

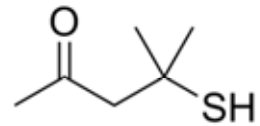
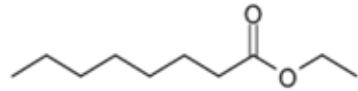
La biosynthèse des arômes dans la baie de raisin

Philippe Hugueney, INRA Colmar

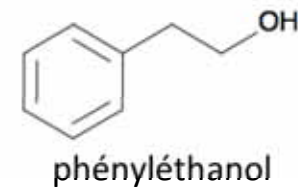
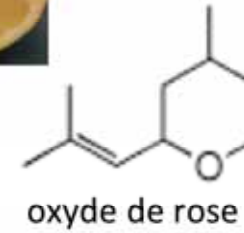
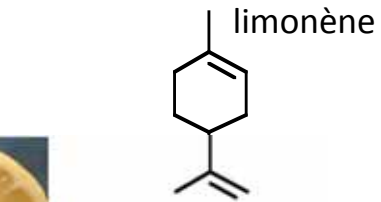


Les arômes des vins

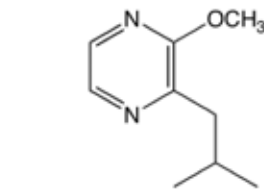
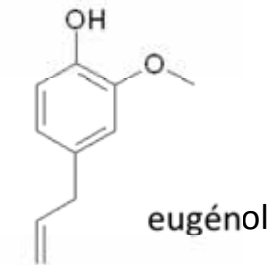
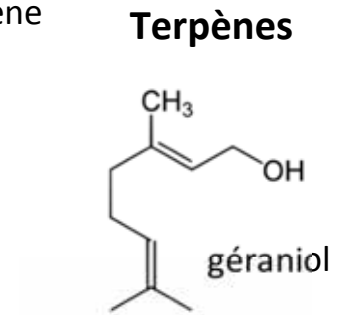
Esters d'acides gras



Thiols

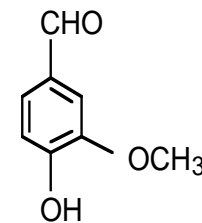


Composés aromatiques

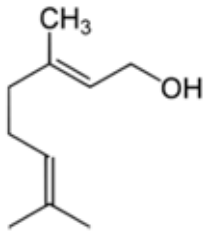


Pyrazines

vanilline



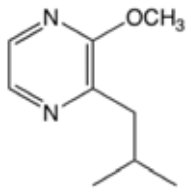
Les arômes variétaux



Terpénols



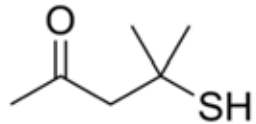
Muscats
Gewurztraminer



Pyrazines



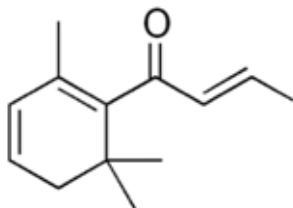
Sauvignons
Cabernet sauvignon



Thiols



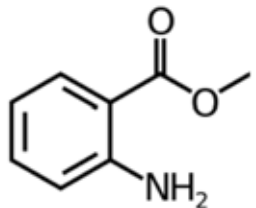
Sauvignons



Norisoprénoïdes



Riesling,
Gewurztraminer

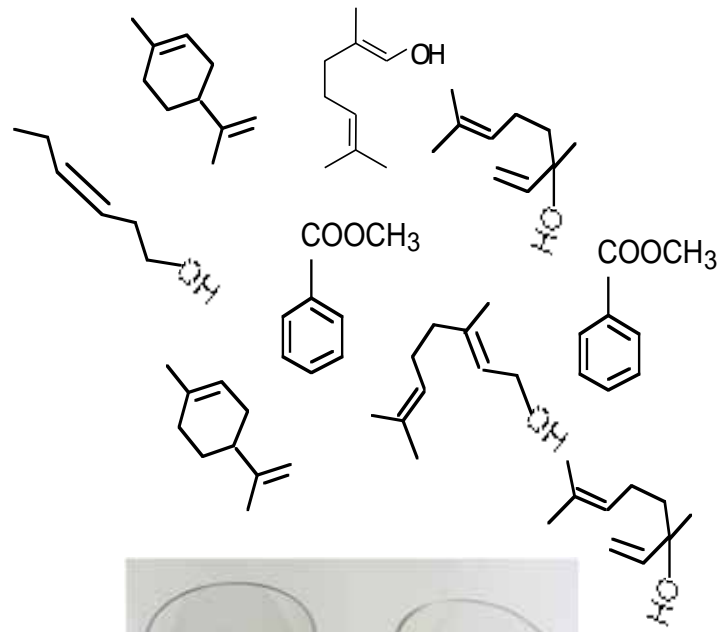


Méthyl anthranilate



Concord (*V. labrusca*)

Ou en est la recherche ?

