



WINN FELINE FOUNDATION

For the Health and Well-being of All Cats

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IMPROVING THE FELINE REFERENCE GENOME

PROJECT STUDIES: Improving the Feline Reference Genome with PacBio Sequencing

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Final report summary, MT14-009 and W15-008

This summary describes the progress associated with generating PacBio sequence data and aiding the improvement of the feline genome syndrome. Both projects had a later start due to the wait for a newer PacBio instrument (the Sequel) and improved sequencing reagents which leads to the benefit of enhanced sequence output per dollar.

With the Sequel, the Sequencing core is generating ~ 25-30X coverage with the data expected to be ready for analysis in January, 2017. With this wait, the project is in position to perform a whole genome de novo assembly which is anticipated to capture up to 98% of the euchromatic sequence. The new genome assembly is therefore anticipated to demonstrate considerable improvement over the current genome assembly, including a more accurate and complete gene set. The comprehensive analyses (including a new domestic cat gene annotation) could be ready by the end of 2017.

In addition, the project has evaluated the efficacy of targeted PacBio sequencing to resolve very complex repetitive sequences. Their experiment was to use 6 ampliconic BAC clones from the cat Y chromosomes. Six randomly ampliconic clones were selected. PacBio long-read sequencing were able to fully reconstruct each BAC clone in a single config. They have now followed up with sequencing another 70 Y clones using this approach combined with a modified Illumina protocol to ensure accuracy. Also, pools of BAC clones with this new approach to generate a nearly finished sequence from an additional 165X chromosome BAC clones that cover gaps in the current genome assembly.

The anticipated goal: a better and more complete cat genome for genetic referencing.

Two manuscripts are anticipated for 2017 from the results of these studies.

Summary prepared by Dr, Vicki Thayer © 2016

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