Future work

To better understand the nature of the aPKC^{TS} allele concerning to its kinase function and activity we will perform *in vitro* kinase assays under different temperatures. It is also interesting to test if we can complement the aPKC^{TS} maternal phenotype by overexpressing *aPKC^{TS}*. This would argue towards the quantitative model regarding aPKC^{TS}. In the case of *aPKC^{PB1}* allele we intent to confirm that mutant aPKC^{PB1} do not interact with PAR6 biochemically.

If aPKC^{TS} is abnormally interacting with some proteins, resulting in the observed phenotypes, it would be interesting to identify by immunoprecipitation and then by mass spectrometry analyses, which are the proteins that aPKC^{TS} is not interacting with.

Taking advantage of the aPKC^{TS} zygotic phenotype, we would like to do a dominant enhancer/suppressor screen, using deficiencies covering the *Drosophila* genome.

To better understand the formation of the follicular epithelium, during mesenquimal to epithelial transition of PFCs, we will take benefit of Par6-GFP and DE-Cad-GFP lines, expressed both in mutant and WT background, and perform *in vivo* analyses of this MET process.