

De, V., I. K. Wilke, and H. Ruden. 1993. [Bacterial reducing qualities of copper-containing and non-copper-containing materials. I. Contamination and sedimentation in humid and dry conditions]. *Zentralbl.Hyg.Umweltmed.* 195:66-87.

Abstract: In this examination the bactericide qualities of different materials were tested. Particularly the effect of humidity was examined. 3 materials containing copper ("copper", "brass" and "brass sheet") and 2 materials not containing copper ("polyamide B" and "high-grade steel") were tested. The surfaces of the 5 types of material were contaminated with a suspension of 2 different bacteria species (*Staphylococcus aureus* and *Micrococcus luteus*). After defined exposure times the survival rate of the microorganisms on the surfaces was determined by the standardized method of the "Guidelines of the German Society of Hygiene and Microbiology". Additionally the sedimentation of airborne microorganisms on the materials was tested by determining the number of colony-forming-units after defined exposure times. In further examinations the materials were contaminated by hands, which were dipped into a suspension of different microorganisms (*Micrococcus luteus*, *Staphylococcus aureus*, *Enterococcus faecium*, *Escherichia coli*, *Enterobacter cloacae* and *Pseudomonas aeruginosa*). The following ways of contaminating the test materials were chosen: single contamination with wet hands, repeated contamination with wet and dry hands. After defined exposure times the survival rate of the microorganisms on the surfaces was determined. The results show, a bactericide quality of copper depends on the percent of copper-content of the tested materials, exposure time, humidity, frequency of contamination and bacteria species. Humidity and only single contamination cause a reduction of bacteria. Reduction of gram-negative bacteria is more easily than reduction of gram-positive bacteria. *Enterococcus faecium* shows the highest, *Pseudomonas aeruginosa* the lowest reduction rate of bacteria in the following sequence: *Enterococcus faecium*, *Escherichia coli*, *Enterobacter cloacae*, *Micrococcus luteus*, *Staphylococcus aureus* and *Pseudomonas aeruginosa*.