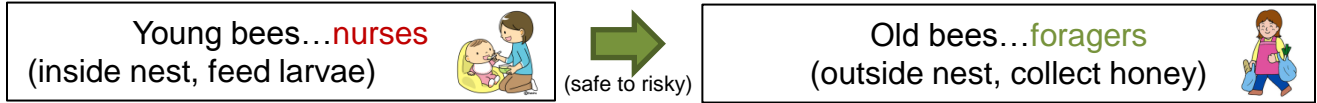


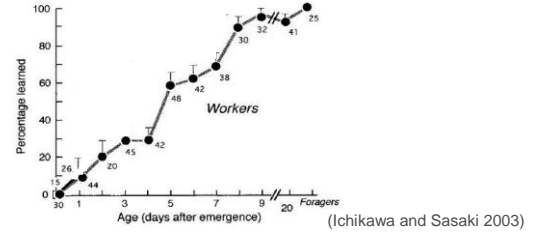
the European honeybee, *Apis mellifera*OHironori Sakamoto¹, Norichika Ogata², Tetsuhiko SASAKI¹ (¹Tamagawa Univ. ²Japan Bio-data)**Introduction**

Worker honeybees change their task with aging



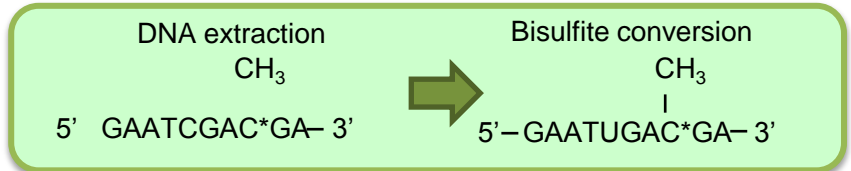
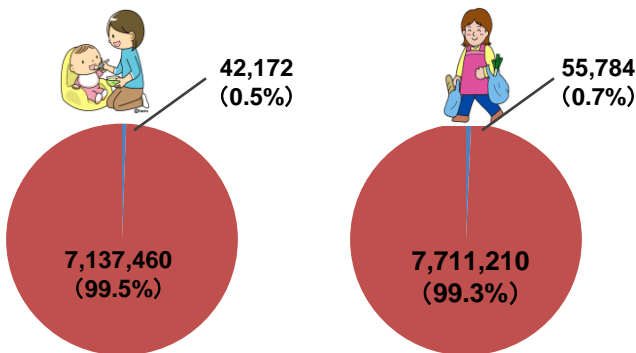
Learning ability increases with aging (nurse << forager)

➔ Does epigenetic mechanism regulate brain function ?
We focused on **DNA methylation**

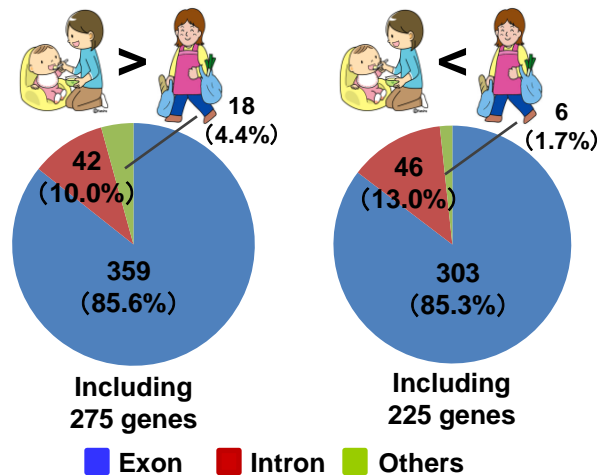
**Materials and Methods**

Compare genome-wide methylation pattern of brains between nurses and foragers by bisulfite sequencing using a next-generation sequencer

- DNA methylation occurs at C of CG (GpG) dinucleotides
- Bisulfite treatment converts unmethylated C to U
- Next generation sequencer can read more than 6 Gb (60, 000, 000, 000 bases) /run

**Results and Conclusions****1. < 1% of CpG sites were methylated.**

■ methylated ■ Not methylated binomial test, FDR<0.05

2. Differently methylated CpG sites were exon-located.**3. Differently methylated genes regulated gene expression**

Predicted function	remarkable genes
histone modification	<i>Sir-2</i> , <i>Hdac3</i>
DEAD-box helicase	<i>LOC726768</i>
chromatin remodeling	<i>Iswi</i>
neural development	<i>big brain</i>

4. Methylation-patterns were brain-specific.