

About Räikkönen et al 2013

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It was suggested that I should share my views on this recent study. It is available at:

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0067218>

Speculations based on the study seem a blatant misuse of both statistics and genetics. However, none of the misleading speculations are claimed as results in the abstract. Thus, the authors themselves do not regard these speculations well supported conclusions. But the authors spread the “news” that malformations become more frequent each year in newspapers (DN

<http://www.dn.se/nyheter/sverige/missbildningar-okar-hos-vargstammen/>) and other media

(<http://sverigesradio.se/sida/artikel.aspx?programid=2108&artikel=5623157>)

Many Swedish scientists (including me), believe that immigration now is sufficient and that the conservation status should be stated favourable. The authors claim that their speculations become less relevant when these conditions are met, which reduces the relevance of the speculations.

The results and statistical evaluation the speculations are based on are presented in Fig 3. That figure is rather informative. But it can be misunderstood, it is not complete and the discussion and statistics are misleading.

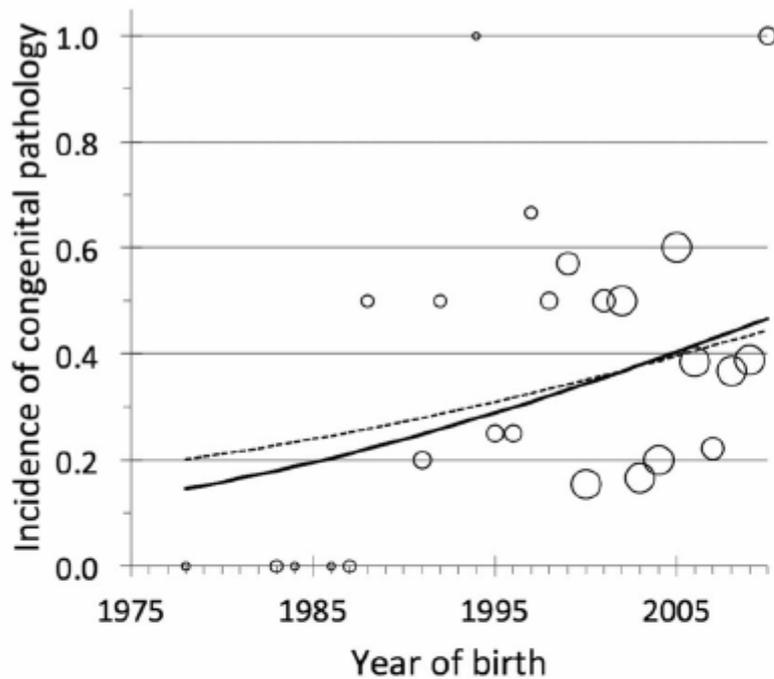


Figure 3. The relationship between year of birth and incidence of congenital pathology. We included 171 Scandinavian wolves born between 1978 and 2010. The wolf born in 1978 is the founding immigrant female. The solid line is the predicted logistic regression line, which includes an estimate for the slope and intercept. The dashed line is the weighted average of two models, the model that includes an estimate of the slope and intercept and a model including only an intercept (i.e., assumes no trend). Each circle is the proportion of wolves observed for a particular year with some kind of congenital pathology. The size of each circle represents the number of wolves observed each year. There are five sizes of circle, representing sample sizes of 1, 2–3, 4–6, 7–9, and 9 to 19.
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First look at Figure 3 and forget about everything, which is not in the figure. Figure 3 shows the trend and the population size. According to the trend lines and the circle sizes, the larger the population grows, the more frequent abnormalities occur. It seems rather weird and not trustworthy to use these results to argue for a higher population size to remedy the problems the Fig 3 illustrates.

Look in Figure 3 again. There are two distinct groups of wolves: those born before 1988 and those born after 1987. For the group <88 no single wolf had any deformation. For the group 87< deformations were rather frequent in all cohorts. This is *very* striking! Theoretically it could be e.g. a disease, which need some time to find and establish in a new host, but this type of biological explanation seem far-fetched. Part of the reason could be that criteria, techniques applied and material quality change over time, thus for compatibility the values <88 should be somewhat higher, but this seems very hypothetical.

”Den första vargen (Leksandhanen) som bevisligen hade grava ryggsproblem hade inavelsgrad noll och var som till Gillhovshannen, den tredje invandraren! Det var således troligen den hanen som förde in problemen i stammen! Gillhovshannen var den varg som satte sprätt på vargstammens utveckling och vars gener finns spridda i en stor del av populationen!” (Glöerssen pers comm). The founding male was thus not included in the study, but suffered relevant problems, which is an indication that “F=0” need not be equivalent to problem free. The third founder may add genetic problems in addition to those caused by inbreeding. That the founding father suffered congenital problems demonstrates that the problem need not be evolutionary severe.

The pedigree and annual rate of inbreeding of the Swedish wolf population is available in a report by Åkesson (2012).

<http://www.viltskadecenter.se/images/stories/Publikationer/sl%E4ktr%E4d%20varg%202011%20rapport.pdf>

The reports by Rääkkönen and Åkesson seem compatible with an assumption that all wolves considered in <88 have F=0 (no formal inbreeding) and belong to the founding family group of the Scandinavian population.

