JULIA SEGRE

CANDIDATE STATEMENT

I would be honored to serve as American Society of Microbiology (ASM)'s President. Three years ago, I joined the ASM Board of Directors to advance innovative ways to connect with and serve members. I now want to amplify implementation of ASM's commitments to equity, diversity, access, inclusion, and accountability.

ASM is my scientific home. My lab at NIH uses genomics to characterize the human skin microbiome (bacteria, fungi, viruses) and track hospital outbreaks. In addition, I recently served in the White House Office of Science and Technology Policy to coordinate federal priorities for pandemic readiness. I bring experience nurturing interactions between clinical and basic scientists, developing policies for antimicrobial stewardship, and engaging in effective public outreach. I am an elected member of American Academy Microbiology, National Academy Medicine, National Academy Sciences.

I invest in approaches to ensure all individuals feel they belong in science and institutions work toward their success.

ASM-RELATED ACTIVITIES

- Board of Directors Programmatic Committee (BDPC), Member, July - December 2021
- ASM Board of Directors, At-large Member, 2020-2023
- American Academy of Microbiology Fellow, elected 2015

BIOGRAPHICAL SKETCH

NAME: SEGRE, Julia A., Ph.D.

eRA COMMONS USER NAME (credential, e.g., agency login): JulieSegre

POSITION TITLE: Senior Investigator, Microbial Genomics Section; Chief, Translational Functional Genomics Branch, National Human Genome Research Institute, NIH

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Amherst College, Amherst, MA	B.A.	1983-1987	Mathematics
Massachusetts Institute of Technology, Cambridge, MA	Ph.D.	1989-1995	Genetics and Genomics
University of Chicago, Chicago, IL	Postdoc	1996-2000	Cell Biology, Genetics

A. Personal Statement

I am a Senior Investigator leading the Microbial Genomics Section, and Chief of the Translational and Functional Genomics Branch of NHGRI. I have extensive expertise in genomics, skin biology, and microbiology, having trained in the laboratories of Drs. Eric Lander and Elaine Fuchs. Since joining the NHGRI Intramural Program as an Investigator in 2000, I have established a highly productive independent research program as well as a leadership role in the Human Microbiome Project. I am the PI of an IRB-approved research protocol to study skin microbial diversity of healthy volunteers and patients with atopic dermatitis and primary immunodeficiencies. I am the co-PI on protocols to explore the microbiome of NIH Clinical Center patients to study nosocomial transmission of microbial pathogens. I work collaboratively with epidemiologists and clinical microbiologists to track and stem outbreaks of drug resistant hospital-acquired microbial infections. I have strong analytical research experience that enables me to effectively lead a trans-disciplinary group of researchers focused on microbial genomic studies. I have significant personal and professional interest in mentorship and skills required for collaboration, as demonstrated by my media communication, editorial writing, awards, and service on committees, within my institution, societies and alumni institution. I am committed to scientific communities that recognize, integrate and champion equity, diversity and inclusion. I invest in institution-centered approaches that will change the culture of science to ensure that all individuals feel they belong in science and that institutions work toward their success. In addition to my research role at NIH, I was 'on detail' to the Office of Science and Technology Policy (OSTP) to help coordinate federal priorities for pandemic readiness.

B. Positions, Scientific Appointments, and Honors

Positions and Employment

1989-1995 Graduate Student, Laboratory of Dr. Eric Lander, Whitehead Institute Genome Center, Massachusetts Institute of Technology
1996-2000 Postdoctoral Fellow, Laboratory of Dr. Elaine Fuchs, University of Chicago
2000-2007 Investigator, Genetics and Molecular Biology Branch, NHGRI, NIH
2007-present Senior Investigator with Tenure, Microbial Genomics Section, NHGRI, NIH
2013-present Chief of Translational and Functional Genomics Branch, NHGRI
2021-2022 Assistant Director for Health and Life Sciences, Office of Science Technology and Policy, Executive Office of the President (White House)

