

Tavis K. Anderson

CONTACT INFORMATION

Virus and Prion Research Unit
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EDUCATION

Rutgers University, New Brunswick, New Jersey, USA
Ph.D., Ecology and Evolution, October 2009.
Dissertation: Food web networks and parasite diversity.
Advisor: Michael V.K. Sukhdeo

The University of Queensland, Brisbane, Queensland, Australia
B.Sc., First Class Honours, December 2001.
Advisor: Ian D. Whittington and Leslie A. Chisholm

The University of Queensland, Brisbane, Queensland, Australia
B.Sc., Parasitology, December 2000.

PROFESSIONAL HISTORY

National Animal Disease Center, USDA-ARS, Ames, Iowa, USA

Research Biologist, Virus and Prion Research Unit, 2019 - present
ORISE Established Research Scientist, Virus and Prion Research Unit, 2015 - 2019
Affiliate Faculty, Department of Computer Science, Iowa State University, 2020 - present
Affiliate Faculty, Veterinary Microbiology & Preventive Medicine, College of Veterinary Medicine, Iowa State University, 2017 - present

Georgia Southern University, Statesboro, Georgia, USA

Assistant Professor of Parasitology, Department of Biology, 2013 - 2015
Adjunct Faculty, Institute for Interdisciplinary STEM Education, 2014 - 2015
Adjunct Assistant Professor of Parasitology, Department of Biology, 2015 - present

National Animal Disease Center, USDA-ARS, Ames, Iowa, USA

Research Associate, Virus and Prion Research Unit, September 2012 - July 2013
Advisor: Amy L. Vincent

University of Wisconsin-Madison, Madison, Wisconsin, USA

Research Associate, School of Veterinary Medicine, August 2009 - August 2012.
Advisor: Tony L. Goldberg

The University of Adelaide, Adelaide, South Australia, Australia

Research Officer, December 2001 - August 2002.
Advisor: Ian D. Whittington and Leslie A. Chisholm

GRANTS AND FELLOWSHIPS

Active:

2021-current, NIH-NIAID Centers of Excellence for Influenza Research and Response, "Swine Influenza Surveillance and Risk Assessment." Center Director: Scott Hensley (University of Pennsylvania); PI: Amy Vincent (USDA-ARS); Co-Investigator: Tavis K. Anderson (USDA-ARS).

2020-current, USDA-APHIS-VS-National Veterinary Services Laboratory, Interagency Agreement,

“USDA Influenza A Virus in Swine Surveillance System – genomic epidemiology and evolution.” Co-Investigators: Tavis K. Anderson and Amy L. Vincent (USDA-ARS).

2020-current, USDA-NIFA-AFRI, “Transmission bottlenecks and within-host evolutionary dynamics of influenza A virus.” PI: Daniela De Souza Rajao (UGA). Co-I: Tavis K. Anderson and Amy L. Vincent (USDA-ARS); Daniel Perez (UGA).

2020-current, Coalition for Epi Response Engagement & Science (CERES Seed funding), “Demystifying the Argasid-Swine Interface.” PI: Gabriel Hamer (Texas A&M). Co-I: Beatriz Martinez Lopez and Alda Pires (UC-Davis); Sarah Hamer, Peter Teel, Alex Pauvolid and Tammi Johnson (Texas A&M); Job Lopez (Baylor College of Med.); Kim Pepin, Andrew Golnar, and Nathan Snow (USDA-APHIS); Tavis K. Anderson (USDA-ARS).

2019-current, CDC-Influenza Division, Interagency Agreement, “The study of influenza A viruses in the swine host.” PI: Amy L. Vincent, Tavis K. Anderson (USDA-ARS), and C. Todd Davis (CDC).

Prior:

2020-2021, DARPA/BTO, “Rapid evolution of influenza A viruses in swine results in zoonotic viruses with human pandemic potential.” PI: Phillip Gauger (ISU). Co-PI: Tavis K. Anderson (USDA-ARS), Oliver Eulenstein (ISU), Ganwu Li (ISU), Amy Vincent (USDA-ARS).

2016-2021, National Pork Board/USDA-ARS, “United States Swine Pathogen Database.” PI: Kay S. Faaberg (USDA-ARS). Co-Investigators: Tavis K. Anderson, Kelly M. Lager (USDA-ARS), Diego Diel (SDSU), Dick Hesse (KSU), Phillip Gauger (ISU), Stephanie Rossow (UMN).

2016-2019, Iowa State University, Presidential Initiative for Interdisciplinary Research, “Development and integration of bioinformatics tools to characterize, monitor, and rapidly recognize emerging influenza viruses in swine through data driven science.” PI: Phillip C. Gauger (Iowa State University). Co-PI: Pat Halbur, Zhengyuan Zhu, Iddo Friedberg, Oliver Eulenstein, Nicholas Gabler, Emily Berg (Iowa State University) and Amy Vincent (USDA-ARS). Collaborators: 1 of 12 Tavis K. Anderson (USDA-ARS).

2015-2019, National Science Foundation, Division of Integrative Organismal Systems Core Programs (13-600), “From complex environments to underlying mechanisms: A network approach to multi-trait tradeoffs.” PI: Zachary Stahlschmidt (University of the Pacific), Tavis Anderson (USDA-ARS).

2016-2018, Merck Animal Health, “Investigation of vaccine associated enhancement of disease (VAERD) in pigs administered with multivalent hemagglutinin and neuraminidase replicon particle vaccine.” PI: Amy L. Vincent, Tavis K. Anderson (USDA-ARS).

2016-2018, National Pork Board, “Heterologous prime-boost vaccination protocols using whole inactivated influenza A virus vaccines to drive improved heterologous cross-protection.” PI: Amy L. Vincent (USDA-ARS), Phillip C. Gauger (Iowa State University). Co-Investigators: Daniela S. Rajao, Tavis K. Anderson, Eugenio J. Abente (USDA-ARS).

2016-2018, National Pork Board, “Adaptation of a human seasonal H3 influenza A virus to efficiently infect and replicate in the swine host.” PI: Amy L. Vincent (USDA-ARS). Co-Investigators: Daniela S. Rajao, Eugenio J. Abente, Tavis K. Anderson (USDA-ARS), Phillip C. Gauger (Iowa State University).

2014-2015, Merck Animal Health, “Swine Influenza Vaccines: Identification of conserved residues in swine H1 and H3 viruses, and the identification of wild-type viruses for vaccine development.” PI: Tavis Anderson (USDA-ARS).

2014, USDA-ARS, Specific Cooperative Agreement (#58-3625-4-070), “Antigenic properties and characterization of the global evolution of influenza A viruses (IAV) in swine.” PI: Amy L. Vincent (USDA-ARS). Co-PI: Tavis Anderson (Georgia Southern).

2011, National Science Foundation, Ecology and Evolution of Infectious Diseases, Workshop Scholarship.

2010, The American Society of Tropical Medicine and Hygiene, Travel Scholarship.

2002-2009, Graduate Awards and Fellowships (Total Awards: \$45,000): New England Complex Systems Institute, Workshop Scholarship, 2008; New Jersey Mosquito Control Association, Educational Scholarship Grant, 2006, (\$1000); American Society of Parasitology, Willis A. Reid Jr. Research Grant, 2005, (\$1000); Pennsylvania Arabian Horse Association, Research Grant, Co-PI: Michael V.K. Sukhdeo, Sarah Ralston, 2005 (\$1000); Rutgers University, Equine Science Center, State Equine Initiative Grant, Co-PI: Michael V.K. Sukhdeo, Lisa Reed, Scott Crans, Robert Kent, 2005, (\$10,000); Pennsylvania Arabian Horse Association, Research Grant, Co-PI: Michael V.K. Sukhdeo, Sarah Ralston, 2004, (\$2000); Rutgers University, Equine Science Center, State Equine Initiative Grant, Co-PI: Michael V.K. Sukhdeo, Jennifer Gruener, Wayne Crans, 2004 (\$30,000).

BOOK CHAPTERS

4. **Anderson, T.K.**, Chang, J., Arendsee, Z.W., Venkatesh, D., Souza, C.K., Kimble, J.B., Lewis, N.S., Davis, C.T., and Vincent, A.L. (2021). Swine influenza A viruses and the tangled relationship with humans. **In:** *Influenza: The Cutting Edge* (Eds. Y. Kawaoka and G. Neumann). pp. 1-24. Cold Spring Harbor Perspectives in Medicine 11 (3), a038737. doi: 10.1101/cshperspect.a038737.

3. Vincent, A.L., **Anderson, T.K.** and Lager, K.M.. (2020). A Brief Introduction to Influenza A Virus in Swine. **In:** *Animal Influenza Virus (Methods in Molecular Biology 1161)* (Ed. E. Spackman). pp. 249-271. Springer.

2. **Anderson, T.K.** and Sukhdeo, M.V.K. (2016). The worm’s eye view of community ecology. **In:** *A Century of Parasitology: Discoveries, ideas, and lessons learned by scientists who published in The Journal of Parasitology 1914-2014* (Eds. John Janovy, Jr. and Gerald W. Esch). pp. 110-130. John Wiley and Sons.

