Developing Proteomic Genotyping for the Common Good

UC Davis Proteomics

Proteomics.ucdavis.edu
blusky=@ucdproteomics.bsky.social
UC Davis Proteomics Core

• Established 2005
• Averages between 3-5 Staff Scientists and 3-5 undergraduate students
• Over 150 Authored publications by core scientists
  • Many more non authored (= acknowledged)
• 3 successful NIH S10 grants
• Generates typically between 600-800K a year in revenue
• Offers Online and in person (hands on classes) almost every year
  • https://video.ucdavis.edu/playlist/details/0_4jkc4swu - Online Videos
• Usually involved and spearheads several international proteins studies a year though the ABRF Proteomics Research group
  • 2020-2021 Pandemic Proteomic Beer Study
  • 2021-2022 Prote“omlet” egg glycopeptide study
• Only academic lab in the world that still does Edman sequencing and Amino Acid analysis
UC Davis Genome Center
proteomics.ucdavis.edu

ucdavis.edu

Genome Center Passes 1 Million COVID-19 Tests, Helping Keep Posit... UC Davis’s asymptomatic COVID-19 testing program completed its one millionth test this week, a little more than a year since the campus ...
Some of the samples in our Core Facility in the last year or so

- Human Hair & Skin & Fingermarks & 11K year old human teeth!
- Grape Sap
- Bull sperm cells
- Ferret Sperm
- Yeast/Beer
- Egg Whites
- All sorts of BioID experiments
- All sorts of PTMS (phospho, Sumo, ubiq)
- All sorts of livers, Fish, mouse, human
- Walnut Bark and Pellicle (walnut skin)
- Tardigrades
- Horse Lung Lavage (horse snot)
- Dog tissue
- Sea Otter hearts (diseased cardiomyopathy, very fibrotic)
- Brain inclusion bodies
- Bovine uterine fluid
- Isolated HDL particles from serum
- Wheat
- Milk - human, cow, formula
- Plasma, human, mouse
- Mouse Knee tissue
- Covid Nasal Swabs
- Some weird sample that was green!
Horse Snot
Collaboration
with the
Proteomics Core
Here at OHSU

Study identifies possible factor in newborn foals being prone to lung infections

Newborn foals appear to have a lower relative abundance of immune-related proteins in their lung lavage fluid than older foals and adult horses, researchers report.
You want me to put this in my mass spec?
2023 course was last month
Sample prep/ LCMS / analysis
Virtual Class

- We did a virtual Pandemic Class available here

https://video.ucdavis.edu/playlist/details/0_4jkc4swu
Proteomics Community Building

Every other week clubhouse chat

Our Proteomics radio hour has been getting more popular
The 2021 ABRF Beer Study: Beer Proteomics at the Global Scale

- Preprint with 74 of co-authors is soon to be out!
- Largest beer proteomics resource ever (we think)

Brett Phinney, Andrew Marcus, Glen Fox, Hua Ding, Laura E Herring, Pratik D. Jagtap, Joanna Kirkpatrick, Vikas Kumar, Mukul K Midha, Leroy Martin, Magnus Palmblad, Baozhen Shan, Paul M Stemmer, Yan Wang, Dan Polasky, Austin Carr, Michael Shortreed, Benjamin A. Neely

The Fundemic Beer Project

MassIVE MSV000088080

The 2020 ABRF Beer Study: beer proteomics at the global scale

357 injections
Complexity & Variation: Isoforms and Proteoforms

Gene → mRNA → Isoforms → PTMs → Proteoforms

- Glycosylation
- Phosphorylation
- Acetylation
A typical workflow in bottom-up proteomics experiment

1. Homogenization/Cell lysis
2. Protein precipitation
3. Denature, Reduce, Alkylate
4. Proteolytic digestion
5. LC-MS/MS

Cell cultures, Primary cells, Frozen tissues, FFPE, Biofluids, Exosomes, Secretome, etc.
Shotgun Proteomics

Complex Mixtures ($10^3$) of proteins are digested using a protease into peptides ($10^6$)

Peptides are Separated and fed into a Mass Spectrometer
Zoomed in. Tons of peptides!!
From: https://www.sciencedirect.com/science/article/pii/S2667237521000035
If the most abundant protein represents the length of California, the least abundant proteins represent the length of *E. coli*. Most analytical methods only have $10^4$ to $10^5$ dynamic range. Representing the size of a 747.

