

Musa bioinformatics course (2013/11/20)

Practical session 4

Annotation with flat files

Goal

The results obtained with different annotation software are often different concerning the number of potential coding sequences and / or their limits. The **Artemis** curation tool

<http://www.sanger.ac.uk/resources/software/artemis/> allows to highlight these differences and work yourself on manual correction of these annotations.

To compare a syntenic region between two *Musa acuminata* haplotypes (e.g. *M. acuminata* subgroup Cavendish cv. Grande Naine and the wild diploid genotype *M. acuminata* ssp. *burmannicoides* Calcutta 4), we can use the **Artemis Comparison Tool** <http://www.sanger.ac.uk/resources/software/act/>. We visualize syntenic blocks on a region containing genes coding for pectin methylesterase (PME) (Mbeguie, et al., 2009).

Task 1: Annotate a gene with Artemis

Start with Artemis <ftp://ftp.sanger.ac.uk/pub4/resources/software/artemis/artemis.pdf>

- Launch Artemis with MaC88K20 sequence
- Look at the interface, create entry, load entry, create and copy features.
- Change feature length
- Use new entry to improve gene annotation; Load Eugene automatic prediction
- Change feature: add intron
- Edit automatic prediction.
- Use interactive blast search to improve Gene annotation
- Comparison with expert manual annotation

Task 2: Annotation transfer using ACT

- Visualize synteny with dot plot (Gepard)
- Start with ACT
- Compare BACs MaC88K20 with Ma4_30C11
- Transfer annotation from one BAC to another

Task 3: Find, describe and annotate a Transposable element (TE)

- Generate a dotplot to visualize repeats
- Find specific features onto dot plot, (microsatellite, retroelements...)
- Find LTR
- Create LTR retroelement annotation with Artemis

Mbeguie, A.M.D., *et al.* (2009) Expression patterns of cell wall-modifying genes from banana during fruit ripening and in relationship with finger drop, *J Exp Bot*, **60**, 2021-2034.