Committee/Service

2020-present Board of Directors, American Society of Microbiology
2011–2017 Board of Trustees, Amherst College, Amherst, MA
2013-2015 Working Group Member, PCAST Report on Combating Antibiotic Resistance, Council of Advisors on Science and Technology, Executive Office of President Obama
2016 Briefing for President Obama at the White House on microbiome research

2017-present NIH Anti-Harassment Committee developing and implementing policies to combat harassment
2017-2021 Member, NIH Equity Committee
2020-2021 co-chair of Intramural Program NIH UNITE initiative to address structural racism in science
2021-present Scientific Advisory Board, Duchossois Family Institute, University of Chicago
2015-2021 Member, Scientific Advisory Board, Genome Canada
2017-2021 Member, Executive Scientific Committee, NIAID Systems Biology Antimicrobial Resistance
2017-present Scientific Advisory Board, Damon Runyon Cancer Research Fund
2020-present Editorial Board, Cell
2013-2019 Associate Editor, *Genome Research;* Associate Editor, Genome Biology
2013- present Executive Committee and Member, NIH Women in Science
2018-2021 Mentor, NIH Distinguished Scholars Program, tenure track investigators committed to diversity
2016-2019 Chair or co-Chair, NHGRI tenure track recruitment search committee
2017-2019 Co-Chair, NIH wide 'Stadtman' tenure track recruitment committee in Genetics & Genomics
2019-present Organizer, Cold Spring Harbor Labs Microbiome Meeting
2017 Organizer, Keystone Microbiome Meeting
2006-present Chair NIAID Systems Biology AI-16-080; Chair, NIGMS Microbial Dynamics: GM-14-001; Member, AI-14-062; AI-14-064; GM-12-011,13-001; AI-ZAR1-XZ-M1 (others)

Honors

1986 Brown Prize for overall top student in class, Amherst College
1987 Phi Beta Kappa, *Summa cum laude,* Amherst College
1987 Breusch Prize for best senior honors thesis in Mathematics, Amherst College
1988 Watson Foundation/I.B.M. Fellowship
1996 Damon Runyon-Walter Winchell Cancer Research Fund Postdoctoral Award
2000 Burroughs Wellcome Career Development Award
2011 NIH Clinical Center Director's Award for tracking Acinetobacter *baumannii* outbreak
2012 NIH Director's Award for tracking *Klebsiella pneumonaie* outbreak
2013 Service to America Medal, Federal Employee of the Year
2014 Chanel Prize for skin research excellence
2015 Elected Fellow of American Academy of Microbiology
2019 Elected National Academy of Medicine
2020 Elected American Academy of Arts and Sciences
2022 Elected National Academy of Sciences

C. Contributions to Science

1. Defining the functional topographic microbial communities of human skin. We explored the bacterial, fungi and viral communities of diverse human skin sites. Our studies demonstrated that biogeography and individuality shape the structural and functional composition of the human skin microbiome. We analyzed skin samples from healthy volunteers to describe bacterial communities, fungal communities and shotgun metagenomics for a multi-kingdom analysis. We found that despite the skin's constant exposure to the external environment, its microbial communities were largely stable. Strain and SNV-level analysis demonstrate that individuals maintain, rather than reacquire prevalent microbes. In addition to scientific accomplishments, we created an infrastructure combining team science and translational research. (* denotes co-senior author)

Grice EA, Kong HH, …, Turner ML, **Segre JA** (2008) A diversity profile of the human skin microbiota. *Genome Res*, 18:1043-50.

Grice EA, Kong HH, Conlan, S, … Murray, PR, Green, ED, Turner ML, **Segre JA** (2009) Topographical and Temporal Diversity of the Human Skin Microbiome. *Science*, 324: 1190-2.

Oh J, Conlan S, Polley E, **Segre JA***, Kong HH* (2012): Shifts in human skin and nares microbiota of healthy children and adults. *Genome Med*. Oct 10;4(10):77.

Conlan S, Mijares LA, NISC…, Kong HH, Murray PR **Segre JA** (2012) *Staphylococcus epidermidis* pan-genome sequence analysis reveals diversity of skin commensal and hospital infection-associated isolates. *Genome Biology,* Jul 25;13(7):R64.

