

ORIENTATESI

Cdl in Chimica e Scienze Chimiche

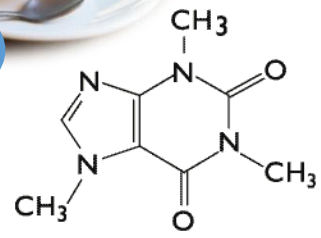
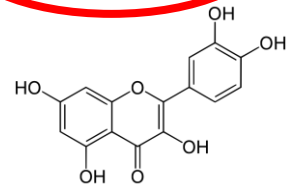
**Scegli i tuoi
esperimenti con...**

METABOLITI

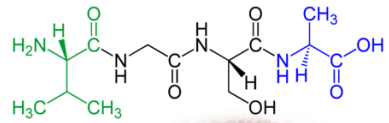
Phytochemicals



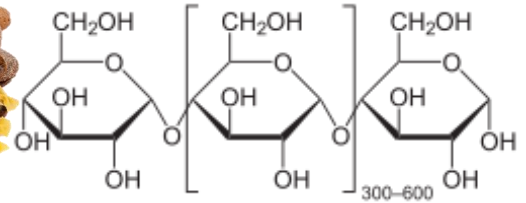
Polifenoli



Amminoacidi e proteine



Carboidrati



METABOLITI.....secondari

I metaboliti secondari sono una categoria di molecole bioattive che funzionano a basse concentrazioni e che vengono utilizzati principalmente per definire relazioni tra piante e altri organismi. Sono composti spesso cellula / tessuto o organo specifici che possono essere sintetizzati costitutivamente a livello basso ma che possono subire incrementi in seguito a risposte esterne come regolatori della crescita, condizioni di stress biotici o abiotici piuttosto che fasi di sviluppo e stagionalità.

UNTARGETED vs TARGETED



@persona 1

@persona 2

@persona 3

@persona 4

IMPRONTA DIGITALE

**Informazione Unica per
l'alimento**

**Utile per valutazione della
qualità e dello stato di salute...**

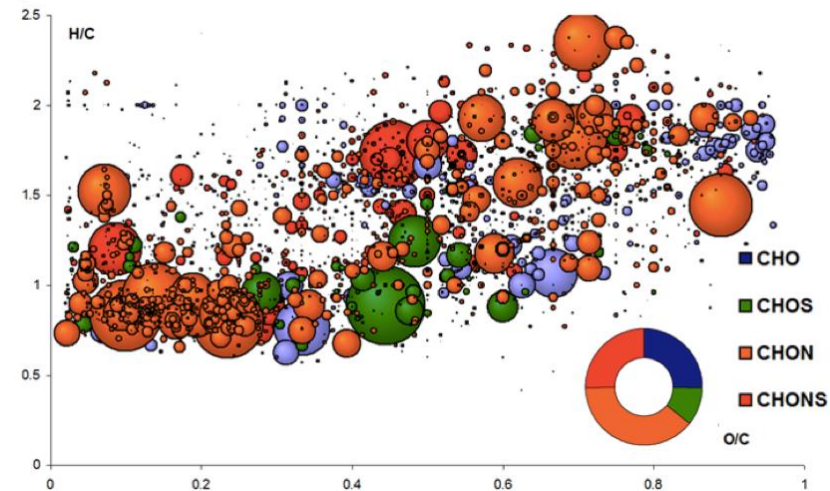
**...e per la tracciabilità e la
certificazione**