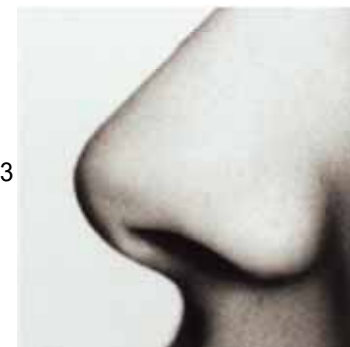
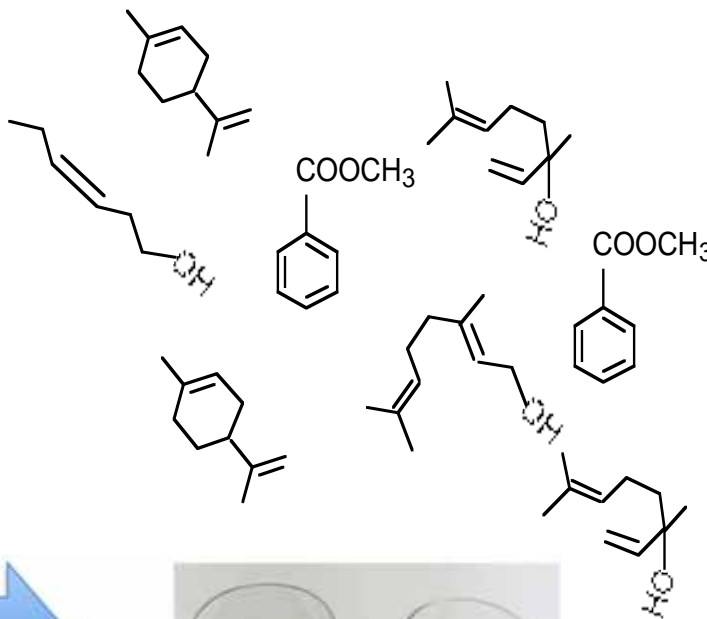


Nature des arômes



Ou en est la recherche ?

Influence des terroirs



Biosynthèse des arômes



Nature des arômes



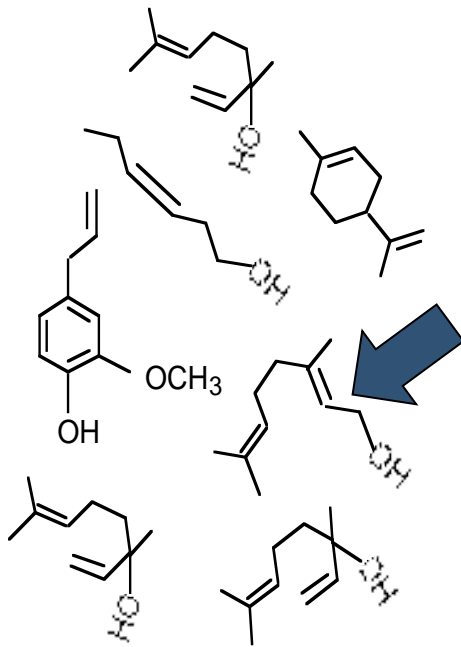
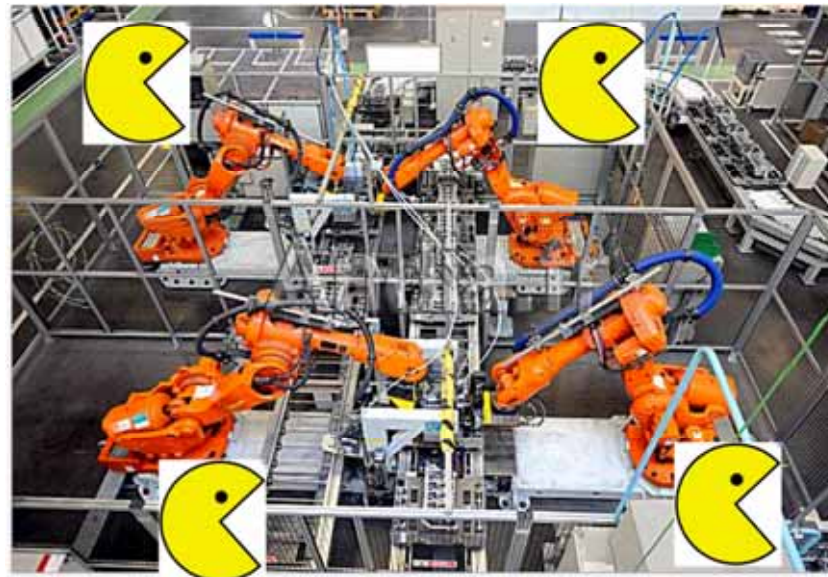
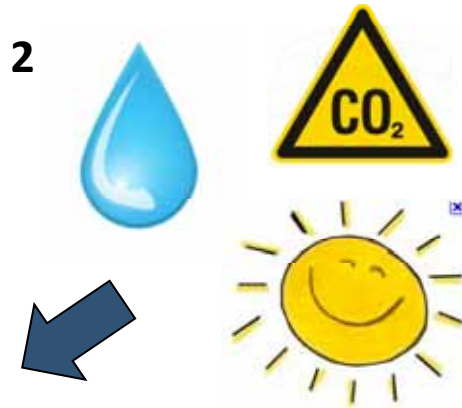
Lien entre nature et perception des arômes