1. Vincent, A.L., Lager, K.M. and **Anderson, T.K.**. (2014). A Brief Introduction to Influenza A Virus in Swine. **In:** *Animal Influenza Virus (Methods in Molecular Biology 1161)* (Ed. E. Spackman). pp. 243-258. Springer.

PUBLICATIONS

61. Kaplan, B.S., **Anderson, T.K.**, Chang, J., Santos, J., Perez, D., Lewis, N.S., and Vincent, A.L. (*in press*). Evolution and antigenic phenotypes of N2 neuraminidase genes from human seasonal influenza A viruses following two separate introductions into swine in the United States. *Journal of Virology* XX:XX.

60. Staton, M., Cannon, E., Sanderson, L., Wegrzyn, J., **Anderson, T.K.**, Buehler, S., Cobo-Simon, I., Faaberg, K., Grau, E., Guignon, V., Gunoskey, J., Inderski, B., Jung, S., Lager, K., Main, D., Poelchau, M., Ramnath, R., Richter, P., West, J., and Ficklin, S. (*in press*). Tripal, a community update after 10 years of supporting open source, standards-based genetic, genomic and breeding databases. *Briefings in Bioinformatics* XX:XX.

59. Zeller, M.A., Gauger, P.C., Arendsee, Z.W., Souza, C.K., Vincent, A.L., and **Anderson, T.K.** (2021). Machine learning prediction and experimental validation of antigenic drift in H3 influenza A viruses in swine. *mSphere* 6 (2), e00920-20. Preprint at *bioRxiv*: 2020.05.29.123828.

58. Powell, J.D., Abente, E.J., Chang, J., Souza, C.K., Rajao, D.S., **Anderson, T.K.**, Zeller, M.A.,

- Gauger, P.C., Lewis, N.S., and Vincent, A.L. (2021). Characterization of contemporary 2010.1 H3N2 swine influenza A viruses circulating in United States pigs. *Virology* 553, 94-101.
57. Nicholson, T.L., Waack, U., **Anderson, T.K.**, Zaia, S.R., Goertz, I., Eppinger, M., Hau, S.J., Brockmeier, S.L., Bayles, D.O., and Shore, S.M. (2020). Comparative Virulence and Genomic Analysis of *Streptococcus suis* Isolates. *Frontiers in Microbiology* 11: 620843.
56. Kaplan, B.S., Kimble, J.B., Chang, J., **Anderson, T.K.**, Gauger, P.C., Janas-Martindale, A., Killian, M.L., Bowman, A.S., and Vincent, A.L. (2020). Aerosol transmission from infected swine to ferrets of a swine H3N2 virus collected from an agricultural fair and associated with human variant infections. *Journal of Virology* 94 (16), e01009-20.
55. Rambo-Martin, B.L., Keller, M.W., Wilson, M.M., Nolting, J.M., **Anderson, T.K.**, Vincent, A.L., Bagal, U., Jang, Y., Neuhaus, E.B., Davis, C.T., Bowman, A.S., Wentworth, D.E., and Barnes, J.R. (2020). Influenza A Virus Field Surveillance at a Swine-Human Interface. *mSphere* 5: e00822-19.. Preprint at *bioRxiv*: 585588.
54. Sharma, A., Zeller, M.A., Li, G., Harmon, K.M., Zhang, J., Hoang, H., **Anderson, T.K.**, Vincent, A.L., and Gauger, P.C. (2020). Diagnostic detection of live attenuated influenza vaccine virus and evidence of reassortment in United States swine. *The Journal of Veterinary Diagnostic Investigation* 32 (2): 301-311.
53. Alfieri, J.M. and **Anderson, T.K.** (2019). Local and regional urbanization: correlates of parasite community composition and richness in the salt marsh fish, *Fundulus heteroclitus*. *PLoS ONE* 14(12): e0225896. Preprint at *bioRxiv*: 404756.
52. Tabaszewski, P., Gorecki, P., **Anderson, T.K.**, Markin, A. and Eulenstein, O. (2019). Consensus of all Solutions for Intractable Phylogenetic Tree Inference. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* doi: 10.1109/TCBB.2019.2947051.
51. Chang, J.*, **Anderson, T.K.***, Zeller, M.A.*, Gauger, P.C., Vincent, A.L. (2019). octoFLU: Automated Classification for Evolutionary Origin of Influenza A Virus Gene Sequences Detected in U.S. swine. *Microbiology Resource Announcements* 8 (32): e00673-19. Github repo: <https://github.com/flu-crew/octoFLU>. *These authors contributed equally.
50. Markin, A., **Anderson, T.K.**, Vadali, V.S.K.T., and Eulenstein, O. (2019). Robinson-Foulds Reticulation Networks. *Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics* 77-86. Preprint at *bioRxiv*: 642973.
49. Register, K.B., Jelinski, M.D., Waldner, M., Boatwright, W.D., **Anderson, T.K.**, Hunter, D.L., Hamilton, R.G., Burrage, P., Shury, T., Bildfell, R., Wolff, P.L., Miskimins, D., Derscheid, R.J., and Woodbury, M.R. (2019). Comparison of multilocus sequence types found among recent North American isolates of *Mycoplasma bovis* from cattle, bison and deer. *The Journal of Veterinary Diagnostic Investigation* 31 (6): 899-904.
48. Walia, R.R.*, **Anderson, T.K.***, and Vincent, A.L. (2019). Regional patterns of genetic diversity in swine influenza A viruses in the United States from 2010 to 2016. *Influenza and Other Respiratory Viruses* 13(3): 262-273. *These authors contributed equally.
47. Bolton, M.J., Abente, E.A., Venkatesh, D., Stratton, J.A., Zeller, M., **Anderson, T.K.**, Lewis, N.S., and Vincent, A.L. (2019). Antigenic evolution of H3N2 influenza A viruses in swine in the United States from 2012 to 2016. *Influenza and Other Respiratory Viruses* 13(1): 83-90.
46. Zeller, M.A., Li, G., Harmon, K., Zhang, J., Vincent, A.L., **Anderson, T.K.**, and Gauger,

- P. C. (2018). Complete genome sequences of two novel human-like H3N2 influenza A viruses A/swine/Oklahoma/65980/2017(H3N2) and A/swine/Oklahoma/65260/2017(H3N2) detected in swine in the United States. *Microbiology Resource Announcements* 7(20): e01203-18.
45. Zeller, M.A., **Anderson, T.K.**, Walia, R.R., Vincent, A.L., and Gauger, P.C. (2018). ISU FLUture: a veterinary diagnostic laboratory web-based platform to monitor the temporal genetic patterns of influenza A virus in swine. *BMC Bioinformatics* 19(1): 397.
44. Chen, Q., Wang, L., Yang, C., Zheng, Y., Gauger, P.C., **Anderson, T.K.**, Harmon, K.M., Zhang, J., Yoon, K-J., Main, R.G., and Li, G. (2018). The emergence of novel sparrow delta-coronaviruses in the United States more closely related to porcine deltacoronaviruses than sparrow deltacoronavirus HKU17. *Emerging Microbes and Infections* 7(1): 105.
43. Nelson, C.W., Sibley, S.D., Hamer, G.L., Newman, C.M., **Anderson, T.K.**, Walker, E.D., Kitron, U.D., Brawn, J.D., Ruiz, M.O., and Goldberg, T.L. (2018). Selective constraint and adaptive potential of West Nile virus within and among naturally infected avian hosts and mosquito vectors. *Virus Evolution* 4(1): vey013.
42. Rajao, D.S., **Anderson, T.K.**, Kitikoon, P., Stratton, J., Lewis, N.S., and Vincent, A.L. (2018). Antigenic and genetic evolution of contemporary swine H1 influenza viruses in the United States. *Virology* 518: 45-54.
41. van Geelen, A.G.M., **Anderson, T.K.**, Lager, K.M., Das, P.B., Otis, N.J., Montiel, N.A., Miller, L.C., Kulshreshtha, V., Buckley, A.C., Brockmeier, S.L., Zhang, J., Gauger, P.C., Harmon, K.M. and Faaberg, K.S. (2018). Porcine Reproductive and Respiratory Disease Virus: Evolution and Recombination Yields Distinct ORF5 RFLP 1-7-4 Viruses with Individual Pathogenicity. *Virology* 513: 168-179.
40. Gao, S., **Anderson, T.K.**, Walia, R.R., Dorman, K.S., Janas-Martindale, A., and Vincent, A.L. (2017). The genomic evolution of H1 influenza A viruses from swine detected in the United States between 2009 and 2016. *Journal of General Virology* 98: 2001-2010.
39. Bowman, A.S., Walia, R.R., Nolting, J.M., Vincent, A.L., Zentkovich, M.M., Lorbach, J.N., Lauterbach, S.E., **Anderson, T.K.**, Davis, C.T., Zanders, N., Jones, J., Jang, Y., Lynch, B., Rodriguez, M.R., Blanton, L., Lindstrom, S.E., Wentworth, D.E., Schiltz, J., Killian, M.L., Averill, J.J., Forshey, T. (2017). Emerging influenza A (H3N2) virus in swine responsible for zoonotic transmission at agricultural fairs, Michigan and Ohio, USA, 2016. *Emerging Infectious Diseases* 23: 1551-1555.
38. Newman, C.M., Krebs, B.L., **Anderson, T.K.**, Hamer, G.L., Ruiz, M.O., Brawn, J.D., Brown, W.M., Kitron, U.D., and Goldberg, T.L. (2017). Culex flavivirus during West Nile virus epidemic and inter-epidemic years in Chicago, USA. *Vector-Borne and Zoonotic Diseases* 17: 567-575.
37. Vincent, A.L., Perez, D.R., Rajao, D.S., **Anderson, T.K.**, Abente, E.J., Walia, R.R., and Lewis, N.S. (2017). The future of influenza A virus vaccines for swine. *Veterinary Microbiology* 206: 35-44.
36. Abente, E.J., Kitikoon, P., Lager, K.M., Gauger, P.C., **Anderson, T.K.** and Vincent, A.L. (2017). A highly pathogenic avian influenza virus H5N1 with 2009 pandemic H1N1 internal genes demonstrated increased replication and transmission in pigs. *Journal of General Virology* 98: 18-30.
35. Zhang, Y., Aebermann, B.D., **Anderson, T.K.**, Burke, D.F., Dauphin, G., Gu, Z., He, S., Kumar, S., Larsen, C.N., Lee, A.J., Li, X., Macken, C.M., Mahaffey, C., Pickett, B.E., Reardon, B., Smith, T., Stewart, L., Suloway, C., Sun, G., Tong, L., Vincent, A.L., Walters, B., Zaremba, S., Zhao,

