

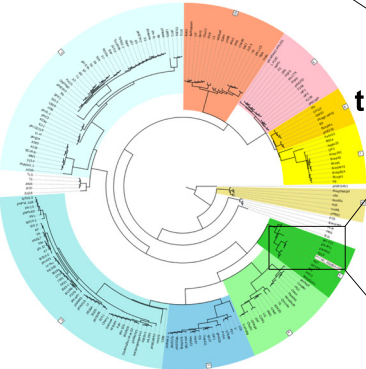
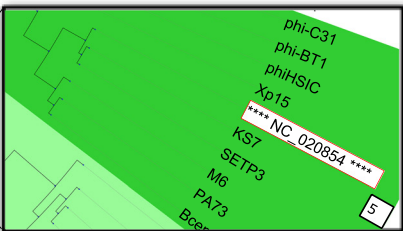
Identification of the various components
of the head-neck-tail module

- Name of the query : **NC_020854**
 - Number of sequences analyzed : **64**
 - Category to which the Query Phage was assigned : **Siphoviridae Type1 (Cluster 5)** (read more about this category)
 - Graphical Summary of the Superfamilies Detected ([Help on Superfamily names](#)):
- Click on the image to download it as png (download in pdf or svg format)



- Classification of the Query Phage with respect to other related Phages in *Adacme* (Query Phage in test box with red border and white background):

Click on the image to download it as png (download in pdf or svg format)

Clustering with the phages sharing
the most similar head-neck-tail module

- Table of the Phage Superfamilies Detected :

Protein Superfamily	Index in the Query	Sequence Header	Detection Method
MCP	1	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Portal	27	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Terminase	75	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Ad1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Hc1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Tc1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Tail	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Bsp	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Sheath	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Ad1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Hc1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Tc1	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Tail	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Bsp	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)
Sheath	NOT FOUND	NC_020854.1_adm1_WF_007670111.1	HHsearch (proba=100.00%)

NB : Matched obtained with a Hitsearch probability between 70 % and 90 % should be considered with caution.
Check that the canonical intergene below is not violated in that case.

- Intergene Distances Exceeding the Threshold Distance (Mean_IntergeneDist+2*Std_Dev) Observed in Reference Phages from Adacme:

Protein Superfamilies	Observed Intergene Distance	Threshold Intergene Distance
Ad1<->MCP	8	2
Tc1<->Ad1	25	4
Terminase<->Ad1	9	3

- Highest Identities of Proteins of the Query Phage with at least 3 Proteins in Adacme Phages :

Protein Superfamily	Corresponding Protein in Adacme	Adacme Phage	Seq. Identity (%)
MCP	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	29 %
Portal	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	27 %
Terminase	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	26 %
Ad1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Hc1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Tc1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Tail	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Bsp	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Sheath	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Ad1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Hc1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Tc1	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Tail	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Bsp	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %
Sheath	proteins/nc_020854.1_adm1_WF_007670111.1	Ad1	23 %

Profile-profile alignments
for the detected components

Ne1	1	HHsearch (proba=100.00%)
Tc1	1	HHsearch (proba=99.96%)

Unusual inter-gene distances

Proteins Superfamilies	Threshold Intergene Distance
Ad1<->Hc1	2
Tc1<->Ad1	4
Ne1<->Ad1	3

Sequence identities
to the closest related phages

Ne1	RTP	21 %
	phiHSIC	21 %
	BcepGomr	20 %