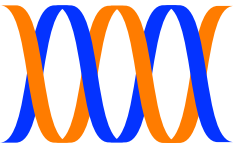


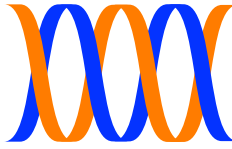
Comment les arômes de la baie de raisin sont ils fabriqués?

Gène 1  Enzyme 1

Gène 2  Enzyme 2



Enzyme 3  Gène 3

Enzyme 4  Gène 4

Déterminants de la qualité aromatique des vins?

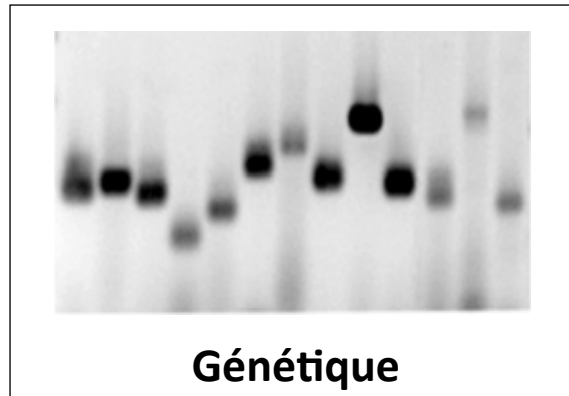
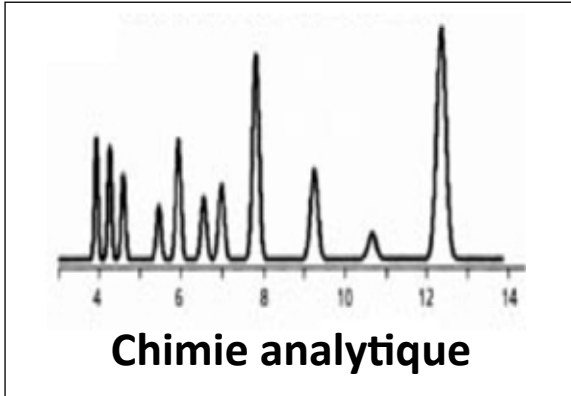
Comment les arômes sont-ils fabriqués?

→ identifier les gènes impliqués

Projet de recherche "Vitaroma"



