Ryan K. Waples, PhD
Hans Rosling Center for Population Health,
Box 351617, Seattle, WA 98195-1617

April 2022
ryan.waples@gmail.com
(206)-432-6664

EDUCATION

Bachelor of Arts in Biology Wesleyan University
Middletown, CT *August 2000 – May 2004*

Master of Science University of Washington
School of Aquatic and Fishery Sciences *March 2014 – Dec. 2015*
Thesis: Population genomics of Puget Sound chum salmon:
The legacy of the salmonid whole genome duplication

PhD University of Copenhagen
advisors: Dr. Ida Moltke and Dr. Anders Albrechtsen *April 2016 – April 2019*
Thesis: Relatedness, admixture and the genetic history of Greenland-European contact

LICENSURE

Not applicable

PROFESSIONAL POSITIONS

Undergraduate Research Assistant Wesleyan University, Middletown, CT
Laboratory of Dr. Sonia Sultan *2002 — 2004*

Lab Manager Wesleyan University, Middletown, CT
Laboratory of Dr. Sonia Sultan *2005 – 2006*

Research Technician Vanderbilt University, Nashville, TN
Laboratory of Dr. Daniel Funk *2006 — 2007*

Fisheries Geneticist, Fisheries Biologist (50% time) NOAA NWFSC, Seattle, WA
Conservation Biology Division, Genetics and Evolution Program *2010 — 2013*

Research Scientist (50% time) University of Washington, Seattle, WA
Laboratory of Dr. Jim and Lisa Seeb *2010 — 2014*

Postdoctoral Scholar University of Copenhagen, Denmark
with Dr. Ida Moltke *April 2019 – March 2020*

Postdoctoral Fellow University of Washington, Seattle, WA
with Dr. Sharon Browning *July 2020 – current*

HONORS, AWARDS, SCHOLARSHIPS

2014 James E Wright Graduate Award - presented annually by the Genetics Section of the American Fisheries Society to recognize excellence in graduate-level work in fisheries genetics.

2015 American Genetic Association Award - to attend and present a poster at the 2015 American Genetic Association Presidential Symposium.

PROFESSIONAL ACTIVITIES

Peer reviewer for: *Bioinformatics, Molecular Ecology, Molecular Ecology Resources, Genetics, Heredity, Journal of Heredity, Evolutionary Applications, BMC Bioinformatics, PCIEvolBiol, PLOS Genetics, American Journal of Human Genetics*

BIBLIOGRAPHY

* indicates equal contributions

Journal Articles (peer reviewed)

[1] R. S. Waples and **R. K. Waples**. “Inbreeding effective population size and parentage analysis without parents”. In: *Molecular Ecology Resources* 11 Suppl 1 (Mar. 2011), pp. 162–171.

[2] S. E. Sultan, T. Horgan-Kobelski, L. M. Nichols, C. E. Riggs, and **R. K. Waples**. “A resurrection study reveals rapid adaptive evolution within populations of an invasive plant”. In: *Evol. Appl.* 6.2 (Feb. 2013), pp. 266–278.

[3] W. A. Larson, L. W. Seeb, M. V. Everett, **R. K. Waples**, W. D. Templin, and J. E. Seeb. “Genotyping by sequencing resolves shallow population structure to inform conservation of Chinook salmon (Oncorhynchus tshawytscha)”. In: *Evol. Appl.* 7.3 (Mar. 2014), pp. 355–369.

[4] M. T. Limborg, **R. K. Waples**, J. E. Seeb, and L. W. Seeb. “Temporally isolated lineages of pink salmon reveal unique signatures of selection on distinct pools of standing genetic variation”. In: *J. Hered.* 105.6 (Nov. 2014), pp. 741–751.

[5] L. W. Seeb, **R. K. Waples**, M. T. Limborg, K. I. Warheit, C. E. Pascal, and J. E. Seeb. “Parallel signatures of selection in temporally isolated lineages of pink salmon”. In: *Molecular Ecology* 23.10 (May 2014), pp. 2473–2485.

[6] M. T. Limborg, **R. K. Waples**, F. W. Allendorf, and J. E. Seeb. “Linkage Mapping Reveals Strong Chiasma Interference in Sockeye Salmon: Implications for Interpreting Genomic Data”. In: *G3* 5.11 (Sept. 2015), pp. 2463–2473.

[7] G. J. McKinney, L. W. Seeb, W. A. Larson, D. Gomez-Uchida, M. T. Limborg, M. S. O. Brieuc, M. V. Everett, K. A. Naish, **R. K. Waples**, and J. E. Seeb. “An integrated linkage map reveals candidate genes underlying adaptive variation in Chinook salmon (Oncorhynchus tshawytscha)”. In: *Molecular Ecology Resources* 16.3 (May 2016), pp. 769–783.