H., Zhou, L., Zmasek, C., Klem, E.B., and Scheuermann, R.H. (2017). Influenza Research Database: An Integrated Bioinformatics Resource for Influenza Virus Research. *Nucleic Acids Research* 45: D466-D474.

34. **Anderson, T.K.**, Macken, C.A., Lewis, N.S., Scheuermann, R.H., Van Reeth, K., Brown, I.H., Swenson, S.L., Simon, G., Saito, T., Berhane, Y., Ciacci-Zanella, J., Pereda, A., Davis, C.T., Donis, R.O., Webby, R.J., and Vincent, A.L. (2016). A phylogeny-based global nomenclature system and automated annotation tool for H1 hemagglutinin genes from swine influenza A viruses. *mSphere* 1(6): e00275-16.

33. Abente, E.J., Santos, J., Lewis, N.S., Gauger, P.C., Stratton, J., Skepner, E., **Anderson, T.K.**, Rajao, D.S., Perez, D.R., and Vincent, A.L. (2016). The molecular determinants of antibody recognition and antigenic drift in the H3 hemagglutinin of swine influenza A virus. *Journal of Virology* 90: 8266-8280.

32. Karki, S., Hamer, G.L., **Anderson, T.K.**, Goldberg, T.L., Kitron, U.D., Krebs, B.L., Walker, E.D., Ruiz, M.O. (2016). Effect of Trapping Methods, Weather, and Landscape on Estimates of the Culex Vector Mosquito Abundance. *Environmental Health Insights* 10: 93-103.

31. Abente, E.J., **Anderson, T.K.**, Rajao, D.S., Swenson, S.L., Gauger, P.C., and Vincent, A.L. (2016). The avian-origin H3N2 canine influenza virus has limited replication in swine. *Influenza and Other Respiratory Viruses* 10(5): 429-432.

30. Lewis, N.S., Russell, C.A., Langat, P., **Anderson, T.K.**, Berger, K., Bielejec, F., Burke, D.F., Dudas, G., Fonville, J.M., Fouchier, R.A.M., Kellam, P., Koel, B.F., Lemey, P., Nguyen, T., Nuansrichy, B., Peiris, J.S.M., Saito, T., Simon, G., Skepner, E., Takemae, N., ESNIP3 consortium, Webby, R., Van Reeth, K., Brookes, S.M., Larsen, L., Watson, S.J., Brown, I.H., and Vincent, A.L. (2016). The global antigenic diversity of swine influenza A viruses. *eLife* 5: e12217.

29. Newman, C.M., **Anderson T.K.**, and Goldberg, T.L. (2016). Decreased flight activity in Culex pipiens (Diptera: Culicidae) naturally infected with Culex flavivirus. *Journal of Medical Entomology* 53: 233-236.

28. Rajao, D.S., Gauger, P.C., **Anderson, T.K.**, Lewis, N.S., Abente, E.J., Killian, M.L., Perez, D.R., Sutton, T.C., Zhang, J., and Vincent, A.L. (2015). Novel reassortant human-like H3N2 and H3N1 influenza A viruses detected in pigs are virulent and antigenically distinct from endemic viruses. *Journal of Virology* 89: 11213-11222.

27. McKee, E.M., Walker, E.D., **Anderson, T.K.**, Kitron, U.D., Brawn, J.D., Krebs, B.L., Newman, C.M., Ruiz, M.O., Levine, R.S., Carrington, M.E., Goldberg, T.L., and Hamer, G.L. (2015). West Nile virus antibody decay rate in free-ranging birds. *Journal of Wildlife Diseases* 51: 601-608.

26. **Anderson, T.K.**, Campbell, B.A., Nelson, M.I., Lewis, N.S., Janas-Martindale, A., Killian, M.L., and Vincent, A.L. (2015). Characterization of cocirculating swine influenza A viruses in North America and the identification of a novel H1 genetic clade with antigenic significance. *Virus Research* 201: 24-31.

25. Henningson, J.N., Rajao, D.S., Kitikoon, P., Lorusso, A., Culhane, M.R., Lewis, N.S., **Anderson, T.K.**, Vincent, A.L. (2015). Comparative virulence of wild-type H1N1pdm09 influenza A isolates in swine. *Veterinary Microbiology* 176: 40-49.

24. Krebs, B.L., **Anderson, T.K.**, Goldberg, T.L., Hamer, G.L., Kitron, U.D., Newman, C.M., Ruiz, M.O., Walker, E.D., and Brawn, J.D. (2014). Host group formation decreases exposure to vector-borne disease: a field experiment in a “hotspot” of West Nile virus transmission. *Proceedings*

of the Royal Society B: Biological Sciences 281: 20141586.

23. Kamlangdee, A., Kingstad-Bakke, B., **Anderson, T.K.**, Goldberg, T.L., and Osorio, J.E. (2014). Broad Protection against Avian Influenza using a Modified Vaccinia Ankara Virus Expressing a Mosaic Hemagglutinin gene. *Journal of Virology* 88: 13300-13309.
22. Medeiros, M.C.I., **Anderson, T.K.**, Higashiguchi, J.M., Kitron, U.D., Walker, E.D., Brawn, J.D., Krebs, B.L., Ruiz, M.O., Goldberg, T.L., Ricklefs, R.E., and Hamer, G.L. (2014). An inverse association between West Nile virus serostatus and avian malaria infection status. *Parasites and Vectors* 7: 415.
21. Rajao, D.S., **Anderson, T.K.**, Gauger, P.C., and Vincent, A.L. (2014). Pathogenesis and vaccination of influenza A virus in swine. *Current Topics in Microbiology and Immunology* 385: 307-326.
20. Hamer, G.L., **Anderson, T.K.**, Donovan, D.J., Brawn, J.D., Krebs, B.L., Gardner, A.M., Ruiz, M.O., Brown, W.M., Kitron, U.D., Newman, C.M., Goldberg, T.L., and Walker, E.D. (2014). Dispersal of Adult *Culex* Mosquitoes in an Urban West Nile Virus Hotspot: a Mark-Capture Study Incorporating Stable Isotope Enrichment of Natural Larval Habitats. *PLoS Neglected Tropical Diseases* 8(3): e2768.
19. Lewis, N.S., **Anderson, T.K.**, Kitikoon, P., Skepner, E., Burke, D.F., and Vincent, A.L. (2014). Substitutions near the hemagglutinin receptor binding site determine the antigenic evolution of influenza A H3N2 viruses in U.S. swine. *Journal of Virology* 88: 4752-4763.
18. Kitikoon, P., Gauger, P.C., **Anderson, T.K.**, Culhane, M.R., Swenson, S.L., Loving, C.L., Perez, D.R., and Vincent, A.L. (2013). Serological cross-reactivity of swine influenza virus vaccines to contemporary U.S. swine H3N2 viruses and vaccine efficacy in pigs infected with an H3N2 virus genetically similar to 2011-2012 H3N2v. *Influenza and Other Respiratory Viruses* 7 (S4): 32-41.
17. **Anderson, T.K.**, Nelson, M.I., Kitikoon, P., Swenson, S.L., Korlund, J.A., and Vincent, A.L. (2013). Population dynamics of co-circulating swine influenza A viruses in the United States from 2009-2012. *Influenza and Other Respiratory Viruses* 7 (S4): 42-51.
16. Loving, C.L., Lager, K.M, Vincent, A.L., Brockmeier, S.L, Gauger, P.C., **Anderson, T.K.**, Kitikoon, P., Perez, D.R., and Kehrli, Jr., M.E. (2013). Efficacy of inactivated and live-attenuated influenza virus vaccines in pigs against infection and transmission of emerging H3N2 similar to the 2011-2012 H3N2v. *Journal of Virology* 87: 9895-9903.
15. **Anderson, T.K.**, and Sukhdeo, M.V.K. (2013) Qualitative community stability determines parasite establishment and richness in estuarine marshes. *PeerJ* 1: e92.
14. Peterson, N.A., **Anderson, T.K.**, Jiao-Jun, W., and Yoshino, T.P. (2013). *In silico* analysis of the fucosylation-associated genome of the human blood fluke *Schistosoma mansoni*: cloning and characterization of the enzymes involved in GDP-L-fucose synthesis and Golgi import. *Parasites and Vectors* 6: 201.
13. Kitikoon, P., Nelson, M.I., Killian, M.L, **Anderson, T.K.**, Koster, L., Culhane, M.R., and Vincent, A.L. (2013). Genotype patterns of contemporary reassorted H3N2 virus in U.S. swine. *Journal of General Virology* 94: 1236-1241.
12. **Anderson, T.K.**, and Sukhdeo, M.V.K. (2013). The relationship between community species richness and the richness of the parasite community in *Fundulus heteroclitus*. *Journal of Parasitology* 99: 391-396.