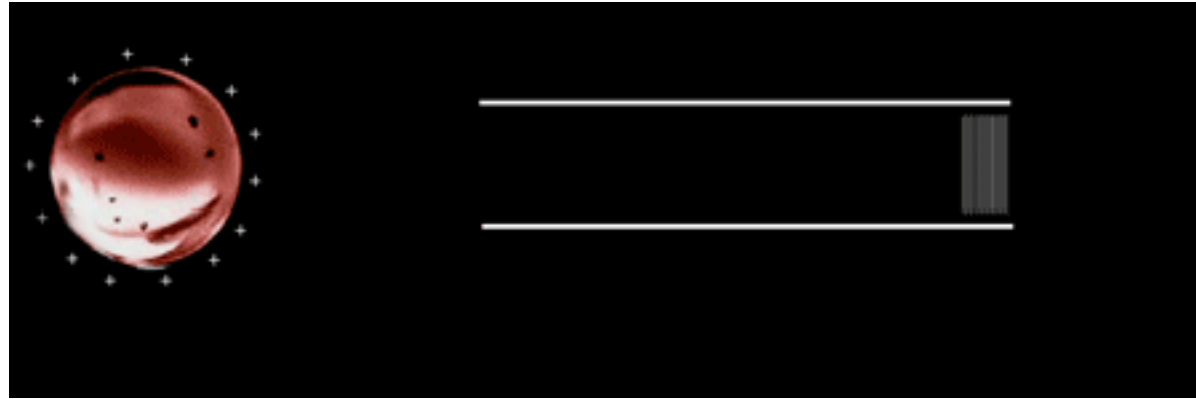
IMPRONTA DIGITALE MOLECOLARE

INFORMAZIONI UNICHE
PER L'ALIMENTO

COSTRUZIONE DELL'
IMPRONTA DIGITALE
MOLECOLARE

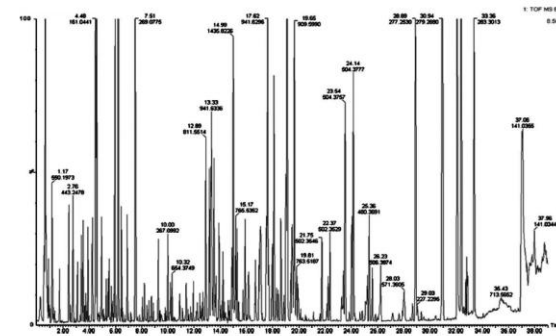
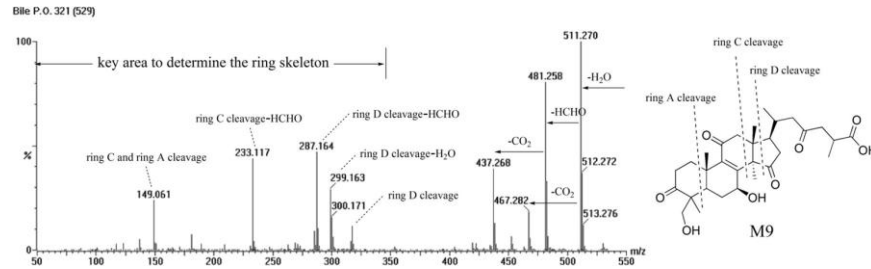


Spettrometria di massa



- E' la tecnica analitica che si basa sulla produzione di ioni da atomi o molecole (*sorgente*) i quali sono poi separati in accordo con il loro rapporto massa/carica (m/z) (*analizzatore*) e infine misurati (*rilevatore*)

