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Dr. Fan Liu is a full professor at Naif Arab University for Security Sciences, previously served as a professor at Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing China and as an assistant professor at Erasmus University Medical Center Rotterdam, the Netherlands. Dr. Liu is a member of the standing committee of the intelligent lifestyle branch of China Geriatric Health Association, the Visigen Consortium, and the forensic genetics branch of the Genetics Society of China. Dr. Liu's research areas include forensic DNA phenotyping, molecular epidemiology, and human appearance omics. He has developed molecular models for predicting human attributes: eye color, hair color, skin color, adult height, male baldness, curly hair, face shape, ancestry, and age. His models for human pigmentation traits find use in forensic settings in various countries, and the age inference model has applications in China's forensic domain. Dr. Liu has published over 100 papers in SCI journals, accumulating more than 4,000 citations with a WoS H-index of 35. Of these, 50 papers list him as a key author in journals such as Nat Genet, Nat Commun, Am J Hum Genet, Curr Bio, and J Invest Dermat. Over 10 of his publications received attention from international media. Dr. Liu is listed in world ranking Top 2% Scientists in the subfield of Legal Medicine updated in the October 2023 database by Stanford and Elsevier, https://elsevier.digitalcommonsdata.com/datasets/btchxktzyw/6.

Research Areas

Molecular Epidemiology; Phenomics; Multiomics; Precision Medicine; Biostatistics; Bioinformatics; Human Complex Trait Genetics; Forensic DNA Phenotyping; Human Appearance Traits.

Work Experience

- **09/2022 to Current** **Professor**, Naif Arab University for Security Sciences, Riyadh, Kingdom of Saudi Arabia.
- **10/2015 to 09/2022** **Professor**, Beijing Institute of Genomics and CNCB, Chinese Academy of Sciences, Beijing, China.
- **10/2015 to 09/2022** **Professor**, School of Future Technology, University Chinese Academy of Sciences, Beijing, China.
- **01/2013 to 10/2015** **Assistant Professor**, Erasmus MC, University Medical Center Rotterdam, Rotterdam, the Netherlands.
- **02/2009 to 12/2012** **Post-doc**, Erasmus MC, University Medical Center Rotterdam, Rotterdam, the Netherlands.

Education

- **09/2004.9 to 02/2009** **PhD** in genetic epidemiology, Department of Genetic Epidemiology, Erasmus MC, University Medical Center Rotterdam, Rotterdam, the Netherlands; Thesis：Methodological Approaches to Study the Genetics of Dementia and Cognitive Function，ISBN 978-90-8559-496-3,

http://repub.eur.nl/resource/pub_15319.

- **09/2002.9 to 09/2004** **MSc** and **DSc** in genetic epidemiology, Department of Genetic Epidemiology, Erasmus MC, University Medical Center Rotterdam, Rotterdam, the Netherlands.
- **09/1994.9 to 06/1999** **BSc** in clinical medicine, Department of Clinical Medicine, Cheeloo College of Medicine, Shandong University, Jinan, Shandong.

Patents

1. WO2011107973 A2 20110909 METHOD FOR PREDICTION OF HUMAN IRIS COLOR.
2. US2011312534 A1 20111222 METHOD FOR PREDICTION OF HUMAN IRIS COLOR.
3. CN201710899133.0, CN109593862A, METHOD AND SYSTEM FOR OBTAINING THE INDIVIDUAL AGE OF CHINESE MALES.
4. CN202110191027.3, CN113373236B, METHOD FOR OBTAINING THE AGE OF INDIVIDUALS OF CHINESE POPULATION.

Software

1. 2017SR716425 AgePrediction: predict age of Chinese males from CpGs.
2. 2018SR922822 AncestryInference: infer genetic decent from SNPs.
3. 2020SR0350636 HAPP_EC: obtain eye color from 2D portrait photos.
4. 2020SR1044984 PCLFP: infer language of Chinese from 2D portrait photos.
5. 2020SR0883343 QHAPP: obtain facial phenotypes from 2D portrait photos.
6. 2020SR1192037 Age Predict: Predict age of Chinese from CpGs.
7. 2020SR1192116 Predict eye color of Chinese from SNPs and CpGs.

8. 2021SR0493745 fastQTLmapping: fast QTL-like analysis of large omics data.
9. 2021SR0523107 InferC: infer genetic ancestry of Chinese from SNPs.
10. 2021SR0579671 InferG: infer living area of Chinese from CpGs.
11. CollapsABEL Detect the effects of compound heterozygote alleles.
12. PedCut Cut complex pedigrees for linkage analysis.
13. Fcn.pl Find consanguineous loops in complex pedigrees.
14. HIrisPlex Predict eye and hair color from SNPs.
15. IrisPlex Predict eye color from SNPs.