11. Peterson, N.A., **Anderson, T.K.** and Yoshino, T.P. (2013). *In silico* analysis of the fucosylation-associated genome of the human blood fluke *Schistosoma mansoni*: cloning and characterization of the fucosyltransferase multigene family. *PLoS ONE* 8(5): e63299.
10. Gardner, A.M., **Anderson, T.K.**, Hamer, G.L., Johnson, D.E., Varela, K.E., Walker, E.D. and Ruiz, M.O. (2013). Terrestrial vegetation and aquatic chemistry influence larval mosquito abundance in catch basins, Chicago, USA. *Parasites and Vectors* 6: 9.
9. Hamer, G.L., **Anderson, T.K.**, Berry, G.E., Makohon-Moore, A.P., Crafton, J.C., Brawn, J.D., Dolinski, A.C., Krebs, B.L., Ruiz, M.O., Muzzall, P.M., Goldberg, T.L., and Walker, E.D. (2013). Prevalence of filarioid nematodes and trypanosomes in American robins and house sparrows, Chicago, USA. *International Journal for Parasitology: Parasites and Wildlife* 2: 42-49.
8. **Anderson, T.K.**, Laegreid, W.W., Cerutti, F., Osorio, F.A., Nelson, E.A., Christopher-Hennings, J. and Goldberg, T.L. (2012). Ranking viruses: measures of positional importance within networks define core viruses for rational polyvalent vaccine development. *Bioinformatics* 28(12): 1624-1632.
7. Hamer, S.A., Goldberg, T.L., Kitron, U.D., Brawn, J.D., **Anderson, T.K.**, Loss, S.R., Walker, E.D. and Hamer, G.L. (2012). Wild birds and the urban ecology of ticks and tick-borne pathogens, Chicago, Illinois, USA, 2005-2010. *Emerging Infectious Diseases* 18(10): 1589-1595.
6. **Anderson, T.K.**, and Sukhdeo, M.V.K. (2011). Host centrality in food web networks determines parasite diversity. *PLoS ONE* 6(10): e26798.
5. Newman, C.M., Cerutti, F., **Anderson, T.K.**, Hamer, G.L., Walker, E.D., Kitron, U.D., Ruiz, M.O., Brawn, J.D. and Goldberg, T.L. (2011). *Culex* flavivirus and West Nile virus mosquito co-infection and positive association in Chicago, USA. *Vector-Borne and Zoonotic Diseases* 11: 1099-1105.
4. Hamer, G.L., Chaves, L.F., **Anderson, T.K.**, Kitron, U.D., Brawn, J.D., Ruiz, M.O. Loss, S.R., Walker, E.D. and Goldberg, T.L. (2011). Spatial variation in *Culex pipiens* host selection and host community competence within an urban focus of West Nile virus transmission. *PLoS ONE* 6(8): e23767.
3. Goldberg, T.L., **Anderson, T.K.** and Hamer, G.L. (2010). West Nile virus may have hitched a ride across the Western United States on *Culex tarsalis* mosquitoes. *Molecular Ecology* 19: 1518-1519.
2. **Anderson, T.K.**, and Sukhdeo, M.V.K. (2010). Abiotic versus biotic hierarchies in the assembly of parasite populations. *Parasitology* 137: 743-754.
1. Raffel, T.R., and **Anderson, T.K.** (2009). A new species of *Hysterothylacium* (Nematoda: Anisakidae) from the stomach of the red-spotted newt, *Notophthalmus viridescens*, from Pennsylvania fishless ponds. *Journal of Parasitology* 95: 1503-1506.

GOVERNMENT
REPORTS

4. Arendsee, Z.W., Young, K., Hufnagel, D., Markin, A., Kimble, B., Souza, C.K., Essen, S., Collins, S., Whittard, E., Torchetti, M.K., Tell, R., Janas-Martindale, A., World Organization for Animal Health/Food and Agriculture Organization (OIE/FAO/OFFLU) Swine Influenza Working Group, Brown, I., Lewis, N., **Anderson, T.K.**, Vincent, A.L., 2021. OFFLU animal influenza report: July 2020 to December 2020. World Health Organization. p. 58.

3. **Anderson, T.K.**, Arendsee, Z.W., Hufnagel, D., Young, K., Souza, C.K., Kimble, B., Brown, I., Essen, S., Collins, S., Byrne, A., Patapiou, P., Lewis, N., Vincent, A.L. 2020. OFFLU animal influenza report: February 2020 to September 2020. World Health Organization. p. 1-58.
2. **Anderson, T.K.**, Arendsee, Z., Chang, J., Kimble, B., Kunzler-Souza, C., Brown, I., Essen, S., Collins, S., Lewis, N., Vincent, A.L., 2020. OFFLU Animal Influenza Report: September 2019 to February 2020. World Health Organization. p. 1-60.
1. **Anderson, T.K.**, Arendsee, Z., Chang, J., Kimble, B., Kunzler-Souza, C., Brown, I., Essen, S., Collins, S., Venkatesh, D. Lewis, N., Vincent, A.L. 2019. OFFLU animal influenza report: February 2019-September 2019. World Health Organization. p. 1-60.

PUBLISHED
PROCEEDINGS

14. **Anderson, T.K.**, Chang, J. Arendsee, Z.W., and Vincent, A.L. (2020). Swine influenza A viruses: quantifying genetic diversity with phylogenetics and the octoFLU pipeline. *Proceedings of the 50th Annual Meeting of the American Association of Swine Veterinarians*.
13. Vincent, A.L., **Anderson, T.K.**, Chang, J. (2019). Evolution of influenza A virus in swine and vaccine selection. *Proceedings of the Iowa Veterinary Medical Association: XX-XX*.
12. Vincent, A.L., Rajao, D., **Anderson, T.K.**, Abente, E.J., and Walia, R.R. (2017). Influenza A virus in swine. *Proceedings of the 16th Chulalongkorn University Veterinary Conference, Bangkok, Thailand: S11*.
11. **Anderson, T.K.**, Walia, R.R., and Vincent, A.L. (2017). Fundamentals of phylogenetic trees and sequence analysis tools for the analyses of swine influenza A viruses. *Proceedings of the 48th Annual Meeting of the American Association of Swine Veterinarians: 3-7 (Seminar 2)*.
10. Zhang, Y., **Anderson, T.K.**, Vincent, A.L., Gauger, P.C., Macken, C.A., and Scheuermann, R.H. (2017). In silico analysis of swine influenza virus sequence data in the Influenza Research Database. *Proceedings of the 48th Annual Meeting of the American Association of Swine Veterinarians: 8-23 (Seminar 2)*.
9. Zeller, M.A., Vincent, A.L., **Anderson, T.K.**, Gauger, P.C. (2017). ISfluView: an interactive online tool for assessing trends in influenza metadata at the Iowa State University Veterinary Diagnostic Laboratory. *Proceedings of the 48th Annual Meeting of the American Association of Swine Veterinarians: 24-26 (Seminar 2)*.
8. Rajao, D.S., Gauger, P.C., **Anderson, T.K.**, Lewis, N.S., Abente, E.J., Killian, M.L., Perez, D.R., Sutton, T.C., Zhang, J., and Vincent, A.L. (2016). Novel reassortant human-like H3N2 and H3N1 influenza A viruses detected in pigs are virulent and antigenically distinct from endemic viruses. *Proceedings of the 47th Annual Meeting of the American Association of Swine Veterinarians*.
7. Vincent, A.L., Rajao, D.S., **Anderson, T.K.**, Abente, E.J., Walia, R., Lewis, N.S. (2016). Considerations for vaccines against influenza A virus in U.S. swine. *Proceedings of the 47th Annual Meeting of the American Association of Swine Veterinarians*.
6. Abente, E.J., Rajao, D.S., Kitikoon, P., **Anderson, T.K.**, Lager, K.M., Gauger, P.C., and Vincent, A.L. (2015). Pathogenesis and transmission studies: Non-swine influenza A viruses in the swine host. *Proceedings of the ISU James D. McKean Swine Disease Conference*.
5. Vincent, A.L., **Anderson, T.K.**, Kitikoon, P., Lewis, N.S., Rajao, D.S., Campbell, B.A. (2014). Connecting the dots between swine influenza A surveillance and vaccines. *Proceedings of the 45th*

Annual Meeting of the American Association of Swine Veterinarians: 527-532.

