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Programme

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P279	THE PHYLOGENETIC EVOLUTION OF PORCINE MRSA IN CHINA	Stefan Schwarz	Jiang Nansong   Jun Li   Andrea Fessler   Yang Wang   Stefan Schwarz   CongMing Wu
P280	Biocide susceptibility in Staphylococcus epidermidis causing infection in pets	Isabel Couto	Sofia Santos Costa   Mafalda Rosa   Adriana Belas   Miguel Viveiros   Maria Constança Pomba   Isabel Couto
P281	A novel genetic locus for niche competition in staphylococci	Mal Horsburgh	Hanaa Ghabban   Josephine Moran   Mal Horsburgh
P282	Development of multidrug resistance in staphylococci driven by efflux	Isabel Couto	Sofia Santos Costa   Adriana Rosato   Miguel Viveiros   Isabel Couto
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P285	Regulation and Specificity of L <sub>Sa</sub> Resistance in Staphylococci, Conferred by ABC-F Protein Vga(A)	Vladimir Vimberg	Vladimir Vimberg   Lenka Nguyen Thi Ngoc   Pauline Cavanagh   Gabriela Balíková Novotná
P286	Diffusion and environmental persistence of pathogenic Staphylococcus capitis isolates Inside a neonatal ICU	Marine Butin	Marine Butin   Yann Dumont   Patricia Martins Simões   Aurane Raphard   Jean-Charles Picaud   Frédéric Laurent

### [P280] BIOCIDES SUSCEPTIBILITY IN STAPHYLOCOCCUS EPIDERMIDIS CAUSING INFECTION IN PETS

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**Aim:** To characterize biocide susceptibility of *Staphylococcus epidermidis* isolates causing infection in pets and evaluate proposed biocide epidemiological cut-off (tentative ECOFF) values.

**Methods:** The study comprised a collection of 17 *S. epidermidis* isolates collected from several infection sources in cats and dogs from 2001 to 2016. Susceptibility to benzalkonium chloride (BAC), cetrimide, chlorhexidine digluconate, tetraphenylphosphonium bromide (TPP), triclosan (TCL) and ethidium bromide (EtBr) was evaluated by microdilution MIC determination. The efflux pump genes *qacA/B*, *qacG*, *qacJ* and *smr*, associated with biocide resistance, and the triclosan resistance gene *sh-fabI* were screened by PCR.

**Results:** The MIC distributions for all biocides and EtBr were analyzed against the tentative ECOFF values proposed for these compounds (see other poster by Costa et al, ISSSI 2018). Non-wild-type (NWT) populations were detected towards BAC (6/17), TPP (8/17) and TCL (4/17) and EtBr (9/17). The NWT populations towards BAC, TPP and EtBr were associated with the presence of either *qacA* or *smr* plasmid-encoded genes, whereas the TCL NWT population was linked to *sh-fabI* carriage. One isolate carrying the *smr* gene was only detected taking into consideration the proposed EtBr ECOFF.

**Conclusion:** This study illustrates the frequently reduced susceptibility towards relevant biocides of *S. epidermidis* infecting pets. It also supports the tentative ECOFF values suggested for BAC, TPP and TCL, as criteria to detect *S. epidermidis* harboring biocide resistance genes. The establishment of such criteria would enable early detection of *S. epidermidis* isolates with a non-wild-type phenotype and improve therapeutics in veterinary medicine.