MASS SPECTROMETRY

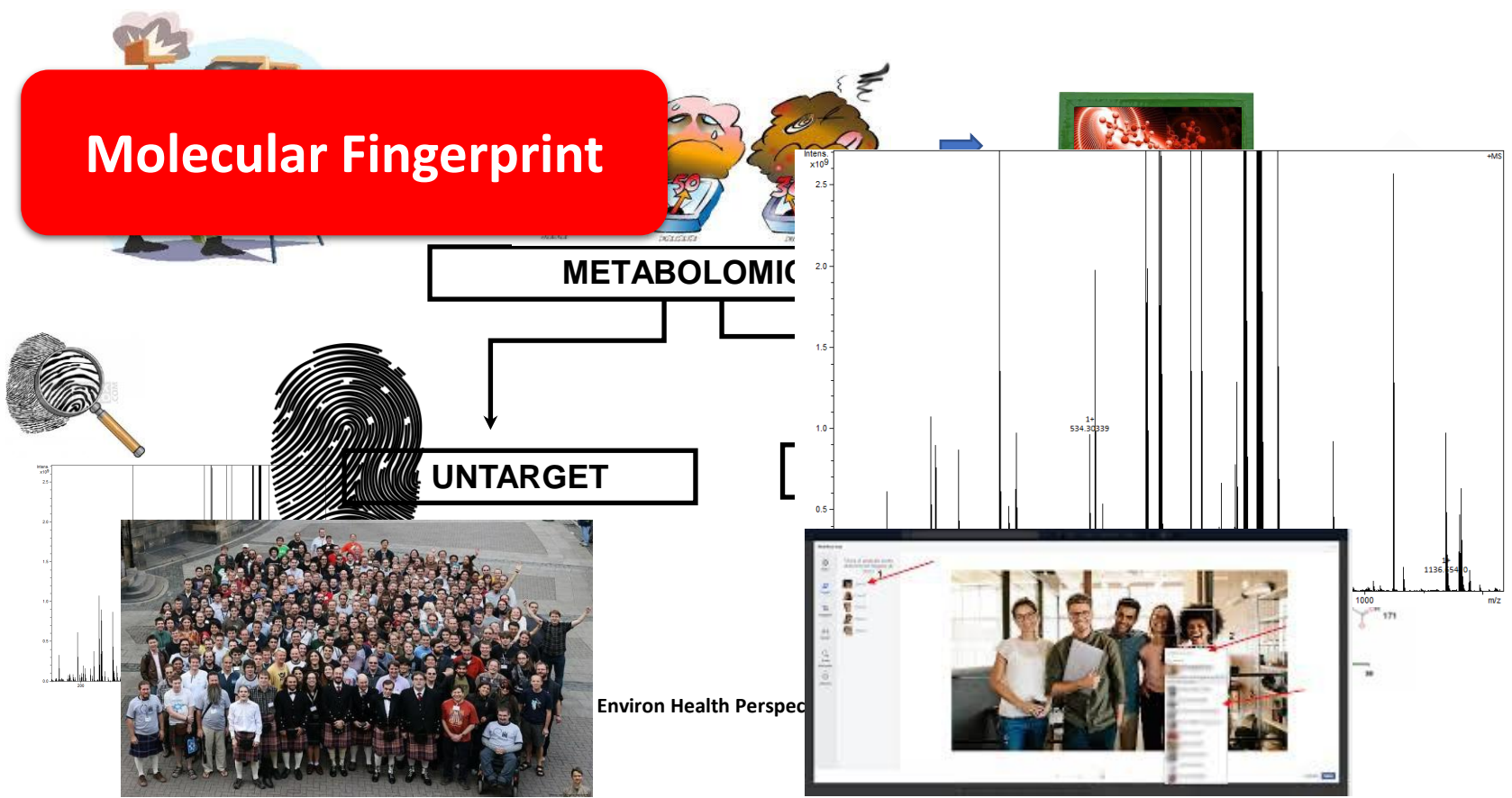


- ✓ Most common technique in Metabolomics
- ✓ High Specificity and Sensibility ($\sim 10^{-15}$ mol)
- ✓ Identification of different classes of Metabolites: **Untarget Analysis**
- ✓ Quantitative Analysis
- ✓ Coupling with Chromatographic techniques (GC-MS and LC-MS)



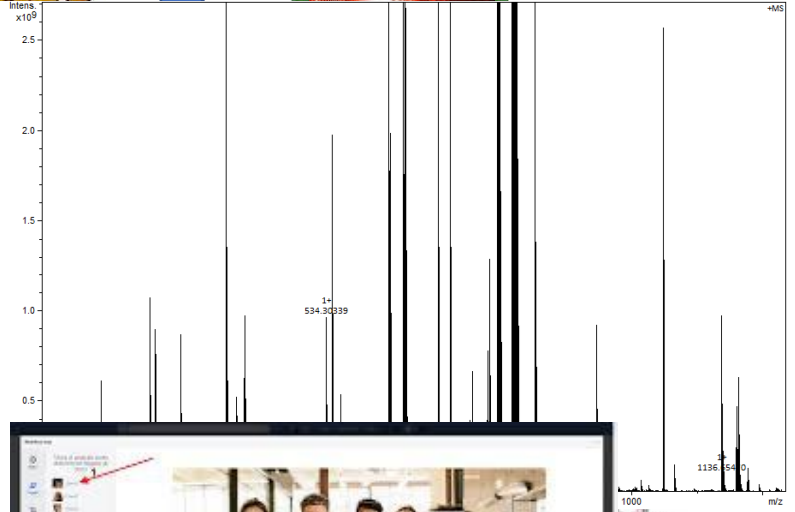
METABOLOMICS

Molecular Fingerprint



METABOLOMIC

UNTARGET

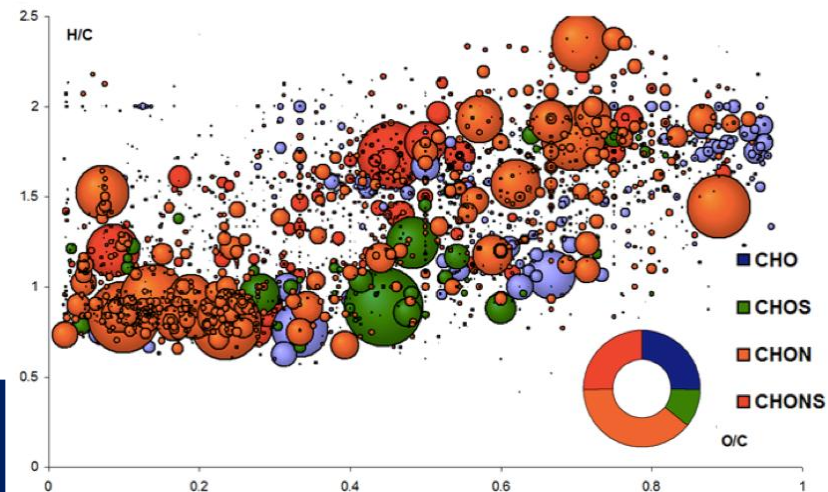


Environ Health Perspec

IMPRONTA DIGITALE MOLECOLARE

Composti	H/C	O/C
Acidi Grassi	1,4-2,3	0-0,3
Peptidi	1,0-2,4	0,2-0,8
Carboidrati	1,0-2,4	0,6-1,0
Polifenoli	0,4-1,4	0,2-0,7
Composti Condensati	0,5-1,2	0-0,4

