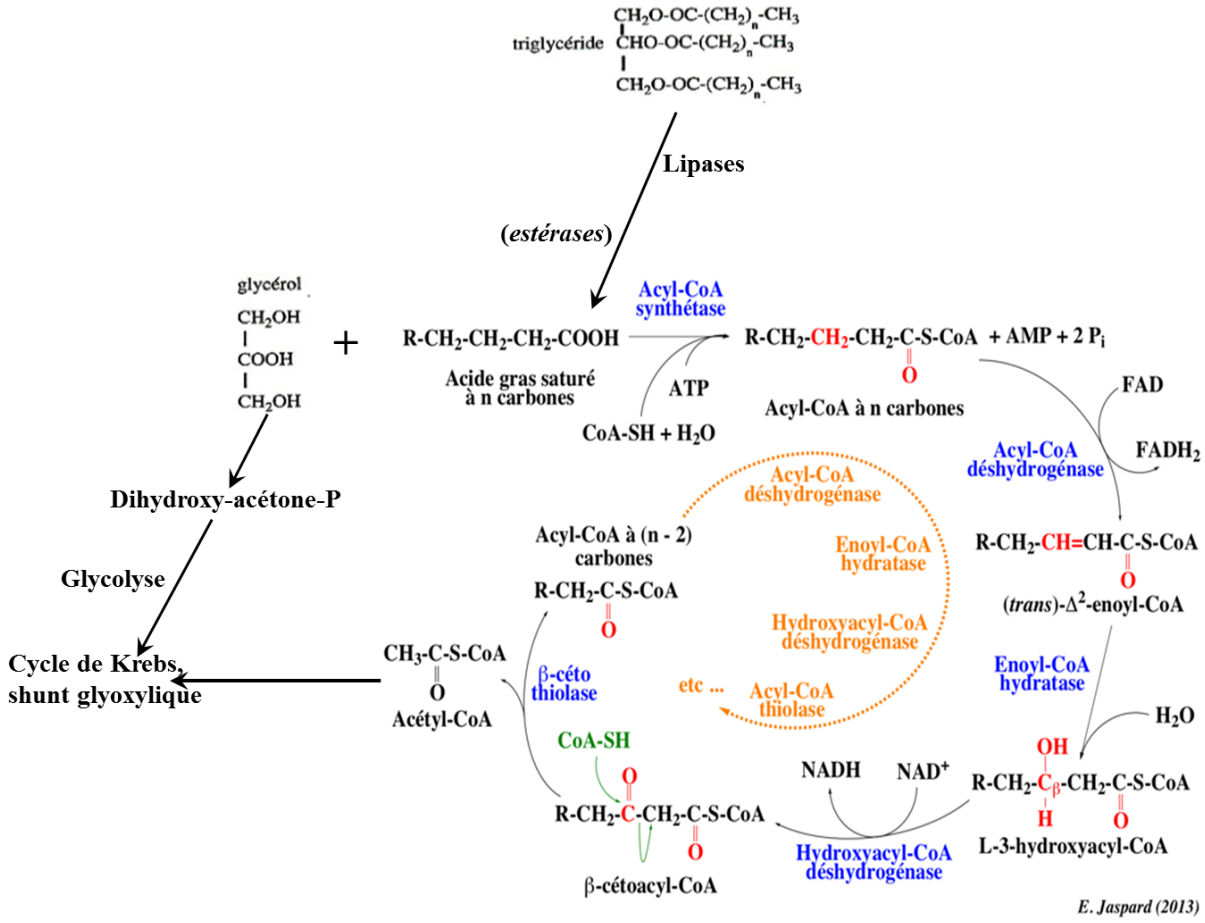
Catabolism of Other Organic Compounds

1- Lipid Degradation

Triglycerides are hydrolyzed into fatty acids and glycerol by lipases or, less specifically, by esterases, which are often extracellular. These lipases are found in molds (Aspergillus, Penicillium, Rhizopus, Geotrichum…), yeasts (Candida, Torulopsis, Saccharomyces, Saccharomycopsis…), and bacteria (Serratia, Pseudomonas, Xanthomonas, Chromobacterium, Alcaligenes, Staphylococcus…).

