Cornelia Vesely, PhD

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Research Ambition

My research is centered on unraveling the mechanisms and consequences of RNA modifications with a particular focus on Adenosine to Inosine (A to I) editing in humans and mice. To study this posttranscriptional process, we use mouse models that either lack certain editases or that have important edited sites fixed genomically. This approach enables me to pinpoint critical regulatory pathways that dictate the site and condition when A- to I changes are introduced, and to study the nature of immune suppressing modifications. Additionally, I am passionate about deciphering the consequences and benefits of certain important editing sites and defining their function under specific stress conditions, aiming to uncover insights that could inform new therapeutic strategies.

Education and Research experience

2016-today **Center for Anatomy and Cell Biology, Medical University of Vienna**
- Project coordinator & Junior principal investigator leading a collaborative consortium for four years (ZK57).
- Postdoctoral position, specialized in identifying non-immunogenic double stranded RNAs and deciphering the role of Filamin A editing in colitis.
- Associated with the collaborative research consortium SFB F80 – RNA DECO, led by Prof. Michael Jantsch
- Co-supervised PhD projects and supervisor of Master and Bachelor students of the University of Vienna as well as a FH Bachelor student and an MPM internship.
- Fulfilled **teaching duties** for undergraduate courses and examinations including Histology practical courses and Thesis seminars. Since 2026: teaching a Block 17 SSM2 practical training.
- Two parental leaves: (2017 and 2018/19)

2014-2016 **CCRI (Children´s Cancer Research Institute), Vienna**
- Postdoctoral position, specialized in determining relapse predictive mutation patters in patients suffering from acute lymphoblastic leukemia.

2013-2014 **Department of Chromosome Biology, University of Vienna**
- Postdoctoral position, specialized in identifying transcriptomic changes in the absence of RNA editing enzymes: ADAR1 and ADAR2.

2009 - 2013 **University of Vienna**
- International PhD Program in RNA Biology (DoktoratsKolleg RNA Biology headed by Andrea Barta) PhD in Molecular Biology.
- Conducted research in RNA biology focusing on microRNAs & A to I editing in mice.
- Research in microRNA maturation in Xenopus oocytes.

2006 - 2009 **University of Natural Resources and Life Sciences (BOKU), Vienna**
- Master of Science

- Master Thesis in Phosphatase research at the Max Perutz Labs (Division of Molecular Genetics). Mapped phosphorylation sites of an important regulatory subunit of Protein Phosphatase 2A (PP2A).

2002 - 2006 **University of Natural Resources and Life Sciences (BOKU), Vienna**
Bachelor in Food Science & Biotechnology

Selected Publications

- Gawish R, Varada R, Deckert F, Hladik A, Steinbichl L, Cimatti L, Milanovic K, Jain M, Torgasheva N, Tanzer A, De Paepe K, Van de Wiele T, Hausmann B, Lang M, Pechhacker M, Ibrahim N, De Vries I, Brostjan C, Sixt M, Gasche C, Boon L, Berry D, Jantsch MF, Pereira FC[+], **Vesely C[+]**. Filamin A editing in myeloid cells reduces intestinal inflammation and protects from colitis. *J Exp Med*. 2025 Sep 1;222(9):e20240109. [+]co-corresponding
https://doi.org/10.1084/jem.20240109
Significance of the study: In this study we revealed that RNA editing of Filamin A (FLNA), specifically the conversion between its Q and R isoforms, critically influences intestinal inflammation and susceptibility to colitis. Using genetically engineered mice expressing fixed FLNA editing states, we demonstrated that the fully edited FLNA-R variant confers strong protection against DSS-induced colitis, while the unedited FLNA-Q variant leads to severe disease. The protective effect of FLNA-R is mediated primarily through myeloid cells, where it diminishes inflammatory responses and neutrophil extracellular trap (NET) formation. Although the microbiome contributes to this phenotype, it is not causal. The study also shows that FLNA editing levels decrease during active colitis in both mice and humans, suggesting translational relevance. These findings highlight FLNA RNA editing as a novel immunomodulatory mechanism in intestinal homeostasis and inflammation, offering a promising therapeutic target via site-directed RNA editing in myeloid cells for inflammatory bowel diseases like ulcerative colitis.