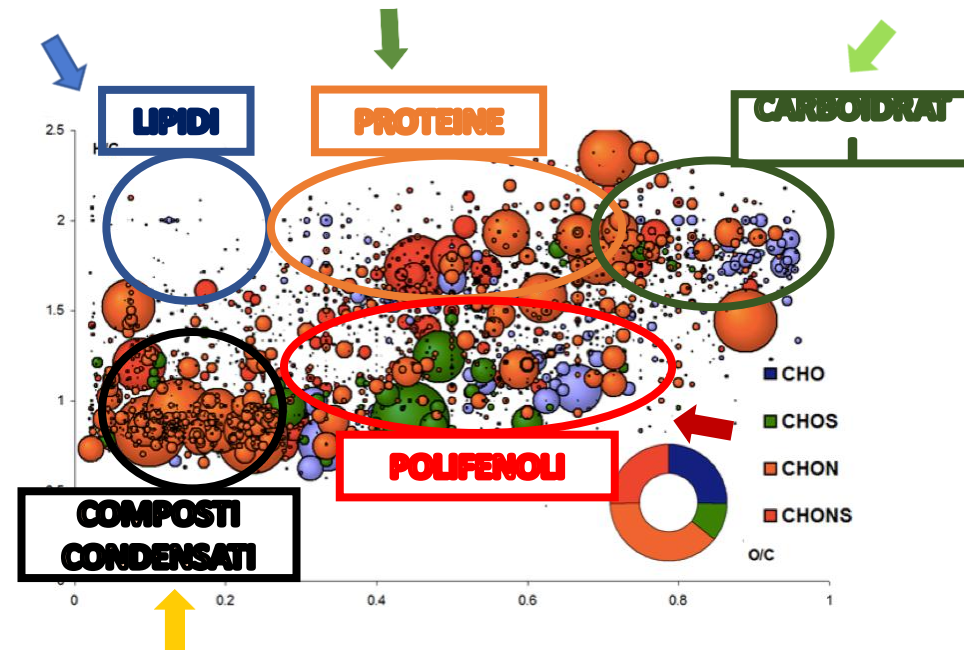
Posizione dei punti = Formula Chimica
 Atomi di Carbonio (C)
 Atomi di Idrogeno (H)
 Atomi di Ossigeno (O)



IMPRONTA DIGITALE MOLECOLARE

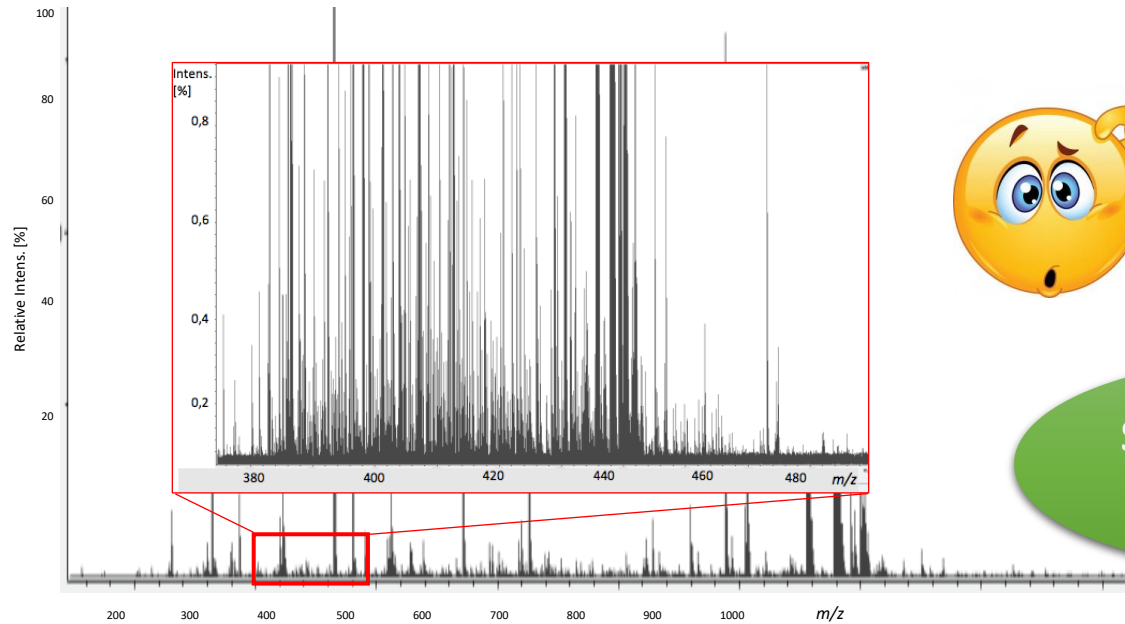


Composti	H/C	O/C
Acidi Grassi	1,4-2,3	0-0,3
Peptidi	1,0-2,4	0,2-0,8
Carboidrati	1,0-2,4	0,6-1,0
Polifenoli	0,4-1,4	0,2-0,7
Composti Condensati	0,5-1,2	0-0,4