4. **Anderson, T.K.**, Kitikoon, P., and Vincent, A.L. (2013). Getting a closer look at USDA swine influenza A surveillance: What can we learn from the genetic data that can help us on the farm? *Proceedings of the Allen D. Leman Swine Conference* 40: 101-104.

3. Vincent, A.L., Kitikoon, P., **Anderson, T.K.** and Loving, C.L. (2013). The growing diversity of H3N2 influenza A virus in swine and the impact on control in swine and at the human animal interface. *Proceedings of the Allen D. Leman Swine Conference* 40: 161-164.

2. Kehrli, Jr., M.E., Vincent, A.L., Gauger, P.C., Kitikoon, P., **Anderson, T.K.**, Loving, C.L., Lager, K.M. (2013). Overview of swine influenza virus vaccine research and technology: What's on the horizon and what do we need to move forward? *Proceedings of the 44th Annual Meeting of the American Association of Swine Veterinarians: 517-520.*

1. Korslund, J.A., Pyburn, D.G., Swenson, S., Schmitt, B., Scott, A., Kasari, E., Martin, B., Tomlinson, S., Vincent, A., Kitikoon, P., **Anderson, T.K.**, and Gomez, T. (2013). USDA surveillance for influenza A virus in swine. *Proceedings of the 44th Annual Meeting of the American Association of Swine Veterinarians: 507-512.*

PATENTS

Osorio, J., Goldberg, T., Kamlangdee, A., Bakke, B. and **Anderson, T.** Broadly reactive mosaic peptide for influenza vaccine. *U.S. Patent Application No. US20150352202A1. issued June 26 2020.*

POPULAR SCIENCE PUBLICATIONS

3. Vincent, A.L., **Anderson, T.K.**, Macken, C.A., Zhang, Y., Lewis, N.S., and Scheuermann, R.H. (2017). OFFLU swine influenza experts develop global nomenclature system and automated annotation tool for H1 hemagglutinin genes of influenza A viruses. *OIE-World Organization for Animal Health, Bulletin* 2017(3): 106-113.

2. Walia, R.R., **Anderson, T.K.**, and Vincent, A.L. (2016). The genetic diversity of contemporary swine influenza A viruses in the United States. **pig333.com: pig to pork.**

1. **Anderson, T.K.**. (2007). Parasites: in sickness can be eco-health. **TrailWalker, December 2007.**

PUBLICATIONS IN REVIEW AND PREPRINTS

Zeller, M.A., Chang, J., Vincent, A.L., Gauger, P.C., and **Anderson, T.K.** (*in review*). Coordinated evolution between N2 neuraminidase and H1 and H3 hemagglutinin genes increased influenza A virus genetic diversity in swine. Submitted to *Virus Evolution*. Preprint at *bioRxiv: 2020.05.29.123828.*

Markin, A., Wagle, S., **Anderson, T.K.**, and Eulenstein, O.E. (*in review*). RF-Net 2: Fast Inference of Virus Reassortment and Hybridization Networks. Submitted to *Bioinformatics*. Preprint at *bioRxiv: 2021.05.05.442676.*

Anderson, T.K., Inderski, B., Diel, D.G., Hause, B.M., Porter, E., Clement, T., Nelson, E.A., Bai, J., Christopher-Hennings, J., Gauger, P.C., Zhang, J., Harmon, K.H., Main, R., Lager, K.M., and Faaberg, K.S. (*in review*). The United States Swine Pathogen Database: integrating veterinary diagnostic laboratory sequence data to monitor emerging pathogens of swine. Submitted to *Database*.

Souza, C.K., **Anderson, T.K.**, Chang, J., Venkatesh, D., Lewis, N.S., Pekosz, A., Shaw-Saliba,

K., Rothman, R.E., Chen, K., and Vincent, A.L. (*in review*). Antigenic distance between North American swine and human seasonal H3N2 influenza A viruses as an indication of zoonotic risk to humans. Submitted to *Journal of Virology*.

INVITED SEMINARS 2021 IAV in Swine Committee, American Association of Swine Veterinarians, Virtual Meeting.
2020 Applied Field Epidemiology Program, The Ohio State University.
2020 J.F. Crow Institute for the Study of Evolution, University of Wisconsin-Madison.
2020 Annual Veterinary Diagnostics Conference, Nanjing, China.
2020 American Association of Swine Veterinarians, Atlanta, GA.
2019 Biologics Committee, 123rd Annual Meeting of the United States Animal Health Association, Providence, RI.
2019 Department of Biology, University of Northern Iowa.
2018 Nanjing Agricultural University, Nanjing, China.
2018 3rd China-USA Swine Industry Forum, Nanjing, China.
2018 Merck Animal Health Swine Virus Symposium, Chicago, Illinois.
2018 Department of Biological Sciences, University of the Pacific.
2017 NebraskaBio/IowaBio Annual Animal Health Symposium.
2016 USDA Research Reviews, 120th Annual Meeting of the United States Animal Health Association.
2016 Symposium, Landscape Change and Infectious Disease Ecology: Applications to Public Health, US-International Association for Landscape Ecology Annual Meeting.
2015 Department of Marine Science, Savannah State University.
2015 Department of Biology, College of Charleston.
2014 Emerging Pathogens Institute, University of Florida.
2014 Centennial Symposium, American Society of Parasitologists, New Orleans, Louisiana.
2014 Department of Wildlife Ecology and Conservation, University of Florida.
2014 College of Science and Mathematics, Georgia Southern University.
2013 Department of Natural Science, University of South Carolina-Beaufort.
2013 American Association of Veterinary Laboratory Diagnosticians, San Diego, CA.
2013 Allen D. Lemman Swine Conference, St. Paul, MN.
2012 Department of Biology, Georgia Southern University.
2010 Evolution Seminar Series, University of Wisconsin-Madison.
2009 Department of Biological Sciences, Florida International University.
2009 Evolution Seminar Series, University of Wisconsin-Madison.
2009 Molecular Parasitology Seminar Series, University of Wisconsin-Madison.

CONFERENCE PRESENTATIONS **Anderson, T.K.**, Zhang, Y., Macken, C., World Organization for Animal Health & Food and Agriculture Organization Influenza Network (OFFLU) Swine Working Group, Scheuermann, R.H., and Vincent, A.L. August 2019. An automated annotation tool and unified nomenclature system for H3 hemagglutinin genes from swine influenza A viruses. Options X for the Control of Influenza. Singapore, Singapore.

Yim-Im, W., **Anderson, T.K.**, Harmon, K., Gauger, P., Main, R., Zhang, J. June 2019. Dynamic changes of PRRSV-2 genetic lineages based on ORF5 sequences in the United States from 2003-2018. The 19th International Symposium of World Association of Veterinary Laboratory Diagnosticians. Chiang Mai, Thailand.

Register, K.B., Jelinski, M.D., Waldner, M., Boatwright, W.D., **Anderson, T.K.**, Hunter, D.L., Hamilton, R.G., Burrage, P., Shury, T., Bildfell, R., Wolff, P.L., Miskimins, D., Derscheid, R.J., and Woodbury, M.R., June 2019. Comparison of Multilocus Sequence Types Found Among Recent North American Isolates of *Mycoplasma bovis* from Cattle, Bison and Deer. ASM Microbe 2019.

San Francisco, California.

Anderson, T.K., Inderski, B., Diel, D.G., Porter, E., Clement, T., Nelson, E.A., Bai, J., Christopher-Hennings, J., Lager, K.M., and Faaberg, K.S. December 2018. The United States Swine Pathogen Database: integrating veterinary diagnostic laboratory sequence data to monitor emerging pathogens of swine. 99th Annual Conference of Research Workers in Animal Diseases (CRWAD). Chicago, Illinois.

Anderson, T.K., Inderski, B., Diel, D.G., Porter, E., Clement, T., Nelson, E.A., Bai, J., Christopher-Hennings, J., Lager, K.M., and Faaberg, K.S. December 2018. The United States Swine Pathogen Database: integrating veterinary diagnostic laboratory sequence data to monitor emerging pathogens of swine. 2018 North American PRRS Symposium. Chicago, Illinois.