Where we need to be to characterize the transcriptome: $4 \times 10^4$ meters, ~marathon
Welcome to the Parker Laboratory
ProteoGenomics

Objectives

• To gain a basic understanding of proteomic genotyping.
• To learn how proteomic information can be useful in a forensic context.
  • Human Hair: Forensic intelligence / human ancestry
  • Human Hair: human identification
  • Fur Hair: Identification of Species Origin
• To learn about applications to Archaeology and Paleontology
  • Proteomic Sex Estimation
Advantages of Protein?

- Protein is intrinsically more stable.

![DNA Structure](image1.png)

Protein

- Less Reactive
- Protein is intrinsically more stable than DNA
  - $1^\circ > 2^\circ > 3^\circ$
- “Pre-Amplified”
- Peptides persist beyond whole proteins
Protein contains genetic information: Proteomic Genotyping

• Genetically Variant Peptides
  • Contains Single Amino Acid Polymorphisms (SAPs)
  • Result of non-synonymous SNPs
  • Detection of GVPs → nsSNP genotype
  • ‘Proteomic Genotyping’

• Allele frequency changes with population ($F_{ST}$)
• Autosomal: Apply Product Rule
• Discrimination: GVPs >> mtDNA

<table>
<thead>
<tr>
<th>SNP</th>
<th>Reference</th>
<th>Variant</th>
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<tbody>
<tr>
<td>rs1732263</td>
<td>...CTGTA...</td>
<td>...TTCTG...</td>
</tr>
<tr>
<td>G1471C</td>
<td>...GTAGAC...</td>
<td>...CAGCC...</td>
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<table>
<thead>
<tr>
<th>SAP</th>
<th>E452D</th>
<th>E452D</th>
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<tr>
<td>GVP</td>
<td>GAFLYEPCGVSTVG</td>
<td>GAFLYDPCG...</td>
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<tr>
<td>M+H</td>
<td>2223.14781 Da</td>
<td>2209.13206 Da</td>
</tr>
</tbody>
</table>

\[ af_{EUR} = 0.96 \quad 0.04 \]
\[ af_{AFR} = 0.79 \quad 0.21 \]

• Do genotyping when no DNA is present!
• Protein Stability >> DNA
• Mass Spectrometry sensitive down to 50 ng
# Genomic content in proteome

## Table 1 | Median autosomal variant sites per genome

<table>
<thead>
<tr>
<th></th>
<th>AFR</th>
<th>AMR</th>
<th>EAS</th>
<th>EUR</th>
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<td>661</td>
<td>347</td>
<td>504</td>
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<td>Mean coverage</td>
<td>8.2</td>
<td>7.6</td>
<td>7.7</td>
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<table>
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<th>Var. sites</th>
<th>Singletons</th>
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<td>SNPs</td>
<td>4.31M</td>
<td>145k</td>
<td>3.64M</td>
<td>120k</td>
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<td>14.8k</td>
<td>3.53M</td>
<td>11.4k</td>
<td>3.60M</td>
<td>14.4k</td>
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<tr>
<td>Indels</td>
<td>625k</td>
<td>-</td>
<td>557k</td>
<td>-</td>
<td>546k</td>
<td>-</td>
<td>546k</td>
<td>-</td>
<td>556k</td>
<td>-</td>
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<td>Large deletions</td>
<td>1.1k</td>
<td>5</td>
<td>949</td>
<td>5</td>
<td>940</td>
<td>7</td>
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<td>153</td>
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<td>158</td>
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<td>157</td>
<td>1</td>
<td>165</td>
<td>1</td>
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<tr>
<td>MEI (Alu)</td>
<td>1.03k</td>
<td>0</td>
<td>845</td>
<td>0</td>
<td>899</td>
<td>1</td>
<td>919</td>
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<td>0</td>
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<td>0</td>
<td>123</td>
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<td>0</td>
<td>56</td>
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<td>53</td>
<td>0</td>
<td>44</td>
<td>0</td>
<td></td>
<td></td>
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<td>MEI (MT)</td>
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<td>5</td>
<td>0</td>
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<td>0</td>
<td>4</td>
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<td>9</td>
<td>0</td>
<td>11</td>
<td>0</td>
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</tbody>
</table>