Kuhnert, N., Dairpoosh, F., Yassin, G., Golon, A., & Jaiswal, R. (2013). What is under the hump? Mass spectrometry based analysis of complex mixtures in processed food—lessons from the characterisation of black tea thearubigins, coffee melanoidines and caramel. *Food & function*, 4(8), 1130-1147

ANALISI DEI METABOLITI



Spettro di Massa ad Alta Risoluzione (HRMS)

Spettrometro di
Massa



Kuhnert, N., Dairpoosh, F., Yassin, G., Golon, A., & Jaiswal, R. (2013). What is under the hump? Mass spectrometry based analysis of complex mixtures in processed food—lessons from the characterisation of black tea thearubigins, coffee melanoidines and caramel. *Food & function*, 4(8), 1130-1147

CALCOLO FORMULE CHIMICHE

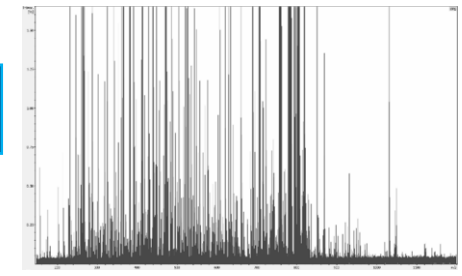
```

64- for(i in seq(1,length(Exp..m.z),1)){
65-   if(N[i]==0 & S[i]==0){
66-     x$HeteroClass[i]<-capture.output(cat(c("N",N[i],"S",S[i]), sep = ""))
67-   } else {
68-     if (N[i]!=0 & S[i]==0){
69-       x$HeteroClass[i]<-capture.output(cat(c("N",N[i]),sep = ""))
70-     } else {
71-       if (N[i]==0 & S[i]!=0){
72-         x$HeteroClass[i]<-capture.output(cat(c("S",S[i]),sep = ""))
73-       } else {
74-         if (N[i]==0 & S[i]==0){
75-           x$HeteroClass[i]<-c("CHO")
76-         }
77-       }
78-     }
79-   }
80- }

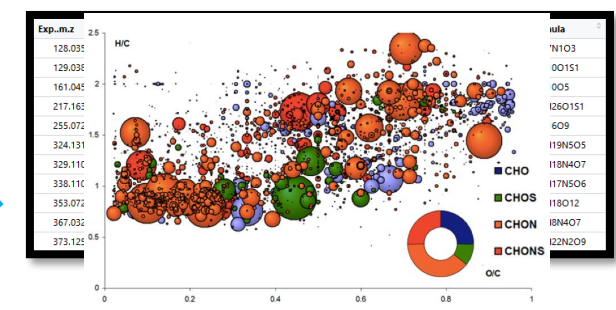
40 vk_diagram<-function(z, manualcolors = c("blue","green","red", "yellow"), title =
41   gsize = FALSE, galpha = FALSE, widjitter = 0.1, xlabel = "o/
42   ylabel = "H/C", legend_title = "Type of Formula"){
43   vkdiagram<-ggplot(data = z, aes(x = OC,y = HC))
44   vkplor<-vkdiagram +
45     geom_point(aes(color = Formula_type, size = Abundance, alpha = 0.5), position
46     scale_colour_manual(legend_title, values = manualcolors) +
47     scale_x_continuous(limits = c(0,1)) +
48     scale_y_continuous(limits = c(0,2.5)) +
49     scale_size(range = c(2,12), guide = gsize) +
50     scale_alpha(guide = galpha) +
51     theme_classic() +
52     theme(axis.title.x = element_text(hjust = 1, face = "bold"),
53           axis.title.y = element_text(hjust = 1, face = "bold")) +
54     xlab(label = xlabel) +
55     ylab(label = ylabel) +
56     ggtitle(label = title)

206 for c in seq(1, maxc, 1){ #obviously our molecules contain at least 1 C and 1
207   for h in seq(1, maxH, 1){ #Based on seven golden rules, a minimum/maximum
208     hcrat = (h)/(c)
209     if 0.2 < hcrat < 3.1:
210       for p in seq(0, maxP, 1){
211         for o in seq(1, maxO, 1){
212           ocrat = (o)/(c)
213           if ocrat < 1.2:
214             for n in seq(0, maxN, 1){
215               ncrat = (n)/(c)
216               if ncrat < 1.3:
217                 for s in seq(0, maxS, 1){
218                   srat = (s)/(c)
219                   rdbe = c - h/2 + n/2 + 1
220                   if (srat < 0.8){
221                     if (rdbe > 0.5){ #Another constraint is a
222                       if (mode2 == "yes"){

