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Leen Beller

Life Sciences

Trainee Patent Attorney

Na haar studies Biomedische Wetenschappen aan de KU Leuven, startte Leen in 2015 haar doctoraat aan het REGA-instituut van de KU Leuven. Gedurende vijf jaren onderzocht ze hoe de darmflora (darmmicrobioom) van gezonde kindjes ontwikkelt in hun eerste levensjaar.

Ze specialiseerde zich in de vele aspecten van de microbiologie en genomics, maar ook in bio-informatica en biostatistiek.

Werkervaring

- Octrooigemachtigde in opleiding, V.O. (2021-heden)
- Doctoraatstudent, Rega Instituut KU Leuven (2015-2021)

Opleiding

- PhD in Biomedical Sciences, KU Leuven (2020)
- MSc in Biomedical Sciences, KU Leuven (2015)
- BSc in Biomedical Sciences, KU Leuven (2013)

Publicaties

- Conceição-Neto, N., Zeller, M., Lefrère, H., De Bruyn, P., Beller, L., Deboutte, W., Yinda, C. K., Lavigne, R., Maes, P., Ranst, M. Van, Heylen, E. & Matthijnsens, J. Modular approach to customise sample preparation procedures for viral metagenomics: A reproducible protocol for virome analysis. *Sci. Rep.* 5, 16532 (2015).
- Yinda, C. K., Zeller, M., Conceição-Neto, N., Maes, P., Deboutte, W., Beller, L., Heylen, E., Ghogomu, S. M., Van Ranst, M. & Matthijnsens, J. Novel highly divergent reassortant bat rotaviruses in Cameroon, without evidence of zoonosis. *Sci. Rep.* 6, 34209 (2016).
- Yinda, C. K., Ghogomu, S. M., Conceição-Neto, N., Beller, L., Deboutte, W., Vanhulle, E., Maes, P., Van Ranst, M. & Matthijnsens, J. Cameroonian fruit bats harbor divergent viruses, including rotavirus H, bastroviruses, and picobirnaviruses using an alternative genetic code. *Virus Evol.* 4, vey008 (2018).
- Theuns, S., Vanmechelen, B., Bernaert, Q., Deboutte, W., Vandenhoe, M., Beller, L., Matthijnsens, J., Maes, P. & Nauwynck, H. J. Nanopore sequencing as a revolutionary diagnostic tool for porcine viral enteric disease complexes identifies porcine kobuvirus as an important enteric virus. *Sci. Rep.* 8, 9830 (2018).
- Vanmechelen, B., Bletsas, M., Laenen, L., Lopes, A. R., Vergote, V., Beller, L., Deboutte, W., Korva, M., Avšič Županc, T., Goüy de Bellocq, J., Gryseels, S., Leirs, H., Lemey, P., Vrancken, B. & Maes, P. Discovery and genome characterization of three new Jeilongviruses, a lineage of paramyxoviruses characterized by their unique membrane proteins. *BMC Genomics* 19, 617 (2018).
- Yinda, C. K., Vanhulle, E., Conceição-Neto, N., Beller, L., Deboutte, W., Shi, C., Ghogomu, S. M., Maes, P., Van Ranst, M. & Matthijnsens, J. Gut Virome Analysis of Cameroonians Reveals High Diversity of Enteric

Viruses, Including Potential Interspecies Transmitted Viruses. *mSphere* 4, (2019).

- Beller, L. & Matthijnssens, J. What is (not) known about the dynamics of the human gut virome in health and disease. *Curr. Opin. Virol.* 37, 52–57 (2019).
- Shi, C., Beller, L., Deboutte, W., Yinda, K. C., Delang, L., Vega-Rúa, A., Failloux, A.-B. & Matthijnssens, J. Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. *Microbiome* 7, 121 (2019).
- Wollants, E., Beller, L., Beuselinck, K., Bloemen, M., Lagrou, K., Reynders, M. & Van Ranst, M. A decade of enterovirus genetic diversity in Belgium. *J. Clin. Virol.* 121, 104205 (2019).
- Deboutte, W., Beller, L., Yinda, C. K., Maes, P., de Graaf, D. C. & Matthijnssens, J. Honey-bee-associated prokaryotic viral communities reveal wide viral diversity and a profound metabolic coding potential. *Proc. Natl. Acad. Sci. U. S. A.* 117, 10511–10519 (2020).
- Thijssen, M., Tacke, F., Beller, L., Deboutte, W., Yinda, K. C., Nevens, F., Laleman, W., Van Ranst, M. & Pourkarim, M. R. Clinical relevance of plasma virome dynamics in liver transplant recipients. *EBioMedicine* 60, 103009 (2020).
- Simsek, C., Corman, V. M., Everling, H. U., Lukashev, A. N., Rasche, A., Maganga, G. D., Binger, T., Jansen, D., Beller, L., Deboutte, W., Gloza-Rausch, F., Seebens-Hoyer, A., Yordanov, S., Sylverken, A., Oppong, S., Sarkodie, Y. A., Vallo, P., Leroy, E. M., Bourgarel, M., Yinda, K. C., Van Ranst, M., Drosten, C., Drexler, J. F. & Matthijnssens, J. At least seven distinct rotavirus genotype constellations in bats with evidence of reassortment and zoonotic transmissions. *MBio* 12, (2021).

Talen

- Nederlands (moedertaal)
- Engels (vloeiend)
- Frans (basis)