[8] B. L. Stockwell, W. A. Larson, **R. K. Waples**, R. A. Abesamis, L. W. Seeb, and K. E. Carpenter. “The application of genomics to inform conservation of a functionally important reef fish (Scarus niger) in the Philippines”. In: *Conserv. Genet.* 17.1 (Feb. 2016), pp. 239–249.

[9] **R. K. Waples**, W. A. Larson, and R. S. Waples. “Estimating contemporary effective population size in non-model species using linkage disequilibrium across thousands of loci”. In: *Heredity* 117.4 (Oct. 2016), pp. 233–240.

[10] **R. K. Waples**, L. W. Seeb, and J. E. Seeb. “Linkage mapping with paralogs exposes regions of residual tetrasomic inheritance in chum salmon (Oncorhynchus keta)”. In: *Molecular Ecology Resources* 16.1 (Jan. 2016), pp. 17–28.

[11] M. W. Ackerman, B. K. Hand, **R. K. Waples**, G. Luikart, R. S. Waples, C. A. Steele, B. A. Garner, J. McCane, and M. R. Campbell. “Effective number of breeders from sibship reconstruction: empirical evaluations using hatchery steelhead”. In: *Evol. Appl.* 10.2 (Feb. 2017), pp. 146–160.

[12] G. J. McKinney, **R. K. Waples**, L. W. Seeb, and J. E. Seeb. “Paralogs are revealed by proportion of heterozygotes and deviations in read ratios in genotyping-by-sequencing data from natural populations”. In: *Molecular Ecology Resources* 17.4 (July 2017), pp. 656–669.

[13] **R. K. Waples**, J. E. Seeb, and L. W. Seeb. “Congruent population structure across paralogous and nonparalogous loci in Salish Sea chum salmon (Oncorhynchus keta)”. In: *Molecular Ecology* 26.16 (Aug. 2017), pp. 4131–4144.

[14] A. Gilly, D. Suveges, K. Kuchenbaecker, M. Pollard, L. Southam, K. Hatzikotoulas, A.-E. Farmaki, T. Bjornland, **R. Waples**, E. V. R. Appel, E. Casalone, G. Melloni, B. Kilian, N. W. Rayner, I. Ntalla, K. Kundu, K. Walter, J. Danesh, A. Butterworth, I. Barroso, E. Tsafantakis, G. Dedoussis, I. Moltke, and E. Zeggini. “Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits”. In: *Nature Communications* 9.1 (Nov. 2018), p. 4674. ISSN: 2041-1723.

[15] G. J. McKinney, **R. K. Waples**, C. E. Pascal, L. W. Seeb, and J. E. Seeb. “Resolving allele dosage in duplicated loci using genotyping-by-sequencing data: A path forward for population genetic analysis”. In: *Molecular Ecology Resources* 18.3 (May 2018), pp. 570–579.

[16] D. W. G. Stanton, P. Frandsen, **R. K. Waples**, R. Heller, I.-R. M. Russo, P. A. Orozco-terWengel, C.-E. T. Pedersen, H. R. Siegismund, and M. W. Bruford. “More grist for the mill? Species delimitation in the genomic era and its implications for conservation”. In: *Conserv. Genet.* 20.1 (Feb. 2019), pp. 101–113.

[17] **R. K. Waples**, A. Albrechtsen, and I. Moltke. “Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data”. In: *Molecular Ecology* 28.1 (Jan. 2019), pp. 35–48.

[18] P. Pečnerová*, G. Garcia-Erill*, X. Liu*, C. Nursyifa*, **R. K. Waples***, C. G. Santander*, L. Quinn, P. Frandsen, J. Meisner, F. F. Stæger, M. S. Rasmussen, A. Brüniche-Olsen, C. Hviid Friis Jørgensen, R. R. da Fonseca, H. R. Siegismund, A. Albrechtsen, R. Heller, I. Moltke, and K. Hanghøj. “High genetic diversity and low differentiation reflect the ecological versatility of the African leopard”. In: *Current Biology* (Feb. 2021).

[19] R. S. Waples, **R. K. Waples**, and E. J. Ward. “Pseudoreplication in genomic-scale data sets”. In: *Molecular Ecology Resources* (Aug. 2021).

[20] **R. K. Waples***, A. L. Hauptmann*, I. Seiding, E. Jørsboe, M. E. Jørgensen, N. Grarup, M. K. Andersen, C. V. L. Larsen, P. Bjerregaard, G. Hellenthal, T. Hansen, A. Albrechtsen, and I. Moltke. “The genetic history of Greenlandic-European contact”. In: *Current Biology* (Mar. 2021).