```

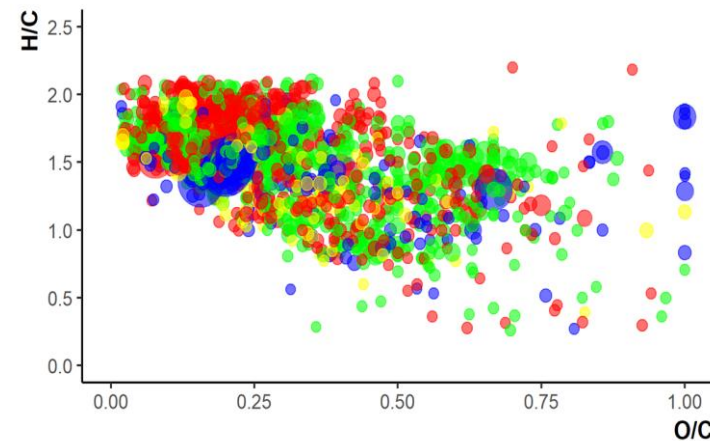
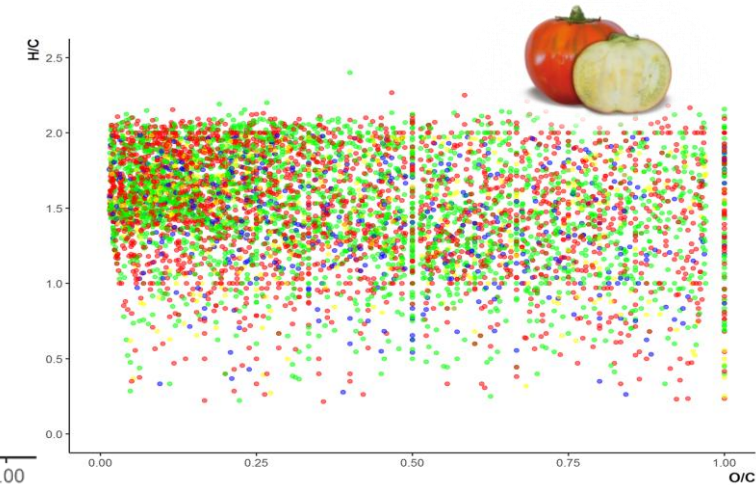
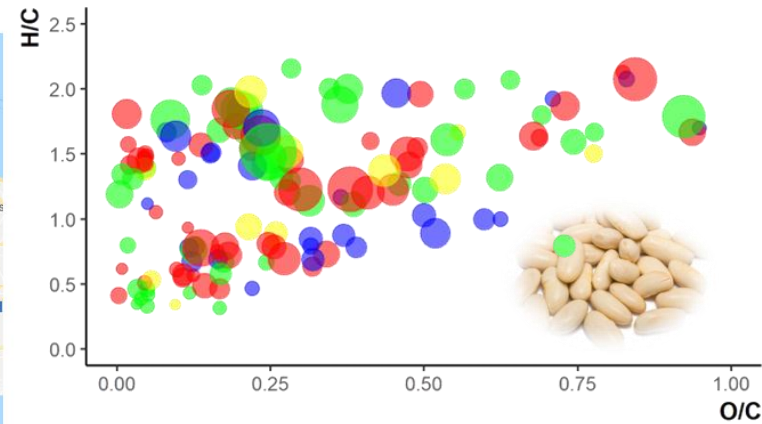


Spettro di massa ad Alta Risoluzione (HRMS)

