Skin microbiome and pH as putative predictor for the development of severe radiodermatitis [Abstract]

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Radiodermatitis is commonly observed in breast cancer patients as an adverse effect during radiotherapy. Several skin diseases are associated with the skin microbiome.

To investigate the impact of the skin microbiome in radiodermatitis, we followed 20 breast cancer patients in a pilot study over 8 weeks before, during and after radiotherapy. Skin swabs were taken from the radiated and the non-radiated breast for 16S rRNA next generation sequencing analysis of the V1-V3 region to investigate the skin microbiome. Furthermore, radiodermatitis severity score and skin pH were assessed weekly from both bodysides.

The global skin microbiome at the β-diversity level did not differ significantly between radiated and non-radiated breast. Likewise, no major differences could be detected between the bodysides when looking at the most abundant bacterial families. The individual skin microbiome could be separated into Corynebacteriaceae-, Staphylococcaceae-, and Propionibacteriaceae- dominated 'epitypes', which remained relatively stable over the observation period. Interestingly, all patients who developed a severe form of radiodermatitis belonged to the epitype Corynebacteriaceae, contrasting to only 25% of patients with mild to moderate radiodermatitis. Additionally, these severe patients had a higher skin pH (median skin pH 6.2) than patients who developed a mild form of radiodermatitis (median skin pH 5.7) at baseline.

In conclusion, the skin microbiome in combination with the skin pH before radiotherapy could be used as a predictive factor for the development of severe radiodermatitis, if confirmed in a larger study.