Functional and Comparative Genomics

Project 2018

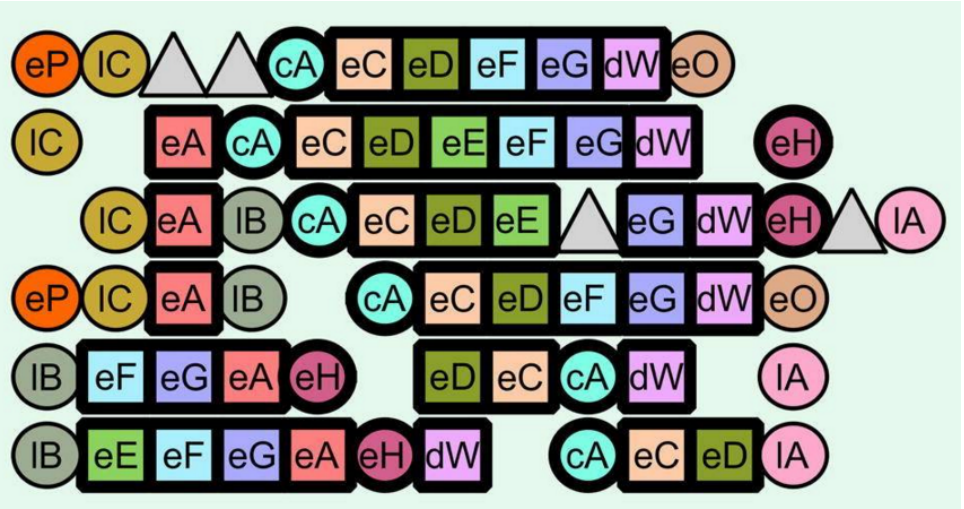
ESCI upf.
School of International Studies

Gene order conservation

Prokaryotes → Operons: groups of genes that are transcribed together and often act in the same metabolic pathway.

Eukaryotes → Gene order is not conserved but it is also not completely random. Some gene clusters have been found and have been related to having similar function, similar expression patterns, being part of protein complexes,… For instance in fungi we have **secondary metabolism gene** clusters.

