Wilma Ziebuhr

Personal data

Name and academic title:	Priv.-Doz. Dr. Wilma Ziebuhr
Date and place of birth:	21st October 1964 in Gera, Germany
Current position:	Principal Investigator and “Akademische Oberrätin”
Institution:	Institute for Molecular Infection Biology, University of Würzburg
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Education

1984-1991	Studies of Medicine, Friedrich-Schiller-University Jena, Germany
1990-1991	Diploma thesis, Clinical Immunology, Friedrich-Schiller-University Jena
1991	State examination in medicine
1991-1994	Doctoral thesis (MD), Institute for Molecular Infection Biology, University of Würzburg

Professional background & positions held

2010-present	Principal Investigator and “Akademische Oberrätin” Institute for Molecular Infection Biology, University of Würzburg
2007-2009	Reader in Bacteriology, Centre for Infection & Immunity, Queen’s University of Belfast, United Kingdom
2003	Habilitation (lecture qualification) in Molecular Infection Biology, University of Würzburg
1996-2006	Principal Investigator, Institute for Molecular Infection Biology, University of Würzburg
1994-1996	Postdoctoral fellow and specialist registrar, Institute for Medical Microbiology, University of Jena

Current research interests

- Antibiotic resistance profiles and mechanisms in coagulase-negative staphylococci from livestock environments
- ncRNA-driven heterogenous gene expression and control in *S. epidermidis* biofilms
- Regulation of methionine metabolism in staphylococci
- Molecular function of mobile genetic elements in staphylococci

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Ten selected publications

1. **Ziebuhr, W**., and Vogel, J. (2015). The end is not the end: remnants of tRNA precursors live on to sponge up small regulatory RNAs.
   Mol Cell *58*, 389-390.

2. Rajan, V., Schoenfelder, S.M., **Ziebuhr, W.**, and Gopal, S. (2015). Genotyping of community-associated methicillin resistant *Staphylococcus aureus* (CA-MRSA) in a tertiary care centre in Mysore, South India: ST2371-SCCmec IV emerges as the major clone.
   Infect Genet Evol *34*, 230-235.

3. Schoenfelder, S.M., Marincola, G., Geiger, T., Goerke, C., Wolz, C., and **Ziebuhr, W**. (2013). Methionine Biosynthesis in *Staphylococcus aureus* Is Tightly Controlled by a Hierarchical Network Involving an Initiator tRNA-Specific T-box Riboswitch.
   PLoS Pathog *9*, e1003606.

4. Makgotlho, P.E., Marincola, G., Schafer, D., Liu, Q., Bae, T., Geiger, T., Wasserman, E., Wolz, C., **Ziebuhr, W.,** and Sinha, B. (2013). SDS Interferes with SaeS Signaling of *Staphylococcus aureus* Independently of SaePQ.
   PLoS One *8*, e71644.

5. Weisser, M., Schoenfelder, S.M., Orasch, C., Arber, C., Gratwohl, A., Frei, R., Eckart, M., Fluckiger, U., and **Ziebuhr, W**. (2010). Hypervariability of biofilm formation and oxacillin resistance in a *Staphylococcus epidermidis* strain causing persistent severe infection in an immunocompromised patient.
   J Clin Microbiol *48*, 2407-2412.

6. Hennig, S., and **Ziebuhr, W.** (2010). Characterization of the Transposase Encoded by IS*256*, the Prototype of a Major Family of Bacterial Insertion Sequence Elements. **J Bacteriol** *192*, 4153-4163.

7. Hennig, S., and **Ziebuhr, W.** (2008). A transposase-independent mechanism gives rise to precise excision of IS*256* from insertion sites in *Staphylococcus epidermidis*.
   J Bacteriol *190*, 1488-1490.

8. Batzilla, C.F., Rachid, S., Engelmann, S., Hecker, M., Hacker, J., and **Ziebuhr, W**. (2006). Impact of the accessory gene regulatory system (Agr) on extracellular proteins, *codY* expression and amino acid metabolism in *Staphylococcus epidermidis*.
   Proteomics *6*, 3602-3613.

9. Loessner, I., Dietrich, K., Dittrich, D., Hacker, J., and **Ziebuhr, W.** (2002). Transposase-dependent formation of circular IS*256* derivatives in *Staphylococcus epidermidis* and *Staphylococcus aureus*.
   J Bacteriol *184*, 4709-4714.

10. **Ziebuhr, W**., Krimmer, V., Rachid, S., Loessner, I., Götz, F., and Hacker, J. (1999). A novel mechanism of phase variation of virulence in *Staphylococcus epidermidis*: evidence for control of the polysaccharide intercellular adhesin synthesis by alternating insertion and excision of the insertion sequence element IS*256*.
    Mol Microbiol *32*, 345-356.