	Kangayam	0.00	Nguni	Amritmahal	0.01	Marhigiana	Umblachery	0.01
Krishna_Valley	Kangayam	0.00	bos_primigenius	Amritmahal	0.01	Arsi	Umblachery	0.01
Yunglin	Kangayam	0.01	Romagnola	Amritmahal	0.01	Nguni	Umblachery	0.01

						bos_primigeniu		
Kosali	Kangayam	0.00	Cinisara	Amritmahal	0.01	s	Umblachery	0.01
Nagori	Kangayam	0.00	Diqin	Amritmahal	0.01	Romagnola	Umblachery	0.01
Nimari	Kangayam	0.00	Tibetan	Amritmahal	0.01	Cinisara	Umblachery	0.01
Ongole	Kangayam	0.00	Kazakh	Amritmahal	0.01	Diqin	Umblachery	0.00
Motu	Kangayam	0.00	Anxi	Amritmahal	0.01	Tibetan	Umblachery	0.01
Mewati	Kangayam	0.00	Weizhou	Amritmahal	0.00	Kazakh	Umblachery	0.01
Mongolian	Kangayam	0.01	Longlin	Amritmahal	0.01	Anxi	Umblachery	0.01
G_Holstein	Kangayam	0.01	Nandan	Amritmahal	0.01	Weizhou	Umblachery	0.00
Menofi	Kangayam	0.01	Anatolian_Black Slavonian_S_Podolia	Murbodner	0.00	Longlin	Umblachery	0.00
Iraqi	Kangayam	0.01	n	Murbodner	0.00	Nandan	Umblachery	0.00
Cabannina	Kangayam	0.01	Fleckvvieh	Murbodner	0.00	Siri	bos_taurus	0.01
Zwergzebu	Kangayam	0.00	Gaolao	Murbodner	0.01	Shweta_Kapila	bos_taurus	0.01
Japanese_black	Kangayam	0.01	Ghhumusari	Murbodner	0.01	Lakhimi	bos_taurus	0.01
Korean_native	Kangayam	0.01	Gangatiri	Murbodner	0.01	Ladakhi	bos_taurus	0.01
Holstein	Kangayam	0.01	Binjarpuri	Murbodner	0.01	Malnad_Gidda	bos_taurus	0.01
Korean_cattle	Kangayam	0.01	Dangi	Murbodner	0.01	Malvi	bos_taurus	0.01
Iranian	Kangayam	0.00	Deoni	Murbodner	0.01	Krishna_Valley	bos_taurus	0.01
Marhigiana	Kangayam	0.01	Red_Sindhi	Murbodner	0.01	Yunglin	bos_taurus	0.01
Arsi	Kangayam	0.01	Sahiwal	Murbodner	0.01	Kosali	bos_taurus	0.01
Nguni	Kangayam	0.01	Red_Kandhari	Murbodner	0.01	Nagori	bos_taurus	0.01
bos_primigenius	Kangayam	0.01	Rathi	Murbodner	0.01	Nimari	bos_taurus	0.01
Romagnola	Kangayam	0.01	Pulikulam	Murbodner	0.01	Ongole	bos_taurus	0.01
Cinisara	Kangayam	0.01	Ponwar	Murbodner	0.01	Motu	bos_taurus	0.01
Diqin	Kangayam	0.01	Punganur	Murbodner	0.01	Mewati	bos_taurus	0.01
Tibetan	Kangayam	0.01	Thutho	Murbodner	0.01	Mongolian	bos_taurus	0.01
Kazakh	Kangayam	0.01	Tharparkar	Murbodner	0.02	G_Holstein	bos_taurus	0.01
Anxi	Kangayam	0.01	Vechur	Murbodner	0.02	Menofi	bos_taurus	0.01
Weizhou	Kangayam	0.00	Umblachery	Murbodner	0.01	Iraqi	bos_taurus	0.01
Longlin	Kangayam	0.01	bos_taurus	Murbodner	0.01	Cabannina	bos_taurus	0.01
Nandan	Kangayam	0.01	Siri	Murbodner	0.01	Zwergzebu	bos_taurus	0.01
Gir	Kankrej	0.00	Shweta_Kapila	Murbodner	0.01	Japanese_black	bos_taurus	0.01
Khariar	Kankrej	0.00	Lakhimi	Murbodner	0.01	Korean_native	bos_taurus	0.01
Kherigarh	Kankrej	0.01	Ladakhi	Murbodner	0.01	Holstein	bos_taurus	0.01
Kenkatha	Kankrej	0.00	Malnad_Gidda	Murbodner	0.01	Korean_cattle	bos_taurus	0.01
Konkan_Kapila	Kankrej	0.00	Malvi	Murbodner	0.01	Iranian	bos_taurus	0.01
Khillar	Kankrej	0.00	Krishna_Valley	Murbodner	0.01	Marhigiana	bos_taurus	0.01
Bargur	Kankrej	0.00	Yunglin	Murbodner	0.01	Arsi	bos_taurus	0.01
Badri	Kankrej	0.00	Kosali	Murbodner	0.01	Nguni	bos_taurus	0.01
						bos_primigeniu		
Bachaur	Kankrej	0.00	Nagori	Murbodner	0.01	s	bos_taurus	0.01
Belahi	Kankrej	0.00	Nimari	Murbodner	0.01	Romagnola	bos_taurus	0.01
Greece_S_Pindos	Kankrej	0.01	Ongole	Murbodner	0.01	Cinisara	bos_taurus	0.01
Katerini	Kankrej	0.01	Motu	Murbodner	0.01	Diqin	bos_taurus	0.01
Skodra_Bu~a	Kankrej	0.01	Mewati	Murbodner	0.01	Tibetan	bos_taurus	0.01
Amritmahal	Kankrej	0.00	Mongolian	Murbodner	0.00	Kazakh	bos_taurus	0.01
Murbodner	Kankrej	0.01	G_Holstein	Murbodner	0.00	Anxi	bos_taurus	0.01
Anatolian_Black	Kankrej	0.01	Menofi	Murbodner	0.00	Weizhou	bos_taurus	0.01
Slavonian_S_Podolia								
n	Kankrej	0.01	Iraqi	Murbodner	0.01	Longlin	bos_taurus	0.01
Fleckvvieh	Kankrej	0.01	Cabannina	Murbodner	0.00	Nandan	bos_taurus	0.01
Gaolao	Kankrej	0.00	Zwergzebu	Murbodner	0.01	Shweta_Kapila	Siri	0.01
Ghhumusari	Kankrej	0.00	Japanese_black	Murbodner	0.00	Lakhimi	Siri	0.01
Gangatiri	Kankrej	0.00	Korean_native	Murbodner	0.00	Ladakhi	Siri	0.01
Binjarpuri	Kankrej	0.00	Holstein	Murbodner	0.01	Malnad_Gidda	Siri	0.01
Dangi	Kankrej	0.00	Korean_cattle	Murbodner	0.00	Malvi	Siri	0.01
Deoni	Kankrej	0.00	Iranian	Murbodner	0.01	Krishna_Valley	Siri	0.01
Red_Sindhi	Kankrej	0.00	Marhigiana	Murbodner	0.01	Yunglin	Siri	0.01
Sahiwal	Kankrej	0.00	Arsi	Murbodner	0.00	Kosali	Siri	0.01
Red_Kandhari	Kankrej	0.00	Nguni	Murbodner	0.00	Nagori	Siri	0.01
Rathi	Kankrej	0.00	bos_primigenius	Murbodner	0.00	Nimari	Siri	0.01
Pulikulam	Kankrej	0.00	Romagnola	Murbodner	0.01	Ongole	Siri	0.01
Ponwar	Kankrej	0.00	Cinisara	Murbodner	0.01	Motu	Siri	0.01
Punganur	Kankrej	0.00	Diqin	Murbodner	0.02	Mewati	Siri	0.01
Thutho	Kankrej	0.00	Tibetan	Murbodner	0.00	Mongolian	Siri	0.01
Tharparkar	Kankrej	0.00	Kazakh	Murbodner	0.00	G_Holstein	Siri	0.01
Vechur	Kankrej	0.00	Anxi	Murbodner	0.00	Menofi	Siri	0.01
Umblachery	Kankrej	0.00	Weizhou	Murbodner	0.01	Iraqi	Siri	0.01
bos_taurus	Kankrej	0.01	Longlin	Murbodner	0.01	Cabannina	Siri	0.01
Siri	Kankrej	0.01	Nandan	Murbodner	0.01	Zwergzebu	Siri	0.01
			Slavonian_S_Podolia					
Shweta_Kapila	Kankrej	0.00	n	Anatolian_Black	0.00	Japanese_black	Siri	0.01
Lakhimi	Kankrej	0.00	Fleckvvieh	Anatolian_Black	0.00	Korean_native	Siri	0.01

