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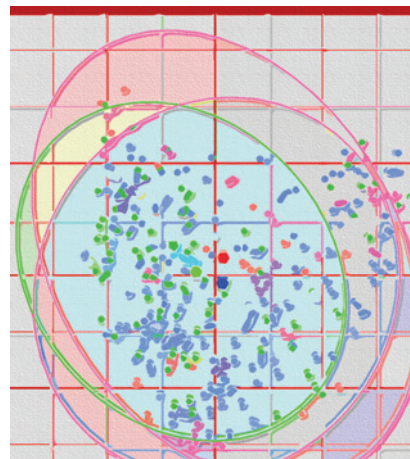
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ABOUT THE COVER

The cover image is adapted from Figure 1 in the article “Tobacco smoking and the fecal microbiome in a large, multi-ethnic cohort,” by Prakash and colleagues. The figure shows beta diversity and ordination of microbiome by smoking status. Increasing evidence suggests that tobacco smoking, a well-known driver of carcinogenesis, influences the gut microbiome; however, these relationships remain understudied in diverse populations. The authors performed an analysis of smoking and the gut microbiome in a subset of 803 adults from the multi-ethnic NYU FAMiLI study. Results showed that the overall composition of the fecal microbiome in former and current smokers differs significantly from that of never smokers, while the taxa *Lachnospira* and *Tenericutes* were depleted, relative to never smokers. These shifts were consistent across racial and ethnic subgroups. The findings suggest common mechanisms of smoking associated microbial change across racial subgroups, regardless of initial microbiome composition. The correlation of these differentials with reactive oxygen species (ROS) exposure pathways may suggest a role for these taxa in the known association between smoking, ROS and carcinogenesis. For more information, see the article beginning on page 1328.



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