

Supplementary Information

Song recording and analysis

At the end of the experiment (after day post hatch 100), each bird was isolated in a sound attenuating box for song recordings. Files containing songs were selected using Sound Explorer (developed by R. Jansen, university of Amsterdam). Raw data (27 sound files; one per bird, each file containing songs used for the analysis) can be downloaded at the following address: doi:10.5061/dryad.7137r

We quantified acoustic similarity between song motifs using a similarity score obtained in Sound Analysis Pro (SAP, version 2.062) from 100 asymmetric pairwise comparisons of each brother's typical motif with its tutor motif and its brother motif. SAP is freely available and can be downloaded at the following address: <http://soundanalysispro.com/>

The similarity procedure implemented in SAP provides 3 components: % similarity, mean accuracy and sequential match. Percentage of similarity is the percentage of similar sounds included in final sections. Mean accuracy is the average local similarity scores across final sections. Sequential match is calculated by sorting the final sections according to their temporal order in reference to the song model, and then examining their corresponding order in the song motif. For statistical analyses, we used only the % similarity.

In asymmetric comparisons, the most similar sound elements of two motifs are compared, independent of their position within a motif. The smallest unit of comparison is 9.26-ms-long sound interval (FFT windows). Each interval is characterized by measures for five acoustic features: pitch, FM, amplitude modulation (AM), Wiener entropy, and pitch goodness. SAP calculates the Euclidean distance between all interval pairs from two songs, over the course of the motif, and determines a p-value for each interval pair. This p-value is based on p-value estimates derived from the cumulative distribution of Euclidean distances across 250,000

sound interval pairs, obtained from 25 random pairs of zebra finch songs. Neighboring intervals that pass the p-threshold value ($p = 0.1$ in this study) form larger similarity segments (70 ms). In asymmetric similarity measurements, we want to judge how good the copy is in reference to the song model. The song model is loaded as “sound 1” and the copies are loaded as “sound 2” in the batch module of the SAP software. Therefore, in our study, song models (tutor motifs) were loaded as “sound 1” and pupil motifs were loaded as “sound 2”. In summary, the amount of sound from the tutor motif that is included into the similarity segments represents the similarity score; it thus reflects how much of the tutor’s song material is found in the pupil motif. This procedure was repeated 25 times, comparing 5 different exemplars of the tutor song with 5 different exemplars of each son’s motif. The mean value of these 25 comparisons was used for statistical analysis.

In our study, since both brothers could have learnt from each other meaning that they could use each other as a song model, there was no reason to choose one brother as a reference rather than the other one. For each pair of siblings, we thus computed the similarity score twice, first using son# 1’s motif as the reference (loaded as “sound 1” in the batch module of SAP), then using son # 2’s motif as the reference. This procedure was repeated 50 times (2 x 25), comparing 5 different exemplars of son# 1’s motif with 5 different exemplars of son# 2’s motif. The mean value of these 50 comparisons was used for statistical analysis.

In summary, using the batch module of SAP, we computed 100 asymmetric comparisons for each triad (father and sons).

Son # 1 bird ID	% similarity	% accuracy	% sequential match
1363	35.2	68.2	63.1
1373	63.3	67.1	59.7
1381	47	71.5	69.1
1386	34.8	73	72.4
1398	58.7	68.9	71.6
1402	64	76.7	60.6
1419	49.4	69.8	55.6
1448	29.8	70.4	72
1451	57.6	69.2	63

Table 1. Similarity scores (mean values) between the song motif of the first son (exposed to the father from dph 35-42) and the song of its father.

Son # 2 bird ID	% similarity	% accuracy	% sequential match
1362	40.8	68.7	56.3
1375	40.1	70.5	69.9
1382	36.5	73.1	73.6
1385	29.4	70.5	75.9
1394	25.8	69.5	75.6
1401	63.4	74.2	61.1
1418	43.5	69.3	63.8
1445	23.6	70	86.2
1449	55.6	69.5	59.4

Table 2. Similarity scores (mean values) between the song motif of the second son (kept in isolation from dph 35-42) and the song of its father.

Brother pair bird ID	% similarity	% accuracy	% sequential match
1363-1362	83	70.7	80.4
1373-1375	54.9	71	54.3
1381-1382	66.5	72.8	54.7
1386-1385	73.8	74.2	60.1
1398-1394	55.7	72.5	54.3
1402-1401	94.8	75.6	100
1419-1418	77	69.3	67
1448-1445	71.5	72.7	44.9
1451-1449	80.7	75.6	27.5

Table 3. Similarity scores (mean values) between the song motifs of the two brothers.

Similarity between songs of unrelated individuals

We also calculated song similarity between unrelated individuals picked randomly by pair in our sample. We observed that % similarity between brothers in our experiment is much higher than similarity between unrelated pupils (mean \pm SE: 73.1 ± 1.4 vs. 33.1 ± 2.4).

The same trend is observed when one compares pairs of related tutor-pupils and unrelated tutor-pupils: son#1-father (related vs. unrelated: mean \pm SE: 48.9 ± 4.4 vs. 32.3 ± 4.2); son#2-father (related vs. unrelated: mean \pm SE: 39.8 ± 4.4 vs. 29.8 ± 4.8).