Human Microbiome Project Consortium. (2012) A framework for human microbiome research. *Nature*. 486(7402):215-21. PMID: 22699610.

Human Microbiome Project Consortium. (2012) Structure, function and diversity of the healthy human microbiome. *Nature*. 2012;486(7402):207-14.

Findley K, Oh J, Yang J, Conlan S, Deming C, NISC …, Kong HH*, **Segre JA*** (2013) Topographic diversity of fungal and bacterial communities in human skin. *Nature*. Jun 20; 498(7454):367-360.

Oh J, Byrd AL, Deming C, Conlan S, NISC, Kong HH*, **Segre JA*** (2014) Biogeography and individuality shape the functional divergence of the human skin metagenome. *Nature* Oct 2;514(7520):59-64.

Oh J, Byrd AL, Park, M, NISC Comparative Sequence Program, Kong HH*, **Segre JA*** (2016) Temporal stability of the human skin microbiome. *CELL* May 5; 165(4): 854-866.

Park J, Schwardt NH, Jo JH, Zhang Z, Pillai V, …Soldin SJ, Yanovski JA, **Segre JA**, Kong HH (2021) Shifts in the skin bacterial and fungal communities of healthy children transitioning through puberty. *J Invest Dermatol*. Jul 9:S0022-202X(21)01421-4.

Saheb Kashaf S, Almeida A, **Segre JA**, Finn RD (2021) Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. *Nat Protoc.* May;16(5):2520-2541.

Saheb Kashaf S, Proctor DM, Deming C, Saary P, Hoelzer M, NISC CompSeqProgram, Taylor ME, Kong HH, **Segre JA***, Almeida A*, Finn RD* (2022) Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. *Nat Microbiology.* Jan;7(1):169-179.

2. Characterizing the skin microbiome of patients with rare and common disorders. Developing animal models to test the function of the skin microbiome in initiating and driving disease. Our bacterial studies with healthy volunteers set the stage to explore the microbial etiology of human dermatologic disorders, which often manifest at stereotypical sites and ages; e.g. atopic dermatitis (AD; commonly known as eczema). We analyzed the bacterial community of AD and primary immune deficient patients' skin. We explored the skin microbiome of animal models of diabetic wound healing and AD. As well, we collaborated with Dr. Belkaid to explore the immunologic response in mouse skin to microbes.

Scharschmidt TC, List K, Grice EA, Szabo R, NISC Comparative Sequencing Program, Renaud G, Lee C-C.R., Wolfsberg TG, Bugge TH, **Segre JA** (2009)**:** Matriptase deficient mice exhibit ichthyotic skin with a selective shift in skin microbiota. *J Inv Derm* 129(10):2435-42.

Grice EA, Snitkin ES, Yockey LJ, Bermudez DM; NISC Comparative Sequencing Program, Liechty KW, **Segre JA** (2010)**:** Longitudinal shift in diabetic wound microbiota correlates with prolonged skin defense response. *Proc Natl Acad Sci* U S A. Aug 17;107(33):14799-804.

Kong HH, Oh J, Deming C, Conlan S, Grice EA, … Murray PR, Turner ML, **Segre, JA** (2012) Temporal shifts in the skin microbiome associated with disease flares and treatment in children with atopic dermatitis, *Genome Res*, May;22(5):850-9.

Naik S, Bouladoux N, …, Kong HH, Campbell DJ, Trinchieri G, **Segre JA**, Belkaid Y (2012) Compartmentalized control of skin immunity by resident commensals, *Science*, 31;337(6098):1115-9.

Oh J, Freeman AF, NISC Comparative Sequence Program, Park M, Sokolic R, Candotti F, Holland SM, **Segre, JA***, Kong HH* (2013) The altered landscape of the human skin microbiome in patients with primary immunodeficiencies, *Genome Res*, Dec;23(12):2103-14

Naik S, Bouladoux N, Linehan JL, Conlan S …, Merad M, **Segre JA**, Belkaid Y (2015) Commensal-dendritic cell dialogue specifies unique skin immune signature. *Nature* Apr 2;520 (7545): 104-8.