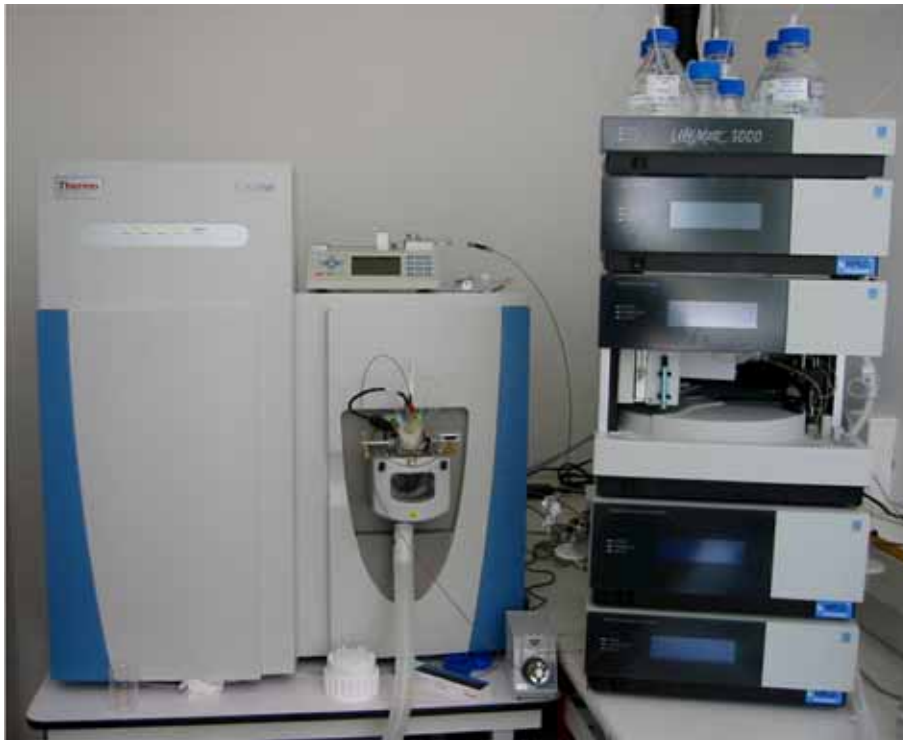
Stratégies



**Identification des gènes
impliqués dans la synthèse
des arômes**

OUTILS: PLATEFORME ANALYTIQUE

→ IDENTIFIER LES COMPOSÉS D'INTÉRÊT



TOUS TYPES DE COMPOSÉS

COMPOSÉS VOLATILS





D. STEYER



Service innovant d'analyse des arômes et
des anti-oxydants dans les boissons

OUTILS: Séquence du génome de La vigne

Vol 449 | 27 September 2007 | doi:10.1038/nature06148

nature

LETTERS

The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla

The French–Italian Public Consortium for Grapevine Genome Characterization*

The analysis of the first plant genomes provided unexpected evidence for genome duplication events in species that had previously been considered as true diploids on the basis of their genetics^{1–3}. These polyploidization events may have had important consequences in plant evolution, in particular for species radiation and adaptation and for the modulation of functional capacities^{4–10}. Here we report a high-quality draft of the genome sequence of grapevine (*Vitis vinifera*) obtained from a highly homozygous genotype. The draft sequence of the grapevine genome is the fourth one produced so far for flowering plants, the second for a woody species and the first for a fruit crop (cultivated for both fruit and beverage). Grapevine was selected because of its important place in the cultural heritage of humanity beginning during the Neolithic period¹¹. Several large expansions of gene families with roles in aromatic features are observed. The grapevine genome has not undergone recent genome duplication, thus enabling the discovery of ancestral traits and features of the genetic organization of flowering plants. This analysis reveals the contribution of three ancestral genomes to the grapevine haploid content. This ancestral arrangement is common to many dicotyledonous plants but is absent from the genome of rice, which is a monocotyledon. Furthermore, we explain the chronology of previously described whole-genome duplication events in the evolution of flowering plants.