Glycerol enters glycolysis at the level of dihydroxyacetone phosphate. Fatty acids, on the other hand, are first activated by ATP in the presence of coenzyme A to form acyl-CoA, which is then oxidized into β-keto-acyl-CoA. After hydrolysis, acetyl-CoA is produced along with an acyl-CoA shortened by two carbon atoms. Oxidation reactions continue as needed according to the length of the carbon chain. The acetyl-CoA formed can then enter the Krebs cycle and the glyoxylate shunt.


triglycéride
Lipases
(estérases)
glycérol
Dihydroxy-acétone-P
Glycolyse
Cycle de Krebs, shunt glyoxylique
Acyl-CoA synthétase
Acide gras saturé à n carbones
ATP
CoA-SH + H2O
Acyl-CoA à n carbones
FAD
FADH2
Acyl-CoA déshydrogénase
(trans)-Δ2-enoyl-CoA
Enoyl-CoA hydratase
H2O
L-3-hydroxyacyl-CoA
NADH
NAD+
Hydroxyacyl-CoA déshydrogénase
β-cétoacyl-CoA
CoA-SH
β-céto thiolase
Acétyl-CoA
Acyl-CoA à (n - 2) carbones
etc ...
Acyl-CoA thiolase
E. Jaspard (2013)

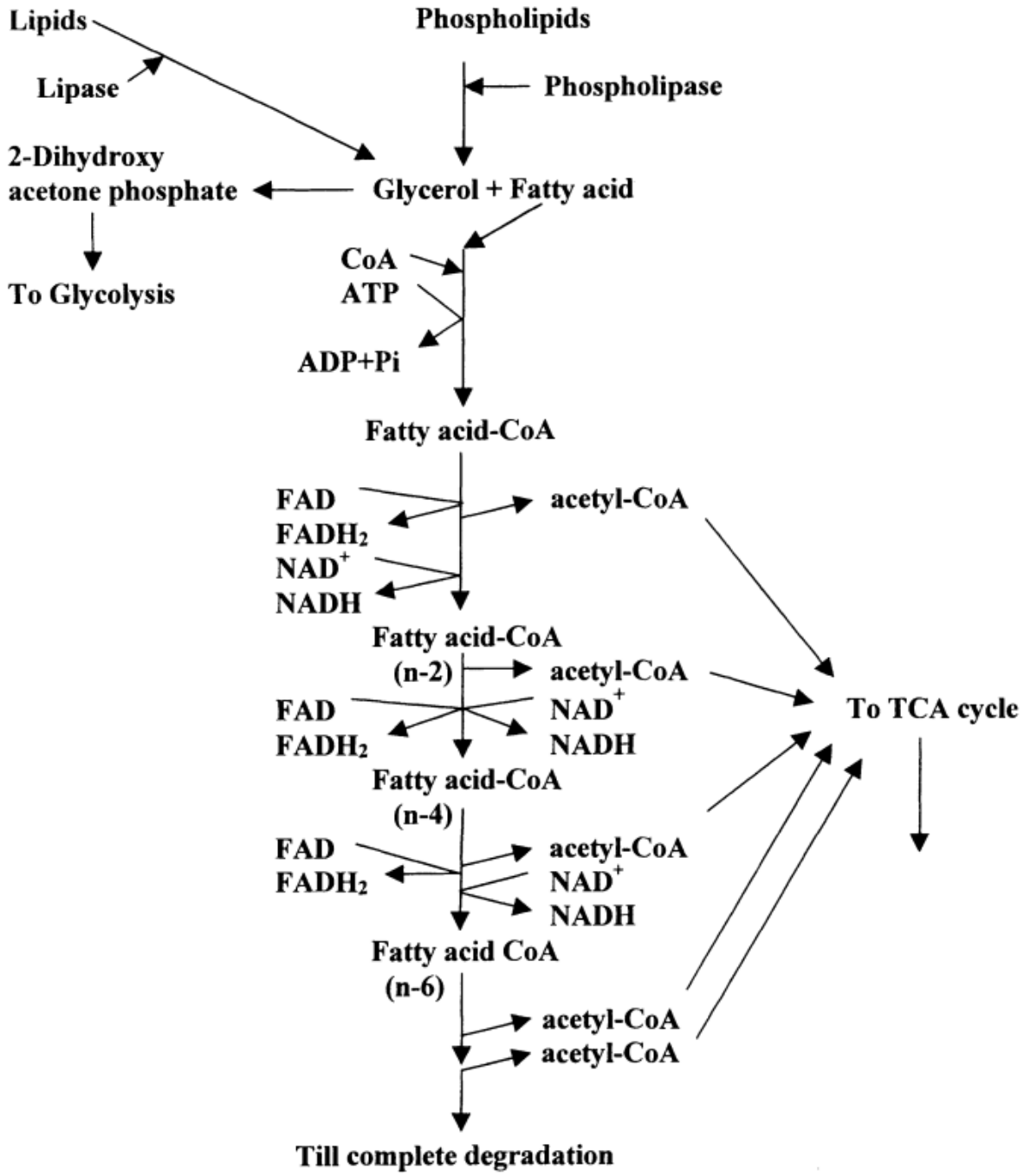


Figure 2. Schéma simplifié de l'utilisation des lipides et phospholipides

2- Catabolism of Hydrocarbons

Many *Pseudomonas* species, other bacterial groups (e.g., *Micrococcus*, actinomycetes), yeasts, and molds are capable of using almost all paraffinic and aromatic hydrocarbons as their sole carbon source.

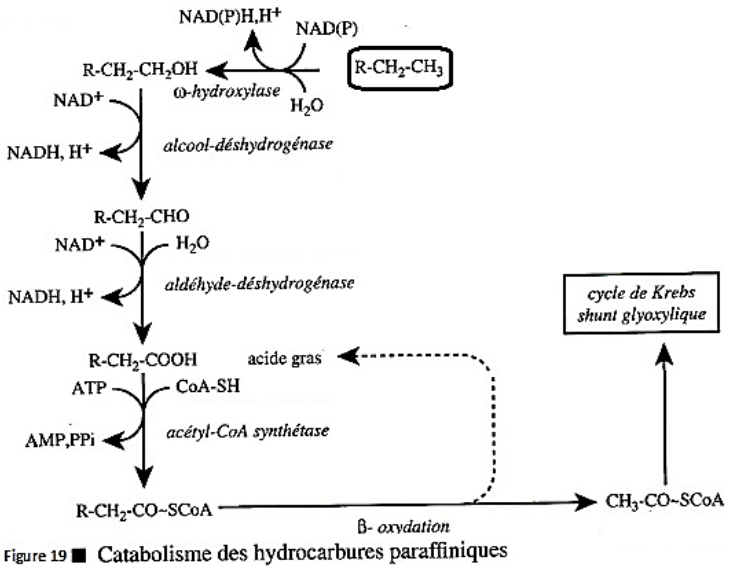


Figure 19 ■ Catabolisme des hydrocarbures paraffiniques

2-1- Paraffinic Hydrocarbons

Paraffinic hydrocarbons are oxidized in successive steps by NAD-dependent dehydrogenases via aldehydes and carboxylic acids. An acyl-CoA synthase activates the resulting monocarboxylic acid into acyl-CoA, which then undergoes β-oxidation, generating acetyl-CoA molecules through successive cleavages. A NADP-dependent ω-hydroxylase is also involved; it is found in various microorganisms, notably in *Pseudomonas oleovorans* grown on hexane.