**Nonsynon** | 12.2k | 139 | 10.4k | 121 | 10.2k | 144 | 10.2k | 116 | 10.3k | 144 |

**Synon** | 13.8k | 78 | 11.4k | 67 | 11.2k | 79 | 11.2k | 59 | 11.4k | 78 |

**Intron** | 2.06M | 7.33k | 1.72M | 6.12k | 1.66M | 7.39k | 1.68M | 5.68k | 1.72M | 7.20k |

**UTR** | 37.2k | 168 | 30.8k | 136 | 30.0k | 169 | 30.0k | 129 | 30.7k | 168 |

**Promoter** | 102k | 430 | 84.3k | 332 | 81.6k | 425 | 82.2k | 336 | 84.0k | 430 |

**Insulator** | 70.9k | 248 | 59.0k | 199 | 57.7k | 252 | 57.7k | 189 | 59.1k | 243 |

**Enhancer** | 354k | 1.32k | 295k | 1.05k | 289k | 1.34k | 288k | 1.02k | 295k | 1.31k |

**TFBSs** | 927 | 4 | 759 | 3 | 748 | 4 | 749 | 3 | 765 | 3 |

**Filtered LoF** | 182 | 4 | 152 | 3 | 153 | 4 | 149 | 3 | 151 | 3 |

**HGMN-DM** | 20 | 0 | 18 | 0 | 16 | 1 | 18 | 0 | 16 | 0 |

**GWAS** | 2.00k | 0 | 2.07k | 0 | 1.99k | 0 | 2.08k | 0 | 2.06k | 0 |

**CinVar** | 28 | 0 | 30 | 1 | 24 | 0 | 29 | 1 | 27 | 1 |

See Supplementary Table 1 for continental population groupings, CNVs, copy-number variants; HGMN-DM, Human Gene Mutation Database disease mutations; k, thousand; LoF, loss-of-function; M, million; MEI, mobile element insertions.

nsSNPs are a small subset of all SNPs

~ 1 nsSNP / 2 proteins
Tandem Mass Spectrometry

• De Novo Sequencing

• Peptide Spectra Matching
  • Match with theoretical sequence
    • Requires reference database
  • Assign a “score”
  • Calculate False Discovery Rate
  • DNA-confirmation/genotyping

• Internal Standards

Proteomics depends on genomics
Proteomics infers the presence of a gene
Wholistic Approach to Crime Scene Management

• What do you do when DNA is missing or degraded:
  • Hair shafts
    • DNA degradation: biological
  • Sexual Assault Evidence
    • DNA degradation
    • Multiple contributors
  • Buried remains
    • DNA degradation: environmental
  • Fingermarks
    • Low copy DNA
    • Highly transferred / mixed
Forensic Use of Hair Shafts

- Hair is ubiquitous
  - 50 to 150 shed per day

- Investigation
  - Ancestry
  - Body Site
  - Identity

- Methods
  - Morphological
  - Analytical
  - Genetic

- **BUT** morphological comparisons are subjective / highly controversial
Proteomic Genotyping from Human Hair

- 508 non-synonymous SNP alleles
- Use inferred genotype to develop random match probabilities
- Optimize sample processing
- Optimize mass spectrometry platform
- Sibship and paternity tests
- Several tissues
  - Hair, Bone, Skin, Semen
- Validations
  - Body site
  - Peroxide
  - Greying hair
  - Storage time

- Hair
  - ~500 proteins, 3 - 4,000 peptides
  - Detect up to 101 GVPs per hair
  - RMPs range up to 1 in $10^{18}$
Side Bar: How many GVPs do you need?