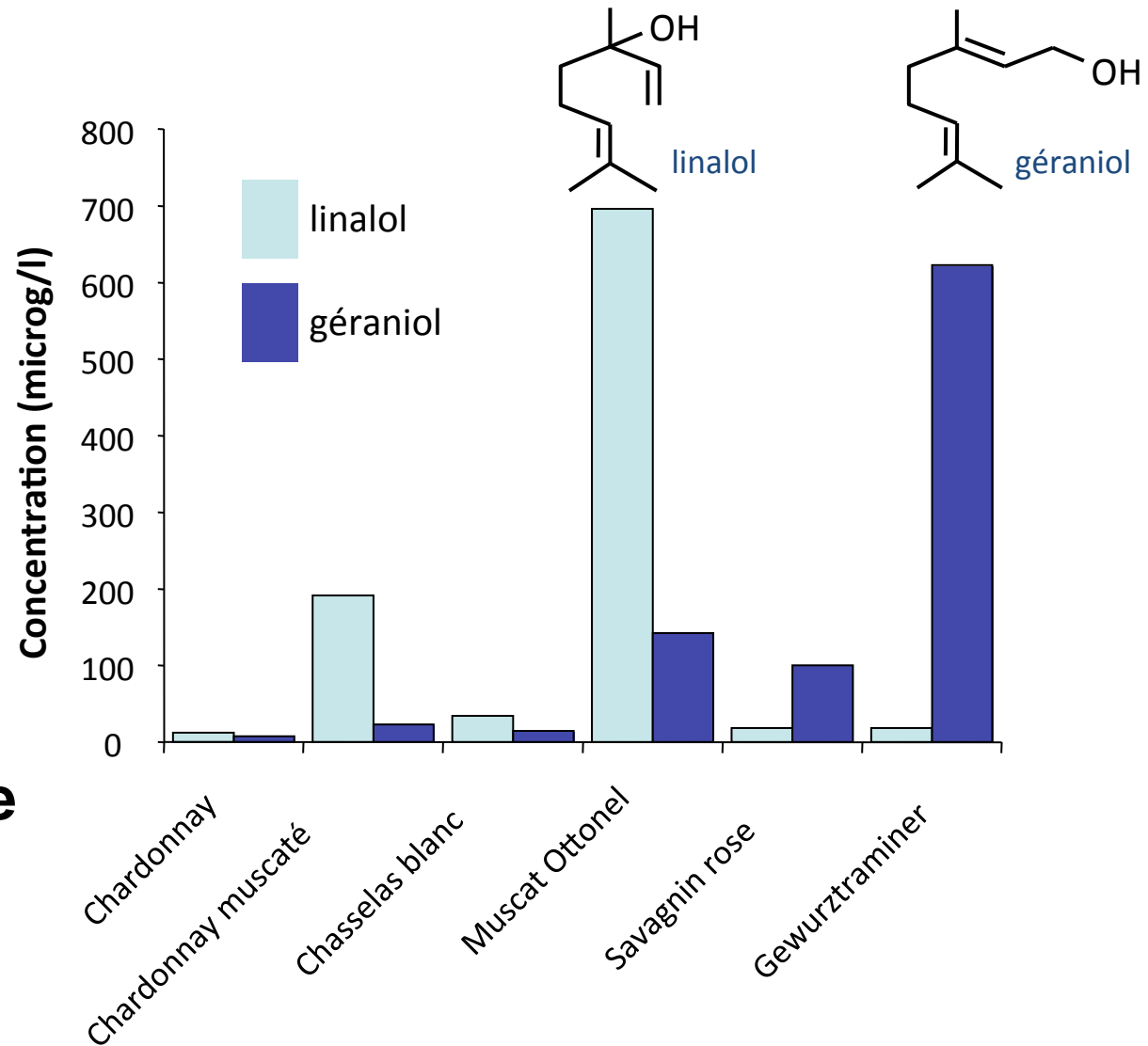
All grapevine varieties are highly heterozygous; preliminary data showed that there was as much as 13% sequence divergence between alleles, which would hinder reliable contig assembly when a whole-genome shotgun strategy was used for sequencing. Our consortium therefore selected the grapevine PN40024 genotype for sequencing. This line, originally derived from Pinot Noir, has been bred close to full homozygosity (estimated at about 93%) by successive selfings, permitting a high-quality whole-genome shotgun assembly.

A total of 6.2 million end-reads were produced by our consortium, representing an 8.4-fold coverage of the genome. Within the assembly, performed with Arachne¹², 316 supercontigs represent putative allelic haplotypes that constitute 11.6 million bases (Mb). These values are in good fit with the 7% residual heterozygosity of PN40024 assessed by using genetic markers. When considering only one of the haplotypes in each heterozygous region, the assembly (Table 1a) consists of 19,577 contigs ($N_{50} = 65.9$ kilobases (kb)), where N_{50} corresponds to the size of the shorter supercontig or contig in a subset representing half of the assembly size) and 3,514 supercontigs ($N_{50} = 2.07$ Mb) totalling 487 Mb. This value is close to the 475 Mb previously reported for the grapevine genome size¹³.