3- Catabolism of Methane and Methanol

Microorganisms capable of growing on methane and methanol as their sole carbon source (e.g., *Pseudomonas*) oxidize methane through the following pathway:

$$CH_4 \xrightarrow{\text{methane monooxygenase}} CH_3OH \xrightarrow{\text{methanol dehydrogenase}} HCHO \xrightarrow{\text{formaldehyde dehydrogenase}} HCOOH \xrightarrow{\text{formate dehydrogenase}}$$

These microorganisms are called **methylotrophs**. They can be **strict methylotrophs** (degrading only methane or methanol) or **facultative methylotrophs** (able to degrade, in addition to methane and methanol, many one- or multi-carbon compounds).

4- Ethanol Degradation

Ethanol can be completely degraded into CO_2 and H_2O, as in certain yeasts (*Brettanomyces*, *Debaryomyces*, *Hansenula*, *Pichia*…), or it can be converted into acetic acid (*Acetobacter*, *Gluconobacter*). In both cases, the first step is the formation of **acetaldehyde**:

$$CH_3CH_2OH \xrightarrow{\text{alcohol dehydrogenase}} CH_3CHO$$

In yeasts, acetaldehyde is oxidized to acetyl-CoA and enters the Krebs cycle:

$$CH_3CHO + CoA + NAD^+ \xrightarrow{\text{acetaldehyde dehydrogenase}} CH_3CO\text{-}CoA + NADH + H^+$$

In acetic acid bacteria, acetaldehyde is further oxidized to acetic acid:

$$CH_3CHO + NAD^+ \xrightarrow{\text{aldehyde dehydrogenase}} CH_3COOH + NADH$$

This degradation is **aerobic**.

In acetic acid bacteria, acetaldehyde is directly converted into acetic acid:

$$CH_3CH_2OH + O_2 \xrightarrow{\text{alcohol dehydrogenase / aldehyde dehydrogenase}} CH_3COOH + H_2O$$

This fermentation, which forms the basis of **vinegar production**, is aerobic. Traditionally, vinegar is produced either by **surface culture** (Orléans process) or by **trickling over wooden**

chips on which bacteria are adsorbed (Schützenbach process). Nowadays, it is produced by **strongly aerated, agitated culture** (acetator, cavitator…).

5- Glycerol Degradation

The catabolism of glycerol has been studied in enterobacteria, lactobacilli, acetic acid bacteria, and *Clostridium butyricum*.

Glycerol is degraded, particularly in acetic acid bacteria, via two pathways (see figure). *Acetobacter suboxydans*, which does not possess a Krebs cycle, can nevertheless metabolize glycerol. This bacterium is used for the production of **dihydroxyacetone**, an intermediate in glycerol degradation. Dihydroxyacetone is used as a tanning agent and in cosmetics.

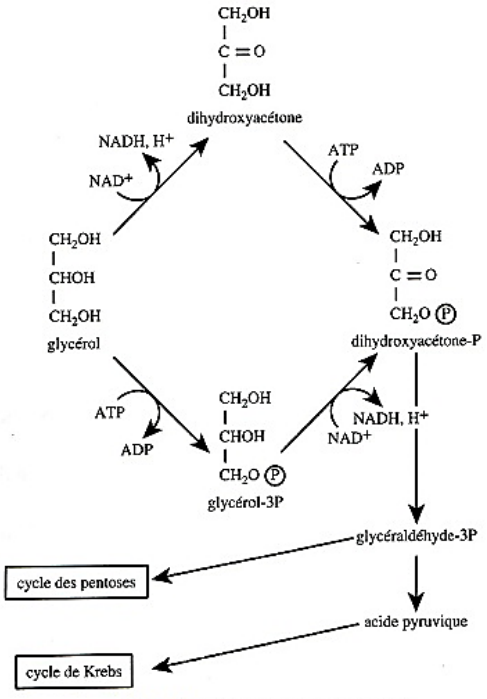


Figure 25 ■ Catabolisme du glycérol

Enterobacteria catabolize glycerol by converting it into dihydroxyacetone or glyceraldehyde-3-phosphate, which are then degraded through the glycolytic pathway. The process is purely fermentative.

Glycerol catabolism in *Escherichia coli* involves a glycerol kinase that produces α-glycerophosphate, which is subsequently converted into dihydroxyacetone phosphate.