- Flanagan K, Gassner K, Lang M, Ozelyte J, Hausmann B, Crepaz D, Pjevac P, Gasche C, Berry D, **Vesely C[+]**, Pereira FC[+]. Human-derived microRNA 21 regulates indole and L-tryptophan biosynthesis transcripts in the gut commensal *Bacteroides thetaiotaomicron*. *mBio*. 2025 Mar 12;16(3):e0392824 [+]co-corresponding
https://doi.org/10.1128/mbio.03928-24
Significance of the study: In this study we revealed a novel host-microbe interaction where the human microRNA miR-21 rapidly associates with diverse gut microbial cells, including Bacteroides thetaiotaomicron. While this association is largely sequence-independent, miR-21 specifically alters bacterial gene expression, notably upregulating an operon involved in indole and L-tryptophan biosynthesis. These metabolites are crucial in regulating host intestinal inflammation and motility. The findings suggest a miR-21-dependent pathway through which the host can modulate gut microbiome function, impacting gastrointestinal conditions like irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD). Importantly, miR-21 levels were found decreased in IBS patient stool samples, indicating its potential role in disease pathogenesis. This work highlights miRNAs as key mediators of gut microbiota-host crosstalk and points to new therapeutic targets for intestinal disorders by modulating microbiome function via miRNAs

- **Vesely C***, Frech C*, Eckert C, Cario G, Mecklenbräuker A, Zur Stadt U, Nebral K, Kraler F, Fischer S, Attarbaschi A, Schuster M, Bock C, Cavé H, von Stackelberg A, Schrappe M, Horstmann MA, Mann G, Haas OA, Panzer-Grümayer R. Genomic and transcriptional landscape of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia. *Leukemia*. 2017 Jul;31(7):1491-1501.
https://doi.org/10.1038/leu.2016.365
Significance of the study: With this study we provided a comprehensive genomic and transcriptional analysis of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia (ALL), revealing critical insights into relapse mechanisms. It shows that while P2RY8-CRLF2 fusions are often lost at relapse and thus dispensable for disease recurrence, alterations in the lymphoid transcription factor IKZF1 are strongly associated with relapse and poor prognosis. IKZF1 alterations are stable from diagnosis to relapse and confer stem cell-like properties, impaired differentiation, and drug resistance. Additionally, mutations activating JAK/STAT and RTK/Ras pathways are frequent but unstable, often replaced by different mutations at relapse. These findings highlight IKZF1 as a key driver of relapse, impacting leukemic cell self-renewal and bone marrow niche homing, and suggest that targeting aberrant IKAROS signaling or related pathways could be a promising therapeutic strategy in these high-risk leukemias.

- **Vesely C**, Tauber S, Sedlazeck FJ, Tajaddod M, von Haeseler A, Jantsch MF. ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. *Nucleic Acids Res*. 2014 Oct 29;42(19):12155-68.
https://doi.org/10.1093/nar/gku844.

Significance of the study: In this study we revealed that ADAR2 significantly influences both the sequence and abundance of mature microRNAs (miRNAs) in the adult mouse brain. We identified 48 novel editing events, many occurring within miRNA seed regions, which can drastically alter miRNA targeting and function. We found that ADAR2 not only edits miRNAs to retarget them but also modulates their processing efficiency, exemplified by miR-497 whose processing is enhanced by ADAR2-mediated editing. Additionally, changes in miRNA abundance in ADAR2-deficient brains occur independently of editing, suggesting that ADAR2 binding alone affects miRNA maturation. These findings highlight ADAR2's multifaceted role in fine-tuning gene regulation in the brain through editing-dependent and -independent mechanisms, emphasizing its importance in neural function and development.

- Muggenhumer D*, **Vesely C***, Nimpf S, Tian N, Yongfeng J, Jantsch MF. Drosha protein levels are translationally regulated during Xenopus oocyte maturation. *Mol Biol Cell*. 2014 Jul 1;25(13):2094-104. https://doi.org/10.1091/mbc.E13-07-0386.
Significance of the study: We showed that Drosha protein levels and pri-miRNA processing are translationally regulated during Xenopus oocyte maturation, with Drosha activity being low in stage VI oocytes but dramatically increased upon maturation to eggs. This increase is linked to poly(A) tail extension of Drosha mRNA, enhancing translation without changes in mRNA levels. The findings highlight Drosha as a rate-limiting factor in miRNA biogenesis during early development and demonstrate that RNA editing can modulate pri-miRNA processing by altering RNA structure. These findings provide insight into developmental control of miRNA maturation and gene regulation.

