

Excerpt on the calculation errors of the review by Lamb 2008 including the two tables referred to.

One important point is that the litter size was analyzed using the breeding pair as the denominator rather than the delivering breeding pair. The number of deliveries in the F3 (3rd generation) matings dropped off for both control and GM test groups and there was no explanation for this decline (see second row of Table 36). This should have been addressed. The decline in fertility resulted in an apparent decrease in litter size that is an artifact of the denominator that they used (see fourth row Table 36). This might best be illustrated by a fictitious example. If one cohabited 20 pairs and only one pair delivered a litter of 10 animals, the mean litter size would be 10; not 0.5 as would have been reported by the authors. If the proper denominator was used, the litter size did not change for either group compared to the other generations. The authors did not report the number of litters analyzed at weaning, so we cannot determine whether or not a similar error was made in the number of weanings/pair. Without the individual animal data, we cannot test the statistical findings either. In the end, the authors did not see a treatment effect in this study, but the computational errors raise concern about other examinations in such an important data set.

The authors also divided the MG study litters into less than 8 and greater than 8 pups per litter. I have never seen this approach to litter analysis and wonder why and when they chose to make this comparison. No rationale is provided for this approach. These data are very difficult to interpret and have dubious scientific meaning. The various charts lead to a good deal of discussion, but do not really aid in the data interpretation.

The RACB study has similar issues that do affect the authors' interpretation of their study. In Table 59 they report data similar to the MG study. Instead of multiple generations, the table shows multiple litters across the study. One odd point is that they had one pair that never delivered any litters. There is no explanation for this, and that is inconsistent with the MG study. They probably should have analyzed the data with and without this pair in the study because it is not likely related to the treatment. This amplifies the error of using the wrong denominator because the litter size is understated for the treated group throughout the study because they again divided by the pairs cohabited without considering the actual litter size for those mated pairs that actually delivered litters. They have made the same mistake on the number of pups at birth per pair and on number of pups at weaning per pair.

The authors' computational approach results in some key misstatements in Table 59. In 3rd litter for the GM group the mean number of pups per litter is incorrect and should be 9.41, not 9.06. For the 4th litter, the GM group should be 8.65 pups per litter, not 7.21. Similar mistakes are presented for the pups weaned and the numbers for the GM are consistently understated. For example, the 4th litter had an average of 9.11 weaned pups per litter, not 7.21 and the 3rd litter had 12.18 weaned pups per litter not 9.06.

Tables 36 and 59 from the original study of

Velimirov, A., Binter, C., Zentek, J., & Herzog, U. (2008)

Biological effects of transgenic maize NK603xMON810 fed in long term reproduction studies in mice, Report, Herausgeber, Medieninhaber und Hersteller: Bundesministerium für Gesundheit, Familie und Jugend, Sektion IV Radetzkystraße 2, 1031 Wien. ISBN 978-3-902611-24-6 pp 109 Forschungsberichte der Sektion IV Band 3/2008 (Report) <http://www.botanischergarten.ch/Food/Velimirov-Austrian-Maize-Study-20081111.pdf> AND <http://www.botanischergarten.ch/Food/Velimirov-Austrian-Maize-Study-German-Abstract-20081111.pdf>

Table 36: **Reproduction data of mice fed 33% isogenic (ISO) or genetically modified (GM) corn in their diet over several generations**

traits	Parental reproduction							
	F0		F1		F2		F3	
	ISO	GM	ISO	GM	ISO	GM	ISO	GM
Pairs/group	18	18	24	24	24	24	22	22
Deliveries/group	17	18	23	22	19	21	16	14
Non deliveries/group	5.6%	0.0%	4.2%	8.3%	20.8%	12.5%	27.3%	36.4%
Number of pups at birth/pair	10.28 ± 0.980	10.22 ± 0.629	8.25 ± 0.778	7.88 ± 0.779	8.42 ± 1.025	8.92 ± 0.875	6.59 ± 1.046	5.68 ± 1.10
Sum of pups at birth/group	185	184	198	189	202	208	145	125
Number of pups at weaning/ pair	8.39 ± 0.936	7.67 ± 0.792	8.00 ± 0.766	6.96 ± 0.786	7.96 ± 0.928	7.63 ± 0.850	6.45 ± 1.040	5.23 ± 1.03
Sum of pups at weaning/ group	151	138	192	167	191	183	142	115
Sum of pup losses/group	34	46	6	22	11	25	3	10
Pup losses/group	2.06 ± 0.683	2.61 ± 0.837	0.26 ± 0.157	1.00 ± 0.510	0.58 ± 0.289	2.95 ± 0.631	0.19 ± 0.136	0.71 ± 0.322

Values represent means and standard error, means that do not share a common superscript are significantly different ($p < 0.05$)

Table 59: **Reproduction data of mice fed 33% isogenic (ISO) or genetically modified (GM) corn in their diet over several generations**

traits	Parental reproduction							
	1st litter		2nd litter		3rd litter		4th litter	
	ISO	GM	ISO	GM	ISO	GM	ISO	GM
Pairs/group	24	24	24	24	24	24	24	24
Deliveries/group	24	23	24	23	24	22	24	20
Non deliveries/group	0	1	0	1	0	2	0	4
Weaned litters/group	24	23	24	23	24	17	24	19
Number of pups at birth/pair	9.00 ± 0.614	8.22 ± 0.590	10.83 ± 0.473	10.65 ± 0.649	11.92 ^a ± 0.496	9.68 ^b ± 0.688	11.38 ^a ± 0.462	8.21 ^b ± 1.077
Sum of pups at birth/group	216	189	260	245	286	213	273	197
Number of pups at weaning/ pair	8.33 ± 0.560	8.13 ± 0.560	10.04 ± 0.480	9.83 ± 0.550	10.58 ± 0.454	9.06 ± 0.820	9.79 ^a ± 0.525	7.21 ^b ± 0.985
Sum of pups at weaning/ group	200	187	241	226	254	207	235	173
Pup losses/group	0.67 ± 0.305	0.09 ± 0.060	0.79 ± 0.289	0.83 ± 0.375	1.33 ^a ± 0.433	0.12 ^b ± 0.081	1.58 ± 0.371	1.00 ± 0.376
Sum of pup losses/group	16	2	19	19	32	2	38	24

Values represent means and standard error, means that do not share a common superscript are significantly different ($p < 0.05$)