Chart, scatter chart

Description automatically generated Chart, scatter chart

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Description automatically generated Chart, line chart

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Description automatically generated Chart, histogram

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Timeline

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Timeline

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A picture containing website

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. It is best to examine genetic differentiation between multiple populations using all the data simultaneously. This can be

accomplished using Nei’s genetic distance and Nei’s genetic identity. Genetic distance

estimates range between zero (genetically identical populations) and 1 and can be interpreted

as a percent. Nei’s identity ranges between zero (genetically unrelated) and 1 (genetically

identical). Nei’s D can be useful when examining multiple, distantly related species.

References:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Codominant data template | genalexformat | Pairwise Population Matrix of Nei **Genetic Distance** |  |  |  |
| Northern | Kinapak | Hawani | Perpaluktok | Southern |  |
| 0.000 |  |  |  |  | Northern |
| 0.333 | 0.000 |  |  |  | Kinapak |
| 0.035 | 0.376 | 0.000 |  |  | Hawani |
| 0.329 | 0.445 | 0.303 | 0.000 |  | Perpaluktok |
| 0.202 | 0.397 | 0.163 | 0.275 | 0.000 | Southern |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| Codominant data template | genalexformat | Pairwise Population Matrix of Nei **Genetic Identity** |  |  |  |
| Northern | Kinapak | Hawani | Perpaluktok | Southern |  |
| 1.000 |  |  |  |  | Northern |
| 0.717 | 1.000 |  |  |  | Kinapak |
| 0.965 | 0.686 | 1.000 |  |  | Hawani |
| 0.720 | 0.641 | 0.738 | 1.000 |  | Perpaluktok |
| 0.817 | 0.672 | 0.849 | 0.760 | 1.000 | Southern |

Fst in males and female for dispersal

See whats going on which ones are most indangered based on inbreeding

Diagram, map

Description automatically generated

SEX DISPERSAL

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Genetic differentiation (pairwise FST) between regional walrus samples based on microsatellite and mtDNA variation** | | | | | | | |
|  | Nms | Nmt | Northern | Kinapak | Hawani | Perpaluktok | Southern |
| Northern | 15 | 19 | – | 0.454 | 0.392 | 0.597 | 0.446 |
| Kinapak | 20 | 23 | 0.208 | – | 0.344 | 0.698 | 0.389 |
| Hawani | 79 | 47 | 0.033 | 0.221 | – | 0.511 | 0.398 |
| Perpaluktok | 43 | 37 | 0.188 | 0.257 | 0.175 | – | 0.433 |
| Southern | 15 | 19 | 0.143 | 0.241 | 0.120 | 0.195 | – |
|  |

Table 1. Genetic differentiation (pairwise FST) between regional walrus samples based on microsatellite and mtDNA variation. *N*ms = sample size in microsatellite analyses; *N*mt = sample size in mtDNA analyses. Estimates based on mtDNA variation above diagonal, with estimates based on microsatellite variation below.