[21] M. K. Andersen, L. Skotte, E. Jørsboe, R. Polito, F. F. Stæger, P. Aldiss, K. Hanghøj, **R. K. Waples**, C. G. Santander, N. Grarup, I. K. Dahl-Petersen, L. J. Diaz, M. Overvad, N. K. Senftleber, B. Søborg, C. V. Larsen, C. Lemoine, O. Pedersen, B. Feenstra, P. Bjerregaard, M. Melbye, M. E. Jørgensen, N. J. Færgeman, A. Koch, T. Moritz, M. P. Gillum, I. Moltke, T. Hansen, and A. Albrechtsen. “Loss of Sucrase-Isomaltase Function Increases Acetate Levels and Improves Metabolic Health in Greenlandic Cohorts”. In: *Gastroenterology* 162.4 (Apr. 2022), 1171–1182.e3. issn: 0016-5085.

Preprints (not peer reviewed)

[22] E. Jørsboe, M. K. Andersen, L. Skotte, F. F. Stæger, N. J. Færgeman, K. Hanghøj, C. G. Santander, N. K. Senftleber, L. J. Diaz, M. Overvad, **R. K. Waples**, F. Geller, P. Bjerregaard, M. Melbye, C. V. L. Larsen, B. Feenstra, A. Koch, M. E. Jørgensen, N. Grarup, I. Moltke, A. Albrechtsen, and T. Hansen. “An LDLR missense variant poses high risk of familial hypercholesterolemia in 30% of Greenlanders and offers potential for early cardiovascular disease intervention”. In: *medRxiv* (Jan. 2022).

Patents and Other Intellectual Property

Publicly Available Software

LDadmix	Software to estimate the haplotype frequencies and linkage disequilibrium in the ancestral populations of admixed samples. link: https://github.com/rwaples/LDadmix
lai-sim	Snakemake pipeline that simulates genetic data under multiple demographic models and infers local ancestry with three methods. link: https://github.com/rwaples/lai-sim

Funding History

2020	Postdoctoral fellowship funded by NHGRI Genome Training Grant awarded to the University of Washington. T32 training grant HG000035 (PI: Evan Eichler). Renewed in 2021.

Public Health Practice Activities

(None)

CONFERENCES AND SYMPOSIA

Invited seminars

- *Where did the European ancestors of the Greenlanders come from?* Bioinformatics Research Centre seminar series. Aarhus University, Denmark, 2019.

Conference presentations (selected)

- *How to Use Reduced-Representation Genomic Methods to Estimate Contemporary Effective Population Size.* American Fisheries Society Annual Meeting. Quebec, Canada, 2014.
- *Linkage mapping with paralogs.* Presidential Symposium of the American Genetic Association. (poster). Bainbridge Island, WA, USA, 2015.
- *LDadmix: a method to estimate LD in the ancestral populations of admixed samples.* Probabilistic modeling in Genomics. (poster). Aarhus University, Denmark, 2017.
- *LDadmix: a method to estimate LD in the ancestral populations of admixed samples.* Annual meeting of the Society for Molecular Biology and Evolution. (poster). Austin, TX, USA, July 2017.
- *Allele frequency-free inference of close familial relationships from genotypes or low depth sequencing data.* Probabilistic modeling in Genomics. (poster). Cold Spring Harbor, NY, USA, Nov. 2018.
- *Where did the European ancestors of the Greenlanders come from?* Greenland Science Week. Nuuk, Greenland, Dec. 2019.
- *Understanding recent admixture with ternary ancestry fractions.* Probabilistic modeling in Genomics. (poster). Cold Spring Harbor, NY, USA (virtual), Apr. 2021.

UNIVERSITY SERVICE

University of Copenhagen

2016 Co-organizer of PhD Day at Bio, one-day scientific conference with more than 200 participants at the University of Copenhagen. Included moderating a live panel debate and inviting and hosting international speakers.

OTHER ACTIVITIES

2019 Co-organizer for EPIC, a monthly Copenhagen-area Population Genetics lunch seminar series.

2019-2020 Co-organizer for a manuscript-in-preparation group, facilitating structured feedback for draft manuscripts, held at the University of Copenhagen.

TEACHING HISTORY

2014 Teaching assistant, Shellfish Biology, Masters course, University of Washington

2016 Teaching assistant, Introduction to Python for Bioinformatics, Masters course, University of Copenhagen

2017 Teaching assistant and guest lecturer, Population genetics, Masters course, University of Copenhagen.

2018 Teaching assistant and guest lecturer, Population genetics, Masters course, University of Copenhagen.

2021 BIOST 581 - Statistical Genetics Seminar (Autumn quarter) Co-taught with Dr. Sharon Browning. Dept. of Biostatistics, University of Washington.

ADVISING AND FORMAL MENTORING

2021 Mentor for an undergraduate research project through the UW Undergraduate Research Program (Summer 2021 - Fall 2021)