

Katherine B. Gettings, Ph.D.
Research Biologist
Applied Genetics Group
Forensics@NIST
November 9, 2020

SNPCHAT: The forensic marker
that could be your new BFF

NIST
National Institute of
Standards and Technology
U.S. Department of Commerce

1

What is a SNP?

How can identity SNPs be used?

How do current prediction methods perform?

Topics to Cover

What info do SNPs provide?

How are ancestry and phenotype SNP panels developed?

2

Single Nucleotide Polymorphism

Allele 1: TAGGATCGTGCCGATGACTG
Allele 2: TAGGATCGTACCGATGACTG

A/A Homozygous A/G Heterozygous G/G Homozygous

3

Single Nucleotide Polymorphism

Population A

Population B

4

Single Nucleotide Polymorphism

Population A, B, C...

Population Z

5

SNP Information

- IISNP** Individual Identification SNP
- AISNP** Ancestry Informative SNP
- PISNP** Phenotype Informative SNP
- LISNP** Lineage Informative SNP

Available online at www.elsevier.com
 ScienceDirect
 Research article
 Report on ISFG SNP Panel Discussion
 J.M. Butler^{1,*}, B. Budowle², P. Gill³, K.K. Kidd⁴, C. Phillips⁵,
 P.M. Schneider⁶, J.M. Kollman⁷, N. Morling⁸
¹Forensic Science International, Genetic Subgroup Series 1 (2006) 471-477
²National Institute of Standards and Technology, Gaithersburg, MD, USA
³Yale University, New Haven, CT, USA
⁴Medical Research Service, Department of Defense, Bethesda, MD, USA
⁵University of Colorado at Boulder, Boulder, CO, USA
⁶University of Granada, Granada, Spain
⁷University of Cologne, Cologne, Germany

6

SNP Information

LISNP-Lineage

7

SNP Information

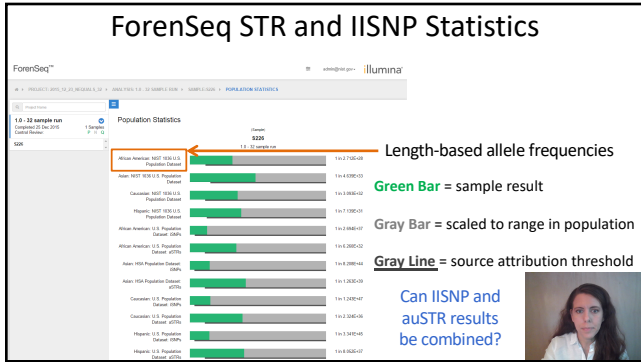
IISNP-Individual Identification

- Balancing has occurred in all populations
- Allele frequencies are similar within and between populations
- High heterozygosity

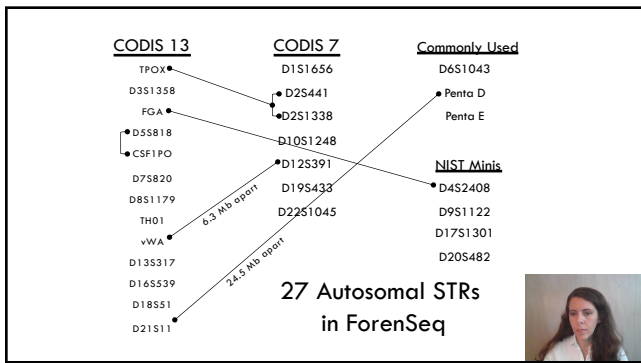
8

IISNP Benefits for Degraded DNA

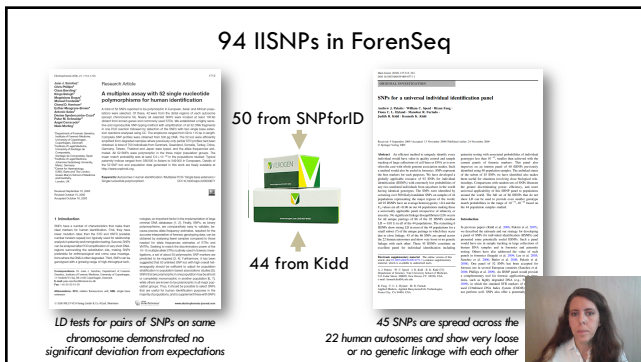
9



10



11



12

LD in casework

Collaboration to evaluate in NIST 1036 with Andreas Tillmar, National Board of Forensic Medicine

Ideally confirm with multiple sample sets from same population, multiple methods

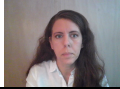
Designing panel/assay: Evaluate LD, eliminate loci as needed based on informativeness

Implementing established panel/assay:

Best – Determine haplotype frequency for pair or block
• for polymorphic loci the sample size would be unfeasible

Alternative – Exclude one of the two markers during validation
• Keep the more informative, similar to assay design

Problematic – Exclude one of the two markers case-by-case
• RMP vs Kinship



13

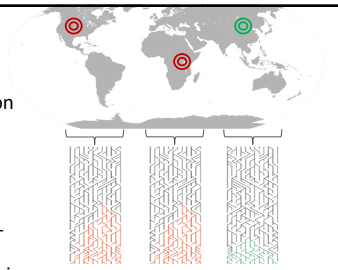
SNP Information

Ancestry Information

- Population specific fixation has occurred
- Low heterozygosity

Examples

- Malaria resistance in Sub-Saharan Africa
- Lighter skin pigmentation in Europe



14

Ancestry SNP Assay Evaluation Criteria

Does the SNP panel target the populations of interest?