Ladakhi	Kankrej	0.00	Gaolao	Anatolian_Black	0.01	Holstein	Siri	0.01
Malnad_Gidda	Kankrej	0.00	Ghhumusari	Anatolian_Black	0.01	Korean_cattle	Siri	0.01
Malvi	Kankrej	0.00	Gangatiri	Anatolian_Black	0.01	Iranian	Siri	0.01
Krishna_Valley	Kankrej	0.00	Binjharपुरi	Anatolian_Black	0.01	Marhigiana	Siri	0.01
Yunglin	Kankrej	0.01	Dangi	Anatolian_Black	0.01	Arsi	Siri	0.01
Kosali	Kankrej	0.00	Deoni	Anatolian_Black	0.01	Nguni	Siri	0.01
Nagori	Kankrej	0.00	Red_Sindhi	Anatolian_Black	0.01	bos_primigenius	Siri	0.01
Nimari	Kankrej	0.00	Sahiwal	Anatolian_Black	0.01	s	Siri	0.01
Ongole	Kankrej	0.00	Red_Kandhari	Anatolian_Black	0.01	Romagnola	Siri	0.01
Motu	Kankrej	0.00	Rathi	Anatolian_Black	0.01	Cinisara	Siri	0.01
Mewati	Kankrej	0.00	Pulikulam	Anatolian_Black	0.01	Diqin	Siri	0.01
Mongolian	Kankrej	0.01	Ponwar	Anatolian_Black	0.01	Tibetan	Siri	0.01
G_Holstein	Kankrej	0.01	Punganur	Anatolian_Black	0.01	Kazakh	Siri	0.01
Menofi	Kankrej	0.01	Thutho	Anatolian_Black	0.01	Anxi	Siri	0.01
Iraqi	Kankrej	0.01	Tharparkar	Anatolian_Black	0.02	Weizhou	Siri	0.01
Cabannina	Kankrej	0.01	Vechur	Anatolian_Black	0.02	Longlin	Siri	0.01
Zwergzebu	Kankrej	0.00	Umlachery	Anatolian_Black	0.01	Nandan	Siri	0.01
Japanese_black	Kankrej	0.01	bos_taurus	Anatolian_Black	0.01	Lakhimi	Shweta_Kapila	0.01
Korean_native	Kankrej	0.01	Siri	Anatolian_Black	0.01	Ladakhi	Shweta_Kapila	0.00
Holstein	Kankrej	0.00	Shweta_Kapila	Anatolian_Black	0.01	Malnad_Gidda	Shweta_Kapila	0.00
Korean_cattle	Kankrej	0.01	Lakhimi	Anatolian_Black	0.01	Malvi	Shweta_Kapila	0.00
Iranian	Kankrej	0.00	Ladakhi	Anatolian_Black	0.01	Krishna_Valley	Shweta_Kapila	0.00
Marhigiana	Kankrej	0.01	Malnad_Gidda	Anatolian_Black	0.01	Yunglin	Shweta_Kapila	0.01
Arsi	Kankrej	0.01	Malvi	Anatolian_Black	0.01	Kosali	Shweta_Kapila	0.00
Nguni	Kankrej	0.01	Krishna_Valley	Anatolian_Black	0.01	Nagori	Shweta_Kapila	0.00
bos_primigenius	Kankrej	0.01	Yunglin	Anatolian_Black	0.01	Nimari	Shweta_Kapila	0.00
Romagnola	Kankrej	0.01	Kosali	Anatolian_Black	0.01	Ongole	Shweta_Kapila	0.00
Cinisara	Kankrej	0.01	Nagori	Anatolian_Black	0.01	Motu	Shweta_Kapila	0.00
Diqin	Kankrej	0.00	Nimari	Anatolian_Black	0.01	Mewati	Shweta_Kapila	0.00
Tibetan	Kankrej	0.01	Ongole	Anatolian_Black	0.01	Mongolian	Shweta_Kapila	0.01
Kazakh	Kankrej	0.01	Motu	Anatolian_Black	0.01	G_Holstein	Shweta_Kapila	0.01
Anxi	Kankrej	0.01	Mewati	Anatolian_Black	0.01	Menofi	Shweta_Kapila	0.01
Weizhou	Kankrej	0.00	Mongolian	Anatolian_Black	0.00	Iraqi	Shweta_Kapila	0.01
Longlin	Kankrej	0.00	G_Holstein	Anatolian_Black	0.00	Cabannina	Shweta_Kapila	0.01
Nandan	Kankrej	0.00	Menofi	Anatolian_Black	0.00	Zwergzebu	Shweta_Kapila	0.00
Khariar	Gir	0.00	Iraqi	Anatolian_Black	0.01	Japanese_black	Shweta_Kapila	0.01
Kherigarh	Gir	0.01	Cabannina	Anatolian_Black	0.00	Korean_native	Shweta_Kapila	0.01
Kenkatha	Gir	0.00	Zwergzebu	Anatolian_Black	0.01	Holstein	Shweta_Kapila	0.01
Konkan_Kapila	Gir	0.00	Japanese_black	Anatolian_Black	0.00	Korean_cattle	Shweta_Kapila	0.01
Khillar	Gir	0.00	Korean_native	Anatolian_Black	0.00	Iranian	Shweta_Kapila	0.00
Bargur	Gir	0.00	Holstein	Anatolian_Black	0.01	Marhigiana	Shweta_Kapila	0.01
Badri	Gir	0.00	Korean_cattle	Anatolian_Black	0.00	Arsi	Shweta_Kapila	0.01
Bachaur	Gir	0.00	Iranian	Anatolian_Black	0.01	Nguni	Shweta_Kapila	0.01
Belahi	Gir	0.00	Marhigiana	Anatolian_Black	0.01	bos_primigenius	Siri	0.01
Greece_S_Pindos	Gir	0.01	Arsi	Anatolian_Black	0.00	s	Shweta_Kapila	0.01
Katerini	Gir	0.01	Nguni	Anatolian_Black	0.00	Romagnola	Shweta_Kapila	0.01
Skodra_Bu [≈] a	Gir	0.01	bos_primigenius	Anatolian_Black	0.00	Cinisara	Shweta_Kapila	0.01
Amritmahal	Gir	0.00	Romagnola	Anatolian_Black	0.01	Diqin	Shweta_Kapila	0.01
Murbodner	Gir	0.01	Cinisara	Anatolian_Black	0.01	Tibetan	Shweta_Kapila	0.01
Anatolian_Black	Gir	0.01	Diqin	Anatolian_Black	0.02	Kazakh	Shweta_Kapila	0.01
Slavonian_S_Podolia	Gir	0.01	Tibetan	Anatolian_Black	0.00	Anxi	Shweta_Kapila	0.01
n	Gir	0.01	Fleckvvieh	Anatolian_Black	0.00	Weizhou	Shweta_Kapila	0.00
Fleckvvieh	Gir	0.01	Kazakh	Anatolian_Black	0.00	Longlin	Shweta_Kapila	0.01
Gaolao	Gir	0.00	Anxi	Anatolian_Black	0.00	Nandan	Shweta_Kapila	0.01
Ghhumusari	Gir	0.00	Weizhou	Anatolian_Black	0.01	Ladakhi	Lakhimi	0.00
Gangatiri	Gir	0.00	Longlin	Anatolian_Black	0.01	Malnad_Gidda	Lakhimi	0.00
Binjharपुरi	Gir	0.00	Nandan	Anatolian_Black	0.01	Malvi	Lakhimi	0.00
Dangi	Gir	0.00	Fleckvvieh	Slavonian_S_Podolia	0.00	Krishna_Valley	Lakhimi	0.00
Deoni	Gir	0.00	Gaolao	n	0.01	Yunglin	Lakhimi	0.01
Red_Sindhi	Gir	0.00	Ghhumusari	Slavonian_S_Podolia	0.01	Kosali	Lakhimi	0.00
Sahiwal	Gir	0.00	Gangatiri	n	0.01	Nagori	Lakhimi	0.00
Red_Kandhari	Gir	0.00	Binjharपुरi	Slavonian_S_Podolia	0.01	Nimari	Lakhimi	0.00
Rathi	Gir	0.00	Dangi	n	0.01	Ongole	Lakhimi	0.00
Pulikulam	Gir	0.00	Deoni	Slavonian_S_Podolia	0.01	Motu	Lakhimi	0.00
				n	0.01	Mewati	Lakhimi	0.00

Ponwar	Gir	0.00	Red_Sindhi	Slavonian_S_Podolia n	0.01	Mongolian	Lakhimi	0.01
Punganur	Gir	0.00	Sahiwal	Slavonian_S_Podolia n	0.01	G_Holstein	Lakhimi	0.01
Thutho	Gir	0.00	Red_Kandhari	Slavonian_S_Podolia n	0.01	Menofi	Lakhimi	0.01
Tharparkar	Gir	0.00	Rathi	Slavonian_S_Podolia n	0.01	Iraqi	Lakhimi	0.01
Vechur	Gir	0.00	Pulikulam	Slavonian_S_Podolia n	0.01	Cabannina	Lakhimi	0.01
Umblachery	Gir	0.00	Ponwar	Slavonian_S_Podolia n	0.01	Zwergzebu	Lakhimi	0.00
bos_taurus	Gir	0.01	Punganur	Slavonian_S_Podolia n	0.01	Japanese_black	Lakhimi	0.01
Siri	Gir	0.01	Thutho	Slavonian_S_Podolia n	0.01	Korean_native	Lakhimi	0.01
Shweta_Kapila	Gir	0.00	Tharparkar	Slavonian_S_Podolia n	0.01	Holstein	Lakhimi	0.01
Lakhimi	Gir	0.00	Vechur	Slavonian_S_Podolia n	0.01	Korean_cattle	Lakhimi	0.01
Ladakhi	Gir	0.00	Umblachery	Slavonian_S_Podolia n	0.01	Iranian	Lakhimi	0.00
Malnad_Gidda	Gir	0.00	bos_taurus	Slavonian_S_Podolia n	0.01	Marhigiana	Lakhimi	0.01
Malvi	Gir	0.00	Siri	Slavonian_S_Podolia n	0.01	Arsi	Lakhimi	0.01
Krishna_Valley	Gir	0.00	Shweta_Kapila	Slavonian_S_Podolia n	0.01	Nguni bos_primigenius	Lakhimi	0.01
Yunglin	Gir	0.01	Lakhimi	Slavonian_S_Podolia n	0.01	Romagnola	Lakhimi	0.01
Kosali	Gir	0.00	Ladakhi	Slavonian_S_Podolia n	0.01	Cinisara	Lakhimi	0.01
Nagori	Gir	0.00	Malnad_Gidda	Slavonian_S_Podolia n	0.01	Diqin	Lakhimi	0.00
Nimari	Gir	0.00	Malvi	Slavonian_S_Podolia n	0.01	Tibetan	Lakhimi	0.01
Ongole	Gir	0.00	Krishna_Valley	Slavonian_S_Podolia n	0.01	Kazakh	Lakhimi	0.01
Motu	Gir	0.00	Yunglin	Slavonian_S_Podolia n	0.01	Anxi	Lakhimi	0.01
Mewati	Gir	0.00	Kosali	Slavonian_S_Podolia n	0.01	Weizhou	Lakhimi	0.00
Mongolian	Gir	0.01	Nagori	Slavonian_S_Podolia n	0.01	Longlin	Lakhimi	0.00
G_Holstein	Gir	0.01	Nimari	Slavonian_S_Podolia n	0.01	Nandan	Lakhimi	0.01
Menofi	Gir	0.01	Ongole	Slavonian_S_Podolia n	0.01	Malnad_Gidda	Ladakhi	0.00
Iraqi	Gir	0.01	Motu	Slavonian_S_Podolia n	0.01	Malvi	Ladakhi	0.00
Cabannina	Gir	0.01	Mewati	Slavonian_S_Podolia n	0.01	Krishna_Valley	Ladakhi	0.00
Zwergzebu	Gir	0.00	Mongolian	Slavonian_S_Podolia n	0.00	Yunglin	Ladakhi	0.01
Japanese_black	Gir	0.01	G_Holstein	Slavonian_S_Podolia n	0.00	Kosali	Ladakhi	0.00
Korean_native	Gir	0.02	Menofi	Slavonian_S_Podolia n	0.01	Nagori	Ladakhi	0.00
Holstein	Gir	0.00	Iraqi	Slavonian_S_Podolia n	0.01	Nimari	Ladakhi	0.00
Korean_cattle	Gir	0.01	Cabannina	Slavonian_S_Podolia n	0.01	Ongole	Ladakhi	0.00
Iranian	Gir	0.00	Zwergzebu	Slavonian_S_Podolia n	0.01	Motu	Ladakhi	0.00
Marhigiana	Gir	0.01	Japanese_black	Slavonian_S_Podolia n	0.00	Mewati	Ladakhi	0.00
Arsi	Gir	0.01	Korean_native	Slavonian_S_Podolia n	0.01	Mongolian	Ladakhi	0.01
Nguni	Gir	0.01	Holstein	Slavonian_S_Podolia n	0.00	G_Holstein	Ladakhi	0.01
bos_primigenius	Gir	0.01	Korean_cattle	Slavonian_S_Podolia n	0.01	Menofi	Ladakhi	0.01
Romagnola	Gir	0.01	Iranian	Slavonian_S_Podolia n	0.01			