Rambo-Martin, B.L., Keller, M.W., Wilson, M.M., Nolting, J.M., **Anderson, T.K.**, Vincent, A.L., Bagal, U., Jang, Y., Neuhaus, E.B., Davis, C.T., Bowman, A.S., Wentworth, D.E., and Barnes, J.R. September 2018. In-field surveillance of influenza outbreaks using the portable MinION nanopore sequencer. ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines. Washington, DC.

Zeller, M.A., **Anderson, T.K.**, Vincent, A.L., and Gauger, P.C. June 2018. Automating Genetic Classification for Hemagglutinin and Neuraminidase genes from Influenza A Viruses through Machine Learning Methods. The 25th International Pig Veterinary Society Congress. Chongqing, China.

Anderson, T.K., Zhang, Y., Macken, C., World Organization for Animal Health & Food and Agriculture Organization Influenza Network (OFFLU) Swine Working Group, Scheuermann, R.H., and Vincent, A.L. April 2018. An automated annotation tool and unified nomenclature system for H3 hemagglutinin genes from swine influenza A viruses. The 4th ISIRV International Symposium on Neglected Influenza Viruses. Brighton, United Kingdom.

Souza, C.K., **Anderson, T.K.**, Kaplan, B.S., Gauger, P.C., Abente, E.J., and Vincent, A.L. April 2018. Pathogenesis and transmission in the swine host of influenza A viruses with dominant H1 genome constellations found in US swine herds. The 4th ISIRV International Symposium on Neglected Influenza Viruses. Brighton, United Kingdom.

Kaplan, B.S., **Anderson, T.K.**, Santos, J., Perez, D., Lewis, N.S., and Vincent, A.L. April 2018. Probing the Antigenic differences between N2 Neuraminidase Lineages of North American Swine Influenza A Viruses. The 4th ISIRV International Symposium on Neglected Influenza Viruses. Brighton, United Kingdom.

Souza, C.K., Anderson, T.K., Venkatesh, D., Bolton, M., Detmer, S., Mena, I., Abente, E.J., Lewis, N.S., García-Sastre, A., and Vincent, A.L. April 2018. Antigenic distance of swine and human H3N2 influenza A virus as an indication of risk to human populations. The 4th ISIRV International Symposium on Neglected Influenza Viruses. Brighton, United Kingdom.

Anderson, T.K., Gauger, P.C., Souza, C.K., Walia, R.R., Venkatesh, D., Zeller, M.A., Rajao, D.S., Lewis, N.S., Abente, E.J., Zhang, J. and Vincent, A.L. July 2017. Spatial dissemination and evolution of human-origin H3 influenza A virus in U.S. swine. NIAID Centers of Excellence for Influenza Research and Surveillance Annual Meeting. Athens, Georgia.

Souza, C.K., Venkatesh, D., **Anderson, T.K.**, Bolton, M.J., Schiro, K.F., Abente, E.J., Lewis, N.S., and Vincent, A.L. July 2017. Pandemic risk assessment of swine H3N2 based on antigenic distance from human seasonal vaccine strains. NIAID Centers of Excellence for Influenza Research and Surveillance Annual Meeting. Athens, Georgia.

Anderson, T.K., Gauger, P.C., Souza, C.K., Walia, R.R., Venkatesh, D., Zeller, M.A., Rajao, D.S., Lewis, N.S., Abente, E.J., Zhang, J. and Vincent, A.L. June 2017. Spatial dissemination and evolution of human-origin H3 influenza A virus in U.S. swine. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Zhang, Y., **Anderson, T.K.**, Vincent, A.L., Macken, C.A., Smith, T., Tong, L., Klem, E.B., and Scheuermann, R.H. June 2017. An automated global clade classification tool for H1 hemagglutinin genes from swine influenza A viruses. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Rajao, D.S., Abente, E.J., Bolton, M.J., Gauger, P.C., **Anderson, T.K.**, Sutton, T.C., Perez, D.R., and Vincent, A.L. June 2017. In vitro characterization of naturally occurring and laboratory derived human seasonal H3 influenza A viruses associated with the ability to infect and replicate in swine. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Bolton, M.J., Abente, E.J., Venkatesh, D., Stratton, J.A., Zeller, M.A., **Anderson, T.K.**, Lewis, N.S., and Vincent, A.L. June 2017. Antigenic evolution of H3N2 influenza A viruses in swine in the United States, 2014-16. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Lopes, S., Wilks, S.H., Venkatesh, D., Souza, C.K., **Anderson, T.K.**, Rajao, D.S., Vincent, A.L., and Lewis, N.S. June 2017. Antibody landscaping in the context of whole inactivated vaccines (WIV) against Influenza A Viruses in swine. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Souza, C.K., Venkatesh, D., **Anderson, T.K.**, Lewis, N.S., and Vincent, A.L. June 2017. Antigenic distance between swine and human seasonal H3N2 influenza A virus to assess potential pandemic risk to humans. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Schiro, K.F. **Anderson, T.K.**, Rajao, D.S., Venkatesh, D., Lewis, N.S., and Vincent, A.L. June 2017. Evolutionary diversification of clade 1A.3.3.3 H1 swine influenza A viruses and zoonotic risk in the United States. The 36th meeting of The American Society for Virology. Madison, Wisconsin.

Abente, E.J., Lewis, N.S., Mogler, M., Rajao, D.S., Santos, J., Perez, D., Gauger, P.C., **Anderson, T.K.**, Bolton, M.J. and Vincent, A.L. March 2017. Antigenic diversity in swine H3 influenza A viruses in the United States and the impact on vaccine efficacy. Symposia on Influenza Antigenic Diversity. Athens, Georgia.

Anderson, T.K., Macken, C.A., Lewis, N.S., Scheuermann, R.H., Van Reeth, K., Brown, I.H., Swenson, S.L., Simon, G., Saito, T., Berhane, Y., Ciacci-Zanella, J., Pereda, A., Davis, C.T., Donis, R.O., Webby, R.J., and Vincent, A.L. August 2016. A unified nomenclature system for hemagglutinin genes from swine influenza A viruses (H1N1 and H1N2). Options IX for the Control of Influenza. Chicago, Illinois, USA.

Anderson, T.K.. April 2016. Ecological restoration and qualitative community stability determine parasite establishment and persistence. The US-International Association for Landscape Ecology Annual Meeting. Asheville, North Carolina.

Anderson, T.K., Stratton, J., Macken, C.A., and Vincent, A.L. April 2015. An automated tool for quantifying spatial and temporal dynamics of influenza A in North American swine. The 3rd ISIRV International Symposium on Neglected Influenza Viruses. Athens, Georgia.

Anderson, T.K. and Sukhdeo, M.V.K. July 2014. The worm's eye view of community ecology. The 89th meeting of The American Society of Parasitologists, New Orleans, Louisiana.

Anderson, T.K., Dunn, S.M., Dodd, E.T., and St. Jean, M.G. April 2014. A threshold in ecological stability determines parasite establishment and persistence in estuarine marshes. The annual meeting of The Southeastern Society of Parasitologists, Statesboro, Georgia.

Anderson, T.K. March 2014. A threshold in ecological stability determines parasite establishment and persistence in estuarine marshes. The 1st meeting on Ecology and Evolution of Marine Parasites and Diseases. The Royal Netherlands Institute for Sea Research and Alfred Wegner Institute for Polar and Marine Research. Texel, Netherlands.

Kamlangdee, A., Kingstad-Bakke, B., **Anderson, T.K.**, Goldberg, T.L., and Osorio, J. 2014. MVA-expressing a mosaic hemagglutinin provides broad humoral and cellular immune responses against Influenza A viruses. The 33rd meeting of The American Society for Virology. Fort Collins, Colorado.

Kitikoon, P., Nelson, M.I., Killian, M.L., **Anderson, T.K.**, Koster, L., Culhane, M.R., Vincent, A.L. July 2013. Increased diversity of H3N2 influenza virus in pigs in the United States and implications for pigs and humans. The 32nd meeting of The American Society for Virology. State College, Pennsylvania.

Anderson, T.K., Nelson, M.I., Kitikoon, P., Swenson, S.L., Korslund, J.K., and Vincent, A.L. March 2013. Spatial and temporal dynamics of influenza A in North American swine. The 2nd ISIRV International Symposium on Neglected Influenza Viruses. Dublin, Ireland.

Anderson, T.K., Kitikoon, P., and Vincent, A.L. February 2013. Prediction of broadly protective and cross-reactive influenza isolates using network centrality measures. MISMS workshop on Influenza at the animal-human interface. Padua, Italy.

McKee, E.M., **Anderson, T.K.**, Walker, E.D., Kitron, U. D., Brawn, J. D., Ruiz, M.O., Krebs, B.L., Goldberg, T. L. and Hamer, G.L. May 2012. Does avian herd immunity influence West Nile virus transmission? The 10th Annual Ecology and Evolution of Infectious Disease Conference. Ann Arbor, Michigan.