- **Current**
  - Average GVPs = 77
  - Median RMP = 1 in 1.1 million

- **Projected with heavy-isotope peptides**
  - Average GVPs = 123
  - Median RMP = 1 in 10 trillion

\[\sim 10 \text{ GVPs per order of magnitude}\]
What can we do with this information?

- Optimizing method for forensic lead generation (ancestry) from a single hair
  - ~500 proteins, 3 - 4,000 peptides
  - Detect up to 101 GVPs per hair
  - RMPs range up to 1 in $10^{18}$
  - RMPs change with reference population (1000G)
Ancestry Estimation from Hair

- 132 subjects
  - (>75% DNA sequence, >2000 peptides)
  - ADMIXTURE analysis (% African Ancestry)
- Four populations
  - European to African axis
- Q-Exactive Plus MS
- X!Tandem & GVPFinder:
  - nsSNP profile
- 3 Approaches
  - STRUCTURE
  - PLSDA
  - Likelihood Ratios

```
<table>
<thead>
<tr>
<th></th>
<th>European</th>
<th>Admixed</th>
<th>African</th>
<th>Middle Eastern</th>
<th>All</th>
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<td>n</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>132</td>
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<tr>
<td>-log(RMP)$_{\text{max}}$</td>
<td>14.3</td>
<td>18.4</td>
<td>12.2</td>
<td>10.3</td>
<td>18.4</td>
</tr>
<tr>
<td>-log(RMP)$_{\text{median}}$</td>
<td>6.5</td>
<td>8.7</td>
<td>8.0</td>
<td>6.9</td>
<td>8.8</td>
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<tr>
<td>#GVPs</td>
<td>57 - 101</td>
<td>54 - 98</td>
<td>43 - 88</td>
<td>71 - 90</td>
<td>43 - 101</td>
</tr>
</tbody>
</table>
```
Summary

- Proteomics
  - 43-101 GVPs per hair shaft
  - RMPs up to 1 in $10^{18}$

- STRUCTURE
  - Not work for proteomic genotype data

- PCA / PLS-DA
  - Single populations
    (AFR= 13/21; EUR= 54/65)
  - Mixed ancestry
    (ADX= 7/20)

- Likelihood Ratio
  - 26 orders of magnitude
  - Partitions genetic populations
  - Accuracy = $11 \pm 13\%$
    - (67% of samples = 6.8 $\pm$ 8.3%)
  - Reference population = 1000G

  - Poorer performance with log(LR) values between -2.5 to 2.5.
Conclusion

- Investigative leads
  - Actionable information
  - Data from sample alone
  - Minimize bias
    - Subjective analysis
    - Non-systematic reference population
  - Scientifically based
  - Statistically sound
  - Complement mtDNA

- Ancestral Likelihood Ratio
  - Accuracy = 11 ± 13%
    - (66% of samples = 6.8 ± 8.3%)
    - Uneven: -2.5 < logLR < 2.5
  - Sample population = 1000G

- Human Identification
  - Median RMP = 1 in $10^{8.8}$
Increasing the scope of genetic proteomics

- Other forensic tissues
  - Sexual Assault Evidence
  - Degraded Skeletons
  - Fingermarks

- Wildlife Forensics
  - Identify Species of Origin

- Proteomic Sex Estimation
A statewide ban on the sale of new animal fur products went into effect on **Jan. 1, 2023**, making California the first state in the U.S. to implement such a ban. Its citizens have waited more than three years for the new law to take effect after legislators passed AB 44, sponsored by Assemblymember Laura Friedman. Jan 3, 2023

A Humane World
https://blog.humanesociety.org › 2023/01 › in-a-win-for...

**In a win for animals, California's ban on fur officially takes effect**
It excludes the sale of leather, **dog and cat fur**, cowhides, deer, sheep and goat skin, and anything preserved through taxidermy. It could mark a significant blow to the fur industry that makes products from animals including mink, chinchillas, rabbits and other animals.  

