

LC-MS/MS based metaproteomics allows reaching simultaneously the functional microbiome and human proteins which are differentially expressed

As an example, we compared swabs of the forehead surface of three female subject to the forehead surface of three male subject



Results: summary female vs male skin swabs

	Identified proteins	Quantifiable proteins	Proteins showing statistical variation of abundance
Human	2535	2520	1011
Bacteria	614	609	291
Fungi	375	366	67
Multiple taxa	47	46	16
TOTAL	3571	3541	1385

Identified and differentially expressed proteins



Example: Involved proteins in lipid metabolism

Accession	Description	p-value	Abundances (Grouped): Male	Abundances (Grouped): Female	Abundance Ratio: (Male) / (Female)
Lipid degradation Human proteins					
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens	0,0016	91,8	108,2	0,85
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens	0,0012	76,5	123,5	0,62
P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens	0,0365	85,2	114,8	0,74
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens	0,0045	81,4	118,6	0,69
Q9NZ01	Very-long-chain enoyl-CoA reductase OS=Homo sapiens	0,0097	94,7	105,3	0,90
Lipid synthesis Bacteria proteins					
D4HAF0	Methylmalonyl-CoA carboxyltransferase 12S subunit OS=Propionibacterium acnes (strain SK137)	0,0001	70,8	129,2	0,55
E6D5I9	Methylmalonyl-CoA epimerase OS=Propionibacterium acnes HL110PA4	0,0001	75,9	124,1	0,61
F1UEF3	Methylmalonyl-CoA carboxyltransferase 1.3S subunit OS=Propionibacterium acnes HL043PA1	0,0002	69	131	0,53
D1YD03	Acyl carrier protein OS=Propionibacterium acnes J139	2,45E-06	51,7	148,3	0,35
E4HHT9	Methylmalonyl-CoA mutase, small subunit OS=Propionibacterium humerusii HL044PA1	0,0003	81,9	118,1	0,69
D1YBL3	Methylmalonyl-CoA mutase large subunit OS=Propionibacterium acnes J139	0,0006	78,6	121,4	0,65
A0A0E1YIU8	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (flavodoxin) OS=Propionibacterium acnes HL097PA1	0,0008	79,6	120,4	0,66
D4HDE4	Acyl transferase domain protein OS=Propionibacterium acnes (strain SK137)	2,55E-05	73,4	126,6	0,58
D1YD01	Acyl transferase domain protein OS=Propionibacterium acnes J139	0,0036	78	122	0,64
E4HJA7	Acyl-CoA dehydrogenase, C-terminal domain protein OS=Propionibacterium humerusii HL044PA1	0,0162	84,8	115,2	0,74
E4HGK7	Uncharacterized protein OS=Propionibacterium humerusii HL044PA1	0,0044	69,5	130,5	0,53

For bacteria: synthesis of lipid is upregulated in female group
 For human: degradation of lipid is upregulated in female group



Conclusion

Our LC-MS/MS metaproteomics workflow allows reaching the interoperability of functions between microbiome and host. Coupled to our CORAVALID™ bioinformatics modules, we can get a complete understanding on incurred effects