Using a set of 409 molecular markers from the reference grapevine map¹⁴, 69% of the assembled 487 Mb, arranged into 45 ultracontigs

- 1 consortium
- 2 pays
- 15 laboratoires
- 56 co-auteurs
- 4^{ème} génome de plante séquencé

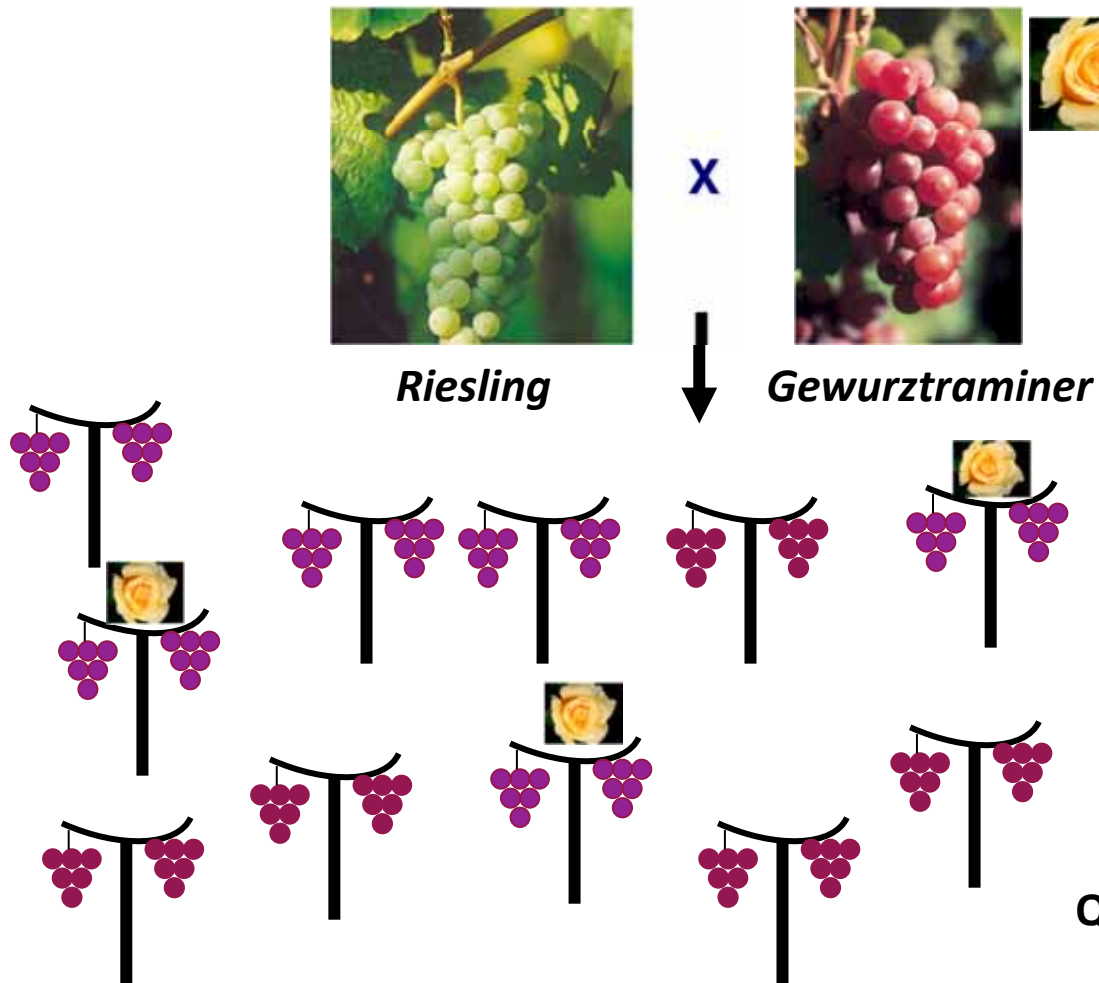
→ Richesse en terpènes



Origine du caractère
aromatique?