Publications: first or corresponding author [1-45] and Co-author (42-97)[46-101]

1. Peng, Q., et al., *Analysis of blood methylation quantitative trait loci in East Asians reveals ancestry-specific impacts on complex traits.* Nat Genet, 2024. **56**(5): p. 846-860.
2. Xu, J., et al., *T cell receptor beta repertoires in patients with COVID-19 reveal disease severity signatures.* Front Immunol, 2023. **14**: p. 1190844.
3. Peng, F., et al., *GWAs Identify DNA Variants Influencing Eyebrow Thickness Variation in Europeans and Across Continental Populations.* J Invest Dermatol, 2023. **143**(7): p. 1317-1322 e11.
4. Lin, S., et al., *Genome-wide epistasis study highlights genetic interactions influencing severity of COVID-19.* Eur J Epidemiol, 2023. **38**(8): p. 883-889.
5. Li, Y., et al., *Combined genome-wide association study of 136 quantitative ear morphology traits in multiple populations reveal 8 novel loci.* PLoS Genet, 2023. **19**(7): p. e1010786.
6. Xiong, Z., et al., *Combining genome-wide association studies highlight novel loci involved in human facial variation.* Nat Commun, 2022. **13**(1): p. 7832.
7. Wang, F., et al., *A Genome-Wide Scan on Individual Typology Angle Found Variants at SLC24A2 Associated with Skin Color Variation in Chinese Populations.* J Invest Dermatol, 2022. **142**(4): p. 1223-1227 e14.
8. Qian, W., et al., *Genetic evidence for facial variation being a composite phenotype of cranial variation and facial soft tissue thickness.* J Genet Genomics, 2022. **49**(10): p. 934-942.
9. Pan, S., et al., *Causal Inference of Genetic Variants and Genes in Amyotrophic Lateral Sclerosis.* Front Genet, 2022. **13**: p. 917142.
10. Han, X., et al., *Identification of novel loci influencing refractive error in East Asian populations using an extreme phenotype design.* J Genet Genomics, 2022. **49**(1): p. 54-62.
11. Qian, Y., et al., *The effects of Tbx15 and Pax1 on facial and other physical morphology in*

mice. FASEB Bioadv, 2021. **3**(12): p. 1011-1019.
12. Qian, Y., et al., *Evidence for CAT gene being functionally involved in the susceptibility of COVID-19.* FASEB J, 2021. **35**(4): p. e21384.
13. Liu, T., et al., *Exome-Wide Association Study Identifies East Asian-Specific Missense Variant MTHFR C136T Influencing Homocysteine Levels in Chinese Populations RH: ExWAS of tHCY in a Chinese Population.* Front Genet, 2021. **12**: p. 717621.
14. Jing, X., et al., *Retraction Note: Predicting adult height from DNA variants in a European-Asian admixed population.* Int J Legal Med, 2021. **135**(6): p. 2151.
15. Feng, Z., et al., *hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context.* Commun Biol, 2021. **4**(1): p. 442.
16. Chen, Y., et al., *The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits.* Forensic Sci Int Genet, 2021. **50**: p. 102395.
17. Yan, J., et al., *A genome-wide association study identifies FSHR rs2300441 associated with follicle-stimulating hormone levels.* Clin Genet, 2020. **97**(6): p. 869-877.
18. Xiong, Z., et al., *Novel genetic loci affecting facial shape variation in humans.* Elife, 2019. **8**.
19. Peng, F., et al., *Genome-Wide Association Studies Identify Multiple Genetic Loci Influencing Eyebrow Color Variation in Europeans.* J Invest Dermatol, 2019. **139**(7): p. 1601-1605.
20. Peng, F., et al., *Validation of methylation-based forensic age estimation in time-series bloodstains on FTA cards and gauze at room temperature conditions.* Forensic Sci Int Genet, 2019. **40**: p. 168-174.
21. Liu, F., et al., *Update on the predictability of tall stature from DNA markers in Europeans.* Forensic Sci Int Genet, 2019. **42**: p. 8-13.
22. Li, Y., et al., *EDAR, LYPLAL1, PRDM16, PAX3, DKK1, TNFSF12, CACNA2D3, and SUPT3H gene variants influence facial morphology in a Eurasian population.* Hum Genet, 2019. **138**(6): p. 681-689.
23. Jing, X., et al., *Predicting adult height from DNA variants in a European-Asian admixed population.* Int J Legal Med, 2019. **133**(6): p. 1667-1679.
24. Liu, F., et al., *Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair.* Hum Mol Genet, 2018. **27**(3): p. 559-575.
25. Li, Y., et al., *[The effect of EDARV370A on facial and ear morphologies in Uyghur population].* Yi Chuan, 2018. **40**(11): p. 1024-1032.
26. Hysi, P.G., et al., *Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability.* Nat Genet, 2018. **50**(5): p. 652-656.
27. Feng, L., et al., *Systematic feature selection improves accuracy of methylation-based forensic age estimation in Han Chinese males.* Forensic Sci Int Genet, 2018. **35**: p. 38-45.
28. Zhong, K., et al., *Genome-wide compound heterozygote analysis highlights alleles associated with adult height in Europeans.* Hum Genet, 2017. **136**(11-12): p. 1407-1417.
29. Zhong, K., et al., *CollapsABEL: an R library for detecting compound heterozygote alleles in genome-wide association studies.* BMC Bioinformatics, 2016. **17**: p. 156.
30. Liu, F., et al., *Prediction of male-pattern baldness from genotypes.* Eur J Hum Genet, 2016. **24**(6): p. 895-902.
31. Liu, F., et al., *The MC1R Gene and Youthful Looks.* Curr Biol, 2016. **26**(9): p. 1213-20.
32. Liu, F., et al., *Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up.* Hum Genet, 2015. **134**(8): p. 823-35.
33. Liu, F., S. Walsh, and M. Kayser, *Of sex and IrisPlex eye colour prediction: a reply to*

