

SAGE analysis of *Anopheles* and *Plasmodium* transcriptomes during the salivary phase of infection.

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Sporozoite transmission during the mosquito bite is a major bottleneck in the *Plasmodium* life cycle. Transmission depends on the capacity of *Plasmodium* sporozoites to invade the salivary glands of their mosquito vector and to survive during several days in close contact with salivary proteins, some of which have biological activities that are potentially deleterious to sporozoites. In addition, during the time-course of their storage in the gland, sporozoites have to undergo a specific genetic program that equips them with the proteins required for hepatocyte invasion and subsequent liver stage development in their vertebrate host. To date, the interactions occurring between salivary gland components and the parasites are largely unknown. With the goal of collecting basic information on salivary gland protein functions and of describing the response of the salivary cells to *Plasmodium* sporozoite invasion, we have initiated a transcriptome analysis of the salivary gland response to *Plasmodium* using SAGE (Serial Analysis of Gene Expression) technology, in the *P.berghei/A.gambiae* model. Four SAGE libraries (two control libraries from non infected salivary glands and two libraries from infected glands at different times after the infecting blood-meal) were characterized and compared.

In total, more than 150000 tags were sequenced, corresponding to about 33000 different tags, coming from both *Anopheles* and *Plasmodium* cDNAs. Statistical comparisons of the libraries reveal tags that are differentially represented in infected/non infected salivary glands. These differentially expressed genes encode proteins involved in essential cellular responses such as stress responses, fatty acid metabolism, innate immunity and as well as secreted proteins that will potentially end up in saliva. The differential expression is being confirmed by quantitative RT-PCR.