Ergot alkaloid gene cluster

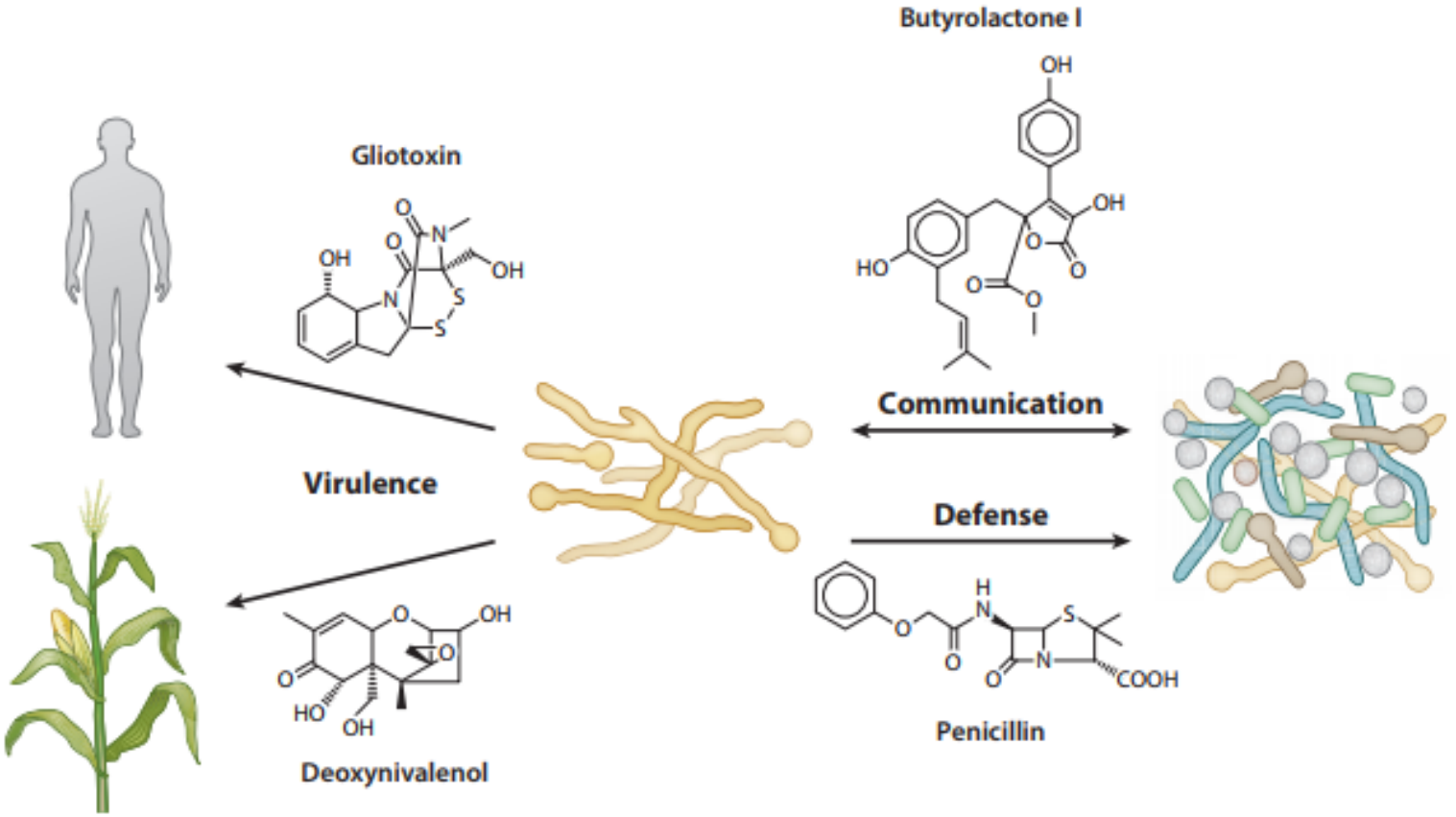


Horizontal acquisition of toxic alkaloid synthesis in a clade of plant associated fungi.

Marcet-Houben M[1], Gabaldón T[2].

Biological aplications of the clusters

Secondary metabolism refers to biosynthetic pathways that synthesize small molecules that are not required for the survival of an organism



Annu Rev Genet. 2016 Nov 23;50:371-392. Epub 2016 Oct 5.

Regulation and Role of Fungal Secondary Metabolites.

Macheleidt J[1], Mattern DJ[1,2], Fischer J[1,2], Netzker T[1,2], Weber J[1,2], Schroeckh V[1], Valiante V[3], Brakhage AA[1,2].