Kennedy EA, … Jo JH, **Segre JA**, Kong HH, Irvine AD (2016). Skin microbiome prior to development of atopic dermatitis: early colonization with commensal staphylococci at 2 months is associated with a lower risk of atopic dermatitis at 1 year. J Allergy Clin Immunol. S0091-6749(16)30893-4.

Byrd AL, Deming C, Cassidy, SKB, Harrison, OJ, Ng W-I, Conlan S, NISC Comparative Sequence Program, Belkaid Y, **Segre JA***, Kong HH*. (2017) *Staphylococcus aureus* and *S. epidermidis* strain diversity underlying human atopic dermatitis. *Science Translational Medicine* Jul5;9(397):eaal4651.

Tirosh O, Conlan S, Deming C, Lee-Lin SQ, Huang X, NISC Comparative Sequencing Program, Su HC, Freeman AF, **Segre JA***, and Kong HH* (2018). Expanded skin virome in DOCK8-deficient patients. *Nature Medicine* Dec;24(12):1815-1821.

Lisco A, Hsu AP, … Proctor DM,…**Segre JA**, Kong HH, Sereti I (2021) Restored NK function shapes skin virome and controls relapsing HPV diseases. *New England Journal of Medicine, Sep 2;385(10):921-929*.

3. Microbial genomics of multi-drug resistant bacterial pathogens to track hospital outbreaks and study acquisition of antibiotic resistance. Working together with clinical microbiologists and hospital epidemiologists, we explored outbreak of multi-drug resistant *A. baumannii* and carbapenem-resistant *Klebsiella pneumoniae.* Together with hospital epidemiologists, we integrated SNP-based genetic data and patient records to reconstruct transmission routes and identify potential weaknesses in hospital practice. Our studies enable non-genomics experts to utilize the growing body of microbial genomic sequence data by designing pipelines distinguish strains circulating within and between hospitals. We have also pioneered the use of new genomic sequence technology to explore plasmid transfer between carbapenem-resistant Enterobacteriaceae and worked across government agencies.

Snitkin ES, Zelazny AM, … Murray PR, **Segre JA** (2011): Genome-wide recombination drives diversification of epidemic strains of Acinetobacter baumannii. *Proc Natl Acad Sci* U S A. 108(33):13758-63.

Snitkin ES, Zelazny AM, Thomas PJ, Stock F, NISC Comp Seq Program, Henderson DK, Palmore TN, **Segre JA** (2012): Tracking a Hospital Outbreak of carbapenem-resistant *Klebsiella pneumoniae* with Whole Genome Sequencing, *Science Translational Medicine,* 4(148):148ra116.

Yang JY, …,**Segre JA*** Snitkin ES*. (2013) Pan-PCR, a computational method for designing bacterial-typing assays based on whole genome sequence data. *J Clin Microbiol*. Mar;51(3):752-8.

Snitkin ES, Zelazny A, Gupta J, Palmore TN, Murray PR, **Segre JA** (2013) Genomic insights into fate of colistin resistance and *Acinetobacter baumannii* during patient treatment. *Genome Res*. 23(7):1155-62.

Conlan S, Thomas PJ, Deming C,…., Korlach J, Henderson DK, Frank KM, Palmore TN, **Segre JA** (2014) Single molecule sequencing to track plasmid diversity of hospital-associated carbapenemase-producing Enterobacteriaceae, *Science Translational Medicine,* Sep 17;6(254):254ra126.

Conlan S, Park M,…Dekker JP,Palmore TN, Frank KM, **Segre JA** (2016). Plasmid Dynamics in KPC-Positive Klebsiella pneumoniae during Long-Term Patient Colonization. MBio. Jun 28;7(3):e00742-16.

Weingarten RA, Johnson RC, Conlan S, …, Palmore TN*, **Segre JA*,** Frank KM*, (2018). Genomic Analysis of Hospital Plumbing Reveals Diverse Reservoir of Bacterial Plasmids Conferring Carbapenem Resistance MBio. Feb 6;9(1):e02011-17.

