

## *Leif Andersson*

### *Curriculum Vitae*

Date of Birth: 17 September, 1954  
Place of Birth: Stockholm, Sweden  
Nationality: Swedish  
Professional Address: Department of Medical Biochemistry and Microbiology  
Uppsala University  
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#### **Current position:**

Professor, Functional Genomics (2006-), Uppsala University  
Professor of Animal Genomics (2016-), Texas A&M University, College Station  
Guest Professor, Molecular Animal Genetics (2006-) Swedish University of Agricultural Sciences, Uppsala

#### **Academic history:**

1979 B.Sc (Chemistry, Biology), University of Stockholm, Stockholm  
1984 Ph.D. (Animal Breeding and Genetics), SLU, Uppsala  
1986 Docent (Animal Breeding and Genetics), SLU, Uppsala  
1986 Research leader, Department of Animal Breeding and Genetics, SLU, Uppsala  
1992 Professor (Animal Genetics), SLU, Uppsala  
2003 Guest professor (Functional Genomics), Uppsala University  
2006 Professor (Functional Genomics), Uppsala University  
2013 Visiting Professor (Animal Genomics) Texas A&M University

#### **Academic milestones:**

>380 scientific publications, >320 original and >60 review articles).

h-index (Web of science): 70 (2016-04-01)

Six granted patent families.

Twenty-nine students mentored to doctorate or licentiate degree (lic=#4 and 7) as main supervisor:

1. Sunna Sigurdardottir. Studies of the class II genes of the major histocompatibility complex in cattle June 6, 1991.
2. Anne Lundén. Marker genes and production traits in domestic animals: an association study with special reference to major histocompatibility complex genes. Dec. 11, 1991.
3. Hans Ellegren. Genome analysis with microsatellite markers. June 11, 1993.
4. Paola Mariani. Genetic mapping of economic trait loci in the pig. Sept. 29, 1995.
5. Maria Johansson Moller. Comparative genome analysis in the pig. Dec. 15, 1995.
6. Sofia Mikko. A comparative analysis of genetic diversity at Mhc DRB loci in some ruminant species. May 16, 1997.
7. Magnus Lindersson. Genome analysis of milk production traits in cattle. Sept. 30, 1997.
8. Lena Marklund. Genome analysis of quantitative trait loci in the pig. Oct. 24, 1997.
9. Stefan Marklund. Applied molecular genetics in domestic animals with particular focus on the horse. Dec. 19, 1997.
10. Anna Törnsten. Physical mapping of important trait loci in the pig. Dec. 15, 2000.
11. Örjan Carlborg. New methods for mapping quantitative trait loci. March 22, 2002.
12. Susanne Kerje. Mapping genes affecting phenotypic traits in chicken. Dec. 16, 2003.
13. Hee-Bok Park. Genetic analysis of quantitative traits using domestic animals: a candidate gene and genome scanning approach. Oct. 28, 2004.

14. Gerli Pielberg. Molecular coat colour genetics. Dominant white in pigs and Greying with age in horses. Dec. 16, 2004.
15. Anne-Sophie Van Laere. From QTL to QTN: Identification of a Quantitative Trait Nucleotide influencing muscle development and fat deposition in the pig. Feb. 11, 2005.
16. Lina Jacobsson. Genetic dissection of growth and fatness using divergent intercrosses in chicken, May 27, 2005.
17. Carolyn Fitzsimmons. Exploring the realm of gene expression differences between White Leghorn and red junglefowl chickens. February 13, 2006.
18. Frida Berg. Genetic analysis of fat metabolism in domestic pigs and their wild ancestor. Sept. 29, 2006.
19. Per Wahlberg. Chicken genomics – linkage and QTL mapping. Jan. 9, 2009.
20. Ellen Markljung. QTL analysis in the pig. From the identification of Quantitative Trait Loci to the understanding of molecular mechanisms. March 13, 2009.
21. Ulrika Gunnarsson. Genetic studies of pigmentation in chicken. April 3, 2009.
22. Anders Hellström. Dissecting phenotypic variation in pigmentation using forward and reverse genetics. November 12, 2010.
23. Elisabeth Sundström. Molecular genetics and mechanisms of pigmentation and melanoma. December 10, 2010.
24. Jonas Eriksson. Genetic and genomic studies in chicken – assigning function to vertebrate genes. February 3, 2012
25. Lin Jiang. Functional studies of genes associated with muscle growth in pigs and hair greying in horses. December 14, 2012.
26. Khurram Maqbool. Bioinformatic analysis of whole genome sequencing data – detection of selective sweeps and structural changes. October 16, 2014.
27. Freyja Imsland, Monogenic traits associated with structural variants in chicken and horse. September 25, 2015.
28. Sangeet Lamichhaney, The genetic basis for adaptation in natural populations. April 29, 2016.
29. Nima Rafati, Exploring genetic diversity in natural and domestic populations through next generation sequencing. March 30, 2017.

