Genetic Parameters and Genetic Trends Of The Sino-European Tai Zumu Composite Line

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Introduction
The creation of a sino-european composite line is considered as the best strategy (Bidanel, JP., Caritez, JC., Gruand, J. et al. 1993; Haley, C., Lee, G., and Ritchie, M. 1995) to take benefit of Chinese breeds mothering abilities and prolificacy. After its creation, it nevertheless takes some time to improve the new line mainly on growth and carcass traits, before using it in a terminal crossbred sow. The GENE+ breeding company created its own sino-european line in 1994-95: the Tai Zumu. This line is now used since 2004 in a two way cross with French Landrace and Large White to produce a terminal sow called Youna. Since 1994-95, the selection was achieved to balance short term and long term objectives. The aim of this communication is to show the genetic response of the breed to the different goals applied during the first 15 years of selection and to discuss the results of an up-dated estimation of the genetic parameters of each recorded trait.

Material and methods
Creation and selection steps of the Tai Zumu line. The Tai Zumu line was created in 1994-95 by mating 34 Chinese sows, (30 pure Meishan and 4 Meishan*Jiaxing F1), with 33 hyper-prolific French Large White boars. A total of 30 F1 boars and 60 F1 sows were kept among 31 litters and next generations were obtained by intercrosses. After two generations of mating without any selection, the breeding improvement was run in 2 main steps. Step 1 from 1997 to 2001 (generation 3 to 6), an index after batch control combining age at 100kg (A100), and backfat thickness (BF100) was used to rank the animals. Then, since 1999, loin depth (LD100) was added to this index. The number of functional teats (NFT) was only considered as a threshold: no animal with less than 16 teats was kept as a future reproducer. Step 2, from 2002 to 2006, a first BLUP evaluation applied to an animal model on a global objective was used after a first computation of genetic parameters. The global objective, took into account (in percent of the global genetic standard deviation) the number of born alive (NBA) for 35%, A100 (11%), LD100 (26%), BF100 (11%) and NFT (17%). Finally, from 2007 until now, step 3, a new global objective was built, with the introduction of the number of weaned piglet from the biological sow (NW) and by slightly changing the weight of the production and teat traits. In 2009, 1070 Tai Zumu sows were used for selection or first stage of multiplication from only 3 nucleus herds.

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Statistical analyses. Average breeding values of females controlled and kept in the nucleus by year of birth were used to estimate genetic trends. They were computed with PEST software (Groeneveld, E., and Kovac, M. 1990) using two separate animal models, one for reproduction and one for production and teat traits. For production and teat traits, fixed effects of the control batch and of the “herd-year-mating type” and random effects of the litter of birth and of the animal were considered. For maternal traits, the parity, the month of farrowing, the covariable of the age at farrowing (nested into parity), were also considered as fixed effects and the random effect of the boar as well as the permanent environment effect of the sow were added. Genetic parameters were firstly calculated in 2002 using restricted maximum likelihood methodology applied to the two multi-trait animal models described above. A new estimation was realized here applying a single multi-trait model using VCE software (Neumaier, A., and Groeneveld, E. 1998).

Results and discussion
Genetic trends for production and teat traits are shown in Figure 1. The first step of the selection (till 2001) is clearly associated with a huge improvement of growth (-8.44 days of age at 100 kg) and a reduction of fatness (-5.48 mm) while during the same time loin depth was decreasing (-1.06 mm) due to a negative correlation with both of these traits (correlations further estimated in 2002).

Figure 1: Genetic trends for Growth (a), carcass (b and c) and teat (d) traits
Taking the number of teats as a threshold to keep new reproducers into the nucleus at each generation was enough to improve the number of functional teats of 0.42 teats. Finally during this step, the genetic value for the number of born alive and weaned piglets of the population (Figure 2) was almost unchanged.

Figure 2: Genetic trends for reproduction traits, number of born alive by litter (a) and number of weaned piglets from the biological sow by litter (b)

During the second step of the selection (from 2002 to 2007), by taking into account correlations between growth and carcass traits in the BLUP evaluation, unfavorable genetic trend on loin depth was rapidly corrected, with a genetic gain of 1.2 mm during this 5 years interval. By introducing the number of functional teats and the number of born alive into the global objective, a more important improvement was made on these two traits comparing to the first step of selection. Nevertheless, from 2002 to 2007, the genetic improvement on growth and on backfat thickness was not at all as expected. One reason may be found in the elimination of one morphologic type of animals into the population. Very thin animals, mainly obtained by a correlated selection of one marker gene on chromosome 7 (Riquet, J., Laval, G., Iannuccelli, N. et al. 2006), animals that were also characterized by a high development and some legs problems, have been culled quickly from the population. But another explanation might be found in the genetic parameters.

The genetic parameters calculated here in 2010 (Table 1), showed quite high heritability estimates, but classical for these different kind of traits, but above all, unfavorable correlations between reproduction traits and age and backfat at 100kg.

Table 1: Estimates of genetic parameters in the Tai Zumu line

<table>
<thead>
<tr>
<th></th>
<th>A100</th>
<th>BF100</th>
<th>LD100</th>
<th>NFT</th>
<th>NBA</th>
<th>NW</th>
</tr>
</thead>
<tbody>
<tr>
<td>A100</td>
<td>0.43</td>
<td>0.51</td>
<td>0.27</td>
<td>0.09</td>
<td>0.30</td>
<td>0.27</td>
</tr>
<tr>
<td>BF100</td>
<td>0.60</td>
<td>0.23</td>
<td>0.00</td>
<td>0.27</td>
<td>0.26</td>
<td></td>
</tr>
<tr>
<td>LD100</td>
<td>0.34</td>
<td>0.51</td>
<td>-0.11</td>
<td>-0.02</td>
<td>0.18</td>
<td>0.92</td>
</tr>
<tr>
<td>NFT</td>
<td></td>
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<td>NBA</td>
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<td>NW</td>
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<td>0.14</td>
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aHeritability estimates on the diagonal and genetic correlations above the diagonal. (All standard deviation for heritability and correlation estimates were equal or lower than 0.02, and 0.07 respectively)
On the contrary, reproduction and loin depth could be considered as not or slightly positively correlated. The other unfavorable correlations between LD100 and A100, either than between LD100 and BF100 and between age and backfat, correlations previously observed in 2002, could still be noticed, in the same range.

Unfavorable correlations were already observed between backfat, growth, and maternal traits in a similar study (Burlot, T., Zhang, S., Naveau, J. et al. 1998), on another sino-european composite line. One explanation might be found in the persistence of linkage disequilibrium after the composite line creation. But if in the past years (e.g. Tribout, T., Bidanel, JP., and Garreau, H. 1998), reproduction and growth and carcass traits were considered as uncorrelated, more recent publications in Large White or Landrace dam lines seemed to show moderate unfavorable correlations (Tribout, T., and Bidanel JP. 2008). To our knowledge, it is also the first time that correlations between loin depth and other traits of growth and carcass in a dam line are reported.

**Conclusion**

During the 15 first years of selection of the Tai Zumu composite line, an important genetic improvement could have been made: -12.4 days of growth, -5.5 mm of backfat, +1.06 mm of loin depth, +2.24 functional teats, and +0.65 born alive and weaned piglet. The genetic parameters calculated for this communication will led to a new model for BLUP evaluation in order to better take into account the correlations between maternal and production traits. Identify markers able to separate the linkage between maternal and production traits could also be useful to manage the selection of this line in the future.

**References**