Martinez-Cadenas et al. Forensic Sci Int Genet, 2014. **9**: p. e5-6.
34. Liu, F., et al., *Common DNA variants predict tall stature in Europeans.* Hum Genet, 2014. **133**(5): p. 587-97.
35. Liu, F., B. Wen, and M. Kayser, *Colorful DNA polymorphisms in humans.* Semin Cell Dev Biol, 2013. **24**(6-7): p. 562-75.
36. Jacobs, L.C., et al., *Comprehensive candidate gene study highlights UGT1A and BNC2 as new genes determining continuous skin color variation in Europeans.* Hum Genet, 2013. **132**(2): p. 147-58.
37. Liu, F., et al., *A genome-wide association study identifies five loci influencing facial morphology in Europeans.* PLoS Genet, 2012. **8**(9): p. e1002932.
38. Liu, F., et al., *Detecting low frequent loss-of-function alleles in genome wide association studies with red hair color as example.* PLoS One, 2011. **6**(11): p. e28145.
39. Liu, F., et al., *Digital quantification of human eye color highlights genetic association of three new loci.* PLoS Genet, 2010. **6**(5): p. e1000934.
40. Liu, F., et al., *The apolipoprotein E gene and its age-specific effects on cognitive function.* Neurobiol Aging, 2010. **31**(10): p. 1831-3.
41. Liu, F., et al., *Eye color and the prediction of complex phenotypes from genotypes.* Curr Biol, 2009. **19**(5): p. R192-3.
42. Liu, F., et al., *A study of the SORL1 gene in Alzheimer's disease and cognitive function.* J Alzheimers Dis, 2009. **18**(1): p. 51-64.
43. Liu, F., et al., *An approach for cutting large and complex pedigrees for linkage analysis.* Eur J Hum Genet, 2008. **16**(7): p. 854-60.
44. Liu, F., et al., *A genomewide screen for late-onset Alzheimer disease in a genetically isolated Dutch population.* Am J Hum Genet, 2007. **81**(1): p. 17-31.
45. Liu, F., et al., *Ignoring distant genealogic loops leads to false-positives in homozygosity mapping.* Ann Hum Genet, 2006. **70**(Pt 6): p. 965-70.
46. Han, X., et al., *Novel loci for ocular axial length identified through extreme-phenotype genome-wide association study in Chinese populations.* Br J Ophthalmol, 2024. **108**(6): p. 865-872.
47. Jawad, M., et al., *Evaluation of facial hair-associated SNPs: a pilot study on male Pakistani Punjabi population.* Forensic Sci Med Pathol, 2023. **19**(3): p. 293-302.
48. Chen, Y., et al., *Genetic prediction of male pattern baldness based on large independent datasets.* Eur J Hum Genet, 2023. **31**(3): p. 321-328.
49. Wang, Q., et al., *DNA-based eyelid trait prediction in Chinese Han population.* Int J Legal Med, 2021. **135**(5): p. 1743-1752.
50. Simcoe, M., et al., *Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color.* Sci Adv, 2021. **7**(11).
51. Planterose Jimenez, B., et al., *Equivalent DNA methylation variation between monozygotic co-twins and unrelated individuals reveals universal epigenetic inter-individual dissimilarity.* Genome Biol, 2021. **22**(1): p. 18.
52. Bonfante, B., et al., *A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation.* Sci Adv, 2021. **7**(6).
53. Pardo, L.M., et al., *Principal component analysis of seven skin-ageing features identifies three main types of skin ageing.* Br J Dermatol, 2020. **182**(6): p. 1379-1387.
54. Liebrechts-Akkerman, G., et al., *Explaining sudden infant death with cardiac arrhythmias: Complete exon sequencing of nine cardiac arrhythmia genes in Dutch SIDS cases highlights new and known DNA variants.* Forensic Sci Int Genet, 2020. **46**: p. 102266.
55. Maas, S.C.E., et al., *Validated inference of smoking habits from blood with a finite DNA*