Cinisara	Gir	0.01	Marhigiana	Slavonian_S_Podolia	0.01	Iraqi	Ladakhi	0.01
Diqin	Gir	0.00	Arsi	Slavonian_S_Podolia	0.00	Cabannina	Ladakhi	0.01
Tibetan	Gir	0.01	Nguni	Slavonian_S_Podolia	0.00	Zwergzebu	Ladakhi	0.00
Kazakh	Gir	0.01	bos_primigenius	Slavonian_S_Podolia	0.00	Japanese_black	Ladakhi	0.01
Anxi	Gir	0.01	Romagnola	Slavonian_S_Podolia	0.01	Korean_native	Ladakhi	0.01
Weizhou	Gir	0.00	Cinisara	Slavonian_S_Podolia	0.01	Holstein	Ladakhi	0.01
Longlin	Gir	0.00	Diqin	Slavonian_S_Podolia	0.02	Korean_cattle	Ladakhi	0.01
Nandan	Gir	0.00	Tibetan	Slavonian_S_Podolia	0.00	Iranian	Ladakhi	0.00
Kherigarh	Khariar	0.01	Kazakh	Slavonian_S_Podolia	0.00	Marhigiana	Ladakhi	0.01
Kenkatha	Khariar	0.00	Anxi	Slavonian_S_Podolia	0.00	Arsi	Ladakhi	0.01
Konkan_Kapila	Khariar	0.00	Weizhou	Slavonian_S_Podolia	0.01	Nguni	Ladakhi	0.01
Khillar	Khariar	0.00	Longlin	Slavonian_S_Podolia	0.01	bos_primigenius	Ladakhi	0.01
Bargur	Khariar	0.00	Nandan	Slavonian_S_Podolia	0.01	Romagnola	Ladakhi	0.01
Badri	Khariar	0.00	Gaolao	Fleckvvieh	0.01	Cinisara	Ladakhi	0.01
Bachaur	Khariar	0.00	Ghhumusari	Fleckvvieh	0.01	Diqin	Ladakhi	0.00
Belahi	Khariar	0.00	Gangatiri	Fleckvvieh	0.01	Tibetan	Ladakhi	0.01
Greece_S_Pindos	Khariar	0.01	Binjharपुरi	Fleckvvieh	0.01	Kazakh	Ladakhi	0.01
Katerini	Khariar	0.01	Dangi	Fleckvvieh	0.01	Anxi	Ladakhi	0.01
Skodra_Bu ^o a	Khariar	0.01	Deoni	Fleckvvieh	0.01	Weizhou	Ladakhi	0.00
Amritmahal	Khariar	0.00	Red_Sindhi	Fleckvvieh	0.01	Longlin	Ladakhi	0.00
Murbodner	Khariar	0.01	Sahiwal	Fleckvvieh	0.01	Nandan	Ladakhi	0.01
Anatolian_Black	Khariar	0.01	Red_Kandhari	Fleckvvieh	0.01	Malvi	Malnad_Gidda	0.00
Slavonian_S_Podolia	Khariar	0.01	Rathi	Fleckvvieh	0.01	Krishna_Valley	Malnad_Gidda	0.00
Fleckvvieh	Khariar	0.01	Pulikulam	Fleckvvieh	0.01	Yunglin	Malnad_Gidda	0.01
Gaolao	Khariar	0.00	Ponwar	Fleckvvieh	0.01	Kosali	Malnad_Gidda	0.00
Ghhumusari	Khariar	0.00	Punganur	Fleckvvieh	0.01	Nagori	Malnad_Gidda	0.00
Gangatiri	Khariar	0.00	Thutho	Fleckvvieh	0.01	Nimari	Malnad_Gidda	0.00
Binjharपुरi	Khariar	0.00	Tharparkar	Fleckvvieh	0.02	Ongole	Malnad_Gidda	0.00
Dangi	Khariar	0.00	Vechur	Fleckvvieh	0.01	Motu	Malnad_Gidda	0.00
Deoni	Khariar	0.00	Umblachery	Fleckvvieh	0.01	Mewati	Malnad_Gidda	0.00
Red_Sindhi	Khariar	0.00	bos_taurus	Fleckvvieh	0.01	Mongolian	Malnad_Gidda	0.01
Sahiwal	Khariar	0.00	Siri	Fleckvvieh	0.01	G_Holstein	Malnad_Gidda	0.01
Red_Kandhari	Khariar	0.00	Shweta_Kapila	Fleckvvieh	0.01	Menofi	Malnad_Gidda	0.01
Rathi	Khariar	0.00	Lakhimi	Fleckvvieh	0.01	Iraqi	Malnad_Gidda	0.01
Pulikulam	Khariar	0.00	Ladakhi	Fleckvvieh	0.01	Cabannina	Malnad_Gidda	0.01
Ponwar	Khariar	0.00	Malnad_Gidda	Fleckvvieh	0.01	Zwergzebu	Malnad_Gidda	0.00
Punganur	Khariar	0.00	Malvi	Fleckvvieh	0.01	Japanese_black	Malnad_Gidda	0.01
Thutho	Khariar	0.00	Krishna_Valley	Fleckvvieh	0.01	Korean_native	Malnad_Gidda	0.02
Tharparkar	Khariar	0.00	Yunglin	Fleckvvieh	0.01	Holstein	Malnad_Gidda	0.00
Vechur	Khariar	0.00	Kosali	Fleckvvieh	0.01	Korean_cattle	Malnad_Gidda	0.01
Umblachery	Khariar	0.00	Nagori	Fleckvvieh	0.01	Iranian	Malnad_Gidda	0.00
bos_taurus	Khariar	0.01	Nimari	Fleckvvieh	0.01	Marhigiana	Malnad_Gidda	0.01
Siri	Khariar	0.01	Ongole	Fleckvvieh	0.01	Arsi	Malnad_Gidda	0.01
Shweta_Kapila	Khariar	0.00	Motu	Fleckvvieh	0.01	Nguni	Malnad_Gidda	0.01
Lakhimi	Khariar	0.00	Mewati	Fleckvvieh	0.01	bos_primigenius	Malnad_Gidda	0.01
Ladakhi	Khariar	0.00	Mongolian	Fleckvvieh	0.00	Romagnola	Malnad_Gidda	0.01
Malnad_Gidda	Khariar	0.00	G_Holstein	Fleckvvieh	0.00	Cinisara	Malnad_Gidda	0.01
Malvi	Khariar	0.00	Menofi	Fleckvvieh	0.00	Diqin	Malnad_Gidda	0.00
Krishna_Valley	Khariar	0.00	Iraqi	Fleckvvieh	0.01	Tibetan	Malnad_Gidda	0.01
Yunglin	Khariar	0.01	Cabannina	Fleckvvieh	0.00	Kazakh	Malnad_Gidda	0.01
Kosali	Khariar	0.00	Zwergzebu	Fleckvvieh	0.01	Anxi	Malnad_Gidda	0.01
Nagori	Khariar	0.00	Japanese_black	Fleckvvieh	0.00	Weizhou	Malnad_Gidda	0.00
Nimari	Khariar	0.00	Korean_native	Fleckvvieh	0.00	Longlin	Malnad_Gidda	0.00
Ongole	Khariar	0.00	Holstein	Fleckvvieh	0.01	Nandan	Malnad_Gidda	0.00
Motu	Khariar	0.00	Korean_cattle	Fleckvvieh	0.00	Krishna_Valley	Malvi	0.00
Mewati	Khariar	0.00	Iranian	Fleckvvieh	0.01	Yunglin	Malvi	0.01
Mongolian	Khariar	0.01	Marhigiana	Fleckvvieh	0.01	Kosali	Malvi	0.00
G_Holstein	Khariar	0.01	Arsi	Fleckvvieh	0.00	Nagori	Malvi	0.00
Menofi	Khariar	0.01	Nguni	Fleckvvieh	0.00	Nimari	Malvi	0.00

Iraqi	Khariar	0.01	bos_primigenius	Fleckvvieh	0.00	Ongole	Malvi	0.00
Cabannina	Khariar	0.01	Romagnola	Fleckvvieh	0.01	Motu	Malvi	0.00
Zwergzebu	Khariar	0.00	Cinisara	Fleckvvieh	0.01	Mewati	Malvi	0.00
Japanese_black	Khariar	0.01	Diqin	Fleckvvieh	0.02	Mongolian	Malvi	0.01
Korean_native	Khariar	0.01	Tibetan	Fleckvvieh	0.00	G_Holstein	Malvi	0.01
Holstein	Khariar	0.00	Kazakh	Fleckvvieh	0.00	Menofi	Malvi	0.01
Korean_cattle	Khariar	0.01	Anxi	Fleckvvieh	0.00	Iraqi	Malvi	0.01
Iranian	Khariar	0.00	Weizhou	Fleckvvieh	0.01	Cabannina	Malvi	0.01
Marhigiana	Khariar	0.01	Longlin	Fleckvvieh	0.01	Zwergzebu	Malvi	0.00
Arsi	Khariar	0.01	Nandan	Fleckvvieh	0.01	Japanese_black	Malvi	0.01
Nguni	Khariar	0.01	Ghhumusari	Gaolao	0.00	Korean_native	Malvi	0.02
bos_primigenius	Khariar	0.01	Gangatiri	Gaolao	0.00	Holstein	Malvi	0.00
Romagnola	Khariar	0.01	Binjharपुरi	Gaolao	0.00	Korean_cattle	Malvi	0.01
Cinisara	Khariar	0.01	Dangi	Gaolao	0.00	Iranian	Malvi	0.00
Diqin	Khariar	0.00	Deoni	Gaolao	0.01	Marhigiana	Malvi	0.01
Tibetan	Khariar	0.01	Red_Sindhi	Gaolao	0.00	Arsi	Malvi	0.01
Kazakh	Khariar	0.01	Sahiwal	Gaolao	0.00	Nguni	Malvi	0.01
Anxi	Khariar	0.01	Red_Kandhari	Gaolao	0.00	bos_primigenius	Malvi	0.01
Weizhou	Khariar	0.00	Rathi	Gaolao	0.00	Romagnola	Malvi	0.01
Longlin	Khariar	0.00	Pulikulam	Gaolao	0.00	Cinisara	Malvi	0.01
Nandan	Khariar	0.00	Ponwar	Gaolao	0.01	Diqin	Malvi	0.00
Kenkatha	Kherigarh	0.01	Punganur	Gaolao	0.00	Tibetan	Malvi	0.01
Konkan_Kapila	Kherigarh	0.01	Thutho	Gaolao	0.00	Kazakh	Malvi	0.01
Khillar	Kherigarh	0.01	Tharparkar	Gaolao	0.00	Anxi	Malvi	0.01
Bargur	Kherigarh	0.01	Vechur	Gaolao	0.00	Weizhou	Malvi	0.00
Badri	Kherigarh	0.01	Umblachery	Gaolao	0.00	Longlin	Malvi	0.00
Bachaur	Kherigarh	0.01	bos_taurus	Gaolao	0.01	Nandan	Malvi	0.00
Belahi	Kherigarh	0.01	Siri	Gaolao	0.01	Yunglin	Krishna_Valley	0.01
Greece_S_Pindos	Kherigarh	0.01	Shweta_Kapila	Gaolao	0.01	Kosali	Krishna_Valley	0.00
Katerini	Kherigarh	0.01	Lakhimi	Gaolao	0.01	Nagori	Krishna_Valley	0.00
Skodra_Bu ^o a	Kherigarh	0.01	Ladakhi	Gaolao	0.00	Nimari	Krishna_Valley	0.00
Amritmahal	Kherigarh	0.01	Malnad_Gidda	Gaolao	0.00	Ongole	Krishna_Valley	0.00
Murbodner	Kherigarh	0.01	Malvi	Gaolao	0.00	Motu	Krishna_Valley	0.00
Anatolian_Black	Kherigarh	0.01	Krishna_Valley	Gaolao	0.00	Mewati	Krishna_Valley	0.00
Slavonian_S_Podolia	Kherigarh	0.01	Yunglin	Gaolao	0.01	Mongolian	Krishna_Valley	0.01
n	Kherigarh	0.01	Kosali	Gaolao	0.00	G_Holstein	Krishna_Valley	0.01
Fleckvvieh	Kherigarh	0.01	Nagori	Gaolao	0.00	Menofi	Krishna_Valley	0.01
Gaolao	Kherigarh	0.01	Nimari	Gaolao	0.00	Iraqi	Krishna_Valley	0.01
Ghhumusari	Kherigarh	0.01	Ongole	Gaolao	0.00	Cabannina	Krishna_Valley	0.01
Gangatiri	Kherigarh	0.01	Motu	Gaolao	0.00	Zwergzebu	Krishna_Valley	0.00
Binjharपुरi	Kherigarh	0.01	Mewati	Gaolao	0.00	Japanese_black	Krishna_Valley	0.01
Dangi	Kherigarh	0.01	Mongolian	Gaolao	0.01	Korean_native	Krishna_Valley	0.02
Deoni	Kherigarh	0.01	G_Holstein	Gaolao	0.01	Holstein	Krishna_Valley	0.00
Red_Sindhi	Kherigarh	0.01	Menofi	Gaolao	0.01	Korean_cattle	Krishna_Valley	0.01
Sahiwal	Kherigarh	0.01	Iraqi	Gaolao	0.01	Iranian	Krishna_Valley	0.00
Red_Kandhari	Kherigarh	0.01	Rathi	Gaolao	0.01	Marhigiana	Krishna_Valley	0.01
Pulikulam	Kherigarh	0.01	Cabannina	Gaolao	0.00	Arsi	Krishna_Valley	0.01
Ponwar	Kherigarh	0.01	Zwergzebu	Gaolao	0.01	Nguni	Krishna_Valley	0.01
Punganur	Kherigarh	0.01	Japanese_black	Gaolao	0.01	bos_primigenius	Krishna_Valley	0.01
Thutho	Kherigarh	0.01	Korean_native	Gaolao	0.01	s	Krishna_Valley	0.01
Tharparkar	Kherigarh	0.01	Holstein	Gaolao	0.01	Romagnola	Krishna_Valley	0.01
Vechur	Kherigarh	0.01	Korean_cattle	Gaolao	0.01	Cinisara	Krishna_Valley	0.01
Umblachery	Kherigarh	0.01	Iranian	Gaolao	0.00	Diqin	Krishna_Valley	0.00
bos_taurus	Kherigarh	0.01	Marhigiana	Gaolao	0.01	Tibetan	Krishna_Valley	0.01
Siri	Kherigarh	0.01	Arsi	Gaolao	0.01	Kazakh	Krishna_Valley	0.01
Shweta_Kapila	Kherigarh	0.01	Nguni	Gaolao	0.01	Anxi	Krishna_Valley	0.01
Lakhimi	Kherigarh	0.01	bos_primigenius	Gaolao	0.01	Weizhou	Krishna_Valley	0.00
Ladakhi	Kherigarh	0.01	Romagnola	Gaolao	0.01	Longlin	Krishna_Valley	0.00
Malnad_Gidda	Kherigarh	0.01	Cinisara	Gaolao	0.01	Nandan	Krishna_Valley	0.00
Malvi	Kherigarh	0.01	Diqin	Gaolao	0.01	Kosali	Yunglin	0.01
Krishna_Valley	Kherigarh	0.01	Tibetan	Gaolao	0.01	Nagori	Yunglin	0.01
Yunglin	Kherigarh	0.01	Kazakh	Gaolao	0.01	Nimari	Yunglin	0.01
Kosali	Kherigarh	0.01	Anxi	Gaolao	0.01	Ongole	Yunglin	0.01
Nagori	Kherigarh	0.01	Weizhou	Gaolao	0.00	Motu	Yunglin	0.01
Nimari	Kherigarh	0.01	Longlin	Gaolao	0.01	Mewati	Yunglin	0.01
Ongole	Kherigarh	0.01	Nandan	Gaolao	0.01	Mongolian	Yunglin	0.01
Motu	Kherigarh	0.01	Gangatiri	Ghhumusari	0.00	G_Holstein	Yunglin	0.01
Mewati	Kherigarh	0.01	Binjharपुरi	Ghhumusari	0.00	Menofi	Yunglin	0.01
Mongolian	Kherigarh	0.01	Dangi	Ghhumusari	0.00	Iraqi	Yunglin	0.01
G_Holstein	Kherigarh	0.01	Deoni	Ghhumusari	0.00	Cabannina	Yunglin	0.01
Menofi	Kherigarh	0.01	Red_Sindhi	Ghhumusari	0.00	Zwergzebu	Yunglin	0.01
			Sahiwal	Ghhumusari	0.00	Japanese_black	Yunglin	0.01