Genes that usually form part of secondary metabolism gene clusters

Signature genes

Non-ribosomal peptide syntahses (NRPS)
Polyketide synthases (PKS)
DMATS

Genes used for tayloring the pathway

Oxidoreducates, methyltransferases, acyltransferases, glycosyltransferases

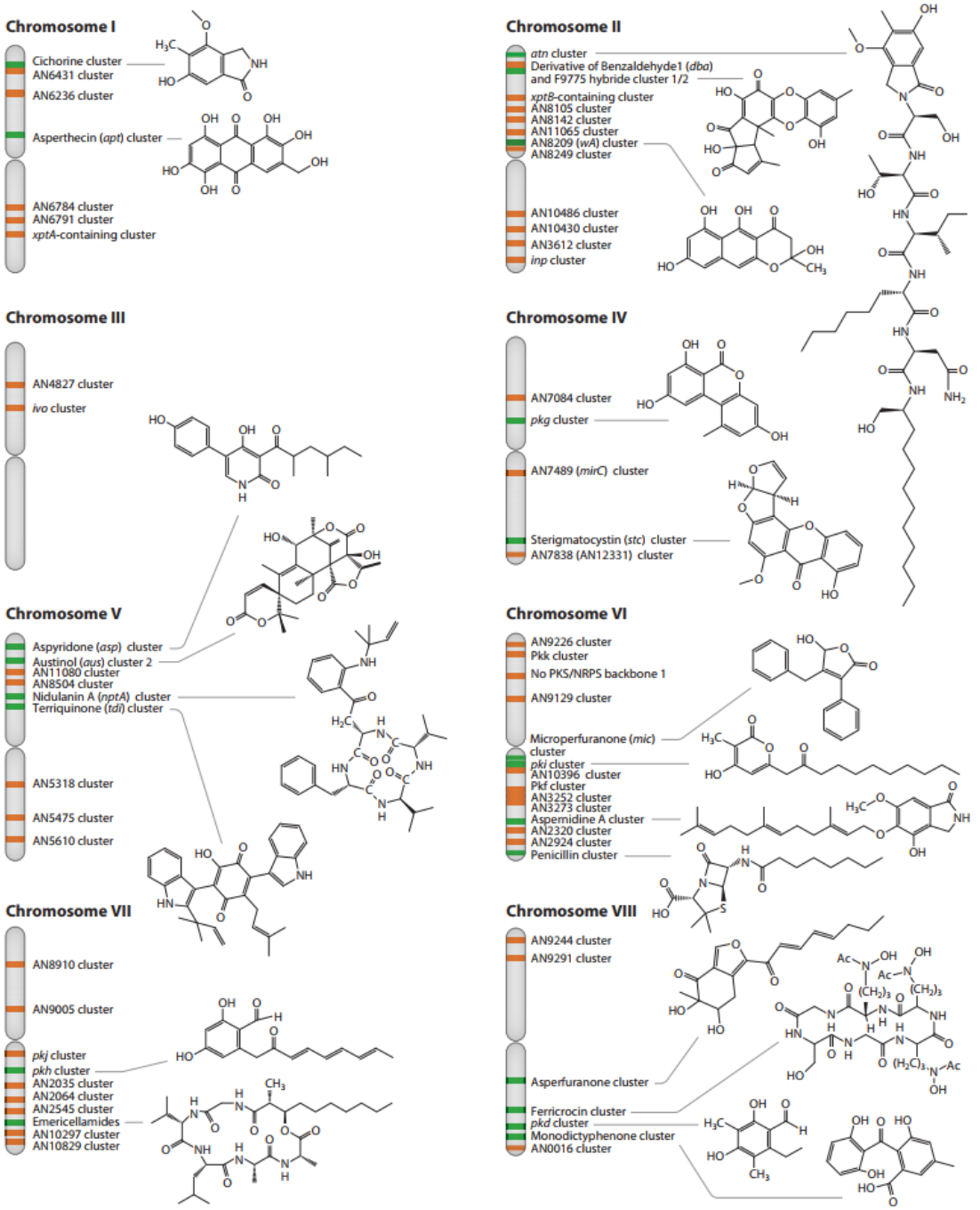
Regulators

Transporters

Genes used for metabolite resistance

Some of the genes will be essential and will be there for all the species that have the cluster.
Other genes may or may not be there, depending on the species.

Aspergillus nidulans



Out of 68 identified secondary metabolism gene clusters, we only know the compounds produced by 20 of them.

Most secondary metabolism gene clusters are silenced under normal circumstances, making it difficult to experimentally determine their activity.

Bikaverin:
In *Fusarium fujikuroi* the synthesis of bikaverin is induced by nitrogen starvation and acidic pH, and it is favored by other factors, such as aeration, sulfate and phosphate starvation, or sucrose availability

Annu Rev Genet. 2016 Nov 23;50:371-392. Epub 2016 Oct 5. Paperpile

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Appl Microbiol Biotechnol. 2010 Jun;87(1):21-9. doi: 10.1007/s00253-010-2551-1. Epub 2010 Apr 8.

Bikaverin production and applications.

Limón MC[1], Rodríguez-Ortiz R, Avalos J.

Objective of the project.

You will be grouped in pairs and given a predicted secondary metabolism gene cluster that has between 9 and 10 genes.

You will use any tools at your disposal to give a broad view of what the genes in the cluster do and how they have evolved. You can be as imaginative as you want, but what needs to be there is for each gene is:

1.- Functional annotation (Description, GO terms associated, conserved Pfam domains, EC code, are they secreted, transmembrane proteins, CAZY proteins, peptidases, etc.)

2.- Metabolic information

3.- Evolutionary information (orthologs, paralogs, duplication events, loss events, horizontal gene transfer events,…)

4.- Is the cluster or part of it conserved in other species? Is the internal gene order in the cluster conserved?

Timetable

Day	What you should be able to do
8th of May	Functional annotation and metabolism, orthology prediction
1st of June	Everything
8th of June	Everything
15th of June	Deliver the written report of your findings

Each group will be assigned a responsible tutor that will be able to help you out with questions and doubts.

The report will be at maximum 10 pages long (Times New Roman, 12) with 3-4 figures. It will be written as a paper, so it needs to contain these parts:

→ Abstract (200 – 300 words)

→ Introduction

→ Materials and Methods

→ Results and Discussion

→ Conclusions

→ References