PhénoFinlait
Cheap and large scale analysis methods to quantify milk fatty acids and proteins content

*F. Faucon-Lahalle[1,2],
B. Huquet[1], F. Barillet[3], M. Brochard[1],
G. Miranda[3], H. Larroque[3], O. Leray[4],
I. Palhière[3], J.L. Peyraud[3],
P. Martin[3] and M. Ferrand[1]*

**[1]Institut de l'Elevage ;
[2]CNIEL ; [3]INRA ;
[4]Actilait**

Context

• Evolution of **milk quality concept:**
nutritive > sanitary clean > **healthy fine composition**
• Lack of **analysis methods** for milk fatty acid (FA) and
individual protein (IP) usable at **high scale**

The french answer: PhénoFinlait research program

• Implication of every partners of french dairy industry, 1,500 commercial
farms, 3 species (cow, ewe, goat) and 7 breeds
• First objectives: develop analysis method to determine milk FA profile,
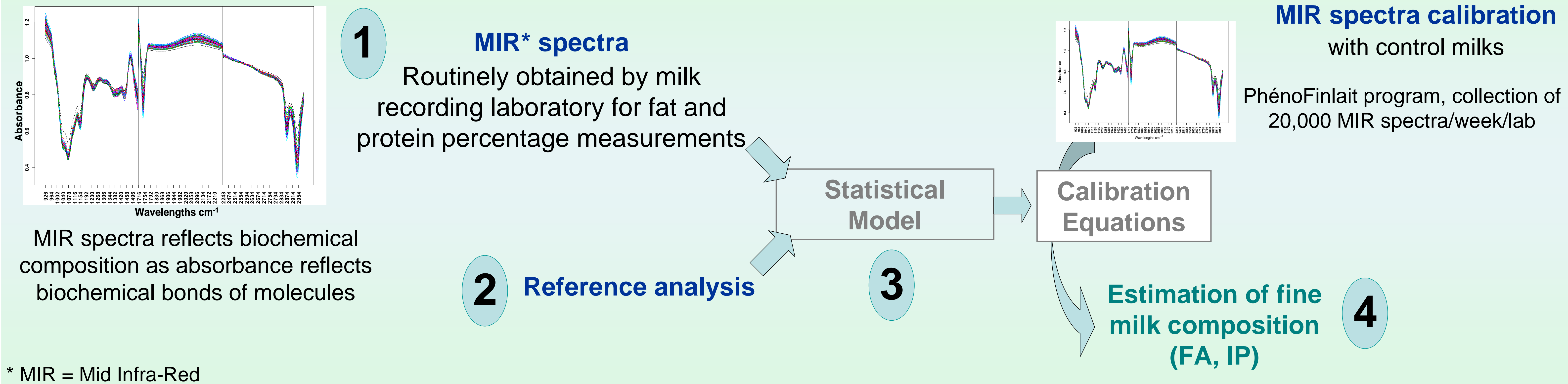create reference analysis method to determine milk IP profile

General principle of a cheap and large scale analysis method

1 **MIR* spectra**
Routinely obtained by milk
recording laboratory for fat and
protein percentage measurements

MIR spectra reflects biochemical
composition as absorbance reflects
biochemical bonds of molecules