Stratégie → Analyses génétiques

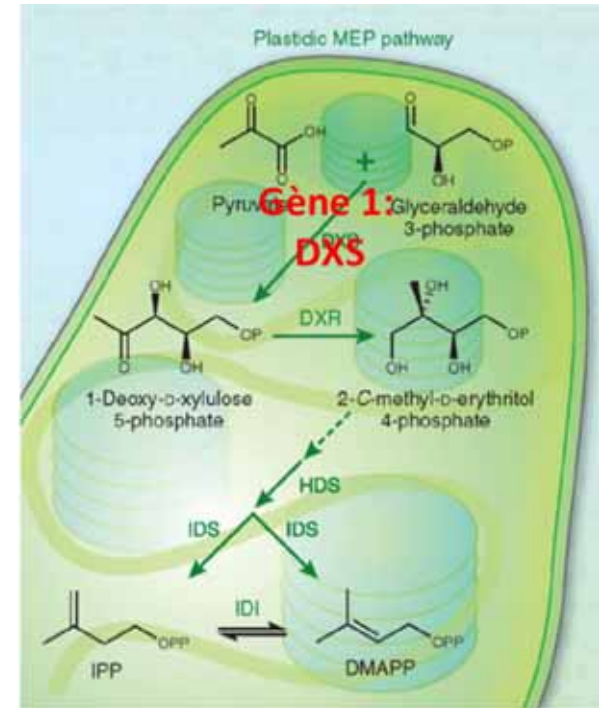
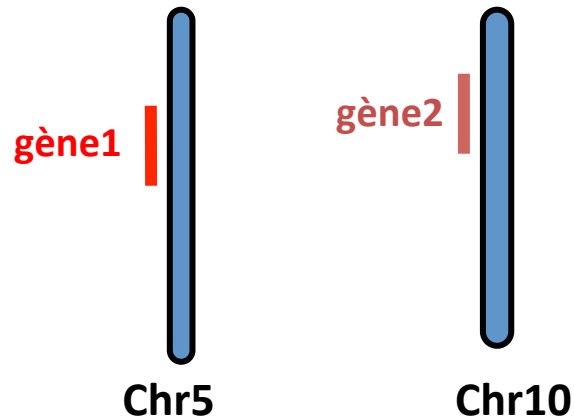
Stratégie: Analyses génétiques



Question:
Quel sont les gènes responsables?

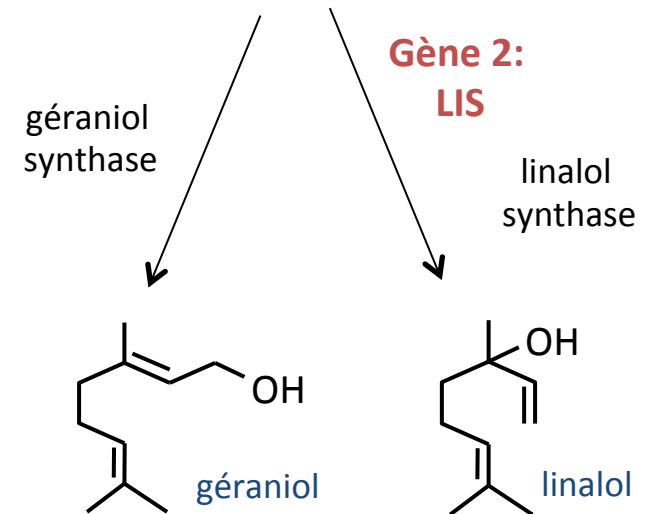
Analyse génétique du caractère aromatiques

Analyse génétique du caractère aromatique (Duchêne et al., 2009)



Gène 1: contenu en terpénols

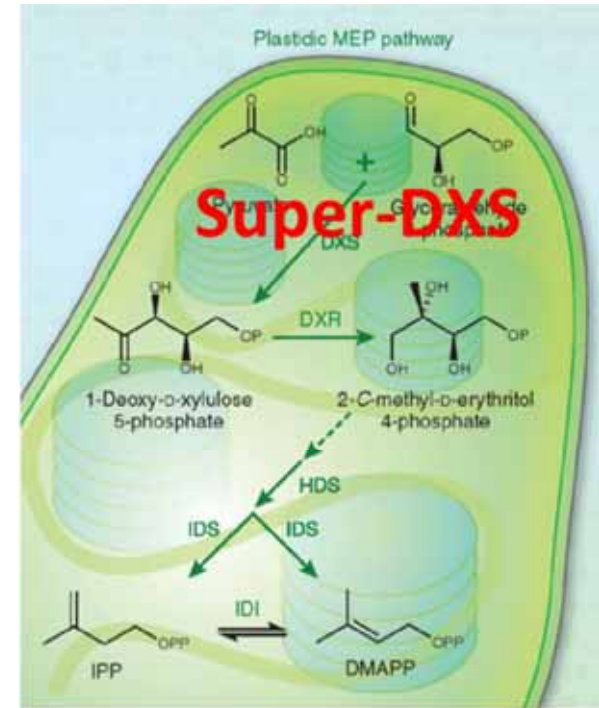
Gène 2: rapport géraniol / linalol



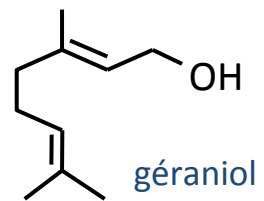
super-producteur naturel de terpènes

→ cas unique chez les végétaux → applications à d'autres modèles

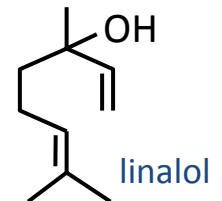
Deux mutations suffisent à expliquer l'origine des cépages aromatiques