Oct 13, 2019

The Guardian

[https://www.theguardian.com/world/oct/fur-ban-california](https://www.theguardian.com/world/oct/fur-ban-california)

**California becomes first US state to ban animal fur products**
(B) “Fur product” does not include any of the following:

(i) A **dog or cat fur product**, as defined in Section 1308 of Title 19 of the United States Code, as that section read on January 1, 2020.

(ii) An animal skin or part thereof that is to be converted into leather, which in processing will have the hair, fleece, or fur fiber completely removed.
Statement of Problem: Phylogenetic Proteomics

- Fur is a major challenge in wildlife forensics.
- Easier to traffic.
- Manufacture requires
  - High temperatures
  - Low pH
  - ± formaldehyde
  - ± peroxide, bleach
- High Failure rate for DNA bar coding! (<3%)

<table>
<thead>
<tr>
<th>Case samples</th>
<th>Skin</th>
<th>Hair</th>
<th>Hoof/Horn</th>
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<tbody>
<tr>
<td>elk shoulder mount</td>
<td>X</td>
<td>X</td>
<td>n/a</td>
</tr>
<tr>
<td>exotic cat vest</td>
<td>X</td>
<td>X</td>
<td>n/a</td>
</tr>
<tr>
<td>kangaroo leather gloves</td>
<td>X</td>
<td>X</td>
<td>n/a</td>
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<tr>
<td>kangaroo pelt</td>
<td>X</td>
<td>X</td>
<td>n/a</td>
</tr>
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<td>kangaroo pelt</td>
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<tr>
<td>mountain goat taxidermied hoof</td>
<td>X</td>
<td>X</td>
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<td>mountain lion pelt</td>
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<td>painted zebra hide</td>
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<tr>
<td>zebra hide coasters</td>
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<td>n/a</td>
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<tr>
<td>zebra skin</td>
<td>√</td>
<td>X</td>
<td>n/a</td>
</tr>
</tbody>
</table>

n/a = source material not available
X = no DNA results obtained
√ = DNA results obtained
Proteomics on Non-Model Organisms

- **Theory: Peptide Spectra Matching Efficiency**
  - Efficiency down with evolutionary distance
  - nsSNPs
    - Individual
    - Common Minor Allele
    - Major Allele
    - Population Specific
    - Species-Specific

- **Practice: Potential confounding effects**
  - Some species closely related
    - Lion and leopard ~3-4 million yrs
  - Some proteins do not change much with evolution.
  - Protein modifications confused for species specific amino acids
  - Not all proteomes are equal
Sidebar: Felidae Phylogenetics

• Forensic Challenge
  • Related species
    • Eg. Lion and Leopard
  • How good can you resolve a population with proteomics?
Identify Species Origin of Felidae Fur

• 5 fur Species Samples
  • Panthera leo (tiger)
  • Panthera pardus (leopard)
  • Panthera tigris (tiger)
  • Puma concolor (puma)
  • Acinonyx jubatus (cheetah)

• 6 samples
  • 3 skin
  • 3 fur hair

1. Process using an optimized hair protocol.
2. Proteomic mass spectrometry
3. Search raw data with species-specific reference protein databases
4. Measure PSM
Example of Protein Coverage

Proline

Alanine
Identify Species Origin of Felidae Fur

Other Factors?
• More stringent searches = no effects
• Protein coverage vs total peptides = no effect
• Human contamination = has an effect
Summary: Phylogenetic Proteomics

- Resolve Lion and Leopard (just)
- Changes can be more pronounced at the protein level
- Species specific peptides can be identified and detected!

- Peptide Sequence Matching is reliable for faster analysis, with no need for development of targeted assays.

- Future work
  - Targeted assays
  - Species specific QQQ assay.
  - More unknown samples!
Statement of Problem: Proteomic Sex Estimation

- Skeletons mostly do not have sexually dimorphic markers
  - Non-adults: male/female skeletons alike
  - Degraded: pelvis bone is fragile, other markers ambiguous.
  - Together most skeletons cannot be sexed.

