Letter to the Editor: A response to Huhtanen and Hristov (2018)

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We thank the journal for this opportunity to respond to the issues raised by P. Huhtanen and A. N. Hristov in their letter to the editor (Huhtanen and Hristov, 2018). We hope this response will resolve a persistent misunderstanding that is also reflected in the statement by Hammond et al. (2016): "... the need for high throughput methodology, e.g. for screening large numbers of animals for genomic studies, does not in itself justify the use of methods that are inaccurate, imprecise, or biased." In this response, we will clarify that even if measurements are inaccurate, imprecise, or biased, they might provide valuable information for selective breeding.

In a discussion on the use of the so-called sniffer method to obtain phenotypes for selective breeding to reduce methane emission of dairy cows, 3 effects should be distinguished: systematic environmental effects, random errors, and systematic errors. Herein, we will discuss the effects of these 3 aspects.

One of the issues raised by Huhtanen and Hristov (2018) is that measurements of methane by using the sniffer method are significantly influenced by external conditions. Indeed, the effects of specific conditions during the day of measurement, farm, automatic milking system, and sensor explained 56% of the total variation in our data (van Engelen et al., 2018). Consequently, we believe that the setup of the sniffer method as used in our experiments is not suited for ranking herds, for example, or for assessing the effect of diets on methane emission. However, this does not imply that sniffer measurements cannot be used for the genetic evaluation of animals for methane emission potential. A mixed model analysis in combination with the pedigree or genotypic data of cows allows for a separation of systematic environmental and genetic effects on the sniffer methane measurements (Henderson, 1984). Therefore, the "bias" introduced by, for example, weather conditions during the day of measurement or location of the

automatic milking system in the barn is accounted for in the statistical model and not reflected in the EBV.

In addition to effects of external conditions, sniffer methane measurements are affected by random errors such as those caused by differences in sampling distance and the cow's head movement (e.g., Wu et al., 2018). These are indeed factors that will increase variation in sniffer methane measurements. However, the sniffer method allows collection of methane measurements each time a cow is being milked, and these repeated observations can be used to reduce effects of random errors. Several studies have shown that methane phenotypes derived from sniffer measurements are repeatable (Lassen et al., 2012; Bell et al., 2014; van Engelen et al., 2018), demonstrating that significant differences do exist between cows. Moreover, heritabilities ranging from approximately 0.10 to 0.30 (Lassen and Løvendahl, 2016; Pszczola et al., 2017; van Engelen et al., 2018) indicate that part of these between-cow differences are genetic in nature. These results are promising and suggest that the sniffer method provides useful data to selectively breed cows that emit less methane.

A third issue is the possible existence of systematic errors due to differences between cows in, for example, behavior during milking or exhalation rate. Such systematic errors are more serious because they cannot be reduced by repeated observations or accounted for in the statistical analyses and they might be relevant for selective breeding but only if the systematic error is partly genetic. This raises questions about what is actually reflected by EBV for methane emission based on sniffer measurements. Are these only genetic differences in methane emission or do they also partly reflect genetic differences in other traits? For example, cows showing restless behavior during milking, which is partly due to genetic differences between cows, might have lower sniffer methane levels because of sampling distance. Knowledge of variation in sniffer methane measurements due to such systematic errors is limited and certainly requires further investigation, as was pointed out by Wu et al. (2018). However, even if genetic differences in sniffer methane partly reflect differences in other traits, this does not disqualify the use of sniffer methane measurements for selective breeding.

Received August 27, 2018.

Accepted August 27, 2018.

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In animal breeding, we distinguish between traits we measure—sometimes referred to as index or indicator traits—and traits we would like to improve—the breeding goal traits. Sniffer methane should be considered an indicator trait for “true” methane emission, and the response to selection is a function of the genetic correlation between both. Sniffer methane, therefore, provides valuable information when the genetic correlation with true methane emission is sufficiently strong, irrespective of whether sniffer methane does or does not take biologically realistic values. To illustrate, heart girth measurements can be used as an indicator for the breeding goal trait BW (Koenen and Groen, 1998), even though both traits are expressed on completely different scales.

We acknowledge that there remain important outstanding issues that need to be resolved before selection on sniffer methane can be implemented. First, we need an estimate of the genetic correlation between sniffer methane and true methane emission. Global data sets on enteric methane emission, largely based on climate respiration chambers, such as described by Niu et al. (2018), could play an important role in estimating this genetic correlation, provided that pedigree information or DNA samples of the cows are available. Second, breeding goals for dairy cattle consist of many different traits; therefore, relationships between methane emission and other breeding goal traits, such as milk production, health, fertility, and feed intake, need to be estimated to avoid undesired correlated responses. Furthermore, all breeding programs require monitoring for possible negative effects on traits not routinely recorded. Therefore, as pointed out by Huhtanen and Hristov (2018), selection for reduced methane emission requires monitoring for traits such as digesta passage rate or cell wall digestibility.

When given the choice, accurate and unbiased measurements are preferred. However, such measurements are seldom available on a large scale and at reasonable cost. We agree with Huhtanen and Hristov (2018) that the current state-of-the-art methane measurements using the sniffer method are “noisy” and biased by environmental conditions. However, inaccurate and biased

sniffer methane phenotypes do not automatically imply inaccurate and biased methane breeding values. Therefore, the disqualification of sniffer methane for selective breeding by Huhtanen and Hristov (2018) is premature and not supported by facts.

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