methylation marker set. Eur J Epidemiol, 2019. **34**(11): p. 1055-1074.
56. Liang, Q.S., et al., *Pigmentation Phenotype Prediction of Chinese Populations from Different Language Families.* Fa Yi Xue Za Zhi, 2019. **35**(5): p. 553-559.
57. Du, Z., et al., *Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome.* Genomics Proteomics Bioinformatics, 2019. **17**(3): p. 229-247.
58. Wu, S., et al., *Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans.* PLoS Genet, 2018. **14**(9): p. e1007640.
59. Visconti, A., et al., *Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure.* Nat Commun, 2018. **9**(1): p. 1684.
60. Pospiech, E., et al., *Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA.* Forensic Sci Int Genet, 2018. **37**: p. 241-251.
61. Lech, K., et al., *Investigation of metabolites for estimating blood deposition time.* Int J Legal Med, 2018. **132**(1): p. 25-32.
62. Jiao, H.Y., et al., *[Assessment of Height Prediction Model Based on SNPs Loci].* Fa Yi Xue Za Zhi, 2018. **34**(2): p. 132-137.
63. Hamer, M.A., et al., *Facial Wrinkles in Europeans: A Genome-Wide Association Study.* J Invest Dermatol, 2018. **138**(8): p. 1877-1880.
64. Duffy, D.L., et al., *Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways.* Nat Commun, 2018. **9**(1): p. 4774.
65. Chaitanya, L., et al., *The HIrisPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation.* Forensic Sci Int Genet, 2018. **35**: p. 123-135.
66. Wollstein, A., et al., *Novel quantitative pigmentation phenotyping enhances genetic association, epistasis, and prediction of human eye colour.* Sci Rep, 2017. **7**: p. 43359.
67. Walsh, S., et al., *Global skin colour prediction from DNA.* Hum Genet, 2017. **136**(7): p. 847-863.
68. Neumann, A., et al., *Predicting hair cortisol levels with hair pigmentation genes: a possible hair pigmentation bias.* Sci Rep, 2017. **7**(1): p. 8529.
69. Caliebe, A., et al., *Likelihood ratio and posterior odds in forensic genetics: Two sides of the same coin.* Forensic Sci Int Genet, 2017. **28**: p. 203-210.
70. Zubakov, D., et al., *Human age estimation from blood using mRNA, DNA methylation, DNA rearrangement, and telomere length.* Forensic Sci Int Genet, 2016. **24**: p. 33-43.
71. Lech, K., et al., *Evaluation of mRNA markers for estimating blood deposition time: Towards alibi testing from human forensic stains with rhythmic biomarkers.* Forensic Sci Int Genet, 2016. **21**: p. 119-25.
72. Tagliabue, E., et al., *MC1R gene variants and non-melanoma skin cancer: a pooled-analysis from the M-SKIP project.* Br J Cancer, 2015. **113**(2): p. 354-63.
73. Pasquali, E., et al., *MC1R variants increased the risk of sporadic cutaneous melanoma in darker-pigmented Caucasians: a pooled-analysis from the M-SKIP project.* Int J Cancer, 2015. **136**(3): p. 618-31.
74. Jacobs, L.C., et al., *IRF4, MC1R and TYR genes are risk factors for actinic keratosis independent of skin color.* Hum Mol Genet, 2015. **24**(11): p. 3296-303.
75. Jacobs, L.C., et al., *A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots.* J Invest Dermatol, 2015. **135**(7): p. 1735-1742.
76. Hamer, M.A., et al., *Validation of image analysis techniques to measure skin aging features*