- **Vesely C***, Tauber S*, Sedlazeck FJ, von Haeseler A, Jantsch MF. Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. *Genome Res*. 2012 Aug;22(8):1468-76. https://doi.org/10.1101/gr.133025.111.
Significance of the study: In this study we revealed that adenosine deaminases acting on RNA (ADARs), particularly ADAR2, significantly influence the abundance and sequence of embryonic microRNAs (miRNAs) in mice. Using transgenic embryos deficient in ADAR1 and ADAR2, we demonstrated that loss of ADAR2 leads to reproducible changes in specific miRNA levels and their target mRNAs, independent of editing events. Despite the general low frequency of editing at early embryonic stages, we identified novel editing sites, that potentially alter miRNA targeting. We highlight that ADARs affect miRNA processing not only through editing but also by binding to miRNA precursors, impacting miRNA maturation. These findings enhance the understanding of RNA editing's role in miRNA regulation during development, suggesting that altered miRNA expression, rather than editing per se, may contribute to phenotypic outcomes in ADAR-deficient embryos.

Conference and Presentations

2026 National Center of Competence in Research, RNA & Disease final Symposium, St. Moritz, Switzerland, **oral presenter**

2025 Gordon Research Conference RNA Modifications in Lucca, Italy, **oral presenter**

2023 National Cancer Institute RNA Biology Symposium, Washington DC, USA, poster presenter
Nucleic Acid Immunity Meeting, Dresden, Germany, poster presenter

2022 Vienna RNA Conference on RNA Modification and Processing, Vienna, Austria, **oral presenter**

2021 2nd Annual SFB RNA DECO Retreat, Mutters, Austria, **oral presenter**

2013 RNA Society meeting in Davos, Switzerland, **oral presenter**

2011 Gordon Research Conference Editing and Modification of RNA and DNA in Galveston, USA, poster presenter

Past Grants and Awards

2019 Young independent researcher grant (ZK 57-B28), **Principal investigator and Coordinator role**

2015 KAPSCH Next-Generation Sequencing Grant

2014 Vienna Biocenter PhD Award

Full Publication list

Varada R*, Leuchtenberger AF*, **Vesely C***, Kaczmarek B, Khosravi HM, Mandl TC, Milanovic K, Honarmand Tamizkar K, Rajendra V, Senoner H, Steinbichl L, Borojevic M, Sombke A, Schmidt K, Eckhard M, Hofacker IL, Walkley C, Heraud-Farlow JE, Picardi E, Bernecky C and Jantsch MF. *Distinguishing self from non-self RNA by editing-specific inosine patterns.* 2026 - under Revision in Nucleic Acids Research

Gawish R, Varada R, Deckert F, Hladik A, Steinbichl L, Cimatti L, Milanovic K, Jain M, Torgasheva N, Tanzer A, De Paepe K, Van de Wiele T, Hausmann B, Lang M, Pechhacker M, Ibrahim N, De Vries I, Brostjan C, Sixt M, Gasche C, Boon L, Berry D, Jantsch MF, Pereira FC, **Vesely C**. *Filamin A editing in myeloid cells reduces intestinal inflammation and protects from colitis.* J Exp Med. 2025 Sep 1;222(9):e20240109. doi: 10.1084/jem.20240109.

Flanagan K, Gassner K, Lang M, Ozelyte J, Hausmann B, Crepaz D, Pjevac P, Gasche C, Berry D, **Vesely C***, Pereira FC*. *Human-derived microRNA 21 regulates indole and L-tryptophan biosynthesis transcripts in the gut commensal Bacteroides thetaiotaomicron*. mBio. 2025 Mar 12;16(3):e0392824. doi: 10.1128/mbio.03928-24