Iraqi	Kherigarh	0.01	Red_Kandhari	Ghhumusari	0.00	Korean_native	Yunglin	0.01
Cabannina	Kherigarh	0.01	Rathi	Ghhumusari	0.00	Holstein	Yunglin	0.01
Zwergzebu	Kherigarh	0.01	Pulikulam	Ghhumusari	0.00	Korean_cattle	Yunglin	0.01
Japanese_black	Kherigarh	0.01	Ponwar	Ghhumusari	0.00	Iranian	Yunglin	0.01
Korean_native	Kherigarh	0.01	Punganur	Ghhumusari	0.00	Marhigiana	Yunglin	0.01
Holstein	Kherigarh	0.01	Thutho	Ghhumusari	0.00	Arsi	Yunglin	0.01
Korean_cattle	Kherigarh	0.01	Tharparkar	Ghhumusari	0.00	Nguni	Yunglin	0.01
Iranian	Kherigarh	0.01	Vechur	Ghhumusari	0.00	bos_primigenius	Yunglin	0.01
Marhigiana	Kherigarh	0.01	Umblachery	Ghhumusari	0.00	s	Yunglin	0.01
Arsi	Kherigarh	0.01	bos_taurus	Ghhumusari	0.01	Romagnola	Yunglin	0.01
Nguni	Kherigarh	0.01	Siri	Ghhumusari	0.01	Cinisara	Yunglin	0.01
bos_primigenius	Kherigarh	0.01	Shweta_Kapila	Ghhumusari	0.00	Diqin	Yunglin	0.01
Romagnola	Kherigarh	0.01	Lakhimi	Ghhumusari	0.00	Tibetan	Yunglin	0.01
Cinisara	Kherigarh	0.01	Ladakhi	Ghhumusari	0.00	Kazakh	Yunglin	0.01
Diqin	Kherigarh	0.01	Malnad_Gidda	Ghhumusari	0.00	Anxi	Yunglin	0.01
Tibetan	Kherigarh	0.01	Malvi	Ghhumusari	0.00	Weizhou	Yunglin	0.01
Kazakh	Kherigarh	0.01	Krishna_Valley	Ghhumusari	0.00	Longlin	Yunglin	0.01
Anxi	Kherigarh	0.01	Yunglin	Ghhumusari	0.01	Nandan	Yunglin	0.01
Weizhou	Kherigarh	0.01	Kosali	Ghhumusari	0.00	Nagori	Kosali	0.00
Longlin	Kherigarh	0.01	Nagori	Ghhumusari	0.00	Nimari	Kosali	0.00
Nandan	Kherigarh	0.01	Nimari	Ghhumusari	0.00	Ongole	Kosali	0.00
Konkan_Kapila	Kenkatha	0.00	Ongole	Ghhumusari	0.00	Motu	Kosali	0.00
Khillar	Kenkatha	0.00	Motu	Ghhumusari	0.00	Mewati	Kosali	0.00
Bargur	Kenkatha	0.00	Mewati	Ghhumusari	0.00	Mongolian	Kosali	0.01
Badri	Kenkatha	0.00	Mongolian	Ghhumusari	0.01	G_Holstein	Kosali	0.01
Bachaur	Kenkatha	0.00	G_Holstein	Ghhumusari	0.01	Menofi	Kosali	0.01
Belahi	Kenkatha	0.00	Menofi	Ghhumusari	0.01	Iraqi	Kosali	0.01
Greece_S_Pindos	Kenkatha	0.01	Iraqi	Ghhumusari	0.01	Cabannina	Kosali	0.01
Katerini	Kenkatha	0.01	Cabannina	Ghhumusari	0.01	Zwergzebu	Kosali	0.00
Skodra_Bu~a	Kenkatha	0.01	Zwergzebu	Ghhumusari	0.00	Japanese_black	Kosali	0.01
Amritmahal	Kenkatha	0.00	Japanese_black	Ghhumusari	0.01	Korean_native	Kosali	0.02
Murbodner	Kenkatha	0.01	Korean_native	Ghhumusari	0.02	Holstein	Kosali	0.00
Anatolian_Black	Kenkatha	0.01	Holstein	Ghhumusari	0.00	Korean_cattle	Kosali	0.01
Slavonian_S_Podolia	Kenkatha	0.01	Korean_cattle	Ghhumusari	0.01	Iranian	Kosali	0.00
n	Kenkatha	0.01	Iranian	Ghhumusari	0.00	Marhigiana	Kosali	0.01
Fleckvvieh	Kenkatha	0.01	Marhigiana	Ghhumusari	0.01	Arsi	Kosali	0.01
Gaolao	Kenkatha	0.00		Ghhumusari	0.00	Nguni	Kosali	0.01
Ghhumusari	Kenkatha	0.00		Ghhumusari	0.01	bos_primigenius	Kosali	0.01
Gangatiri	Kenkatha	0.00	Arsi	Ghhumusari	0.01	s	Kosali	0.01
Binjharपुरi	Kenkatha	0.00	Nguni	Ghhumusari	0.01	Romagnola	Kosali	0.01
Dangi	Kenkatha	0.00	bos_primigenius	Ghhumusari	0.01	Cinisara	Kosali	0.01
Deoni	Kenkatha	0.00	Romagnola	Ghhumusari	0.01	Diqin	Kosali	0.00
Red_Sindhi	Kenkatha	0.00	Cinisara	Ghhumusari	0.01	Tibetan	Kosali	0.01
Sahiwal	Kenkatha	0.00	Diqin	Ghhumusari	0.00	Kazakh	Kosali	0.01
Red_Kandhari	Kenkatha	0.00	Tibetan	Ghhumusari	0.01	Anxi	Kosali	0.01
Rathi	Kenkatha	0.00	Kazakh	Ghhumusari	0.01	Weizhou	Kosali	0.00
Pulikulam	Kenkatha	0.00	Anxi	Ghhumusari	0.01	Longlin	Kosali	0.00
Ponwar	Kenkatha	0.00	Weizhou	Ghhumusari	0.00	Nandan	Kosali	0.00
Punganur	Kenkatha	0.00	Longlin	Ghhumusari	0.00	Nimari	Nagori	0.00
Thutho	Kenkatha	0.00	Nandan	Ghhumusari	0.00	Ongole	Nagori	0.00
Tharparkar	Kenkatha	0.00	Binjharपुरi	Ghhumusari	0.00	Motu	Nagori	0.00
Vechur	Kenkatha	0.00	Dangi	Ghhumusari	0.00	Mewati	Nagori	0.00
Umblachery	Kenkatha	0.00	Deoni	Ghhumusari	0.00	Mongolian	Nagori	0.01
bos_taurus	Kenkatha	0.01	Red_Sindhi	Ghhumusari	0.00	G_Holstein	Nagori	0.01
Siri	Kenkatha	0.01	Sahiwal	Ghhumusari	0.00	Menofi	Nagori	0.01
Shweta_Kapila	Kenkatha	0.00	Red_Kandhari	Ghhumusari	0.00	Iraqi	Nagori	0.01
Lakhimi	Kenkatha	0.00	Rathi	Ghhumusari	0.00	Cabannina	Nagori	0.01
Ladakhi	Kenkatha	0.00	Pulikulam	Ghhumusari	0.00	Zwergzebu	Nagori	0.00
Malnad_Gidda	Kenkatha	0.00	Ponwar	Ghhumusari	0.00	Japanese_black	Nagori	0.01
Malvi	Kenkatha	0.00	Punganur	Ghhumusari	0.00	Korean_native	Nagori	0.02
Krishna_Valley	Kenkatha	0.00	Thutho	Ghhumusari	0.00	Holstein	Nagori	0.00
Yunglin	Kenkatha	0.01	Tharparkar	Ghhumusari	0.00	Korean_cattle	Nagori	0.01
Kosali	Kenkatha	0.00	Vechur	Ghhumusari	0.00	Iranian	Nagori	0.00
Nagori	Kenkatha	0.00	Umblachery	Ghhumusari	0.00	Marhigiana	Nagori	0.01
Nimari	Kenkatha	0.00	bos_taurus	Ghhumusari	0.01	Arsi	Nagori	0.01
Ongole	Kenkatha	0.00	Siri	Ghhumusari	0.01	Nguni	Nagori	0.01
Motu	Kenkatha	0.00		Ghhumusari	0.01	bos_primigenius	Nagori	0.01
Mewati	Kenkatha	0.00	Shweta_Kapila	Ghhumusari	0.00	s	Nagori	0.01
Mongolian	Kenkatha	0.01	Lakhimi	Ghhumusari	0.00	Romagnola	Nagori	0.01
G_Holstein	Kenkatha	0.01	Ladakhi	Ghhumusari	0.00	Cinisara	Nagori	0.01
Menofi	Kenkatha	0.01	Malnad_Gidda	Ghhumusari	0.00	Diqin	Nagori	0.00
	Kenkatha	0.01	Malvi	Ghhumusari	0.00	Tibetan	Nagori	0.01
	Kenkatha	0.01	Krishna_Valley	Ghhumusari	0.00	Kazakh	Nagori	0.01