from facial photographs. Skin Res Technol, 2015. **21**(4): p. 392-402.
77. Walsh, S., et al., *Developmental validation of the HIrisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage.* Forensic Sci Int Genet, 2014. **9**: p. 150-61.
78. Pospiech, E., et al., *The common occurrence of epistasis in the determination of human pigmentation and its impact on DNA-based pigmentation phenotype prediction.* Forensic Sci Int Genet, 2014. **11**: p. 64-72.
79. Liebrechts-Akkerman, G., et al., *PHOX2B polyalanine repeat length is associated with sudden infant death syndrome and unclassified sudden infant death in the Dutch population.* Int J Legal Med, 2014. **128**(4): p. 621-9.
80. Lao, O., et al., *GAGA: a new algorithm for genomic inference of geographic ancestry reveals fine level population substructure in Europeans.* PLoS Comput Biol, 2014. **10**(2): p. e1003480.
81. Jacobs, L.C., et al., *Intrinsic and extrinsic risk factors for sagging eyelids.* JAMA Dermatol, 2014. **150**(8): p. 836-43.
82. Walsh, S., et al., *The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA.* Forensic Sci Int Genet, 2013. **7**(1): p. 98-115.
83. Keating, B., et al., *First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip.* Int J Legal Med, 2013. **127**(3): p. 559-72.
84. Walsh, S., et al., *DNA-based eye colour prediction across Europe with the IrisPlex system.* Forensic Sci Int Genet, 2012. **6**(3): p. 330-40.
85. Raimondi, S., et al., *Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies.* BMC Med Res Methodol, 2012. **12**: p. 116.
86. Walsh, S., et al., *IrisPlex: a sensitive DNA tool for accurate prediction of blue and brown eye colour in the absence of ancestry information.* Forensic Sci Int Genet, 2011. **5**(3): p. 170-80.
87. Schuur, M., et al., *Genetic risk factors for cerebral small-vessel disease in hypertensive patients from a genetically isolated population.* J Neurol Neurosurg Psychiatry, 2011. **82**(1): p. 41-4.
88. Liebrechts-Akkerman, G., et al., *Postnatal parental smoking: an important risk factor for SIDS.* Eur J Pediatr, 2011. **170**(10): p. 1281-91.
89. Broer, L., et al., *Association of HSP70 and its co-chaperones with Alzheimer's disease.* J Alzheimers Dis, 2011. **25**(1): p. 93-102.
90. Branicki, W., et al., *Model-based prediction of human hair color using DNA variants.* Hum Genet, 2011. **129**(4): p. 443-54.
91. Boehringer, S., et al., *Genetic determination of human facial morphology: links between cleft-lips and normal variation.* Eur J Hum Genet, 2011. **19**(11): p. 1192-7.
92. Zubakov, D., et al., *Estimating human age from T-cell DNA rearrangements.* Curr Biol, 2010. **20**(22): p. R970-1.
93. Schol-Gelok, S., et al., *A genome-wide screen for depression in two independent Dutch populations.* Biol Psychiatry, 2010. **68**(2): p. 187-96.
94. Ikram, M.A., et al., *The GAB2 gene and the risk of Alzheimer's disease: replication and meta-analysis.* Biol Psychiatry, 2009. **65**(11): p. 995-9.
95. Estrada, K., et al., *A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation.* Hum Mol Genet, 2009. **18**(18): p. 3516-24.

96. van den Boogaard, M.J., et al., *The MSX1 allele 4 homozygous child exposed to smoking at periconception is most sensitive in developing nonsyndromic orofacial clefts.* Hum Genet, 2008. **124**(5): p. 525-34.
97. Kayser, M., et al., *Three genome-wide association studies and a linkage analysis identify HERC2 as a human iris color gene.* Am J Hum Genet, 2008. **82**(2): p. 411-23.
98. Hoppenbrouwers, I.A., et al., *Maternal transmission of multiple sclerosis in a dutch population.* Arch Neurol, 2008. **65**(3): p. 345-8.
99. Berends, A.L., et al., *Familial aggregation of preeclampsia and intrauterine growth restriction in a genetically isolated population in The Netherlands.* Eur J Hum Genet, 2008. **16**(12): p. 1437-42.
100. Gonzalez-Zuloeta Ladd, A.M., et al., *IGF-1 CA repeat variant and breast cancer risk in postmenopausal women.* Eur J Cancer, 2007. **43**(11): p. 1718-22.
101. Arias-Vasquez, A., et al., *Relationship of the Ubiquilin 1 gene with Alzheimer's and Parkinson's disease and cognitive function.* Neurosci Lett, 2007. **424**(1): p. 1-5.