Epigenetics of brain development in workers of the European honeybee, *Apis mellifera*

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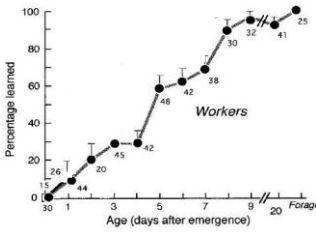
Introduction

Worker honeybees change their task with aging

Young bees…nurses (inside nest, feed larvae) → (safe to risky) → Old bees…foragers (outside nest, collect honey)

Learning ability increases with aging (nurse << forager)



(Ichikawa and Sasaki 2003)

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

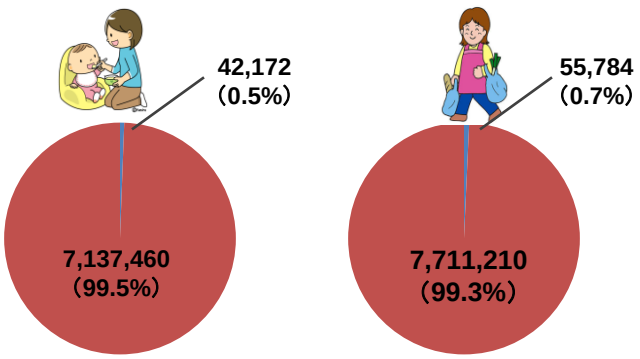
- DNA methylation occurs at C of CG (GpG) dinucleotides
- Bisulfite treatment converts unmethylated C to U

DNA extraction: 5' GAATCGAC*GA– 3'
Bisulfite conversion: 5'–GAATUGAC*GA– 3' (C* = CH_3)

- Next generation sequencer can read more than 6 Gb (60, 000, 000, 000 bases) /run

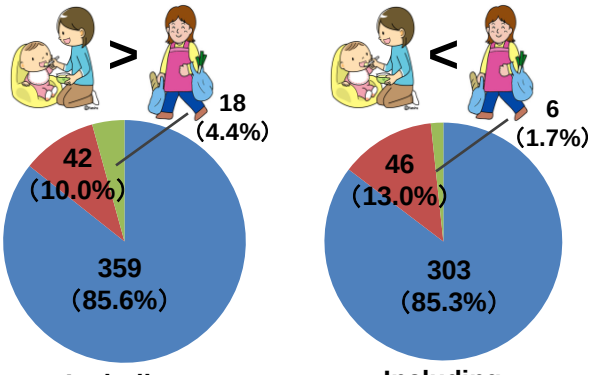
Results and Conclusions

1. < 1% of CpG sites were methylated.



methylated Not methylated binomial test, FDR<0.05

2. Differently methylated CpG sites were exon-located.



Exon Intron Others

3. Differently methylated genes regulated gene expression

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

4. Methylation-patterns were brain-specific.