Iraqi	Kenkatha	0.01	Yunglin	Gangatiri	0.01	Anxi	Nagori	0.01
Cabannina	Kenkatha	0.01	Kosali	Gangatiri	0.00	Weizhou	Nagori	0.00
Zwergzebu	Kenkatha	0.00	Nagori	Gangatiri	0.00	Longlin	Nagori	0.00
Japanese_black	Kenkatha	0.01	Nimari	Gangatiri	0.00	Nandan	Nagori	0.01
Korean_native	Kenkatha	0.02	Ongole	Gangatiri	0.00	Ongole	Nimari	0.00
Holstein	Kenkatha	0.00	Motu	Gangatiri	0.00	Motu	Nimari	0.00
Korean_cattle	Kenkatha	0.01	Mewati	Gangatiri	0.00	Mewati	Nimari	0.00
Iranian	Kenkatha	0.00	Mongolian	Gangatiri	0.01	Mongolian	Nimari	0.01
Marhigiana	Kenkatha	0.01	G_Holstein	Gangatiri	0.01	G_Holstein	Nimari	0.01
Arsi	Kenkatha	0.01	Menofi	Gangatiri	0.01	Menofi	Nimari	0.01
Nguni	Kenkatha	0.01	Iraqi	Gangatiri	0.01	Iraqi	Nimari	0.01
bos_primigenius	Kenkatha	0.01	Cabannina	Gangatiri	0.01	Cabannina	Nimari	0.01
Romagnola	Kenkatha	0.01	Zwergzebu	Gangatiri	0.00	Zwergzebu	Nimari	0.00
Cinisara	Kenkatha	0.01	Japanese_black	Gangatiri	0.01	Japanese_black	Nimari	0.01
Diqin	Kenkatha	0.00	Korean_native	Gangatiri	0.02	Korean_native	Nimari	0.01
Tibetan	Kenkatha	0.01	Holstein	Gangatiri	0.00	Holstein	Nimari	0.00
Kazakh	Kenkatha	0.01	Korean_cattle	Gangatiri	0.01	Korean_cattle	Nimari	0.01
Anxi	Kenkatha	0.01	Iranian	Gangatiri	0.00	Iranian	Nimari	0.00
Weizhou	Kenkatha	0.00	Marhigiana	Gangatiri	0.01	Marhigiana	Nimari	0.01
Longlin	Kenkatha	0.00	Arsi	Gangatiri	0.01	Arsi	Nimari	0.01
Nandan	Kenkatha	0.00	Nguni	Gangatiri	0.01	Nguni	Nimari	0.01
Khillar	Konkan_Kapila	0.00	bos_primigenius	Gangatiri	0.01	bos_primigenius	Nimari	0.01
Bargur	Konkan_Kapila	0.00	Romagnola	Gangatiri	0.01	Romagnola	Nimari	0.01
Badri	Konkan_Kapila	0.00	Cinisara	Gangatiri	0.01	Cinisara	Nimari	0.01
Bachaur	Konkan_Kapila	0.00	Diqin	Gangatiri	0.00	Diqin	Nimari	0.00
Belahi	Konkan_Kapila	0.00	Tibetan	Gangatiri	0.01	Tibetan	Nimari	0.01
Greece_S_Pindos	Konkan_Kapila	0.01	Kazakh	Gangatiri	0.01	Kazakh	Nimari	0.01
Katerini	Konkan_Kapila	0.01	Anxi	Gangatiri	0.01	Anxi	Nimari	0.01
Skodra_Buena	Konkan_Kapila	0.01	Weizhou	Gangatiri	0.00	Weizhou	Nimari	0.00
Amritmahal	Konkan_Kapila	0.00	Longlin	Gangatiri	0.00	Longlin	Nimari	0.00
Murbodner	Konkan_Kapila	0.01	Nandan	Gangatiri	0.01	Nandan	Nimari	0.01
Anatolian_Black	Konkan_Kapila	0.01	Dangi	Binjharपुरi	0.00	Motu	Ongole	0.00
Slavonian_S_Podoliana	Konkan_Kapila	0.01	Deoni	Binjharपुरi	0.00	Mewati	Ongole	0.00
Fleckvvieh	Konkan_Kapila	0.01	Red_Sindhi	Binjharपुरi	0.00	Mongolian	Ongole	0.01
Gaolao	Konkan_Kapila	0.00	Sahiwal	Binjharपुरi	0.00	G_Holstein	Ongole	0.01
Ghhumusari	Konkan_Kapila	0.00	Red_Kandhari	Binjharपुरi	0.00	Menofi	Ongole	0.01
Gangatiri	Konkan_Kapila	0.00	Rathi	Binjharपुरi	0.00	Iraqi	Ongole	0.01
Binjharपुरi	Konkan_Kapila	0.00	Pulikulam	Binjharपुरi	0.00	Cabannina	Ongole	0.01
Dangi	Konkan_Kapila	0.00	Ponwar	Binjharपुरi	0.00	Zwergzebu	Ongole	0.00
Deoni	Konkan_Kapila	0.00	Punganur	Binjharपुरi	0.00	Japanese_black	Ongole	0.01
Red_Sindhi	Konkan_Kapila	0.00	Thutho	Binjharपुरi	0.00	Korean_native	Ongole	0.02
Sahiwal	Konkan_Kapila	0.00	Tharparkar	Binjharपुरi	0.00	Holstein	Ongole	0.00
Red_Kandhari	Konkan_Kapila	0.00	Vechur	Binjharपुरi	0.00	Korean_cattle	Ongole	0.01
Rathi	Konkan_Kapila	0.00	Umblachery	Binjharपुरi	0.00	Iranian	Ongole	0.00
Pulikulam	Konkan_Kapila	0.00	bos_taurus	Binjharपुरi	0.01	Marhigiana	Ongole	0.01
Ponwar	Konkan_Kapila	0.00	Siri	Binjharपुरi	0.01	Arsi	Ongole	0.01
Punganur	Konkan_Kapila	0.00	Shweta_Kapila	Binjharपुरi	0.00	Nguni	Ongole	0.01

Thutho	Konkan_Kapila	0.00	Lakhimi	Binjharpuri	0.00	bos_primigenius	Ongole	0.01
Tharparkar	Konkan_Kapila	0.00	Ladakhi	Binjharpuri	0.00	Romagnola	Ongole	0.01
Vechur	Konkan_Kapila	0.00	Malnad_Gidda	Binjharpuri	0.00	Cinisara	Ongole	0.01
Umblachery	Konkan_Kapila	0.00	Malvi	Binjharpuri	0.00	Diqin	Ongole	0.00
bos_taurus	Konkan_Kapila	0.01	Krishna_Valley	Binjharpuri	0.00	Tibetan	Ongole	0.01
Siri	Konkan_Kapila	0.01	Yunglin	Binjharpuri	0.01	Kazakh	Ongole	0.01
Shweta_Kapila	Konkan_Kapila	0.00	Kosali	Binjharpuri	0.00	Anxi	Ongole	0.01
Lakhimi	Konkan_Kapila	0.00	Nagori	Binjharpuri	0.00	Weizhou	Ongole	0.00
Ladakhi	Konkan_Kapila	0.00	Nimari	Binjharpuri	0.00	Longlin	Ongole	0.00
Malnad_Gidda	Konkan_Kapila	0.00	Ongole	Binjharpuri	0.00	Nandan	Ongole	0.00
Malvi	Konkan_Kapila	0.00	Motu	Binjharpuri	0.00	Mewati	Motu	0.00
Krishna_Valley	Konkan_Kapila	0.00	Mewati	Binjharpuri	0.00	Mongolian	Motu	0.01
Yunglin	Konkan_Kapila	0.01	Mongolian	Binjharpuri	0.01	G_Holstein	Motu	0.01
Kosali	Konkan_Kapila	0.00	G_Holstein	Binjharpuri	0.01	Menofi	Motu	0.01
Nagori	Konkan_Kapila	0.00	Menofi	Binjharpuri	0.01	Iraqi	Motu	0.01
Nimari	Konkan_Kapila	0.00	Iraqi	Binjharpuri	0.01	Cabannina	Motu	0.01
Ongole	Konkan_Kapila	0.00	Cabannina	Binjharpuri	0.01	Zwergzebu	Motu	0.00
Motu	Konkan_Kapila	0.00	Zwergzebu	Binjharpuri	0.00	Japanese_black	Motu	0.01
Mewati	Konkan_Kapila	0.00	Japanese_black	Binjharpuri	0.01	Korean_native	Motu	0.01
Mongolian	Konkan_Kapila	0.01	Korean_native	Binjharpuri	0.02	Holstein	Motu	0.00
G_Holstein	Konkan_Kapila	0.01	Holstein	Binjharpuri	0.00	Korean_cattle	Motu	0.01
Menofi	Konkan_Kapila	0.01	Korean_cattle	Binjharpuri	0.01	Iranian	Motu	0.00
Iraqi	Konkan_Kapila	0.01	Iranian	Binjharpuri	0.00	Marhigiana	Motu	0.01
Cabannina	Konkan_Kapila	0.01	Marhigiana	Binjharpuri	0.01	Arsi	Motu	0.01
Zwergzebu	Konkan_Kapila	0.00	Arsi	Binjharpuri	0.01	Nguni	Motu	0.01
Japanese_black	Konkan_Kapila	0.01	Nguni	Binjharpuri	0.01	bos_primigenius	Motu	0.01
Korean_native	Konkan_Kapila	0.02	bos_primigenius	Binjharpuri	0.01	Romagnola	Motu	0.01
Holstein	Konkan_Kapila	0.00	Romagnola	Binjharpuri	0.01	Cinisara	Motu	0.01
Korean_cattle	Konkan_Kapila	0.01	Cinisara	Binjharpuri	0.01	Diqin	Motu	0.00
Iranian	Konkan_Kapila	0.00	Diqin	Binjharpuri	0.00	Tibetan	Motu	0.01
Marhigiana	Konkan_Kapila	0.01	Tibetan	Binjharpuri	0.01	Kazakh	Motu	0.01
Arsi	Konkan_Kapila	0.01	Kazakh	Binjharpuri	0.01	Anxi	Motu	0.01
Nguni	Konkan_Kapila	0.01	Anxi	Binjharpuri	0.01	Weizhou	Motu	0.00
bos_primigenius	Konkan_Kapila	0.01	Weizhou	Binjharpuri	0.00	Longlin	Motu	0.00
Romagnola	Konkan_Kapila	0.01	Longlin	Binjharpuri	0.00	Nandan	Motu	0.01
Cinisara	Konkan_Kapila	0.01	Nandan	Binjharpuri	0.00	Mongolian	Mewati	0.01
Diqin	Konkan_Kapila	0.00	Deoni	Dangi	0.00	G_Holstein	Mewati	0.01