- DNA:
  - X-/Y-chromosome Markers
  - Sensitive, but DNA is often missing
  - Low copy number → error rate
Amelogenin Genes are Expressed in Enamel

The most characterized sex-chromosome markers are expressed in the most robust tissue!

- Amino acid differences occur between them
  - AMELX_HUMAN
  - AMELY_HUMAN
- Amelogenin peptides can be extracted from enamel tissue
  - AMELY_HUMAN
  - CA-ALA-554 B85D, ~1000 BP
Amelogenin Genes are Expressed in Enamel

- Peptides can be measured
  - Total Ion Current (TIC)
- Combine all peptide signals that are specific to AMELX_HUMAN or AMELY_HUMAN
- Male (◼) and Female (●) teeth separate into two populations.
  - Signal ranges over 2 orders of magnitude
  - AMELY is about 10% of AMELX
  - 2 outliers
  - Unsexed samples partition as well
Amelogenin Genes are Expressed in Enamel

- Peptides are very stable
- Over 10,000 years no change in signal!
- Male (■) and Female (●) teeth separate into two populations.
  - AMELY is about 10% of AMELX
  - 2 outliers
  - Unsexed samples partition as well
Amelogenin Genes are Expressed in Enamel

• How does Proteomic Sex Estimation compare to other methods?
• Genomic Sex Estimation contradicts some Proteomic Sex Estimates
  • Who is at fault?: Protein, DNA or Both
  • Contradictions only occur in low quality DNA samples!
  • no pattern in protein quality!
• Therefore when estimating sex
  • Proteomic sex estimation > High read (>100K) genomic estimation > Osteology sex estimation.

Genomic Sex Estimation is NOT reliable < 100K reads
Summary: Proteomic Sex Estimation

• **Pros:**
  - Partitions male and female samples
  - Highly sensitive and stable
    - No change over 10K years
  - More reliable than DNA methods, where DNA read < 100K.
  - Potentially much cheaper!

• **Cons:**
  - DNA genotyping is being conducted anyway.
  - If >100K ancient reads, no difference.
  - Osteological sex estimation
    - Only good for ~50% of samples
    - BUT very cheap and fast
    - Confident estimates are reliable (>95%).
A comparison of proteomic, genomic, and osteological methods of archaeological sex estimation

Tammy Buonasera 1,2, Jelmer Eerkens 3, Alida de Flamingh 4, Laurel Engbring 5, Julia Yip 6, Hongjie Li 7, Randall Haas 3, Diane DiGiuseppe 8, Dave Grant 8, Michelle Salemi 9, Charlene Nijmeh 10, Monica Arellano 10, Alan Leventhal 10,11, Brett Phinney 9, Brian F Byrd 5, Ripan S Malhi 4,7,12, Glendon Parker 13

Affiliations  + expand

PMID: 32681049  PMCID: PMC7368048  DOI: 10.1038/s41598-020-68550-w

Free PMC article
9000-year-old grave shows women tackled big game

UC Davis study challenges age-old ‘man-the-hunter hypothesis”
Acknowledgements

- UC Davis
  - Robert Rice
  - Jelmer Eerkens
  - Randy Haas
  - Brett Phinney
  - Zachary Goecker
  - Tammy Buonasera
  - Noreen Karim
  - Julia Yip
  - Jennifer Milan
  - Tina De Leon
  - Victoria Montgomery
  - Ashleigh Matzoll
  - Trevor Borja
  - Rachel Franklin
  - Nicole Slattengren
  - Kyle Burk
  - Daniela Vasquez
  - Jacqui Abad Santos
  - Diana Malachik
  - Michelle Salemi
  - Ashley Spicer
  - Kelly Carrothers
  - Nicole Slattengren

- CFSRE
  - Heather McKiernan
  - Kevin Legg
  - Catherine Brown
  - Phil Danielson (U.Denver)

- Battelle
  - Craig Bartling
  - Lindsey Caitlin
  - Rich Chou

- IUPUI
  - Susan Walsh
  - Bailey Wills
  - Noah Herrick

NIJ 2015-DN-BX-K065
NSF #BCS-1825022