

## Genome wide survey of the Toll-like receptor family in the Mediterranean sea urchin

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Toll-like receptors (TLRs) represent a conserved family of proteins widely expressed in eukaryotes. They play crucial roles in the innate immune system recognizing different pathogen-associated molecular patterns. In mammals the TLR family comprises 10-13 members, while a huge number of TLR-like genes were recovered in *S.purpuratus*[1-3]. The *Paracentrotus lividus* genome project recently generated a new high-quality assembly of the genome that represents a valuable resource also for clarifying the evolutionary origin of immune system. In order to identify TLR genes in *P.lividus*, a genome wide survey was carried out and BLAT searches retrieved 119 TLR genes (PlivTLRs). *Ab initio* gene predictions and *in silico* analyses allowed us to compute gene structures and define TSS, start/stop codons and PolyA sites in the retrieved sequences. Remarkably, differently from other species, several PlivTLR genes possess one or two introns interrupting the coding region and two different predictions were often obtained, both compatible with TLR protein structures. To support predictions and to get functional information, we examined the available *P.lividus* transcriptomes. Based on transcriptomic analysis, more than 50% of PlivTLRs resulted expressed and ~30% of genes without matching sequences probably represent pseudogenes, due to defects in TSS, coding region or PolyA signal. A molecular phylogenetic analysis aiming to classify PlivTLRs and gain insights into TLR evolution is in processing. Comparative genome analyses confirm the massive expansion of such family in sea urchins and suggests that TLRs are likely to function as part of a fundamentally different immune mechanism.

1-3. Rast group (2006, 2012, 2015)