## **Appendix 1**

In the Introduction section, we mentioned that (i) European society "seems largely ignorant of modern developments in commercial pig breeding, and seems to assume that mortality rates must necessarily continue to increase with increasing litter size [...] the notion that mortality rates can actually be *reduced* has not taken hold yet", and that (ii) "many of these views are based on information that is largely out of date (as is so often the case in discussions about livestock production"). We present here one example of such (ii) "information that is largely out of date", cited in a report that was written in 2022 to provide EU policymakers with supposedly sound scientific information. The issue here is that teat number becomes a limiting factor for piglet survival when the number born alive increases above it; one of the relevant points is then how many (functional) teats current (i.e. 2022) sows typically have, bearing in mind that teat number can be just as easily increased by selection (e.g. Marois and Larochelle, 2008, their Table 3; Sevillano et al., 2022, their Figure 1) as litter size can be, so that data recorded at any point in time in the past becomes less and less representative for the current situation.

The EFSA AHAW Panel (2022, p. 180) wrote: "[...] the number of functional teats is crucial, and this number is typically lower than the total number of teats. Ocepek et al. (2016), e.g. found that the proportion of non-functional teats varied between 9.4% and 20.7% in three Norwegian breeds. In recent studies, there are different average numbers of functional teats presented. These numbers varied between 14.2 and 15.1 in sows of a Danish breed (Kobek-Kjeldager et al., 2020), between 12.8 and 14.2 in sows of a German breed (Pustal et al., 2015), between 12.6 and 15.9 in sows of three Norwegian breeds (Ocepek et al., 2016) and was 14.2 in a genetic analysis using a Swedish-Finnish breed (Lundeheim et al., 2013)".

First comment: Ocepek et al. (2016) studied teat morphology and functionality in Norsvin Landrace (NL) sows, NL × Yorkshire sows, and Norsvin Duroc sows, with data recorded in late 2013 and early 2014. At that time, according to FAOstat, the Norwegian sow population formed about 0.3 % of the European one. Norsvin Duroc is a sire line that has never been selected for maternal traits such as litter size or teat number; consistent with that, Ocepek's most unfavourable values quoted by EFSA (12.6 functional teats, 20.7 % non-functional teats) pertain to this sire line and are therefore irrelevant for a study of hyperprolific sows. In the maternal (and therefore relevant) populations in that study, teat number was included in the breeding goal in 2001 to cover only 3 % of the total selection criterion versus 30 % for litter size (https://svineportalen.no/pa-vei-mot-superpurka, our translation from Norwegian). Apart from that, these populations were represented by 12 and 14 sows only; due to this very limited sample size, even the large difference in the proportion of non-functional teats between these three populations (9.4 and 10.4 versus 20.7 %; from Ocepek's Table 3) did not achieve statistical significance ( $F_{113}^2 = 1.7$ , P = 0.19; from Ocepek's Table 4). It follows that this source

cannot be regarded as representative for the current (2022) European pig sector and its maternal breeding populations.

Second comment: Kobek-Kjeldager et al. (2020) analyzed data of 93 Danavl Yorkshire × Landrace sows, recorded in 2017; the Danavl breeding goals have never included teat number. Pustal et al. (2015) recorded their data in 2011-2012 on 120 Porkuss<sup>®</sup> Yorkshire × Landrace sows that had been sourced from that same Danavl breeding programme. For Ocepek et al. (2016), see the previous paragraph. The teat number data of Lundeheim et al. (2013) were recorded in 2007-2009 on Swedish Yorkshire pigs; these authors note that if "there is no genetic correlation between teat number and litter size, number of (functional) teats is to be included in the breeding programme, to secure the piglets' need when litter size is increasing. [...] Including the number of functional teats [...] in the genetic evaluation could easily result in a substantial genetic progress also for this trait". In other words, the breeding goal for this population had not included teat number either.

It follows that these "recent studies", based on 5-15 year old data from populations that had hardly or not at all been selected for teat number, create a seriously biased view of the current (2022) European pig sector and its maternal breeding populations.

