# Curriculum vitae

**Lucia DAXINGER**

Leiden University Medical Centre
Department of Human Genetics

Nationality:
Austria

Education:

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| 2003 | M.S. University of Salzburg, Austria. Genetics |
| 2008 | PhD. University of Vienna, Austria, Genetics<br>Dr. Marjori Matzke<br>Thesis title: 'Genetic analysis of RNA-directed DNA methylation in *Arabidopsis thaliana*' |

Postdoctoral Training:

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| 2008 – 2009 | Dr. Marjori Matzke; Gregor Mendel Institute for Molecular Plant Biology, Vienna, Austria |
| 2009 – 2012 | Prof. Emma Whitelaw; QIMR Berghofer Medical Research Institute, Brisbane, Australia; Erwin Schroedinger Postdoctoral Fellowship; |
| 2013 | Prof. Emma Whitelaw; La Trobe Institute for Molecular Sciences, Melbourne, Australia |

Appointments:

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| 2014 - | Junior group leader; Department of Human Genetics, Leiden University Medical Center, Leiden, The Netherlands. LUMC Fellowship |

International collaborations

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| 2013 – ongoing | Prof Steven E Jacobsen, HHMI, UCLA, USA<br>Project: Characterization of novel epigenetic factors in mammals |
| 2015 – ongoing | Dr Ragnhild Eskeland, University of Oslo, Norway<br>Project: Higher order chromatin structure and nuclear organization during mammalian development |
| Ongoing | Prof Emma Whitelaw, La Trobe Institute for Molecular Sciences, Melbourne, Australia<br>Project: Identification of novel epigenetic factors in mammals |

Invited Presentations

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| October 2017 | Invited speaker, "Maternal and Paternal Intergenerational Programming Effects", Rank Price Funds, Grasmere, Cumbria, UK |
| October 2017 | Invited speaker, "Building Bridges Autumn 2017: Epigenetics in Clinical and Translational Research", Biomedicum Finland, Helsinki, Finland |
| May 2017 | Invited speaker, "Frontiers in Reproductive Epigenetics Symposium", van Andel Research Institute, Grand Rapids, USA |
| April 2015 | Invited seminar, "Paternal effect genes in the mouse", Max Planck Institute for Epigenetics and Immunology, Freiburg, Germany |
| November 2013 | Invited seminar, "Epigenetic regulation in mammals", Leiden University Medical Centre, Leiden, Netherlands |
| April 2013 | Invited seminar, "Genotype, Phenotype, and the Epigenome", Swammerdam Institute for Life Sciences, Amsterdam, Netherlands |
| September 2011 | Invited speaker, "Epigenetics Meeting, Queenstown Research Week", Queenstown, New Zealand |
| December 2010 | Speaker selected from abstract, "1st Max Planck Freiburg Epigenetics meeting", Max Planck Institute for Epigenetics and Immunology, Freiburg, Germany |
| April 2009 | Invited speaker, "Microsymposium on small RNAs", Institute of Molecular Biotechnology, Vienna, Austria |

Research visits

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| Jan – Jun 2002 | Erasmus Research Traineeship, Prof. Jan Kooter (Vrije Universiteit Amsterdam, The Netherlands) |
| September 2005 | Selected Participant "2nd course on Epigenetics", Institute Curie, Paris, France |

Publications: (*equal contribution)

2018

Fransen MF, Benonisson H, van Maren WW, Sow HS, Breukel C, Linssen MM, Claassens JWC, Brouwers C, van der Kaa J, Camps M, Kleinovink JW, Vonk KK, van Heiningen S, Klar N, van Beek L, van Harmelen V, Daxinger L, Nandakumar KS, Holmdahl R, Coward C, Lin Q, Hirose S, Salvatori D, van Hall T, van Kooten C, Mastroeni P, Ossendorp F, Verbeek JS. A Restricted Role for FcγR in the Regulation of Adaptive Immunity. J Immunol. 2018 Apr 15;200(8):2615-2626. doi: 10.4049/jimmunol.1700429. Epub 2018 Mar 9.

2017

van den Boogaard ML, Thijssen PE, Aytekin C, Licciardi F, Kıykım AA, Spossito L, Dalm VA, Driessen GJ, Kersseboom R, de Vries F, van Ostaijen-Ten Dam MM, Ikinciogullari A, Dogu F, Oleastro M, Bailardo E, Daxinger L, Nain E, Baris S, van Tol MJ, Weemaes C, van der Maarel SM. Expanding the mutation spectrum in ICF syndrome: Evidence for a gender bias in ICF2. Clin Genet. 2017 Jan 27.