Post-doctoral students:

1. JinTae-Jeon 1997-2000
2. James Kijas 1997-2001
3. Elisabetta Giuffra 1998-2001
4. Valerie Amarger 1999-2001
5. Martin Braunschweig 2001-2003
6. Robert Fredriksson 2004-2005
7. Meiyang Fang 2004-2007
8. Emmanuelle Bourneuf 2004-2006
9. Xavier Tordoir 2006-2007
10. Greger Larson 2006-2008
11. Anna Golovko 2006-2008
12. Dominic Wright 2006-2008
13. Jennifer Meadows 2008-2010
14. Carl-Johan Rubin 2009-2012
15. Alvaro Martinez Barrio 2010-2014
16. Elizabeth Gilbert 2010-2011
17. Ben Dorshorst 2010-2012
18. Elisabeth Sundström 2012-2014
19. Marta Promerova 2012-2013
20. Ola Wallerman 2012-2014
21. Rajesh Gupta 2012-2014
22. Mats Pettersson 2014-2016
23. Chungang Feng 2014-
24. Ann Staiger 2015-
25. Chao Wang 2015-
26. Muhammad Akhtar Ali 2016-

27. Junfeng Chen 2016-

**Professional experience:**

Member of the Scientific Advisory Board, Gregor Mendel Institute of Molecular Plant Biology, Vienna, Austria (2016-)

Member of the review panel for ERC starting grants (2011-2014)

Member of the Scientific Advisory Board, HudsonAlpha Institute for Biotechnology, Huntsville, AL, USA (2014-).

Member of The Roslin Institute Scientific Advisory Board, Edinburgh, UK (2008-)

Member of the international jury for the Francqui price 2005 and 2008, Belgium

Director, Uppsala Centre for Comparative Genomics (UCG) (2004-2008)

Member of the Scientific Advisory Board of The Institute of Genomic Biology, University of Illinois at Urbana-Champaign (2005-2012)

Member of the editorial boards of Animal Genetics, Mammalian Genome, Animal Biotechnology, Molecular Genetics and Genomics, and Canine Genetics and Epidemiology.

Co-founder and board member of the biotech company Arexis AB (bought by Biovitrum AB 2005)

Co-founder of FunboGen AB (established 2007)

Co-founder of Biocistronics AB (established 2009)

Co-founder of Capilet Genetics AB (established 2011)

More than 100 invited lectures have been given at international meetings or symposia. In addition numerous invited lectures have been given at national universities, industries and academic institutions.

**Some recent key-note and invited lectures:**

Phenotypic evolution in domestic animals – walking in the footsteps of Charles Darwin.

Evolution – The molecular landscape. 74th Cold Spring Harbor Symposium on Quantitative Biology, Cold Spring Harbor, May 2009 (~1,000 delegates)

How selective sweeps in domestic animals inform human medicine. Nobel symposium Genetics in Medicine, Stockholm, June 2010 (~500 delegates)

Structural variation underlying phenotypic diversity in domestic animals. Keystone symposium, Steamboat Springs, January 2011 (200 delegates)

How domestic animals can teach us about the molecular mechanisms underlying phenotypic evolution. Keynote speech at 6<sup>th</sup> international conference on “Advances in Canine and Feline Genomics and Inherited Diseases”, Visby, Sweden, June 2012

How animal genomics can shed light on important biological mechanisms. 34th International Society for Animal Genetics Conference. Xian, July 2014 (>1000 delegates)

