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The phyllosphere microbiome of host trees contributes more than leaf phytochemicals to variation in the *Agrilus planipennis* Fairmaire gut microbiome structure

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The microbiome composition of living organisms is closely linked to essential functions determining the fitness of the host for thriving and adapting to a particular ecosystem. Although multiple factors, including the developmental stage, the diet, and host-microbe coevolution have been reported to drive compositional changes in the microbiome structures, very few attempts have been made to disentangle their various contributions in a global approach. Here, we focus on the emerald ash borer (EAB), an herbivorous pest and a real threat to North American ash tree species, to explore the responses of the adult EAB gut microbiome to ash leaf properties, and to identify potential predictors of EAB microbial variations. The relative contributions of specific host plant properties, namely bacterial and fungal communities on leaves, phytochemical composition, and the geographical coordinates of the sampling sites, to the EAB gut microbial community was examined by canonical analyses. The composition of the phyllosphere microbiome appeared to be a strong predictor of