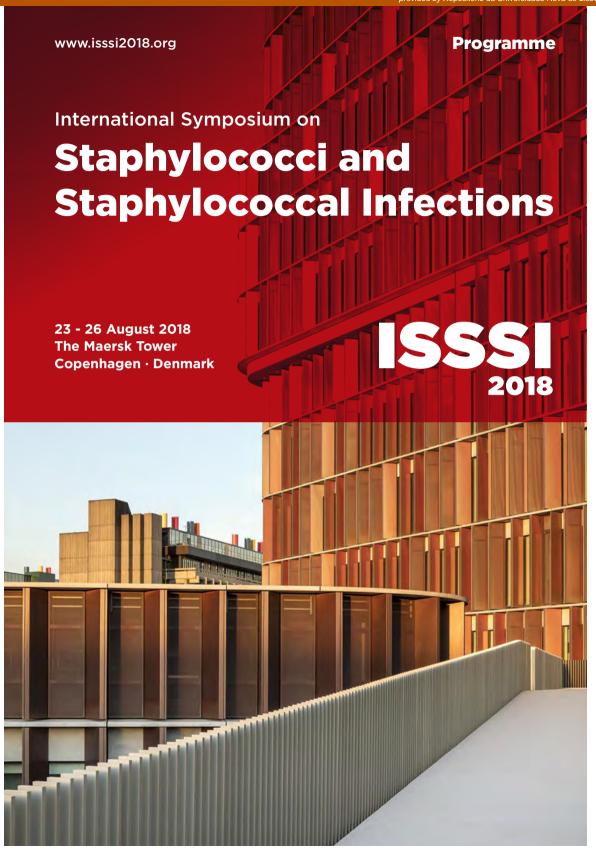
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P278	Global phylogeny of Staphylococcus aureus spa type t127	Øystein Angen	Øystein Angen Patricia Alba Antonio Battisti Ivana Cirkovic Geoffrey Coombs Daum Robert D. Michael David Alessia Franco Daniel Gregson Carl Andreas Grøntvedt Thor Bech Johannesen Hulya Kaya Jesper Larsen Monica Monaco Stephan Monecke Suvi Nykäsenoja Annalisa Pantosti Frieder Schaumburg Marc Stegger Marianne Sunde Sima Tokajian Carmen Torres Deborah Williamson Anders Rhod Larsen
P279	THE PHYLOGENETIC EVOLUTION OF PORCINE MRSA IN CHINA	Stefan Schwarz	Jiang Nansong Jun Li Andrea Fessler Yang Wang Stefan Schwarz CongMing Wu
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P285	Regulation and Specificity of LSa 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

Poster Abstracts

[P280] BIOCIDE SUSCEPTIBILITY IN STAPHYLOCOCCUS EPIDERMIDIS CAUSING INFECTION IN PETS

Sofia Santos Costa ¹, Mafalda Rosa², Adriana Belas³, Miguel Viveiros⁴, Maria Constança Pomba⁵, Isabel Couto⁶

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-fabl* 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.

¹Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisbon, Portugal ²Ihmt/Unl

³Faculty Veterinary Medicine

⁴Unidade de Microbiologia Médica, Instituto de Higiene E Medicina Tropical, Universidade Nova de Lisboa, Lobal Health and Tropical Medicine, Ihmt/Unl, Portugal, Ihmt/Unl, Portugal, Lisboa, Portugal

⁵Antibiotic Resistance Laboratory, Ciisa, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal

⁶Unidade de Microbiologia Médica, Global Health and Tropical Medicine (Ghtm), Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa, Lisboa, Portugal, Lisbon, Portugal