The Atlantic herring – a novel model for studies of molecular evolution and genetic adaptation. Gordon Research Conference on Quantitative Genetics and Genomics, Barga, Italy, February 2015 (>200 delegates)

The genetics of ruff sex. Keystone symposia on Understanding the Function of Human Genome Variation, Uppsala, June 2016 (>500 delegates)

Polygenic basis for ecological adaptation revealed by genome sequencing. Society for Molecular Biology and Evolution, July 2016 (>500 delegates)

### **Recognitions:**

Member of the Royal Swedish Academy of Agriculture and Forestry (2001)  
Member of the Royal Swedish Academy of Sciences (2002)  
Member of the Royal Physiographic Society in Lund (2004)  
Member of the Royal Society of Sciences in Uppsala (2007)  
Member of the European Molecular Biology Organization (EMBO) (2008)  
Foreign associate of the National Academy of Sciences (USA) (2012)  
Member of The Academy of Medicine, Engineering & Science of Texas (2016)

Doctor *honoris causa*, University of Liège, Belgium (2009)  
Wallenberg Scholar, The Knut and Alice Wallenberg Foundation (2012)  
Eminent Scholar in Residence and Visiting Professor of Animal Genomics, Texas A&M  
Institute of Advanced Study (TIAS) Faculty Fellows, USA (2013)  
Honorary Doctor, Texas A&M University, USA (2015)  
Honorary Member for life time, International Society for Animal Genetics (2016)  
The Karl Johan Öbrink lecture 2005, Uppsala Biomedical Centre  
The Osborne Memorial Lecture, University of Edinburgh (2009)

### **Prizes**

Lilly and Sven Thuréus prize in Natural History and Medicine 2004, Royal Society of  
Sciences, Uppsala  
Rosén's Linné-prize in Zoology 2004, Royal Physiographic Society in Lund  
Hilda and Alfred Eriksson's prize in medicine 2012. Royal Swedish Academy of Sciences.  
The Olof Rudbeck Prize 2013. Uppsala Medical Society.  
The Wolf prize in Agriculture 2014, The Wolf foundation, Israel.  
The Nilsson-Ehle Medal 2015, Royal Swedish Academy of Agriculture and Forestry.

### **Other:**

Reviewer for a number of international scientific journals including Nature, Science, Nature  
Review Genetics, Nature Genetics, PLoS Medicine, PLoS Genetics, Genetics, Genomics,  
Genome Research, Bioinformatics and Trends in Genetics.

### **Twelve selected papers, 2000-:**

Milan,D., Jeon,J.-T., Looft,C., Amarger,V., Thelander,M., Robic,A., Rogel-Gaillard,C.,  
Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundström,K., Reinsch,N., Gellin,J.,  
Kalm,E., Le Roy,P., Chardon,P. and **Andersson,L.** 2000. A mutation in PRKAG3  
associated with excess glycogen content in pig skeletal muscle. *Science* 288:1248-  
1251.

Van Laere,A.S., Nguyen,M., Braunschweig,M., Nezer,C., Collette,C., Moreau,L.,  
Archibald,A., Haley,C.S., Buys,N., Tally,M., Andersson,G., Georges,M. and  
**Andersson,L.** 2003. A regulatory mutation in *IGF2* causes a major QTL effect on  
muscle growth in the pig. *Nature* 425:832-836.

Rosengren Pielberg,G., Golovko,A., Sundström,E., Curik,I., Lennartsson,J.,  
Seltenhammer,M.H., Druml,T., Binns,M., Fitzsimmons,C., Lindgren,G., Sandberg,K.,  
Baumung,R., Vetterlein,M., Strömberg,S., Grabherr,M., Wade,C., Lindblad-Toh,K.,  
Pontén,F., Heldin,C.-H., Sölkner,J. and **Andersson,L.** 2008. A cis-acting regulatory