Hamer, G.L. **Anderson, T.K.**, Brawn, J.D., Kitron, U.D., Ruiz, M.O., Goldberg, T.L., and Walker, E.D. March 2012. *Culex* mosquito dispersal in the urban environment. NSF-NIH Ecology and Evolution of Infectious Diseases Symposium. Berkeley, California.

Krebs, B.L., Newman, C.M., **Anderson, T.K.**, Brawn, J. August 2012. Spatio-temporal patterns in communal roosting behavior of American Robins (*Turdus migratorius*) in an urban setting. The 5th North American Ornithological Conference. Vancouver, Canada.

Ruiz, M.O., **Anderson, T.K.**, Hamer, G.L., Walker, E.D., and Kitron, U.D. November 2012. Spatial dynamics of abundance and West Nile virus infection of mosquitoes in a suburban neighborhood. The 61st meeting of The American Society of Tropical Medicine and Hygiene. Atlanta, Georgia.

Anderson, T.K., Laegeid, W.W., Cerutti, F., Osorio, F.A., Nelson, E.A., Christopher-Hennings, J. and Goldberg, T.L. July 2011. Weapons of mass-reduction: applying network statistics to define core PRRSV proteins for rational polyvalent vaccine development. The 30th meeting of The American Society for Virology. Minneapolis, Minnesota.

Hamer, G.L., Chaves, L.F., **Anderson, T.K.**, Kitron, U. D., Brawn, J. D., Ruiz, M.O., Loss, S.R., Walker, E.D. and Goldberg, T. L. June 2011. Fine-scale variation in vector host feeding preferences and force of infection drive localized patterns of West Nile virus transmission. The 9th Annual Ecology and Evolution of Infectious Disease Conference. Santa Barbara, California.

Hamer, G.L., Berry, G.E., Makohon-Moore, A., Crafton, J. **Anderson, T.K.**, Goldberg, T.L., and Walker, E.D. March 2011. Filarioid nematode infections in amplification hosts for West Nile virus. NSF-NIH Ecology and Evolution of Infectious Diseases Symposium. Madison, Wisconsin.

Anderson, T.K., Laegeid, W.W., Cerutti, F., Osorio, F.A., Nelson, E.A., Christopher-Hennings, J. and Goldberg, T.L. December 2010. Weapons of mass-reduction: applying network statistics to define core PRRSV proteins for rational polyvalent vaccine development. International Porcine Reproductive and Respiratory Syndrome Symposium. Chicago, Illinois.

Anderson, T.K., Hamer, G.L., Walker, E.D., Chaves, L.F., Kitron, U.D., Brawn, J.D., Ruiz, M.O. and Goldberg, T.L. November 2010. Pattern formation in the dynamics of West Nile virus amplification in a transmission hot spot in Chicago, U.S.A. The 59th meeting of The American Society of Tropical Medicine and Hygiene. Atlanta, Georgia.

Hamer, G.L., Goldberg, T.L., **Anderson, T.K.**, Kitron, U.D., Chaves, L.F., Brawn, J.D., Ruiz, M.O. Krebs, B., Hood-Nowotny, R., Donovan, D.J., Kaufman, M.G., and Walker, E.D. November 2010. Dispersal of *Culex pipiens* in an urban focus of West Nile virus transmission: a mark-capture study using stable isotopes. The 59th meeting of The American Society of Tropical Medicine and Hygiene. Atlanta, Georgia.

Newman, C.M., Cerutti, F. **Anderson, T.K.**, Hamer, G. L., Walker, E.D., Kitron, U.D., Ruiz, M.O., Brawn, J. D., , and Goldberg, T.L. November 2010. *Culex* flavivirus enhances West Nile virus mosquito infection. The 59th meeting of The American Society of Tropical Medicine and Hygiene. Atlanta, Georgia.

Goldberg, T.L. Kitron, U.D., Ruiz, M.O., Walker, E.D., Brawn, J. D., Hamer, G.L., **Anderson, T.K.**, Chaves, L.F., Bertolotti, L. Amore, G., Cerutti, F., Krebs, B., Newman, C.M. and Goldberg, T.L. November 2010. Transmission, amplification, and evolution of West Nile virus in Chicago, USA. The 59th meeting of The American Society of Tropical Medicine and Hygiene. Atlanta, Georgia.

Anderson, T.K. and Sukhdeo, M.V.K. August 2010. Community stability threshold for parasite establishment and persistence in estuarine marshes. The 95th meeting of The Ecological Society of America. Pittsburgh, Pennsylvania.

Hamer, G.L., Goldberg, T.L. **Anderson, T.K.**, Kitron, U.D., Brawn, J.D., Ruiz, M.O., Loss, S.R., and Walker, E.D. February 2010. Spatial variation in *Culex pipiens* host selection and avian community reservoir competence within an urban focus of West Nile virus transmission. Michigan Mosquito Control Association Meeting. Traverse City, Michigan.

Hamer, G.L., Goldberg, T.L. **Anderson, T.K.**, Kitron, U.D., Brawn, J.D., Ruiz, M.O., Loss, S.R., and Walker, E.D. December 2009. Spatial variation in *Culex pipiens* host selection and avian community reservoir competence within an urban focus of West Nile virus transmission. Entomological Society of America Conference. Indianapolis, Indiana.

Anderson, T.K. and Sukhdeo, M.V.K. August 2009. Abiotic versus biotic: hierarchical factors in the assembly of parasite communities. The 84th meeting of The American Society of Parasitologists, Knoxville, Tennessee.

Anderson, T.K. March 2009. Network structure and disease transmission. Ecology and Evolution Graduate Student Symposium, Princeton University-University of Pennsylvania-Rutgers University. University of Pennsylvania, Philadelphia, PA.

Anderson, T.K. and Sukhdeo, M.V.K. June 2008. Core-periphery structure in food webs drives parasite community assembly in naïve fish hosts. The 83rd meeting of The American Society of

Parasitologists, Arlington, Texas.

Rutherford, A., Maro, J., Korolev, K., **Anderson, T.K.**, Holcomb, J. and Harrington, P. January 2008. Competition and diffusion of information on social networks. New England Complex Systems Institute Workshop, Massachusetts Institute of Technology, Boston.

Anderson, T.K. and Sukhdeo, M.V.K. June 2007. Food web stability drives parasite species diversity. The First North American Parasitology Congress, Merida, Mexico.

Anderson, T.K. and Sukhdeo, M.V.K. August 2005. West Nile Virus: habitat-based spatial heterogeneity. The 90th meeting of The Ecological Society of America. Montreal, Canada.

Anderson, T.K. and Sukhdeo, M.V.K. July 2004. Ecology of West Nile virus: a habitat-based approach to quantifying risk and transmission. The 79th meeting of The American Society of Parasitologists, Philadelphia, Pennsylvania.

Anderson, T.K., Chisholm, L.A. and Whittington, I.D. August 2003. Seasonal patterns and microhabitat selection of monogenean gill parasites from the Giant Shovelnose ray, *Rhinobatos typus* at Heron Island, Great Barrier Reef, Australia. The 78th meeting of The American Society of Parasitologists, Halifax, Nova Scotia.

PROFESSIONAL EXPERIENCE

Teaching

- 2019 Instructor, Phylogenetic methods and sequence analysis, Boehringer Ingelheim Influenza A virus workshop, USDA-ARS, Ames, IA.
- 2017-2018 Instructor, Phylogenetic Methods, Influenza Sequence Analysis and Phylogenetics (Pre-conference workshop, Iowa State University, James D. McKean Swine Disease Conference).
- 2017 Instructor, Zoetis/Boehringer Ingelheim/Hanor, Influenza Sequence Analysis and Phylogenetics Workshop, Iowa State University.
- 2017 Instructor, Phylogenetic Methods, Influenza Sequence Analysis and Phylogenetics (Pre-conference workshop, Annual Meeting of the American Association of Swine Veterinarians).
- 2015 Instructor, Phylogenetic Methods, Computational Methods in Swine Virology (USDA-ARS, USDA-APHIS, National Pork Board Sponsored Workshop).
- 2015 (Spring) Instructor, Current Trends in Biological Research (BIOL3630H: 20 students), and General Biology (BIOL1130 Lecture Section: 230 students), Georgia Southern University.
- 2014 (Fall) Instructor, Parasitology (BIOL5341 Lecture and Lab Sections: 40 students), Georgia Southern University.
- 2014 (Spring) Instructor, Parasitology (BIOL5341 Lecture and Lab Sections: 40 students), Georgia Southern University.
- 2013 (Fall) Instructor, General Biology (BIOL1130 Lecture Section: 230 students), Georgia Southern University.
- 2013 Instructor, Phylogenetic Methods, USDA-NIH MISMS Workshop.
- 2010 Guest lecture, Parasitology, University of Wisconsin-Madison.
- 2008-09 Teaching Assistant, General Biology, Rutgers University.
- 2008 Guest lecturer, Human Parasitology, Rutgers University.
- 2003-08 Instructor, Human Parasitology Lab (146:329: 40 students), Rutgers University.
- 2001 Lab Instructor, Marine Parasitology, The University of Queensland.

