Whole genome *de novo* sequencing of quail and grey partridge

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Introduction

The development in sequencing methodology has enabled whole genome *de-novo* sequencing of species without large commercial interests. In this project, sequencing of quail (*Coturnix coturnix*) and grey partridge (*Perdix perdix*) was initiated to generate information for comparative purposes towards the chicken genome. The amount of sequencing also provides a basis for generating a sequence assembly for each of these species.

Methods

Samples. A single female from each species was sequenced.
Sequencing. Two paired-end libraries were prepared for each species. Insert sizes were approximately 300 bp and approximately 600 bp, respectively. Sequencing was done on an Illumina GAII sequencer. Sequencing was performed using 54 cycles for quail and 101 cycles for grey partridge.
Sequence assembly. A preliminary sequence assembly was constructed using the CLC Genomics Workbench software package.

Data obtained

Quail *de-novo* assembly	
Number of sequence reads	164,470,975
Number of bases	8.4 Gb
Large contigs (>10 kb)	31
Total number of contigs	1,131,878
Average contig size	347 bp
Aggregated length of contigs	393 Mb
N50	355 bp

Grey partridge *de-novo* assembly	
Number of sequence reads	108,850,178
Number of bases	9.5 Gb
Large contigs (>10 kb)	217
Total number of contigs	1,112,419
Average contig size	865 bp
Aggregated length of contigs	963 Mb
N50	1,462 bp


Photo: Alejandro Tores Sánchez, http://www.birdlife.org/


Photo: Mark Desholm, National Environmental Research Institute, Aarhus University, Denmark

Conclusion

- Sufficient sequence data to initiate genome sequencing of quail and grey partridge has been obtained,
- The difference in assembly quality between species is a consequence of the difference in length of the sequence reads (54 cycles versus 101 cycles).
- Additional data will be required before sequence assembly are being performed.
- Specifically will longer sequence reads (especially in quail) be necessary to generate assemblies of a reasonable quality.

Further work

The group would like to invite other research groups with an interest in quail or grey partridge genome sequences to contact us with the aim of establishing a collaborative group for generating genome sequences of these two species.

Interested groups can contact:
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Acknowledgement
This work was part of the EU FP7 financed Quantomics (From sequence to consequence – Tools for the exploitation of livestock genomes) project (KBBE-2A-222664)

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