Tibetan	Konkan_Kapila	0.01	Red_Sindhi	Dangi	0.00	Menofi	Mewati	0.01
Kazakh	Konkan_Kapila	0.01	Sahiwal	Dangi	0.00	Iraqi	Mewati	0.01
Anxi	Konkan_Kapila	0.01	Red_Kandhari	Dangi	0.00	Cabannina	Mewati	0.01
Weizhou	Konkan_Kapila	0.00	Rathi	Dangi	0.00	Zwergzebu	Mewati	0.00
Longlin	Konkan_Kapila	0.00	Pulikulam	Dangi	0.00	Japanese_black	Mewati	0.01
Nandan	Konkan_Kapila	0.00	Ponwar	Dangi	0.00	Korean_native	Mewati	0.02
Bargur	Khillar	0.00	Punganur	Dangi	0.00	Holstein	Mewati	0.00
Badri	Khillar	0.00	Thutho	Dangi	0.00	Korean_cattle	Mewati	0.01
Bachaur	Khillar	0.00	Tharparkar	Dangi	0.00	Iranian	Mewati	0.00
Belahi	Khillar	0.00	Vechur	Dangi	0.00	Marhigiana	Mewati	0.01
Greece_S_Pindos	Khillar	0.01	Umblachery	Dangi	0.00	Arsi	Mewati	0.01
Katerini	Khillar	0.01	bos_taurus	Dangi	0.01	Nguni	Mewati	0.01
Skodra_Bu ^o a	Khillar	0.01	Siri	Dangi	0.01	bos_primigenius	Mewati	0.01
Amritmahal	Khillar	0.00	Shweta_Kapila	Dangi	0.00	Romagnola	Mewati	0.01
Murbodner	Khillar	0.01	Lakhimi	Dangi	0.00	Cinisara	Mewati	0.01
Anatolian_Black	Khillar	0.01	Ladakhi	Dangi	0.00	Diqin	Mewati	0.00
Slavonian_S_Podolia	Khillar	0.01	Malnad_Gidda	Dangi	0.00	Tibetan	Mewati	0.01
Fleckvvieh	Khillar	0.01	Malvi	Dangi	0.00	Kazakh	Mewati	0.01
Gaolao	Khillar	0.00	Krishna_Valley	Dangi	0.00	Anxi	Mewati	0.01
Ghhumusari	Khillar	0.00	Yunglin	Dangi	0.01	Weizhou	Mewati	0.00
Gangatiri	Khillar	0.00	Kosali	Dangi	0.00	Longlin	Mewati	0.00
Binjharपुरi	Khillar	0.00	Nagori	Dangi	0.00	Nandan	Mewati	0.01
Dangi	Khillar	0.00	Nimari	Dangi	0.00	G_Holstein	Mongolian	0.00
Deoni	Khillar	0.00	Ongole	Dangi	0.00	Menofi	Mongolian	0.00
Red_Sindhi	Khillar	0.00	Motu	Dangi	0.00	Iraqi	Mongolian	0.01
Sahiwal	Khillar	0.00	Mewati	Dangi	0.00	Cabannina	Mongolian	0.00
Red_Kandhari	Khillar	0.00	Mongolian	Dangi	0.01	Zwergzebu	Mongolian	0.01
Rathi	Khillar	0.00	G_Holstein	Dangi	0.01	Japanese_black	Mongolian	0.00
Pulikulam	Khillar	0.00	Menofi	Dangi	0.01	Korean_native	Mongolian	0.00
Ponwar	Khillar	0.00	Iraqi	Dangi	0.01	Holstein	Mongolian	0.01
Punganur	Khillar	0.00	Cabannina	Dangi	0.01	Korean_cattle	Mongolian	0.00
Thutho	Khillar	0.00	Zwergzebu	Dangi	0.00	Iranian	Mongolian	0.01
Tharparkar	Khillar	0.00	Japanese_black	Dangi	0.01	Marhigiana	Mongolian	0.01
Vechur	Khillar	0.00	Korean_native	Dangi	0.02	Arsi	Mongolian	0.00
Umblachery	Khillar	0.00	Holstein	Dangi	0.00	Nguni	Mongolian	0.00
bos_taurus	Khillar	0.01	Korean_cattle	Dangi	0.01	bos_primigenius	Mongolian	0.01
Siri	Khillar	0.01	Iranian	Dangi	0.00	Romagnola	Mongolian	0.01
Shweta_Kapila	Khillar	0.00	Marhigiana	Dangi	0.01	Cinisara	Mongolian	0.01
Lakhimi	Khillar	0.00	Arsi	Dangi	0.01	Diqin	Mongolian	0.01
Ladakhi	Khillar	0.00	Nguni	Dangi	0.01	Tibetan	Mongolian	0.00
Malnad_Gidda	Khillar	0.00	bos_primigenius	Dangi	0.01	Kazakh	Mongolian	0.00
Malvi	Khillar	0.00	Romagnola	Dangi	0.01	Anxi	Mongolian	0.00
Krishna_Valley	Khillar	0.00	Cinisara	Dangi	0.01	Weizhou	Mongolian	0.01
Yunglin	Khillar	0.01	Diqin	Dangi	0.00	Longlin	Mongolian	0.01
Kosali	Khillar	0.00	Tibetan	Dangi	0.01	Nandan	Mongolian	0.01
Nagori	Khillar	0.00	Kazakh	Dangi	0.01	Menofi	G_Holstein	0.00
Nimari	Khillar	0.00	Anxi	Dangi	0.01	Iraqi	G_Holstein	0.01
Ongole	Khillar	0.00	Weizhou	Dangi	0.00	Cabannina	G_Holstein	0.00
Motu	Khillar	0.00	Longlin	Dangi	0.00	Zwergzebu	G_Holstein	0.01
Mewati	Khillar	0.00	Nandan	Dangi	0.01	Japanese_black	G_Holstein	0.00
Mongolian	Khillar	0.01	Red_Sindhi	Deoni	0.00	Korean_native	G_Holstein	0.00
G_Holstein	Khillar	0.01	Sahiwal	Deoni	0.00	Holstein	G_Holstein	0.01
Menofi	Khillar	0.01	Red_Kandhari	Deoni	0.00	Korean_cattle	G_Holstein	0.00
Iraqi	Khillar	0.01	Rathi	Deoni	0.00	Iranian	G_Holstein	0.01
Cabannina	Khillar	0.01	Pulikulam	Deoni	0.00	Marhigiana	G_Holstein	0.01
Zwergzebu	Khillar	0.00	Ponwar	Deoni	0.01	Arsi	G_Holstein	0.00
Japanese_black	Khillar	0.01	Punganur	Deoni	0.00	Nguni	G_Holstein	0.00
Korean_native	Khillar	0.02	Thutho	Deoni	0.00	bos_primigenius	G_Holstein	0.00
Holstein	Khillar	0.00	Tharparkar	Deoni	0.00	Romagnola	G_Holstein	0.01
Korean_cattle	Khillar	0.01	Vechur	Deoni	0.00	Cinisara	G_Holstein	0.01
Iranian	Khillar	0.00	Umblachery	Deoni	0.00	Diqin	G_Holstein	0.02
Marhigiana	Khillar	0.01	bos_taurus	Deoni	0.01	Tibetan	G_Holstein	0.00
Arsi	Khillar	0.01	Siri	Deoni	0.01	Kazakh	G_Holstein	0.00
Nguni	Khillar	0.01	Shweta_Kapila	Deoni	0.01	Anxi	G_Holstein	0.00

bos_primigenius	Khillar	0.01	Lakhimi	Deoni	0.01	Weizhou	G_Holstein	0.01
Romagnola	Khillar	0.01	Ladakhi	Deoni	0.00	Longlin	G_Holstein	0.01
Cinisara	Khillar	0.01	Malnad_Gidida	Deoni	0.00	Nandan	G_Holstein	0.01
Diqin	Khillar	0.00	Malvi	Deoni	0.00	Iraqi	Menofi	0.01
Tibetan	Khillar	0.01	Krishna_Valley	Deoni	0.00	Cabannina	Menofi	0.00
Kazakh	Khillar	0.01	Yunglin	Deoni	0.01	Zwergzebu	Menofi	0.01
Anxi	Khillar	0.01	Kosali	Deoni	0.00	Japanese_black	Menofi	0.00
Weizhou	Khillar	0.00	Nagori	Deoni	0.00	Korean_native	Menofi	0.00
Longlin	Khillar	0.00	Nimari	Deoni	0.00	Holstein	Menofi	0.01
Nandan	Khillar	0.00	Ongole	Deoni	0.00	Korean_cattle	Menofi	0.00
Badri	Bargur	0.00	Motu	Deoni	0.00	Iranian	Menofi	0.01
Bachaur	Bargur	0.00	Mewati	Deoni	0.00	Marhigiana	Menofi	0.01
Belahi	Bargur	0.00	Mongolian	Deoni	0.01	Arsi	Menofi	0.00
Greece_S_Pindos	Bargur	0.01	G_Holstein	Deoni	0.01	Nguni	Menofi	0.00
Katerini	Bargur	0.01	Menofi	Deoni	0.01	bos_primigenius	Menofi	0.00
Skodra_Bu ^{ca}	Bargur	0.01	Iraqi	Deoni	0.01	Romagnola	Menofi	0.01
Amritmahal	Bargur	0.00	Cabannina	Deoni	0.01	Cinisara	Menofi	0.01
Murbodner	Bargur	0.01	Zwergzebu	Deoni	0.00	Diqin	Menofi	0.02
Anatolian_Black	Bargur	0.01	Japanese_black	Deoni	0.01	Tibetan	Menofi	0.00
Slavonian_S_Podolia	Bargur	0.01	Korean_native	Deoni	0.01	Kazakh	Menofi	0.00
n	Bargur	0.01	Holstein	Deoni	0.01	Anxi	Menofi	0.00
Fleckvvieh	Bargur	0.01	Holstein	Deoni	0.01	Weizhou	Menofi	0.01
Gaolao	Bargur	0.00	Korean_cattle	Deoni	0.01	Weizhou	Menofi	0.01
Ghhumusari	Bargur	0.00	Iranian	Deoni	0.00	Longlin	Menofi	0.01
Gangatiri	Bargur	0.00	Marhigiana	Deoni	0.01	Nandan	Menofi	0.01
Binjharpuri	Bargur	0.00	Arsi	Deoni	0.01	Cabannina	Iraqi	0.01
Dangi	Bargur	0.00	Nguni	Deoni	0.01	Zwergzebu	Iraqi	0.01
Deoni	Bargur	0.00	bos_primigenius	Deoni	0.01	Japanese_black	Iraqi	0.01
Red_Sindhi	Bargur	0.00	Romagnola	Deoni	0.01	Korean_native	Iraqi	0.01
Sahiwal	Bargur	0.00	Cinisara	Deoni	0.01	Holstein	Iraqi	0.01
Red_Kandhari	Bargur	0.00	Diqin	Deoni	0.01	Korean_cattle	Iraqi	0.01
Rathi	Bargur	0.00	Tibetan	Deoni	0.01	Iranian	Iraqi	0.01
Pulikulam	Bargur	0.00	Kazakh	Deoni	0.01	Marhigiana	Iraqi	0.01
Ponwar	Bargur	0.00	Anxi	Deoni	0.01	Arsi	Iraqi	0.01
Punganur	Bargur	0.00	Weizhou	Deoni	0.00	Nguni	Iraqi	0.01
Thutho	Bargur	0.00	Longlin	Deoni	0.00	bos_primigenius	Iraqi	0.01
Tharparkar	Bargur	0.00	Nandan	Deoni	0.01	Romagnola	Iraqi	0.01
Vechur	Bargur	0.00	Sahiwal	Red_Sindhi	0.00	Cinisara	Iraqi	0.01
Umblachery	Bargur	0.00	Red_Kandhari	Red_Sindhi	0.00	Diqin	Iraqi	0.01
bos_taurus	Bargur	0.01	Rathi	Red_Sindhi	0.00	Tibetan	Iraqi	0.01
Siri	Bargur	0.01	Pulikulam	Red_Sindhi	0.00	Kazakh	Iraqi	0.01
Shweta_Kapila	Bargur	0.00	Ponwar	Red_Sindhi	0.00	Anxi	Iraqi	0.01
Lakhimi	Bargur	0.00	Punganur	Red_Sindhi	0.00	Weizhou	Iraqi	0.01
Ladakhi	Bargur	0.00	Thutho	Red_Sindhi	0.00	Longlin	Iraqi	0.01
Malnad_Gidida	Bargur	0.00	Tharparkar	Red_Sindhi	0.00	Nandan	Iraqi	0.01
Malvi	Bargur	0.00	Vechur	Red_Sindhi	0.00	Zwergzebu	Cabannina	0.01
Krishna_Valley	Bargur	0.00	Umblachery	Red_Sindhi	0.00	Japanese_black	Cabannina	0.00
Yunglin	Bargur	0.01	bos_taurus	Red_Sindhi	0.01	Korean_native	Cabannina	0.00
Kosali	Bargur	0.00	Siri	Red_Sindhi	0.01	Holstein	Cabannina	0.01
Nagori	Bargur	0.00	Shweta_Kapila	Red_Sindhi	0.00	Korean_cattle	Cabannina	0.00
Nimari	Bargur	0.00	Lakhimi	Red_Sindhi	0.00	Iranian	Cabannina	0.01
Ongole	Bargur	0.00	Ladakhi	Red_Sindhi	0.00	Marhigiana	Cabannina	0.01
Motu	Bargur	0.00	Malnad_Gidida	Red_Sindhi	0.00	Arsi	Cabannina	0.00
Mewati	Bargur	0.00	Malvi	Red_Sindhi	0.00	Nguni	Cabannina	0.00
Mongolian	Bargur	0.01	Krishna_Valley	Red_Sindhi	0.00	bos_primigenius	Cabannina	0.00
G_Holstein	Bargur	0.01	Yunglin	Red_Sindhi	0.01	Romagnola	Cabannina	0.01
Menofi	Bargur	0.01	Kosali	Red_Sindhi	0.00	Cinisara	Cabannina	0.01
Iraqi	Bargur	0.01	Nagori	Red_Sindhi	0.00	Diqin	Cabannina	0.02
Cabannina	Bargur	0.01	Nimari	Red_Sindhi	0.00	Tibetan	Cabannina	0.00
Zwergzebu	Bargur	0.00	Ongole	Red_Sindhi	0.00	Kazakh	Cabannina	0.00
Japanese_black	Bargur	0.01	Motu	Red_Sindhi	0.00	Anxi	Cabannina	0.00
Korean_native	Bargur	0.02	Mewati	Red_Sindhi	0.00	Weizhou	Cabannina	0.01
Holstein	Bargur	0.00	Mongolian	Red_Sindhi	0.01	Longlin	Cabannina	0.01
Korean_cattle	Bargur	0.01	G_Holstein	Red_Sindhi	0.01	Nandan	Cabannina	0.01
Iranian	Bargur	0.00	Menofi	Red_Sindhi	0.01	Japanese_black	Zwergzebu	0.01
Marhigiana	Bargur	0.01	Iraqi	Red_Sindhi	0.01	Korean_native	Zwergzebu	0.01
Arsi	Bargur	0.01	Cabannina	Red_Sindhi	0.01	Holstein	Zwergzebu	0.00
Nguni	Bargur	0.01	Zwergzebu	Red_Sindhi	0.00	Korean_cattle	Zwergzebu	0.01
bos_primigenius	Bargur	0.01	Japanese_black	Red_Sindhi	0.01	Iranian	Zwergzebu	0.00
Romagnola	Bargur	0.01	Korean_native	Red_Sindhi	0.01	Marhigiana	Zwergzebu	0.01
Cinisara	Bargur	0.01	Holstein	Red_Sindhi	0.00	Arsi	Zwergzebu	0.01