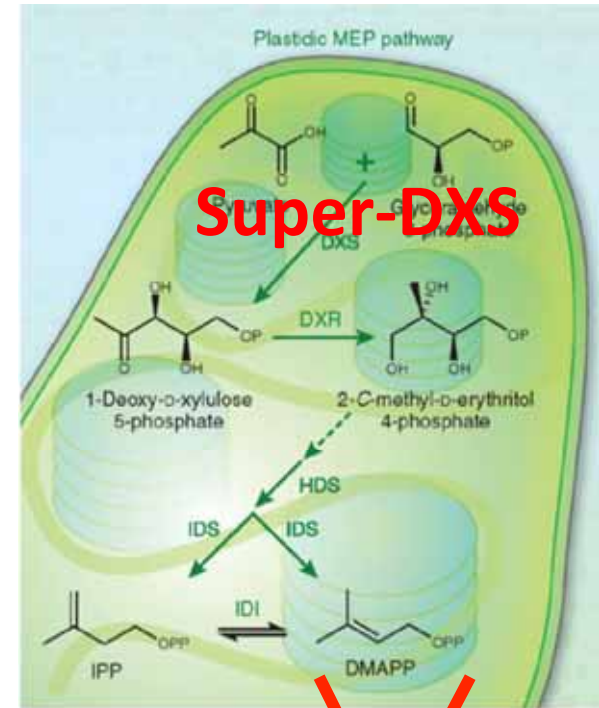
GES
géraniol
synthase



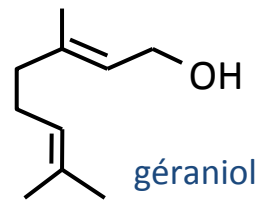
LIS
linalol
synthase



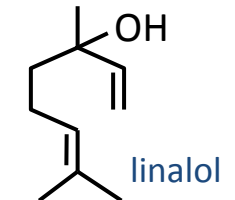
Deux mutations suffisent à expliquer l'origine des cépages aromatiques



GES
géraniol
synthase

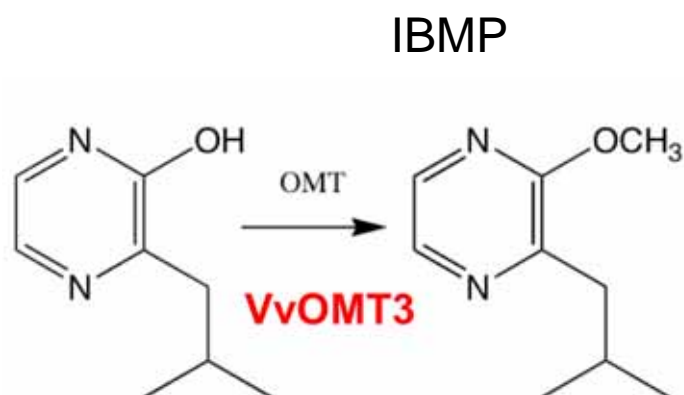


~~**LIS**~~
~~linalol
synthase~~



Caractérisation d'un déterminant majeur de la synthèse des méthoxypyrazines

- Responsable de caractères herbacés (cosse de pois, poivron)
- caractère positif (Sauvignons) ou négatif si trop prononcé
- Seuil de perception olfactive 1ng/L dans l' eau



Plant Physiology[®], June 2013, Vol. 162, pp. 604–615,


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UNIVERSITÉ DE STRASBOURG

ACQUIS

→ Caractérisation de 2 déterminants majeurs de la biosynthèse des arômes



→ maîtrise de ces caractères en création variétale

→ outils pour la maîtrise de ces caractères dans un environnement changeant

Perpectives et directions futures

**Relation entre diversité
des cépages
et diversité des arômes**



**Séquençage des génomes du
Riesling et du Gewurztraminer**



Influence des terroirs



Biosynthèse des arômes

**Alsace → Diversité des terroirs
→ Vins mono-cépages**