It is quite surprising that no single malformations was found for <88. That the founding wolves are assigned F=0, does not mean that they need to be much better than typical for the population they originate from. The founding father was not included in the material and is known to have suffered from malformations. 1987 two wolves sampled from a population with average F=0.25 had no malformations. Wolves in “non-inbred” (or rather “less inbred”) populations have malformations and it seems to be unsatisfactory little data on that to allow firm conclusions what should be expected if the Swedish wolves were less inbred. It may just be good luck in a low number (around 7) that malformations were not observed. As far as I understand it is not “statistically significant” that the absence of malformations in the <88 group is compatible with a frequency of malformations above 0.3. Thus the “true” difference between <88 and 87<, and thus the impact of inbreeding, is almost certainly smaller than it looks like in Fig 3, and may be considerable smaller.

Since the largest circles (numbers) start occurring 4 years are above the regression line and 7 below. Counting only the largest (safest) 2 are above and 6 are below the regression line. Extrapolating that following years are expected to result in higher values is not convincing.

No effort was done by Rääkkönen et al. to link the incidence to the inbreeding of individuals or cohorts. Individual values are not easy to link, for most wolves it is not possible, and it should require that the Grimsö group spend time on the material. But that is no excuse to use a language indicating relationships, which actually are not indicated. But relating with the cohort averages calculated by Åkesson (2012) would be easy (that information is published and need no permission to utilize if inbreeding is read from the diagram) and give a rather fair picture how inbreeding and malformation develop. The authors base their discussion on two assumptions: A) That inbreeding causing malformations increases by year of birth, which it does not after 1987. The average inbreeding for pups born after 87 can be said to roughly average F=0.25, it is F=0.25 both 1987 and 2011 with some variations up and down in between (Åkesson 2012) and actually it sunk to F=0.24 in the last observation; B) That incidence of malformations raise between 1988 and 2010, which it does not seem to do, look at Figure 3! Thus, there is no support for the most annoying speculations.

The data seems to support that a raise in inbreeding with $F=0.25$ causes a “jump” in the “incidence of congenital pathology” with something like 0.1-0.3 in the end of the 80th. But *not* the continuous raise indicated by the trend lines in Fig. 3.

If malformations really continue to rise in wolves born later than 1987, the reason must be something else than inbreeding, as inbreeding has not changed much since that. After 2007 inbreeding is slowly sinking, and when malformations should sink also. The authors seem unaware of this, as they do not discuss reasons for the rise they claim exists in spite of that the inbreeding decreases.

To preserve wolf for ever, there is a need for more wolves in total than recently exists in Scandinavia, but those extra wolves need not be in Scandinavia. A sufficient number may exist in an international genetically connected meta-population and the genetic connection with populations in other areas seems adequate <http://vargweb.wordpress.com/2013/08/26/tillrackligt-manga-vargar-for-evigheten/>. But for conservation up to 100 years and to reduce inbreeding and rise genetic variation, the current Swedish population is already larger than required by EU rules (according to a considerable share of qualified scientists). Actually, I and others believe that selective wolf hunt combined with lower number than today is an effective tool in reducing inbreeding at current immigration. I believe that “Grimso” has started the process of writing a scientific paper, and publically available reports are already available on the issue, besides my published popular discussion papers. It would be better if scientists, stating that they want to discuss the implications of observations, tried to do that in a more objective way than in this paper. It is astonishing that so many wolf-related scientists point at the problems high inbreeding causes with the purpose of actually arguing against efforts reducing inbreeding. Probably high number reduces the effect of a given amount of inbreeding somewhat in some centuries, but low number and selective hunt reduce inbreeding much more efficient and in some decades. Probably what high populations do over centuries is at least as much to reduce inbreeding depression by natural selection, as reduction of formal inbreeding.

The authors are to be criticised for (among other things) speculative alarmist sentences “Each wolf generation (which is about 4 years), the odds... of being born with a congenital anomaly increases by 23%.” This is not supported by the study, where seems no reason to assume a fast increase in the near future. The authors state above Fig 3 “There is good reason to believe the incidence of anomalies among Scandinavian wolves has been increasing substantially over the past three decades.” which is formally true. But it misleads the reader that there are good reasons to believe the incidence has raised the past 15 years and from extrapolation can be assumed to continue to rise. The authors claim: “to avoid further rise of the inbreeding rate the population must increase”. The inbreeding in Scandinavian wolf is the last years slowly *decreasing* (Åkesson 2012)!!!! and the cause is immigration, no-one believe it is thanks to population growth. It is opposite, the sink would have been larger if the immigrant genes were less diluted in a smaller population. If inbreeding is the cause of the problems, it would decrease the last years. The authors make incorrect statements about essentials in Swedish wolf-genetics. Self-respecting responsible scientists should avoid formulating statements, which to the public will give a misleading main message, often seemingly as a result of their scientific study. This seems to be a common habit among scientists, when Swedish wolf is concerned. This habit is one of the reasons why wolf is so controversial in Sweden.

I permit uncontrolled circulation of this document. But I sometimes make (usually minor) mistakes and often update my opinions and sometimes get comments which deserve attention. So if it is

important, you can ask me to get the latest version. I thank Håkan Sand and Gunnar Glöerssen for comments during my “evaluation”. Some more have had the opportunity to comment, but they did not. To offer the authors the chance to correct mistakes or make other comments on this document I have sent this evaluation to the main author some months ago, but not got any comments.