2016

Wu H, Thijssen PE, de Klerk E, Vonk KKD, Wang J, den Hamer B, Aytekin C, van der Maarel SM, Daxinger L. Converging disease genes in ICF syndrome: ZBTB24 controls expression of CDCA7 in mammals. HumMolGenet. 2016 Sep 15;25(18):4041-4051.

Li S, Yen L, Pastor WA, Johnston JB, Shew C, Du J, Liu W, Ho J, Stender B, Clark AT, Burlingame A, *Daxinger L, *Patel DJ, *Jacobsen SE. Mouse MORC3 is an ATP dependent dimer involved in gene silencing that localizes to H3K4me3-marked chromatin. ProcNatlAcadSci USA.2016 Aug 30;113(35):E5108-16.

29. Isbel L, Prokopuk L, Wu H, Daxinger L, Oey H, Spurling A, Lawther A, Hale M, Whitelaw E. Widely interspaced zinc finger motifs, Wiz, binds promoters containing CTCF-binding sites and is required for normal neural function in the mouse. Elife. 2016 Jul 13;5. pii: e15082. doi: 10.7554/eLife.15082.

Daxinger L, Oey H, Isbel L, Whitelaw NC, Youngson NA, Spurling A, Vonk KKD, Whitelaw E. Hypomethylation of ERVs in the sperm of mice haploinsufficient for the histone methyltransferase Setdb1 correlates with a paternal effect on phenotype. Scientific Reports. 2016 Apr 26;6:25004.

2015

Isbel L, Srivastava R, Oey H, Spurling A, Daxinger L, Puthalakath H, Whitelaw E. Trim33 binds and silences a Class of Young Endogenous Retroviruses in the mouse testis; a novel component in the arms race between Retrotransposons and the Host Genome. PloS Genet. 2015 Dec 1;11(12):e1005693.

Daxinger L, Tapscott SE, van der Maarel SM. Genetic and Epigenetic Contributors to FSHD. Current Opinion in Genetics and Development. 2015 Aug;33:56-61.

Harten SK, Oey H, Bourke LM, Bharti V, Isbel L, Daxinger L, Faou P, Robertson N, Matthews JM, Whitelaw E. The recently identified modifier of murine metastable epialleles, Rearranged L-Myc Fusion, is involved in maintaining epigenetic marks at CpG island shores and enhancers. BMC Biol. 2015 Mar 26;13(1):21.

Sorolla A, Tallack MR, Oey H, Harten SK, Daxinger LC, Magor GW, Combes AN, Ilsley M, Whitelaw E, Perkins AC. Identification of novel hypomorphic and null mutations in Klf1 derived from a genetic screen for modifiers of α-globin transgene variegation. Genomics. 2015 Feb;105(2):116-22.

2013

*Daxinger L, *Harten SK, Oey H, Epp T, Isbel L, Huang E, Whitelaw N, Apedaile A, Sorolla A, Yong J, Bharti V, Sutton J, Ashe A, Pang Z, Wallace N, Gerhardt D, Blewitt ME, Jeddeloh JA, Whitelaw E. An ENU mutagenesis screen identifies novel and known genes involved in epigenetic processes in the mouse. Genome Biology. 2013,14:R96.

Roberts AR, Huang E, Jones L, Daxinger L, Chong S, Whitelaw E. Non-telomeric epigenetic and genetic changes are associated with the inheritance of shorter telomeres in mice. Chromosoma. 2013, (9):R96.

Youngson NA, Epp T, Roberts AR, Daxinger L, Ashe A, Huang E, Lester KL, Cox T, Matthews JM, Chong S. and Whitelaw E. No evidence for cumulative effects in a Dnmt3b hypomorph across multiple generations. Mamm Genome. 2013, (5-6):206-17.

2012
You W, Tyczewska A, Spencer M, Daxinger L, Schmid M, Grossniklaus U, Simon SA, Meyers BC, Matzke AJ, Matzke M. Atypical DNA methylation of genes encoding cysteine-rich peptides in Arabidopsis thaliana. BMC Plant Biol. 2012, 12:51.

Daxinger L, Oey H, Apedaile A, Sutton J, Ashe A, Whitelaw E. A forward genetic screen identifies eukaryotic translation initiation factor 3, subunit H (eIF3h), as an enhancer of variegation in the mouse. G3: Genes, Genomes, Genetics. 2012, 2:1393-6.

Daxinger L and Whitelaw E. Understanding transgenerational epigenetic inheritance via the gametes in mammals. Nat Rev Genet. 2012, 13:153-62.