Diqin	Bargur	0.00	Korean_cattle	Red_Sindhi	0.01	Nguni	Zwergzebu	0.01
Tibetan	Bargur	0.01	Iranian	Red_Sindhi	0.00	bos_primigenius	Zwergzebu	0.01
Kazakh	Bargur	0.01	Marhigiana	Red_Sindhi	0.01	Romagnola	Zwergzebu	0.01
Anxi	Bargur	0.01	Arsi	Red_Sindhi	0.01	Cinisara	Zwergzebu	0.01
Weizhou	Bargur	0.00	Nguni	Red_Sindhi	0.01	Diqin	Zwergzebu	0.00
Longlin	Bargur	0.00	bos_primigenius	Red_Sindhi	0.01	Tibetan	Zwergzebu	0.01
Nandan	Bargur	0.00	Romagnola	Red_Sindhi	0.01	Kazakh	Zwergzebu	0.01
Bachaur	Badri	0.00	Cinisara	Red_Sindhi	0.01	Anxi	Zwergzebu	0.01
Belahi	Badri	0.00	Diqin	Red_Sindhi	0.00	Weizhou	Zwergzebu	0.00
Greece_S_Pindos	Badri	0.01	Tibetan	Red_Sindhi	0.01	Longlin	Zwergzebu	0.00
Katerini	Badri	0.01	Kazakh	Red_Sindhi	0.01	Nandan	Zwergzebu	0.01
Skodra_Bu~a	Badri	0.01	Anxi	Red_Sindhi	0.01	Korean_native	Japanese_black	0.00
Amritmahal	Badri	0.01	Weizhou	Red_Sindhi	0.00	Holstein	Japanese_black	0.01
Murbodner	Badri	0.01	Longlin	Red_Sindhi	0.00	Korean_cattle	Japanese_black	0.00
Anatolian_Black	Badri	0.01	Nandan	Red_Sindhi	0.00	Iranian	Japanese_black	0.01
Slavonian_S_Podoliana	Badri	0.01	Red_Kandhari	Sahiwal	0.00	Marhigiana	Japanese_black	0.01
Fleckvvieh	Badri	0.01	Rathi	Sahiwal	0.00	Arsi	Japanese_black	0.00
Gaolao	Badri	0.01	Pulikulam	Sahiwal	0.00	Nguni	Japanese_black	0.00
Ghhumusari	Badri	0.00	Ponwar	Sahiwal	0.00	bos_primigenius	Japanese_black	0.00
Gangatiri	Badri	0.00	Punganur	Sahiwal	0.00	Romagnola	Japanese_black	0.01
Binjharपुरi	Badri	0.00	Thutho	Sahiwal	0.00	Cinisara	Japanese_black	0.01
Dangi	Badri	0.00	Tharparkar	Sahiwal	0.00	Diqin	Japanese_black	0.02
Deoni	Badri	0.01	Vechur	Sahiwal	0.00	Tibetan	Japanese_black	0.00
Red_Sindhi	Badri	0.00	Umblachery	Sahiwal	0.00	Kazakh	Japanese_black	0.00
Sahiwal	Badri	0.00	bos_taurus	Sahiwal	0.01	Anxi	Japanese_black	0.00
Red_Kandhari	Badri	0.00	Siri	Sahiwal	0.01	Weizhou	Japanese_black	0.01
Rathi	Badri	0.00	Shweta_Kapila	Sahiwal	0.00	Longlin	Japanese_black	0.01
Pulikulam	Badri	0.00	Lakhimi	Sahiwal	0.00	Nandan	Japanese_black	0.01
Ponwar	Badri	0.01	Ladakhi	Sahiwal	0.00	Holstein	Korean_native	0.01
Punganur	Badri	0.00	Malnad_Gidda	Sahiwal	0.00	Korean_cattle	Korean_native	0.00
Thutho	Badri	0.00	Malvi	Sahiwal	0.00	Iranian	Korean_native	0.01
Tharparkar	Badri	0.00	Krishna_Valley	Sahiwal	0.00	Marhigiana	Korean_native	0.01
Vechur	Badri	0.00	Yunglin	Sahiwal	0.01	Arsi	Korean_native	0.00
Umblachery	Badri	0.00	Kosali	Sahiwal	0.00	Nguni	Korean_native	0.00
bos_taurus	Badri	0.01	Nagori	Sahiwal	0.00	bos_primigenius	Korean_native	0.00
Siri	Badri	0.01	Nimari	Sahiwal	0.00	Romagnola	Korean_native	0.01
Shweta_Kapila	Badri	0.01	Ongole	Sahiwal	0.00	Cinisara	Korean_native	0.01
Lakhimi	Badri	0.01	Motu	Sahiwal	0.00	Diqin	Korean_native	0.02
Ladakhi	Badri	0.00	Mewati	Sahiwal	0.00	Tibetan	Korean_native	0.00
Malnad_Gidda	Badri	0.00	Mongolian	Sahiwal	0.01	Kazakh	Korean_native	0.00
Malvi	Badri	0.00	G_Holstein	Sahiwal	0.01	Anxi	Korean_native	0.00
Krishna_Valley	Badri	0.00	Menofi	Sahiwal	0.01	Weizhou	Korean_native	0.02
Yunglin	Badri	0.01	Iraqi	Sahiwal	0.01	Longlin	Korean_native	0.01
Kosali	Badri	0.00	Cabannina	Sahiwal	0.01	Nandan	Korean_native	0.01
Nagori	Badri	0.00	Zwergzebu	Sahiwal	0.00	Korean_cattle	Holstein	0.01
Nimari	Badri	0.00	Japanese_black	Sahiwal	0.01	Iranian	Holstein	0.00
Ongole	Badri	0.00	Korean_native	Sahiwal	0.01	Marhigiana	Holstein	0.01
Motu	Badri	0.00	Holstein	Sahiwal	0.00	Arsi	Holstein	0.01
Mewati	Badri	0.00	Korean_cattle	Sahiwal	0.01	Nguni	Holstein	0.01
Mongolian	Badri	0.01	Iranian	Sahiwal	0.00	bos_primigenius	Holstein	0.01
G_Holstein	Badri	0.01	Marhigiana	Sahiwal	0.01	Romagnola	Holstein	0.01
Menofi	Badri	0.01	Arsi	Sahiwal	0.01	Cinisara	Holstein	0.01
Iraqi	Badri	0.01	Nguni	Sahiwal	0.01	Diqin	Holstein	0.01
Cabannina	Badri	0.01	bos_primigenius	Sahiwal	0.01	Tibetan	Holstein	0.01
Zwergzebu	Badri	0.00	Romagnola	Sahiwal	0.01	Kazakh	Holstein	0.01
Japanese_black	Badri	0.01	Cinisara	Sahiwal	0.01	Anxi	Holstein	0.01
Korean_native	Badri	0.01	Diqin	Sahiwal	0.00	Weizhou	Holstein	0.00
Holstein	Badri	0.01	Tibetan	Sahiwal	0.01	Longlin	Holstein	0.01
Korean_cattle	Badri	0.01	Kazakh	Sahiwal	0.01	Nandan	Holstein	0.01
Iranian	Badri	0.00	Anxi	Sahiwal	0.01	Iranian	Korean_cattle	0.01
Marhigiana	Badri	0.01	Weizhou	Sahiwal	0.00	Marhigiana	Korean_cattle	0.01
Arsi	Badri	0.01	Longlin	Sahiwal	0.00	Arsi	Korean_cattle	0.00
Nguni	Badri	0.01	Nandan	Sahiwal	0.01	Nguni	Korean_cattle	0.00
bos_primigenius	Badri	0.01	Rathi	Red_Kandhari	0.00	bos_primigenius	Korean_cattle	0.00
Romagnola	Badri	0.01	Pulikulam	Red_Kandhari	0.00	Romagnola	Korean_cattle	0.01
Cinisara	Badri	0.01	Ponwar	Red_Kandhari	0.00	Cinisara	Korean_cattle	0.01
Diqin	Badri	0.00	Punganur	Red_Kandhari	0.00	Diqin	Korean_cattle	0.02
Tibetan	Badri	0.01	Thutho	Red_Kandhari	0.00	Tibetan	Korean_cattle	0.00