Johnson R,…,Henderson DK, Lau AF, Palmore TN, **Segre JA***. Genomic and Epidemiologic Investigation of an Indolent Hospital Outbreak. *New England Journal of Medicine,* Dec 27;379(26):2529-2539.

Conlan S, Lau AF, Deming C, Spalding CD, Lee-Lin S, … Dekker JP, Frank KM, Palmore TN, **Segre JA** (2019). Plasmid Dissemination and Selection of a Multidrug-Resistant *Klebsiella pneumoniae* Strain during Transplant-Associated Antibiotic Therapy. *MBio*. Oct 8;10(5): e00652-19.

Huang X, Hurabielle C, Drummond RA, Bouladoux N, Desai JV, Sim CK, Belkaid Y, Lionakis MS*, **Segre JA*** (2021) Murine model of colonization with fungal pathogen *Candida auris* to explore skin tropism, host risk factors and therapeutic strategies. *Cell Host Microbe*. Feb 10;29(2):210-221.

Proctor DM, Dangana T, Sexton DJ, …Chiller T, Forsberg K, Black SR, Pacilli M, Lin MY, Litvintseva AP, **Segre JA***, Hayden MK* (2021) Integrated genomic, epidemiologic investigation of *Candida auris* skin colonization in a skilled nursing facility. *Nat Med.* Aug;27(8):1401-1409.

Huang X, Welsh RM, Deming C, Proctor DM, …Chiller T, Jackson BR, Forsberg K, Conlan S, Litvintseva AP, **Segre JA***(2021) Skin metagenomic sequence analysis of early Candida auris outbreaks in United States nursing homes. *mSphere.* Aug 4:e0028721.

Sim CK, Kashaf SS, …, Belkaid Y, Conlan S, **Segre JA** (2022) A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant *Enterobacteriaceae*. Microbiome. 2022 Mar 10;10(1):43.

4. Basic biology of transcriptional regulation of skin barrier development. The majority of my training as a graduate student and postdoctoral fellow focused on the transcriptional regulation of skin barrier development, explored with genomic, genetic and cell biology approaches.

Lisitsyn NA, **Segre JA**, Kusumi K, …, Wigler MH, Lander ES (1994) Direct isolation of polymorphic markers linked to a trait by genetically directed representational difference analysis. *Nat Genet* 6:57-6.

Segre JA, … Nadeau JH, Lander ES (1995) Positional cloning of the *nude* locus: genetic, physical and transcription maps of the region and mutations in mouse and rat. *Genomics* 28:549-559, 1995.

Segre JA, Bauer C, Fuchs E (1999) Klf4 is a transcription factor required for establishing the barrier function of

the skin. *Nat Genet* 22:356-360.

Martin N, Patel S, **Segre JA** (2004) Long-range comparison of human and mouse *Sprr* loci to identify conserved noncoding sequences involved in coordinate regulation. *Genome Res* 14:2430-2438.

Djalilian AR, McGaughey D,…, Ishida-Yamamoto A, **Segre JA** (2006) Connexin 26 regulates epidermal barrier and wound remodeling and promotes psoriasiform response. *J Clin Invest* 116:1243-1253.

de Guzman Strong, C, Wertz PW, … Ho IC, **Pai SY**, **Segre JA** (2006) Lipid defect underlies selective deficiency of an epidermal-specific deletion of *Gata-3*. *J Cell Biol* 175:661-670.

Patel S, … **Segre JA** (2006) Klf4 and corticosteroids activate an overlapping set of transcriptional targets to accelerate *in utero* epidermal barrier acquisition. *Proc Natl Acad Sci* 103:18668.

5. Collaborate with colleagues to develop microbiome projects across multiple systems (recent).

Greathouse KL, White JR, Vargas AJ, …, Deming C, Conlan S, Oh J, **Segre JA**, Harris CC (2018) Interaction between the microbiome and TP53 in human lung cancer. *Genome Biol*. Aug 24;19(1):123.

Harris TA, Gattu S, … Kong HH, **Segre JA**, Hooper LV (2019). Resistin-like Molecule α Provides Vitamin-A-Dependent Antimicrobial Protection in the Skin. *Cell Host Microbe*. Jun 12;25(6):777-788.e8.