Farhat A, Radhouani M, Deckert F, Zahalka S, Pimenov L, Fokina A, Hakobyan A, Oberndorfer F, Brösamlen J, Hladik A, Lakovits K, Meng F, Quattrone F, Boon L, **Vesely C**, Starkl P, Boucheron N, Menche J, van der Veeken J, Ellmeier W, Gorki AD, Campbell C, Gawish R, Knapp S. *An aging bone marrow exacerbates lung fibrosis by fueling profibrotic macrophage persistence*. Sci Immunol. 2025 Mar 28;10(105):eadk5041. doi: 10.1126/sciimmunol.adk5041

Kleinova R, Rajendra V, Leuchtenberger AF, Lo Giudice C, **Vesely C**, Kapoor U, Tanzer A, Derdak S, Picardi E, Jantsch MF. *The ADAR1 editome reveals drivers of editing-specificity for ADAR1-isoforms.* Nucleic Acids Res, 2023 May 22; 51(9):4191-4207. doi: 10.1093/nar/gkad265

Goldeck M, Gopal A, Jantsch MF, Mansouri Khosravi HR, Rajendra V, **Vesely C**. *How RNA editing keeps an I on physiology*. Am J Physiol Cell Physiol. 2022 Nov 1;323(5):C1496-C1511. doi: 10.1152/ajpcell.00191.2022.

Vesely C, Jantsch MF. *An I for an A: Dynamic Regulation of Adenosine Deamination-Mediated RNA Editing.* Genes, 2021, 12, 1026. doi: 10.3390/genes12071026

Pereira FC, Wasmund K, Cobankovic I, Jehmlich N, Herbold CW, Lee KS, Sziranyi B, **Vesely C**, Decker T, Stocker R, Warth B, vonBergen M, Wagner M, Berry D. *Rational design of a microbial consortium of mucosal sugar utilizers reduces Clostridiodes difficile colonization.* Nat Commun, 2020 Oct; 11, 5104. doi: 10.1038/s41467-020-18928-1

Altaf F*, **Vesely C***, Sheikh AM, Munir R, Shah STA, Tariq A. Modulation of ADAR mRNA expression in patients with congenital heart defects. PLOS One, 2019 Apr; 14(4). doi: 10.1371/journal.pone.0200968

Vesely C, Frech C, Eckert C, Cario G, Mecklenbräuker A, Zur Stadt U, Nebral K, Kraler F, Fischer S, Attarbaschi A, Schuster M, Bock C, Cavé H, von Stackelberg A, Schrappe M, Horstmann MA, Mann G, Haas OA, Panzer-Grümayer. *Genomic and transcriptional landscape of P2RY8-CRLF2-positive childhood acute lymphoblastic leukemia*. Leukemia, 2017 Jul; 31(7): 1491-1501. doi: 10.1038/leu.2016.365.

Daryabeigi A, Woglar A, Baudrimont A, Silva N, Paouneskou D, **Vesely C**, Rauter M, Penkner A, Jantsch M, Jantsch V. Nuclear Envelope Retention of LINC Complexes Is Promoted by SUN-1 Oligomerization in the Caenorhabditis elegans Germ Line. Genetics, 2016 Jun; 203(2):733-48. doi: 10.1534/genetics.116.188094.

Mannion NM, Greenwood SM, Young R, Cox S, Brindle J, Read D, Nellåker C, **Vesely C**, Ponting CP, McLaughlin P, Jantsch MF, Dorin J, Adams IR, Scadden ADJ, Öhman M, Keegan LP and O'Connell MA. *The RNA editing enzyme ADAR1 is a key regulator of innate immune responses to RNA.* Cell Reports, 2014 Nov; 9(4): 1482-1494. doi: 10.1007/s00109-016-1416-1

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Muggenhumer D*, **Vesely C***, Tian N, Yongfeng J, Nimpf S, Jantsch MF. *DROSHA protein levels are translationally regulated during Xenopus oocyte maturation.* Mol. Biol. Cell, 2014 Jul 1; 25(13): 2094-2104. doi: 10.1091/mbc.E13-07-0386

Vesely C*, Tauber S*, Sedlazeck FJ, von Haeseler A, Jantsch MF. *Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs.* Genome Research, 2012 Aug; 22(8): 1468-1476. doi:10.1101/gr.133025.111

Jantsch MF and **Vesely C** (2011) *Chapter 7: RNA Binding Domains and RNA Recognition by RNA-Editing Machineries.* RNA Binding Proteins, Landes Bioscience