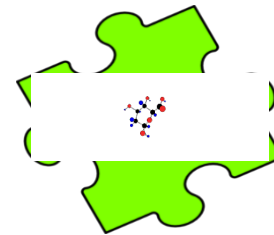
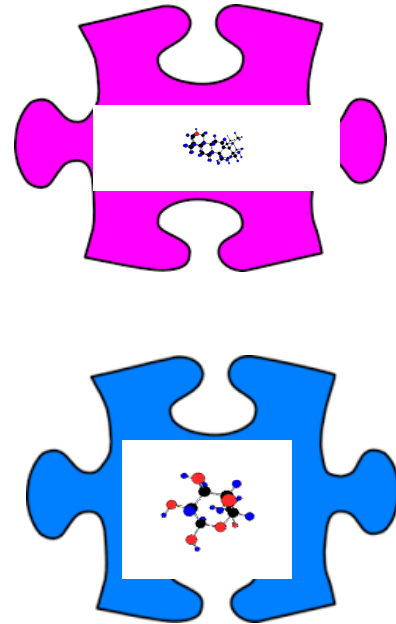
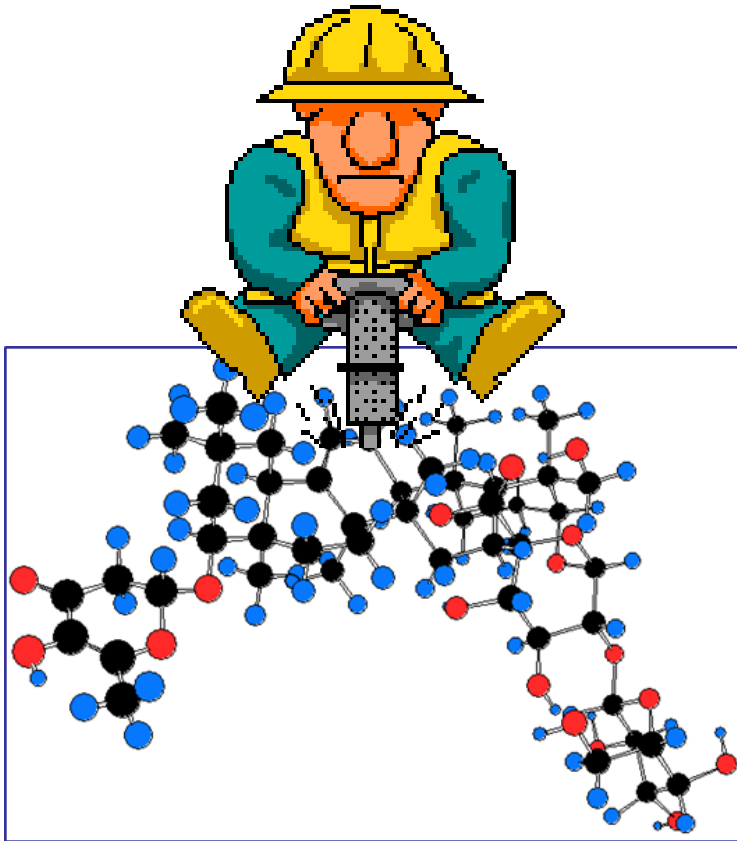


Kuhnert, N., Dairpoosh, F., Yassin, G., Golon, A., & Jaiswal, R. (2013). What is under the hump? Mass spectrometry based analysis of complex mixtures in processed food—lessons from the characterisation of black tea thearubigins, coffee melanoidines and caramel. *Food & function*, 4(8), 1130-1147

