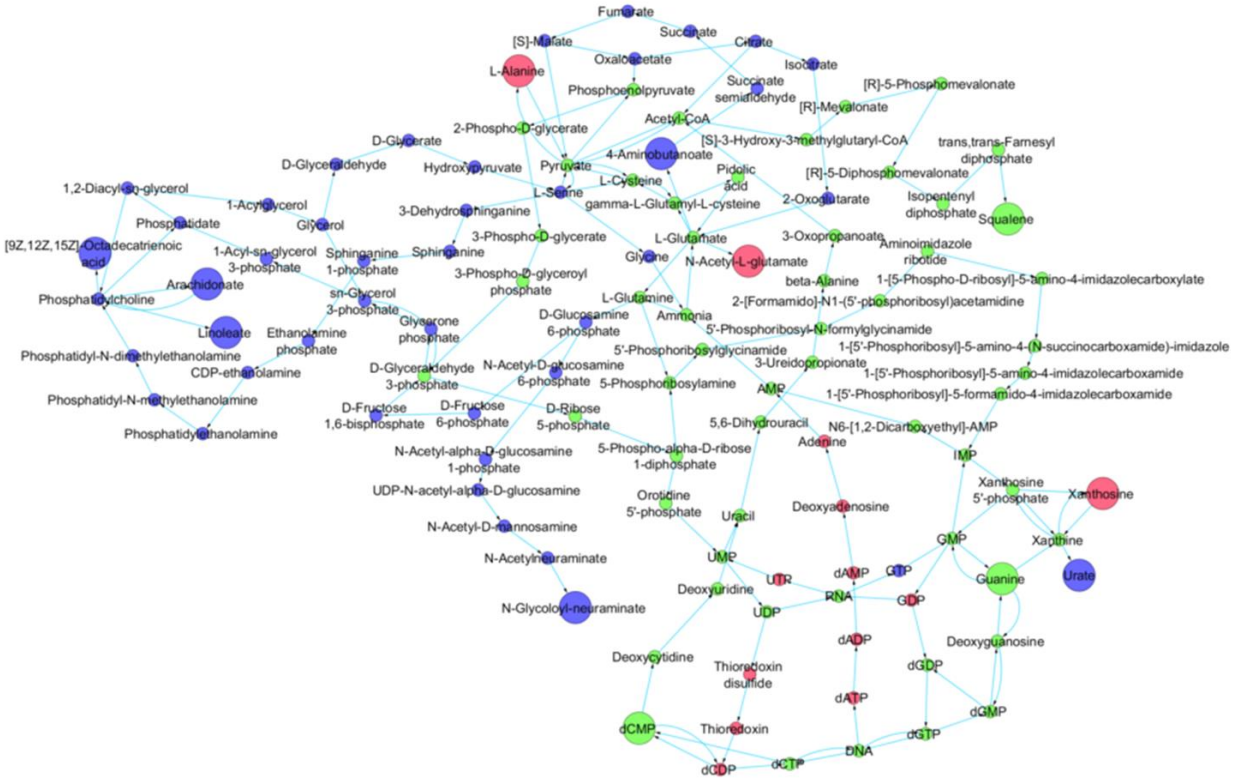
Leticia Abecia is a postdoctoral fellow working in the rumen microbial ecosystem research team at Estación Experimental del Zaidín (CSIC-Spain). My main activity relates to testing different CH_4 mitigation nutritional strategies in ruminants as shown in recent publications (Abecia et al., 2012; 2013; 2014). For my STSM, rumen samples were collected from doe goats at weaning and their offspring one month after weaning, which were receiving an antimethanogenic compound (bromochloromethane), and used for an untargeted metabolomics study with the aim of identifying metabolites whose concentration was related to CH_4 production in the animal. The purpose of the STSM at INRA-Clermont Ferrand with Dr. Diego Morgavi and his team was to learn how to process data obtained from a metabolomics platform (Metabolon platform in our case). For that purpose, following the recommendations from the host institution, it was decided to use the web server MetExplore version 2.4 (http://metexplore.toulouse.inra.fr/metexplore2/). MetExplore was released in 2010 and it is dedicated to the analysis of genome scale metabolic networks. Once registered on the server, KEGG (Kyoto Encyclopedia of Genes and Genomes) database (http://www.genome.jp/kegg/) was used to download the KEGG metabolic pathway for *Capra hircus* that was used as BioSource. From a total of 473 biochemicals detected in the rumen by the platform, only metabolites that were statistically significant in adult goats at weaning were converted to KEGG ID using the following interface: http://cts.fiehnlab.ucdavis.edu/conversion/batch, introduced in MetExplore and mapped with the KEGG database. From 46 metabolites identified, 27 were converted to KEGG ID and only 11 were mapped by the database. However, only 8 biomarkers out of 11 were linked in a sub-network. The same process was repeated with metabolites identified as statistically significant in the rumen of young animals, one month after weaning. This time, only 11 metabolites out of 16 were converted to KEGG ID and the 6 metabolites found in the database were linked in a sub-network. Then, both sub-networks were merged in one and sent to Cytoscape version 3.2. Cytoscape is an open source bioinformatics software platform (http://www.cytoscape.org) for visualizing complex networks and integrating these with any type of attribute data. Cytoscape helped us to visualize biomarkers and be able to study the pathways affected when the animals were treated or untreated with an antimethanogenic compound at two different ages. The results showed that some metabolic pathways were affected in both groups of animals however some others were specific for each group of age. The metabolic pathways affected by bromochloromethane in the rumen of doe goats were higher (blue) than in the undeveloped rumen from offspring (red). The metabolic pathways affected in both groups of age are represented in green in the figure presented below.



Thanks to the STSM, I learnt how to use bioinformatics tools for the analysis of my experiments related with methane emission. The visit to INRA was very useful for me but still more analyses need to be done in order to identify key metabolites and include them as results in a scientific paper that we plan to write together. If the key metabolites identified at the end of the work could be easily determined, this would be highly supportive to establish breeding programs for low methane emitters. METHAGENE would benefit from this information and would be able to propose easy to record and inexpensive proxies for methane emissions to be used for genetic evaluations. To our knowledge, this is the first attempt made to link metabolites in the rumen with the production of methane. In this sense, the STSM will strengthen my research career and the international network of collaborations not only with Diego´s group, but also with other groups involved in the COST Action.