- Varies by country/region

How do the SNPs perform?

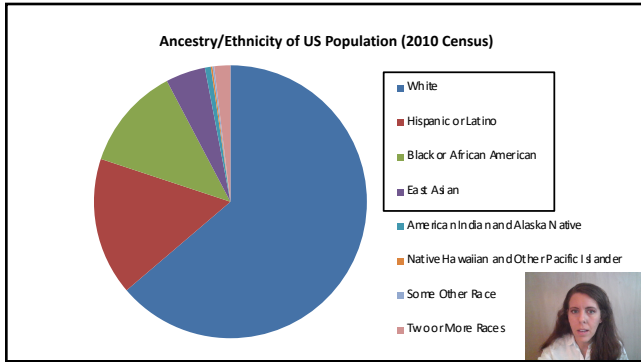
- Interlocus balance
- Heterozygote balance
- Concordance

Does the interpretation model provide reliable predictions?

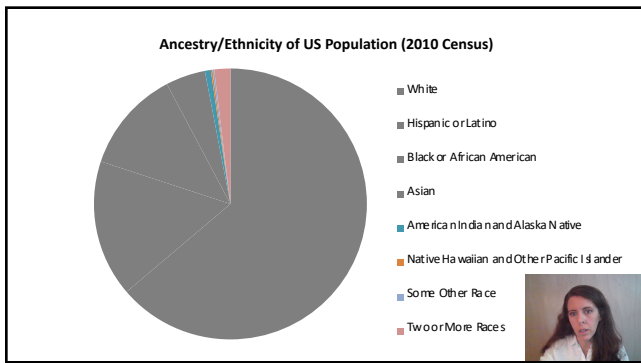
- Dependent on appropriate model training data



15



16



17

SNP Information
AISNP - Ancestry

- S5 Ancestry SNP Panel contains
 - Seldin 128 (with some exceptions)
 - Kidd 55
- ForenSeq contains Kidd 55

Forensic Science International: Genetics
Research Article
Human Mutation

Ancestry Informative Marker Sets for Determining Continental Origin and Admixture Proportions in Common Populations in America



Research Article
Human Mutation

18

SNP Information

PISNP-Phenotype

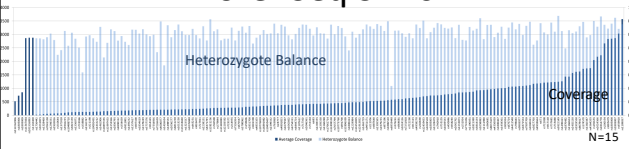
- 24 Hirisplex SNPs
 - ForenSeq
 - S5 Phenotype Panel

The HirisPlex system for simultaneous prediction of hair and eye colour from DNA
 Susan Walsh*, Fan Liu*, Andreas Wellbroin*, Leda Kovacs*, Arwin Ralf*, Agnieszka Kosiniak-Karysta*, Wojciech Branicki**, Manfred Kayser**

19

ForenSeq SNPs



172 SNPs - Identity, Ancestry & Phenotype
 Contains (with a few exceptions):

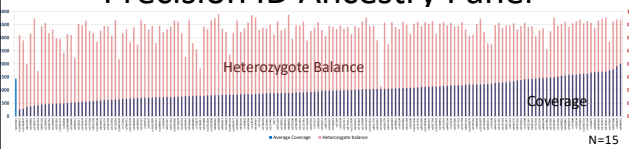
- Kidd 55 for Ancestry
- Kidd 45 + SNPforID52 for Identity
- Hirisplex 24

Left side y-axis = average SNP coverage
 • ranges from 23X to 3567X (>150 fold)

