Perturbed human sub-networks by Fusobacterium nucleatum candidate virulence proteins

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Motivation
Fusobacterium nucleatum is a gram-negative anaerobic species residing in the oral cavity and implicated in several inflammatory processes in the human body. Although F. nucleatum abundance is increased in inflammatory bowel disease subjects and is prevalent in colorectal cancer patients, the causal role of the bacterium in gastrointestinal disorders and the mechanistic details of host cell functions subversion are not fully understood.
Methods
We devised a computational strategy to identify putative secreted F. nucleatum proteins (FusoSecretome) and to infer their interactions with human proteins based on the presence of host molecular mimicry elements. We mapped the FusoSecretome interactors on a binary human interactome and, by using the OCG algorithm, we studied its modular structure of in order to identify host cellular functions that are likely perturbed by F. nucleatum candidate virulence proteins.
Results
FusoSecretome proteins share similar features with known bacterial virulence factors thereby highlighting their pathogenic potential. We show that they interact with human proteins that participate in infection-related cellular processes and localize in established cellular districts of the host-pathogen interface. Our network-based analysis identified 31 functional modules in the human interactome preferentially targeted by 138 FusoSecretome proteins, among which we selected 26 as main candidate virulence proteins, representing both putative and known virulence proteins. Finally, six of the preferentially targeted functional modules are implicated in the onset and progression of inflammatory bowel diseases and colorectal cancer.
Overall, our computational analysis identified candidate virulence proteins potentially involved in the F. nucleatum-human cross-talk in the context of gastrointestinal diseases.