Graduate Advising and Mentorship

- 2020-present, Postdoctoral Associate, Dr. Zeb Arendsee, National Animal Disease Center, USDA-ARS.
- 2020-present, Postdoctoral Associate, Dr. Alexey Markin, National Animal Disease Center, USDA-ARS.
- 2020-present, Postdoctoral Associate, Dr. David Hufnagel, National Animal Disease Center,

- USDA-ARS.
- 2020-2021, M.Sc., Committee, Anugrah Saxena, Graduate Program in Computer Science, Iowa State University.
 - 2018-2020, Ph.D. Committee, Alexey Markin, Graduate Program in Computer Science, Iowa State University.
 - 2018-2019, M.Sc., Committee, Veenanadh Srimathtirumalagudime, Graduate Program in Computer Science, Iowa State University.
 - 2018, Ph.D. external reviewer, The University of Adelaide
 - 2017-present, ORISE Research Assistant, Blake Inderski, National Animal Disease Center, USDA-ARS.
 - 2017-2020, Ph.D. Committee, Fathi Mubarak, Graduate Program in Computer Science, Iowa State University.
 - 2017-present, Ph.D. Committee, Wannarat Yim-Im, Graduate Program in Veterinary Microbiology, Iowa State University.
 - 2016-2018, ORISE Research Assistant, Kelly Schiro, National Animal Disease Center, USDA-ARS.
 - 2014-2016 M.Sc., Advisor, Jamie Alfieri, Department of Biology, Georgia Southern University.
 - 2014-2016 M.Sc., Committee, Keysa Rosas-Rodriguez, Department of Biology, Georgia Southern University.

Undergraduate Advising

- 2015 Undergraduate Advisor, Jackson Tomlinson, Department of Biology, Georgia Southern University.
- 2014 Undergraduate Advisor, Jeyvan Joseph, Department of Biology, Georgia Southern University.
- 2013-2015 Honors Advisor, Sarah Dunn, Department of Biology, Georgia Southern University.
- 2013-2016 Undergraduate Advisor, Emily Dodd, Department of Biology, Georgia Southern University.
- 2013-2015 Undergraduate Advisor, Maria St. Jean, Department of Biology, Georgia Southern University.
- 2011 Undergraduate Advisor, Jeremy Hemberger, Department of Pathobiological Sciences, University of Wisconsin-Madison.
- 2007 Undergraduate Advisor, Jesse Stratowski, Department of Ecology, Evolution and Natural Resources, Rutgers University.
- 2004 Undergraduate Advisor, Jodi Messina, Department of Ecology, Evolution and Natural Resources, Rutgers University.

Service

- 2021 Interview Committee, Infectious Bacterial Diseases Research Unit, USDA-ARS-NADC.
- 2019 Interview Committee, Supervisory Information Technology Specialist, USDA-APHIS
- 2018 Interview Committee, Computational Biologist, USDA-ARS-NADC.
- 2018-present Letters to a Pre-Scientist, Educational Outreach Program Participant.
- 2018-2019 Program Committee, 11th International Conference on Bioinformatics and Computational Biology.
- 2016-present SCINet Policy Working Group, USDA-ARS (the ARS Big Data Initiative).
- 2016-2017 Nominating & Tellers Committee, American Society of Parasitologists.
- 2016-2018 Summer School Outreach (United Way of Story County), National Animal Disease Center, USDA-ARS.
- 2016-present Science Fair (Blood Activity), National Animal Disease Center, USDA-ARS.
- 2015 Section Leader, Science Olympiad, Institute for Interdisciplinary STEM Education.
- 2014-2015 Organizing Committee, Computational Methods in Swine Virology (USDA-ARS, USDA-APHIS, National Pork Board Sponsored Workshop).
- 2014 *Ad hoc* contributor to the USDA-ARS Animal Influenza Viruses Gap Analysis report.

- 2013-2017 Distinguished Service Award/Extramural Awards Committee, American Society of Parasitologists.
- 2013-Present User Advisory Group, Influenza Research Database/Virus Pathogen Resource
- 2013-2014 Organizing Committee, The 2014 Annual Meeting of the Southeastern Society of Parasitologists
- 2010-12 Graduate Committee, Wisconsin Ecology, University of Wisconsin-Madison.
- 2008 Student Volunteer, The 83rd Annual Meeting of The American Society of Parasitologists.
- 2007 Student Volunteer, The First North American Parasitology Congress, Merida, Mexico.
- 2007-09 Judge, North Jersey Science Fair (Captain, Zoology Section 2008-2009).
- 2004-05 Secretary, Ecology and Evolution Graduate Student Association, Rutgers University.
- 2005 Co-Chair Organizing Committee, Disease Ecology Symposium, Princeton University.
- 2001 Student Volunteer, The Forth International Symposium on Monogenea, Brisbane Australia.

REVIEWER FOR

Journal of Animal Ecology, Biological Invasions, Philosophical Transactions of the Royal Society B, PLoS Neglected Tropical Diseases, PLoS ONE, EcoHealth, Journal of Wildlife Diseases, Emerging Infectious Diseases, Bulletin of Mathematical Biology, Veterinary Microbiology, Journal of Parasitology, International Journal for Parasitology, Journal of the Royal Society Interface, Comparative Parasitology, Scientific Reports, Journal of Virology, Journal of General Virology, Parasites and Vectors, Journal of Clinical Microbiology, Journal of Medical Microbiology, Landscape and Urban Planning, Virus Genes, Clinical Infectious Diseases, Journal of Infection and Public Health, Human Vaccines & Immunotherapeutics, Frontiers in Veterinary Science.

-SciLog Fellow, Mitigating Zoonotic Threats *Research Corporation for Science Advancement* (2021-2023)

-Advisory Board, **FluZooMark** (2020-2025).

-Editorial Board, *Pathogens* (2019-present).

-National Science Foundation Panelist (2013, 2014, 2015, 2016, 2017, 2018).

-National Science Foundation, *ad hoc* review (2015, 2016).

-National Pork Board (2010, 2011, 2012, 2013, 2017, 2018: Swine Health Section).

-Genome Canada, *ad hoc* review (2017, 2018).

-National Institutes of Health, Early Career Reviewer Program (2016-2019).

-Consulting: Merck Animal Health (2017, 2018, 2019).

DOCTORAL
COMMITTEE

Michael Sukhdeo (advisor), Steven Handel, Julie Lockwood, Peter Morin.

External Reviewers: Andrew Dobson (Princeton University), Emmett Dennis (The University of Liberia).

POSTDOCTORAL
ADVISOR

Tony L. Goldberg (University of Wisconsin-Madison), Amy L. Vincent (National Animal Disease Center, USDA-ARS).

PROFESSIONAL
SOCIETIES AND
AWARDS

American Society for Virology, Full Member (2017-present)

American Society of Parasitology (2002-present)

The International Society for Influenza and other Respiratory Virus Diseases (2015-present)

The International Society for Computational Biology (2012-present)

Sigma Xi, The Scientific Research Society (2015-present); Committee for Qualifications and Mem-

bership (2021-present)

American Society of Parasitology, Meritorious Award in the Paper Competition (2008)

The University of Queensland, Faculty of Biological and Chemical Sciences, Commendation for High Achievement (2000)

Rutgers University, Graduate School of New Brunswick, Travel Award (2005, 2007-2008)

American Society of Parasitology, Marc Dresden Travel Award (2007-2009)

Georgia Southern University, Faculty Development Grant (2014)

3rd International Symposium on Neglected Influenza Viruses, Merck Animal Health Junior Investigator Best Speaker Award (2015)

PROFESSIONAL
TRAINING

Programming

- R, Python (Midwest Big Data Summer School, 2019, NSF-Midwest Big Data Hub, Iowa State University)
- Python (Midwest Big Data Summer School, 2016, NSF-Midwest Big Data Hub, Iowa State University)
- Python (Python Bootcamp, 2010, The Hacker Within, University of Wisconsin-Madison)
- Matlab, R (New England Complex Systems workshop, 2008, MIT)

Statistics, phylogenetics, and data science

- R, Python (Midwest Big Data Summer School, 2019, NSF-Midwest Big Data Hub, Iowa State University)
- Data Carpentry Workshop (Iowa State University, 2017)
- R, Python (Midwest Big Data Summer School, 2016, NSF-Midwest Big Data Hub, Iowa State University)
- Phylogenetic Methods (NIH-Fogarty International Center, 2013, MISMS workshop on Influenza at the animal-human interface, Padua, Italy)
- Phylogenetic Methods (NSF Ecology and Evolution of Infectious Disease workshop, 2011, University of California-Santa Barbara)
- R (NSF Ecology and Evolution of Infectious Disease workshop, 2011, University of California-Santa Barbara)
- Matlab, R (New England Complex Systems workshop, 2008, M.I.T.)
- SAS (Quantitative Ecology and Evolution, Rutgers University)

REFERENCES

Upon request.