revealed that both programs are equally profitable. However, with use of 2-stage schemes there is more control on rates of inbreeding which is beneficial on the long term.
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Massive transcriptome sequencing in sole

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The rapid development of Next Generation Sequencing (NGS) techniques has transformed the way genomic research and characterization of genomes is done today. They can be applied to a wide variety of biological questions, from the sequencing of complete eukaryotic and prokaryotic genomes and transcriptomes, genome-scale analysis of DNA–protein interactions to metapopulation studies. Ultra-high throughput sequencing of the transcriptome (RNA-seq) has become a powerful and attractive alternative technology for gene discovery, transcript quantification and marker discovery. In this presentation, we focus on the use of NGS in sole transcriptomics. Particularly, we have performed two 454 runs for transcriptome analysis in Senegalese sole. In the first run, we tried to evaluate the defence mechanisms against pathogens throughout a better knowledge of the transcriptome of five immunostimulated organs (a pool of Head kidney, spleen, thymus, brain, gills).
We obtained 723,729 sequencing reads (N50 contig size: 431 base pairs). *De novo* assemblies yielded 117,152 contigs with 191,152 reads remaining as singletons. Based on sequence similarity with known proteins, contig sequences represented approximately 28,000 annotated genes. In the second run we studied the transcriptome after salinity changes in pooled samples of larvae, kidney, brain, intestine and gills. The number of reads was 812,279 with a N50 contig size of 628 bp. The number of contigs achieved was 73,026 of which approximately 35,000 were annotated. The number of singletons was 76,308. At this moment, we are building a database to make all these sequences public. Also, we are using all this information to the design of new and improved high-throughput array tools to be applied in sole physiological studies.
All this information will be complemented with new NGS data from AQUAGENET project (SUDOE Interreg IVB sole). This cooperation project will bring together new genomic data from *S. senegalensis* and *S. solea* species using genome, transcriptome and mapping data in order to build a complete database for genomic resources in sole species.