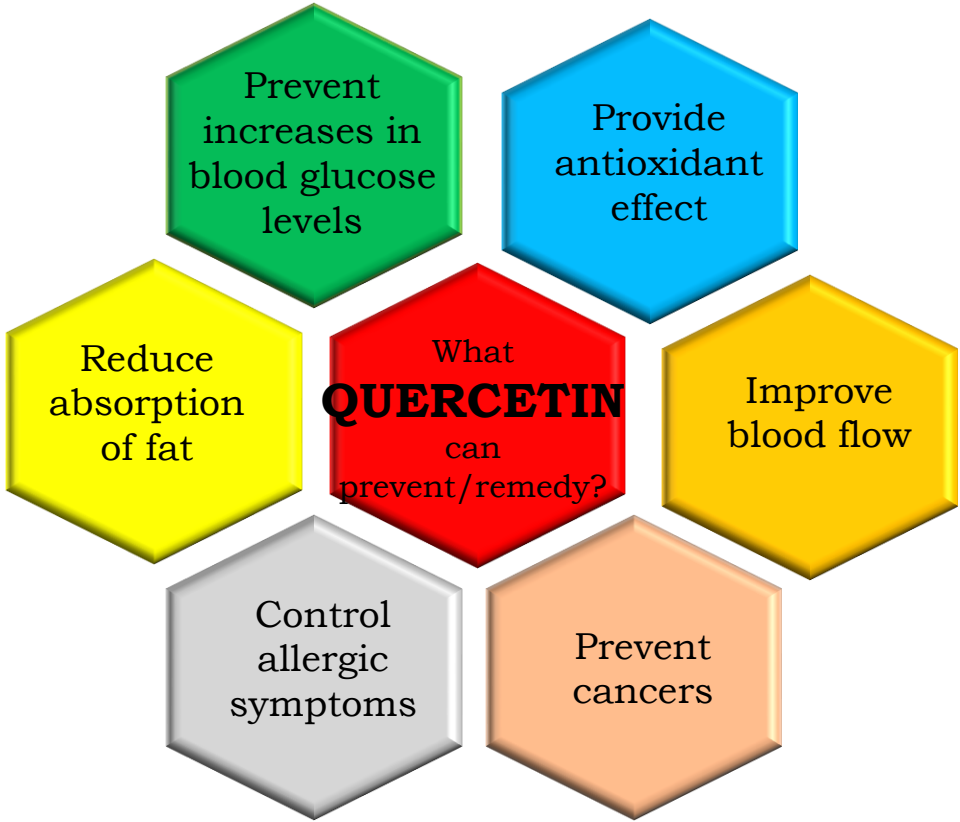
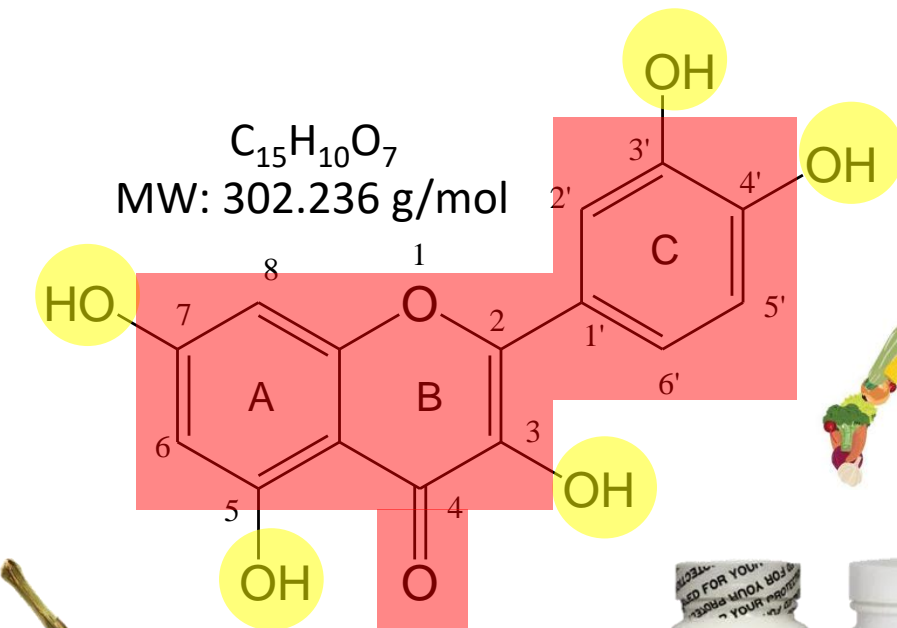
CARTOGRAFIA DEI PRODOTTI TIPICI LUCANI



Caratterizzazione strutturale TARGETED mediante MS/MS



Identificazione TARGETED dei derivati della quercetina nei peperoni di Senise LC-ESI(-)-LTQ-MSMS



Identificazione TARGETED dei derivati della quercetina nei peperoni di Senise LC-ESI(-)-LTQ-MSMS

1.



EXTRACTION

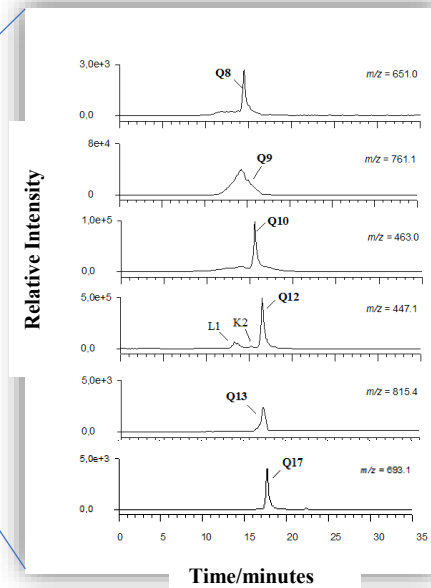
Extraction solvent:
MeOH 100%

2.

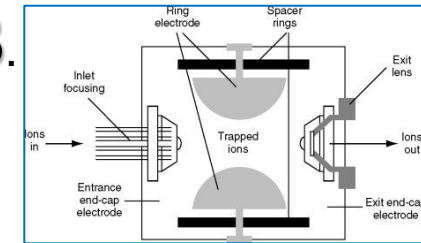


LC SEPARATION

Luna-C18 (2) (150 ×
4.6 mm, 3.0 μm)



3.



STRUCTURAL CHARACTERIZATION

ESI(-) Ionization
LTQ analyzer

Low-Resolution Mass spectrometry

- Resolving power < 10,000 at m/z 868.5
- Error > 5 ppm
- No accurate mass measurements