Right side y-axis = average het balance
 • ranges from 0.42 to 0.94

20

Precision ID Ancestry Panel

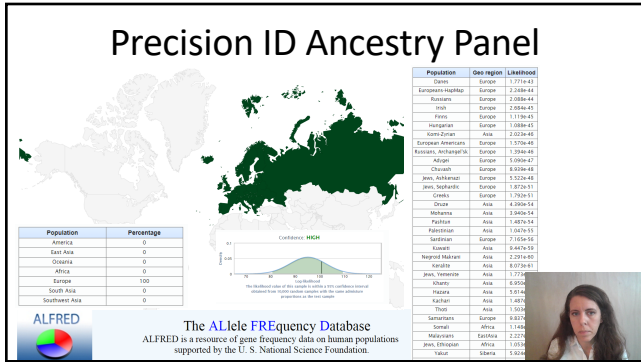


165 SNPs - Ancestry
 Contains Kidd 55 and Seldin 128
 (with exceptions)

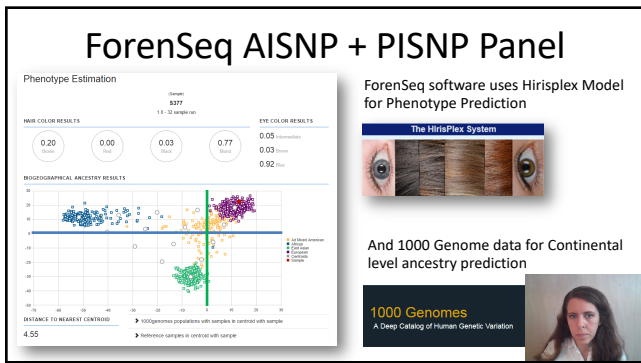
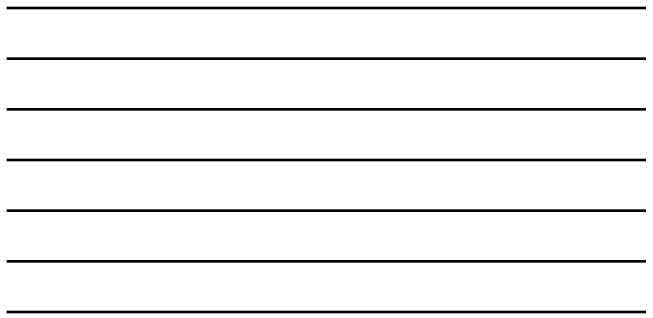
Left side y-axis = average SNP coverage
 • ranges from 264X to 2000X (7.6 fold)

Right side y-axis = average het balance
 • ranges from 0.43 to 0.98

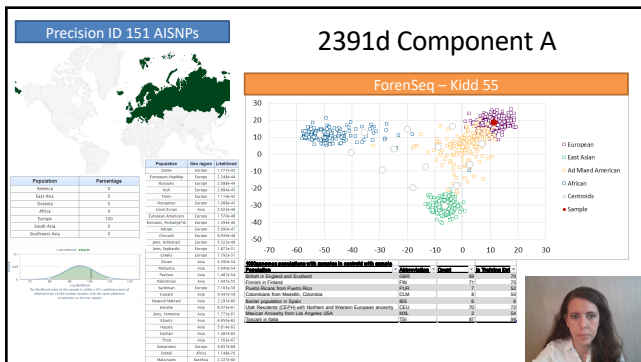
21



22

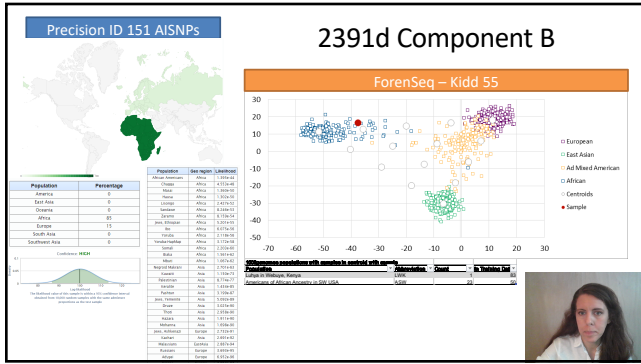


23

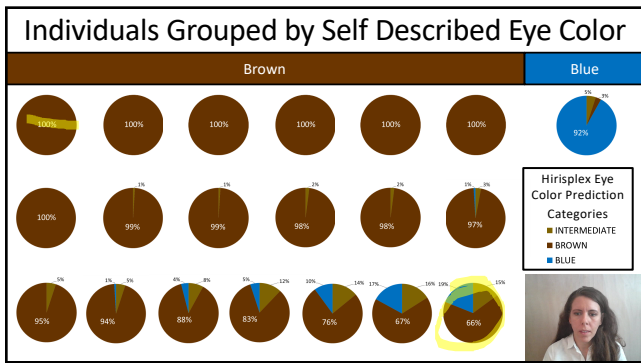


24





25



26

SNP Assays - Conclusions

SNP genotyping performance is different from CE-STR assays

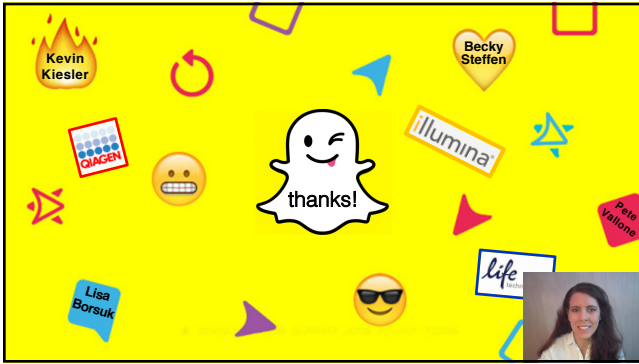
Identity SNP panels are useful for degraded samples

Identity SNP data can be combined with STR data

Linkage Disequilibrium needs to be evaluated

Labs must carefully consider how to convey ancestry and phenotype prediction information

27



28