- mutation causes premature hair greying and susceptibility to melanoma in the horse. *Nature Genetics* 40:1004-1009.
- Markljung,E., Jiang,L., Jaffe,J.D., Mikkelsen,T.S., Wallerman,O., Larhammar,M., Zhang,X., Wang,L., Saenz-Vash,V., Gnirke,A., Lindroth,A.M., Barrés,R., Yan,J., Strömberg,S., De,S., Pontén,F., Lander,E.S., Carr,S.A., Zierath,J.R., Kullander,K., Wadelius,C., Lindblad-Toh,K., Andersson,G., Hjälms,G., and **Andersson,L.** 2009. ZBED6, a novel transcription factor derived from a domesticated DNA transposon regulates IGF2 expression and muscle growth. *PLoS Biology* 7: e1000256.
- Rubin,C.-J., Zody,M.C., Eriksson,J., Meadows,J.R.S., Sherwood,E., Webster,M.T., Jiang,L., Ingman,M., Sharpe,T., Ka,S., Hallböök,F., Besnier,F., Carlborg,Ö., Bed’hom,B., Tixier-Boichard,M., Jensen,P., Siegel,P., Lindblad-Toh,K. and **Andersson,L.** 2010. Whole genome resequencing reveals loci under selection during chicken domestication. *Nature* 464:587-591.
- Andersson LS, Larhammar M, Memic F, Wootz H, Schwochow D, Rubin CJ, Patra K, Arnason T, Wellbring L, Hjälms G, Imsland F, Petersen JL, McCue ME, Mickelson JR, Cothran G, Ahituv N, Roepstorff L, Mikko S, Vallstedt A, Lindgren G, **Andersson,L\***, Kullander K. 2012. Mutations in *DMRT3* affect locomotion in horses and spinal circuit function in mice. *Nature* 488:642-646. (\*corresponding author).
- Carneiro M, Rubin CJ, Di Palma F, Albert FW, Alföldi J, Barrio AM, Pielberg G, Rafati N, Sayyab S, Turner-Maier J, Younis S, Afonso S, Aken B, Alves JM, Barrell D, Bolet G, Boucher S, Burbano HA, Campos R, Chang JL, Duranthon V, Fontanesi L, Garreau H, Heiman D, Johnson J, Mage RG, Peng Z, Queney G, Rogel-Gaillard C, Ruffier M, Searle S, Villafuerte R, Xiong A, Young S, Forsberg-Nilsson K, Good JM, Lander ES, Ferrand N, Lindblad-Toh K, **Andersson L.** Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. *Science* 345: 1074-1079.
- Lamichhaney S, Berglund J, Sällman Almén M, Maqbool K, Grabherr M, Martinez-Barrio A, Promerová M, Rubin C-J, Wang C, Zamani N, Grant BR, Grant PR, Webster MT, **Andersson L.** 2015. Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature* 518:371-375.
- Lamichhaney S, Fan G, Widemo F, Gunnarsson U, Thalmann DS, Hoepfner MP, Kerje S, Gustafson U, Shi C, Zhang H, Chen W, Liang X, Huang L, Wang J, Liang E, Wu Q, Lee SM, Xu X, Höglund J, Liu X, **Andersson L.** 2016. Structural genomic changes underlie alternative reproductive strategies in the ruff (*Philomachus pugnax*). *Nature Genetics* 48:84-88.
- Imsland F, McGowan K, Rubin CJ, Henegar C, Sundström E, Berglund J, Schwochow D, Gustafson U, Imsland P, Lindblad-Toh K, Lindgren G, Mikko S, Millon L, Wade C, Schubert M, Orlando L, Penedo MC, Barsh GS, **Andersson L.** 2016. Regulatory mutations in *TBX3* disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. *Nature Genetics* 48:152-158.
- Lamichhaney S, Han F, Berglund J, Wang C, Sällman Almén M, Webster MT, Grant BR, Grant PR, **Andersson L.** 2016. A beak size locus in Darwin's finches facilitated character displacement during a drought. *Science* 352:470-474.
- Martinez Barrio, A., Lamichhaney, S., Fan, G., Rafati, N., Pettersson, M., Zhang, H., Dainat, J., Ekman, D., Höppner, M., Jern,P., Martin,M., Nystedt,B., Liu, X., Chen, W., Liang, X., Shi, C., Fu, Y., Ma, K., Zhan, X., Feng, C., Gustafson, U., Rubin, C.-J., Sällman Almén, M., Blass, M., Casini, M., Folkvord, A., Laikre, L., Ryman, N., Lee, S.M.-E., Xu,X, **Andersson, L.** 2016. The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. *eLife* 5: e12081.