Singer JR, Blosser EG, … **Segre JA**, Gray MJ, Randolph DA, Weaver CT (2019). Preventing dysbiosis of the neonatal mouse intestinal microbiome protects against late-onset sepsis. *Nat Med* 25(11):1772-1782.

Stacy A, Andrade-Oliveira V, …, Trinchieri G, **Segre JA**, Rehermann B, Belkaid Y (2021) Infection trains the host for microbiota-enhanced resistance to pathogens. *Cell.* Feb 4;184(3):615-627.e17.

Claesen J, Spagnolo JB, … Kong HH, **Segre JA**, … Lemon KP (2021) A *Cutibacterium acnes* antibiotic modulates human skin microbiota composition in hair follicles. *Sci Transl Med.* Nov 18;12(570):eaay5445.

Sakamoto K, Jin S-P, …**Segre JA**, Kong HH, Nagao K (2021) Disruption of the ADAM10-Notch signaling axis leads to dysbiosis and immune-mediated hair follicle destruction. *Immunity*, Oct 12;54(10):2321-2337.

Drummond RA, Desai JV, …, Belkaid Y, **Segre JA**, Lionakis MS (2022) Long-term antibiotic exposure promotes mortality after systemic fungal infection by driving lymphocyte dysfunction and systemic escape of commensal bacteria. Cell Host Microbe. May 7:S1931-3128(22)00219-0.

6. Provide intellectual framework with Perspectives and Commentaries (recent).

Belkaid Y and **Segre JA** (2014) Dialogue between Skin Microbiota and Immunity. *Science* 346(6212)954-9.

Segre JA (2015) Microbial growth dynamics and human disease. *Science*. Sep 4;349(6252):1058-9.

Nagao K, **Segre JA** (2015) "Bringing Up Baby" to Tolerate Germs. *Immunity*. Nov 17;43(5):842-4.

Byrd AL, **Segre JA** (2016) Infectious disease. Adapting Koch's postulates. *Science*. 351(6270): 224-6.

Fischbach MA, **Segre JA** (2016) Signaling Host-Associated Microbial Communities. *Cell* 164(6):1288-300.

Segre JA, Salafsky N (2016) Hominid superorganisms. *Science. 2016 Jul 22;353(6297):350-1.*

Joglekar P, **Segre JA**. (2017) Building a Translational Microbiome Toolbox. *Cell*. Apr 20;169(3):378-380.

Byrd AL, Belkaid, Y, **Segre, JA**, (2018) The human skin microbiome. *Nat Rev Microbiol*. Mar;16(3):143-155.

Guillemin K, **Segre JA** (2019) Frontiers in microbiome studies: viewing vast vistas with roadmap in hand. *Curr Opin Microbiol*. Aug;50:iii-iv.

Harkins CP, Kong HH, **Segre JA** (2019) Manipulating the Human Microbiome to Manage Disease. *JAMA.* Jan 28; 323(4):303-304.

Kong HH, **Segre JA** (2020) Cultivating fungal research. *Science*. Apr 24;368(6489):365-366.

Collins FS, Adams AB, Aklin C, Archer TK, Bernard MA, … Johnson AC, Schwetz T, **Segre JA**, Tabak LA, Hooper MW, Wolinetz C; NIH UNITE (2021) Affirming NIH's commitment to addressing structural racism in the biomedical research enterprise. *Cell*. Jun 10;184(12):3075-3079.

List of Published Work in MyBibliography: http://www.ncbi.nlm.nih.gov/pubmed/?term=segre+ja

Ongoing research projects supported by NIH Division of Intramural Research include:

ZIA HG000180 Segre (PI) GENE-ENVIRONMENT INTERACTIONS AT THE SKIN SURFACE
Explore the diversity of skin microbial communities in healthy volunteers and patients

ZIA HG200382 Segre (PI) MICROBIAL GENOMICS OF HOSPITAL-ASSOCIATED PATHOGENS
Use genomic information to track and model outbreaks, monitor evolution of antibiotic resistance