2011
Naumann U, Daxinger L, Kanno T, Eun C, Long Q, Lorkovic ZJ, Matzke M, Matzke AJ. Genetic Evidence that DNA Methyltransferase DRM2 Has a Direct Catalytic Role in RNA-Directed DNA Methylation in Arabidopsis thaliana. Genetics. 2011, 187:977-9.

2010
Daxinger L, Whitelaw E. Transgenerational epigenetic inheritance: more questions than answers. Genome Res. 2010, 20:1623-8.

*Gao Z, *Liu HL, *Daxinger L, *Pontes O, He X, Qian W, Lin H, Xie M, Lorkovic ZJ, Zhang S, Miki D, Zhan X, Pontier D, Lagrange T, Jin H, Matzke AJ, Matzke M, Pikaard CS, Zhu JK. An RNA polymerase II- and AGO4-associated protein acts in RNA-directed DNA methylation. Nature. 2010, 465:106-9.

Kanno T, Bucher E, Daxinger L, Huettel B, Kreil DP, Breinig F, Lind M, Schmitt MJ, Simon SA, Gurazada SG, Meyers BC, Lorkovic ZJ, Matzke AJ, Matzke M. RNA-directed DNA methylation and plant development require an IWR1-type transcription factor. EMBO Rep. 2010, 11:65-71.

Vrbsky J, Akimcheva S, Watson JM, Turner TL, Daxinger L, Vyskot B, Aufsatz W, Riha K. siRNA-mediated methylation of Arabidopsis telomeres. PLoS Genet. 2010, 6:e1000986.

2009
*Daxinger L, *Kanno T, Bucher E, van der Winden J, Naumann U, Matzke AJ, Matzke M. A stepwise pathway for biogenesis of 24-nt secondary siRNAs and spreading of DNA methylation. EMBO J. 2009, 28:48-57.

Matzke M, Kanno T, Daxinger L, Huettel B, Matzke AJ. RNA-mediated chromatin-based silencing in plants. Curr Opin Cell Biol. 2009, 21:367-76.

2008
Daxinger L, Hunter B, Sheikh M, Jauvion V, Gasciolli V, Vaucheret H, Matzke M, Furner I. Unexpected silencing effects from T-DNA tags in Arabidopsis. Trends Plant Sci. 2008, 13):4-6.

Daxinger L, Kanno T, Matzke M. Pol V transcribes to silence. Cell. 2008, 135:592-4.

*Kanno T, *Bucher E, Daxinger L, Huettel B, Böhmdorfer G, Gregor W, Kreil DP, Matzke M, Matzke AJ. A structural-maintenance-of-chromosomes hinge domain-containing protein is required for RNA-directed DNA methylation. Nat Genet. 2008, 40:670-5.

2007
Matzke M, Kanno T, Huettel B, Daxinger L, Matzke AJ. Targets of RNA - directed DNA methylation. Targets of RNA-directed DNA methylation. Curr Opin Plant Biol. 2007,(5):512-9.

Huettel B, Kanno T, Daxinger L, Bucher E, van der Winden J, Matzke AJ, Matzke M. RNA-directed DNA methylation mediated by DRD1 and Pol IVb: a versatile pathway for transcriptional gene silencing in plants. Biochim Biophys Acta. 2007 May-Jun; 1769(5-6):358-74.

2006
Matzke M, Kanno T, Huettel B, Daxinger L, Matzke AJ. RNA - directed DNA methylation and Pol IVb in *Arabidopsis*. Cold Spring Harb Symp Quant Biol. 2006; 71:449-59.

Huettel B, Kanno T, Daxinger L, Aufsatz W, Matzke AJ, Matzke M. Endogenous targets of RNA-directed DNA methylation and Pol IV in *Arabidopsis*. EMBO J. 2006, 25:2828-36.

2005
Kanno T, Huettel B, Mette MF, Aufsatz W, Jaligot E, Daxinger L, Kreil DP, Matzke M, Matzke AJ. Atypical RNA polymerase subunits required for RNA-directed DNA methylation. Nat Genet. 2005, 37:761-5.

2004
Matzke M, Aufsatz W, Kanno T, Daxinger L, Papp I, Mette MF, Matzke AJM, Genetic analysis of RNA-mediated transcriptional gene silencing, Biochim Biophys Acta. 2004, 167:129-41.

2003
Papp I, Mette MF, Aufsatz W, Daxinger L, Schauer S, Ray A, van der Winden J., Matzke M., Matzke A., Evidence for nuclear processing of plant microRNA and short interfering RNA precursors, Plant Physiol. 2003, 132:1382-90.