2 **Reference analysis**

Statistical Model

3

Calibration Equations

MIR spectra calibration
with control milks

PhénoFinlait program, collection of
20,000 MIR spectra/week/lab

**Estimation of fine
milk composition
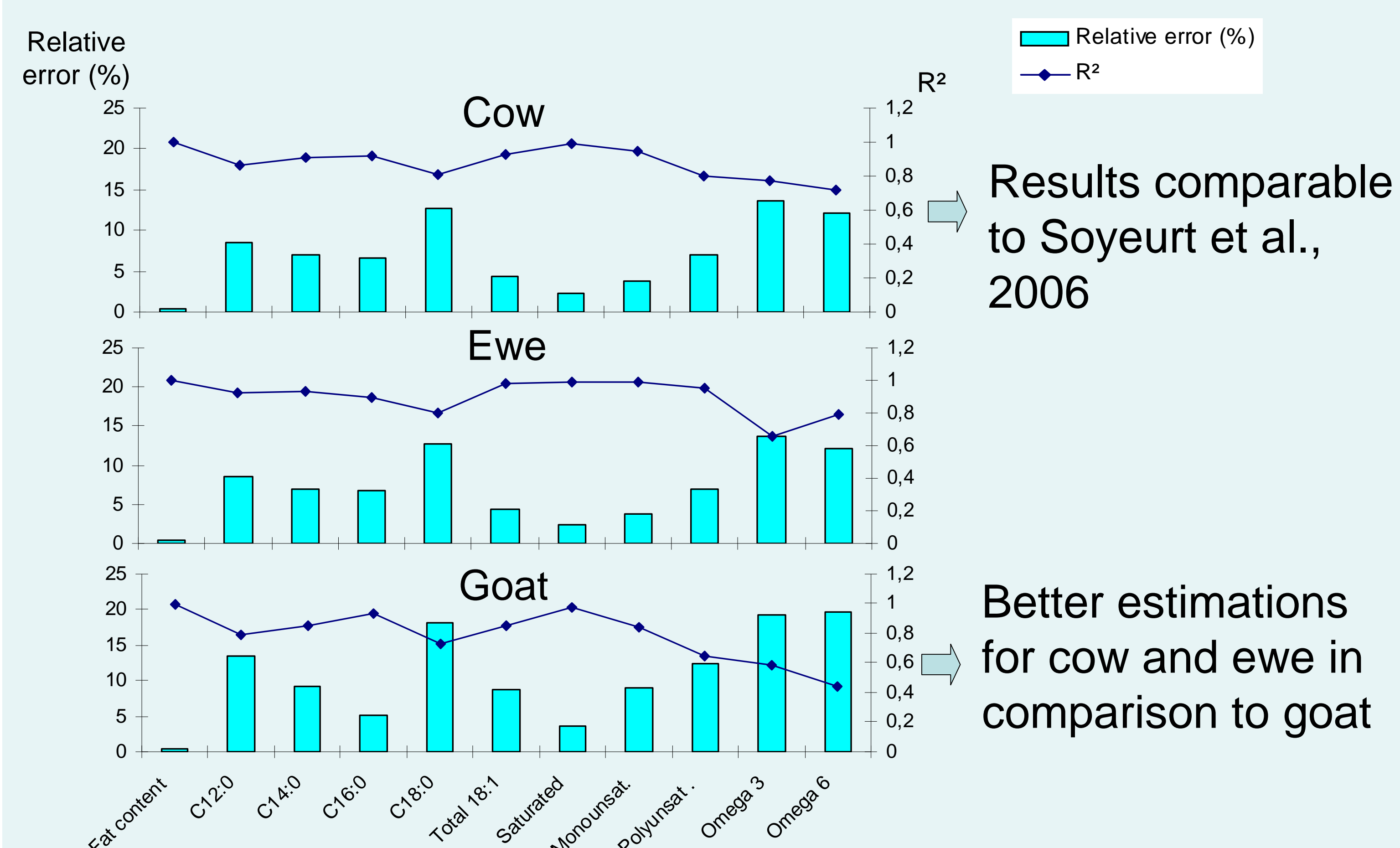(FA, IP)**

4

* MIR = Mid Infra-Red

For fatty acids

2 Gas chromatography: 400 analysis for cows,
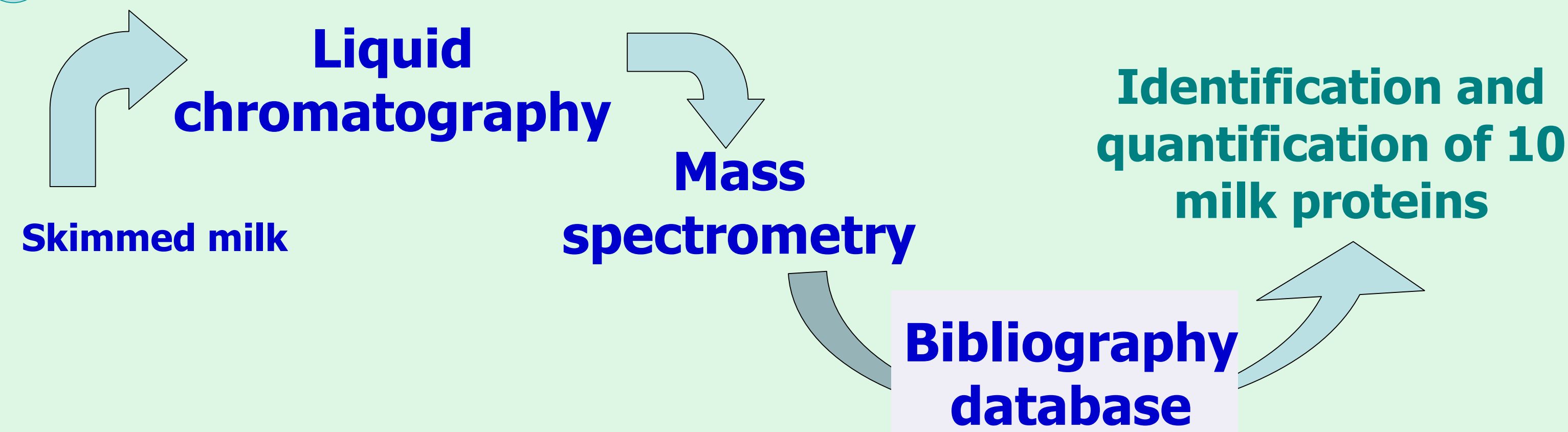200 for ewes and 200 for goats

3 a) **Selection of wavelengths** with genetic
algorithms (Leardi R. 1998, Ferrand 2009)
b) **Partial Least Square (PLS) regression**
(coefficients are applied to wavelengths)

4 Estimations usable for 15 to 20 FA

Results comparable
to Soyeurt et al.,
2006

Better estimations
for cow and ewe in
comparison to goat

For individual proteins

2 Establishment of the reference method:

Liquid chromatography

Skimmed milk

Mass spectrometry

Bibliography database

Identification and quantification of 10 milk proteins

3 Calculation with 67 cow milk samples
Partial Least Square (PLS) regression =>
coefficients are applied to wavelengths

4 Too many variants (genetic, postranscriptional…)
to have good estimations of IP
Necessity to analyze more milk samples (14,000 in
the PhenoFinlait program)

www.phenofinlait.fr