qPCR on available RNAi lines



Materials and Methods and Results

We analyzed the efficiency of the available *FoxP* RNAi lines using RT-qPCR. We extracted RNA from about 20 flies for each genotype (Table 1), following the TriFastTM protocol from peqlab (a VWR company). The RNA was subsequently transcribed into cDNA using the OneStep RT-PCR Kit from QIAGEN (thermocycler program used: 42°C for 2 minutes, 4°C pause until manual restart at 42°C for 30 minutes, 95°C for 3 minutes and finally 10°C ∞). Subsequently, the qPCR was performed. The primers were identical to those used in (Mendoza et al. 2014). For the qPCR reaction we used a Biorad CFX Connect Real-Time PCR Detection System thermocycler and the Biorad CFX manager software to store and analyze the data. Every sample was run in triplicate in a 96-well plate in a total volume of 10 μ l. The mixture contained 5 μ l sybrGreen master mix (QuantiTect SYBR Green from QIAGEN), 0.5 μ l from each primer, 1 μ l of 1:10 diluted cDNA and 3 μ l sterile H₂O (thermocycler program in Table 2). As reference, we used the same reaction mix without cDNA. The experiments were repeated 1 to 3 times.

Fly line	Source	
CS	own laboratory	
UAS-Dcr2;; nSyb-GAL4	Stephan Sigrist	

50200	VDRC
15732	VDRC
15735	VDRC
16899R-2	NIG-Fly
16899R-4	NIG-Fly
TRP26774	?

Table 1: Fly lines used for the experiment

Step	Temperature	Time	Nr. of Cycles
Denaturation	95 °C	3 min	
Denaturation	95 °C	10 s	
Annealing	55 °C	10 s	
Elongation, measurement	72 °C	30 s	GoTo step 2 x39
Denaturation	95 °C	10 s	
Melting curve, measurement	65 °C – 95 °C	+ 0.5 °C / 5s	

Table 2: qPCR thermocycler program

We determined the relative abundances of the mRNAs for all the isoforms of *FoxP* in each RNAi line by calculating the $2^{(-\Delta\Delta Cq)}$ of each line against CS.

References

Mendoza, Ezequiel, Julien Colomb, Jürgen Rybak, Hans-Joachim Pflüger, Troy Zars, Constance Scharff, and Björn Brembs. 2014. "Drosophila FoxP Mutants Are Deficient in Operant Self-Learning." *PloS One* 9 (6): e100648.