Kazakh	Badri	0.01	Tharparkar	Red_Kandhari	0.00	Kazakh	Korean_cattle	0.00
Anxi	Badri	0.01	Vechur	Red_Kandhari	0.00	Anxi	Korean_cattle	0.00
Weizhou	Badri	0.00	Umblachery	Red_Kandhari	0.00	Weizhou	Korean_cattle	0.01
Longlin	Badri	0.00	bos_taurus	Red_Kandhari	0.01	Longlin	Korean_cattle	0.01
Nandan	Badri	0.01	Siri	Red_Kandhari	0.01	Nandan	Korean_cattle	0.01
Belahi	Bachaur	0.00	Shweta_Kapila	Red_Kandhari	0.00	Marhigiana	Iranian	0.01
Greece_S_Pindos	Bachaur	0.01	Lakhimi	Red_Kandhari	0.00	Arsi	Iranian	0.01
Katerini	Bachaur	0.01	Ladakhi	Red_Kandhari	0.00	Nguni	Iranian	0.01
Skodra_Bu~a	Bachaur	0.01	Malnad_Gidda	Red_Kandhari	0.00	bos_primigenius	Iranian	0.01
Amritmahal	Bachaur	0.00	Malvi	Red_Kandhari	0.00	Romagnola	Iranian	0.01
Murbodner	Bachaur	0.01	Krishna_Valley	Red_Kandhari	0.00	Cinisara	Iranian	0.01
Anatolian_Black	Bachaur	0.01	Yunglin	Red_Kandhari	0.01	Diqin	Iranian	0.00
Slavonian_S_Podolia	Bachaur	0.01	Kosali	Red_Kandhari	0.00	Tibetan	Iranian	0.01
n	Bachaur	0.01	Nagori	Red_Kandhari	0.00	Kazakh	Iranian	0.01
Fleckvvieh	Bachaur	0.01	Nagori	Red_Kandhari	0.00	Kazakh	Iranian	0.01
Gaolao	Bachaur	0.00	Nimari	Red_Kandhari	0.00	Anxi	Iranian	0.01
Ghhumusari	Bachaur	0.00	Ongole	Red_Kandhari	0.00	Weizhou	Iranian	0.00
Gangatiri	Bachaur	0.00	Motu	Red_Kandhari	0.00	Longlin	Iranian	0.00
Binjharपुरi	Bachaur	0.00	Mewati	Red_Kandhari	0.00	Nandan	Iranian	0.01
Dangi	Bachaur	0.00	Mongolian	Red_Kandhari	0.01	Arsi	Marhigiana	0.01
Deoni	Bachaur	0.00	G_Holstein	Red_Kandhari	0.01	Nguni	Marhigiana	0.01
Red_Sindhi	Bachaur	0.00	Menofi	Red_Kandhari	0.01	bos_primigenius	Marhigiana	0.01
Sahiwal	Bachaur	0.00	Iraqi	Red_Kandhari	0.01	Romagnola	Marhigiana	0.00
Red_Kandhari	Bachaur	0.00	Cabannina	Red_Kandhari	0.01	Cinisara	Marhigiana	0.00
Rathi	Bachaur	0.00	Zwergzebu	Red_Kandhari	0.00	Diqin	Marhigiana	0.02
Pulikulam	Bachaur	0.00	Japanese_black	Red_Kandhari	0.01	Tibetan	Marhigiana	0.01
Ponwar	Bachaur	0.00	Korean_native	Red_Kandhari	0.01	Kazakh	Marhigiana	0.01
Punganur	Bachaur	0.00	Holstein	Red_Kandhari	0.00	Anxi	Marhigiana	0.01
Thutho	Bachaur	0.00	Korean_cattle	Red_Kandhari	0.01	Weizhou	Marhigiana	0.01
Tharparkar	Bachaur	0.00	Iranian	Red_Kandhari	0.00	Longlin	Marhigiana	0.01
Vechur	Bachaur	0.00	Marhigiana	Red_Kandhari	0.01	Nandan	Marhigiana	0.01
Umblachery	Bachaur	0.00	Arsi	Red_Kandhari	0.01	Nguni	Arsi	0.00
bos_taurus	Bachaur	0.01	Nguni	Red_Kandhari	0.01	bos_primigenius	Arsi	0.00
Siri	Bachaur	0.01	bos_primigenius	Red_Kandhari	0.01	Romagnola	Arsi	0.01
Shweta_Kapila	Bachaur	0.00	Romagnola	Red_Kandhari	0.01	Cinisara	Arsi	0.01
Lakhimi	Bachaur	0.00	Cinisara	Red_Kandhari	0.01	Diqin	Arsi	0.02
Ladakhi	Bachaur	0.00	Diqin	Red_Kandhari	0.00	Tibetan	Arsi	0.00
Malnad_Gidda	Bachaur	0.00	Tibetan	Red_Kandhari	0.01	Kazakh	Arsi	0.00
Malvi	Bachaur	0.00	Kazakh	Red_Kandhari	0.01	Anxi	Arsi	0.00
Krishna_Valley	Bachaur	0.00	Anxi	Red_Kandhari	0.01	Weizhou	Arsi	0.01
Yunglin	Bachaur	0.01	Weizhou	Red_Kandhari	0.00	Longlin	Arsi	0.01
Kosali	Bachaur	0.00	Longlin	Red_Kandhari	0.00	Nandan	Arsi	0.01
Nagori	Bachaur	0.00	Nandan	Red_Kandhari	0.01	bos_primigenius	Nguni	0.00
Nimari	Bachaur	0.00	Pulikulam	Rathi	0.00	Romagnola	Nguni	0.01
Ongole	Bachaur	0.00	Ponwar	Rathi	0.00	Cinisara	Nguni	0.01
Motu	Bachaur	0.00	Punganur	Rathi	0.00	Diqin	Nguni	0.02
Mewati	Bachaur	0.00	Thutho	Rathi	0.00	Tibetan	Nguni	0.00
Mongolian	Bachaur	0.01	Tharparkar	Rathi	0.00	Kazakh	Nguni	0.00
G_Holstein	Bachaur	0.01	Vechur	Rathi	0.00	Anxi	Nguni	0.00
Menofi	Bachaur	0.01	Umblachery	Rathi	0.00	Weizhou	Nguni	0.01
Iraqi	Bachaur	0.01	bos_taurus	Rathi	0.01	Longlin	Nguni	0.01
Cabannina	Bachaur	0.01	Siri	Rathi	0.01	Nandan	Nguni	0.01
Zwergzebu	Bachaur	0.00	Shweta_Kapila	Rathi	0.00	Romagnola	bos_primigenius	0.01
Japanese_black	Bachaur	0.01	Lakhimi	Rathi	0.00	Cinisara	bos_primigenius	0.01
Korean_native	Bachaur	0.02	Ladakhi	Rathi	0.00	Diqin	bos_primigenius	0.02
Holstein	Bachaur	0.00	Malnad_Gidda	Rathi	0.00	Tibetan	bos_primigenius	0.00
Korean_cattle	Bachaur	0.01	Malvi	Rathi	0.00	Kazakh	bos_primigenius	0.01
Iranian	Bachaur	0.00	Krishna_Valley	Rathi	0.00	Anxi	bos_primigenius	0.00
Marhigiana	Bachaur	0.01	Yunglin	Rathi	0.01	Weizhou	bos_primigenius	0.01
Arsi	Bachaur	0.01	Kosali	Rathi	0.00	Longlin	bos_primigenius	0.01
Nguni	Bachaur	0.01	Nagori	Rathi	0.00	Nandan	bos_primigenius	0.01

bos_primigenius	Bachaur	0.01	Nimari	Rathi	0.00	Cinisara	Romagnola	0.00
Romagnola	Bachaur	0.01	Ongole	Rathi	0.00	Diqin	Romagnola	0.02
Cinisara	Bachaur	0.01	Motu	Rathi	0.00	Tibetan	Romagnola	0.01
Diqin	Bachaur	0.00	Mewati	Rathi	0.00	Kazakh	Romagnola	0.01
Tibetan	Bachaur	0.01	Mongolian	Rathi	0.01	Anxi	Romagnola	0.01
Kazakh	Bachaur	0.01	G_Holstein	Rathi	0.01	Weizhou	Romagnola	0.01
Anxi	Bachaur	0.01	Menofi	Rathi	0.01	Longlin	Romagnola	0.01
Weizhou	Bachaur	0.00	Iraqi	Rathi	0.01	Nandan	Romagnola	0.01
Longlin	Bachaur	0.00	Cabannina	Rathi	0.01	Diqin	Cinisara	0.02
Nandan	Bachaur	0.00	Zwergzebu	Rathi	0.00	Tibetan	Cinisara	0.01
Greece_S_Pindos	Belahi	0.01	Japanese_black	Rathi	0.01	Kazakh	Cinisara	0.01
Katerini	Belahi	0.01	Korean_native	Rathi	0.01	Anxi	Cinisara	0.01
Skodra_Bu~a	Belahi	0.01	Holstein	Rathi	0.00	Weizhou	Cinisara	0.01
Amritmahal	Belahi	0.00	Korean_cattle	Rathi	0.01	Longlin	Cinisara	0.01
Murbodner	Belahi	0.01	Iranian	Rathi	0.00	Nandan	Cinisara	0.01
Anatolian_Black	Belahi	0.01	Marhigiana	Rathi	0.01	Tibetan	Diqin	0.02
Slavonian_S_Podolia								
n	Belahi	0.01	Arsi	Rathi	0.01	Kazakh	Diqin	0.01
Fleckvvieh	Belahi	0.01	Nguni	Rathi	0.01	Anxi	Diqin	0.02
Gaolao	Belahi	0.00	bos_primigenius	Rathi	0.01	Weizhou	Diqin	0.00
Ghhumusari	Belahi	0.00	Romagnola	Rathi	0.01	Longlin	Diqin	0.00
Gangatiri	Belahi	0.00	Cinisara	Rathi	0.01	Nandan	Diqin	0.01
Binjharपुरi	Belahi	0.00	Diqin	Rathi	0.00	Kazakh	Tibetan	0.00
Dangi	Belahi	0.00	Tibetan	Rathi	0.01	Anxi	Tibetan	0.00
Deoni	Belahi	0.00	Kazakh	Rathi	0.01	Weizhou	Tibetan	0.01
Red_Sindhi	Belahi	0.00	Anxi	Rathi	0.01	Longlin	Tibetan	0.01
Sahiwal	Belahi	0.00	Weizhou	Rathi	0.00	Nandan	Tibetan	0.01
Red_Kandhari	Belahi	0.00	Longlin	Rathi	0.00	Anxi	Kazakh	0.00
Rathi	Belahi	0.00	Nandan	Rathi	0.00	Weizhou	Kazakh	0.01
Pulikulam	Belahi	0.00	Ponwar	Pulikulam	0.00	Longlin	Kazakh	0.01
Ponwar	Belahi	0.00	Punganur	Pulikulam	0.00	Nandan	Kazakh	0.01
Punganur	Belahi	0.00	Thutho	Pulikulam	0.00	Weizhou	Anxi	0.01
Thutho	Belahi	0.00	Tharparkar	Pulikulam	0.00	Longlin	Anxi	0.01
Tharparkar	Belahi	0.00	Vechur	Pulikulam	0.00	Nandan	Anxi	0.01
Vechur	Belahi	0.00	Umblachery	Pulikulam	0.00	Longlin	Weizhou	0.00
Umblachery	Belahi	0.00	bos_taurus	Pulikulam	0.01	Nandan	Weizhou	0.00
bos_taurus	Belahi	0.01	Siri	Pulikulam	0.01	Nandan	Longlin	0.01

Životopis

Katarina Marić

Kontakt: Ruđera Boškovića 11, Nova Gradiška
+385 99 5258 676
katamaric99@gmail.com
<https://www.linkedin.com/in/katarina-maric/>

Apsolventica sam diplomskog studija Genetika i oplemenjivanje životinja pri Agronomskom fakultetu u Zagrebu.

Obrazovanje: 2021.- trenutno

Diplomski studij • Genetika i Oplemenjivanje životinja • diplomski rad:
Varijabilnost mitogenoma goveda

2018.-2021.

Preddiplomski studij (univ. bacc. ing. agr.) • Ekološka poljoprivreda • završni rad: Otpornost pšenice na priježetveno proklijavanje

2014.-2018.

Opća gimnazija Nova Gradiška

2008.-2014.

Osnovna glazbena škola • Pučko otvoreno učilište Matije Antuna Relkovića • Gitara

2006.-2014.

Osnovna škola "Mato Lovrak"

Ključne sposobnosti: • Organizacija vremena
• Rad u programu R
• Rad u programu SAS
• Rad s Microsoft Office paketima
• Poznavanje programa za obradu genetskih podataka
• Engleski jezik B2
• Vozačka dozvola AM, B

- Komunikacijske vještine
- Analiza i obrada prostornih podataka
- Sviranje gitare

- Iskustvo: 2.10.2023.- trenutno
DHL Express • studentski posao • rad na recepciji
- 1.8.2022.-31.8.2022.
Roto dinamic • studentski posao - ispomoć • rad s kupcima, rad na blagajni
- 12.9.2021.- 30.1.2022.
A1 Hrvatska • Agent u službi za korisnike • komunikacija s korisnicima, rješavanje prigovora, prodaja mobilnih i fiksnih usluga
- 30.6.2021.- 6.9.2021.
A1 Hrvatska • agent u teleprodaji • komunikacija s korisnicima, prodaja mobilnih i fiksnih usluga
- 31.1.2021.- 20.4.2021.
Studio Moderna • telemarketing • komunikacija s kupcima, prodaja Dormeo/Delimano proizvoda
- Aktivnosti: 11.2.2024. – 15.2.2024.
59. hrvatski i 19. međunarodni Simpozij agronoma – predstavljanje rada pod nazivom „Open spatial data in animal protein production in Croatia“
2013. – 2016. Volontiranje u Crvenom križu (prikupljanje dobrovoljnog priloga)
2014. volontiranje u Crvenom križu za vrijeme poplava
- Postignuća: 11.5.2022. – 13.5.2022.
Ljetna škola – certifikat : Molekularna bioraznolikost i oplemenjivanje bilja
13.5.2023. Sudjelovanje u Datathon natjecanju u sklopu projekta Prilagodba informacijskih sustava tijela javnog sektora Portalu otvorenih podataka (Open data) • 1. mjesto u ekonomskom području • 1. mjesto u političkom području

Interesi/hobiji:

- rješavanje sudokua
- čitanje znanstvene fantastike
- književna djela – renesansa
- poezija – romantizam
- filmovi – znanstvena fantastika i fantazija
- adrenalinski sportovi i aktivnosti
- sviranje gitare
- ljubiteljica životinja