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## Appendix 2

Routine EBVs are available for total number born (TNB), number stillborn (NSB), and lactation mortality rate (LAMR). From these, EBVs for number born alive (NBA) and litter size at weaning (LSW) must be derived. Also, the number of litters required to produce 1000 weaned piglets (L1000) and the associated numbers of farrowing and lactation mortalities (FAM, LAM), and their annual changes (dL1000, dFAM, dLAM) must be calculated.

EBVs have an average value of zero, and they are additive but not multiplicative. For multiplication they must be scaled up to the phenotypic level by adding the phenotypic mean value of the trait, calculated across the relevant group of animals. For trait TRT: aTRT = ebvTRT + mTRT, so that ebvTRT = aTRT - mTRT.

- aNBA = aTNB aNSB. Also, mNBA = mTNB mNSB, so that mTNB = mSNB + mNBA. Then aNBA = (ebvTNB + mTNB) - (ebvNSB + mNSB). With that, ebvNBA = aNBA - mNBA = (ebvTNB + mTNB) - (ebvNSB + mNSB) - mNBA = ebvTNB - ebvNSB + mTNB - (mNSB + mNBA) = ebvTNB - ebvNSB. In other words, trait EBVs are indeed additive.
- 2.  $aLSW = (1 aLAMR) \times aNBA$ . Also,  $mLSW = (1 mLAMR) \times mNBA = mNBA mLAMR \times mNBA$ . Then  $aLSW = (1 - ebvLAMR - mLAMR) \times (ebvNBA + mNBA) = mNBA + ebvNBA - mNBA - ebvNBA - mNBA + ebvNBA + mNBA + ebvNBA - mNBA + ebvNBA - mNBA + ebvNBA - mNBA + ebvNBA + mNBA + mNBA + mNBA + ebvNBA + mNBA + mNBA$

$$\label{eq:mlambda} \begin{split} mLAMR \times mNBA - mLAMR \times ebvNBA - ebvLAMR \times mNBA - ebvLAMR \times ebvNBA, \\ so that ebvLSW = aLSW - mLSW = ebvNBA - mLAMR \times ebvNBA - ebvLAMR \times mNBA - ebvLAMR \times ebvNBA = (1 - ebvLAMR - mLAMR) \times ebvNBA - ebvLAMR \times mNBA. \end{split}$$

- 3. L1000 = 1000 / LSW so that  $\frac{dL1000}{dt} = \frac{dL1000}{dLSW} \times \frac{dLSW}{dt} = \frac{-1000}{LSW^2} \times \frac{dLSW}{dt}$ , where  $\frac{dLSW}{dt}$  is the genetic trend in LSW, estimated from ebvLSW.
- 4. FAM = L1000 × NSB. For y =  $x_1 x_2$ ,  $\frac{dy}{dt} = \frac{dx_1}{dt} \bar{x}_2 + \frac{dx_2}{dt} \bar{x}_1$ . Then  $\frac{dFAM}{dt} = \frac{dL1000}{dt} \text{ mNSB} + \frac{dNSB}{dt} \text{ mL1000}$ , where  $\frac{dNSB}{dt}$  is the genetic trend in NSB, estimated from ebvNSB.
- 5. LAM = L1000 × NBA × LAMR. For  $y = x_1 x_2 x_3$ ,  $\frac{dy}{dt} = \frac{dx_1}{dt} \overline{x}_2 \overline{x}_3 + \frac{dx_2}{dt} \overline{x}_1 \overline{x}_3 + \frac{dx_3}{dt} \overline{x}_1 \overline{x}_2$ .

Then  $\frac{dLAM}{dt} = \frac{dL1000}{dt}$  mNBA mLAMR +  $\frac{dNBA}{dt}$  mL1000 mLAMR +  $\frac{dLAMR}{dt}$  mL1000 mNBA where  $\frac{dNBA}{dt}$  and  $\frac{dLAMR}{dt}$  are genetic trends again, estimated from ebvNBA and ebvLAMR.