Plants encode large sets of cell surface pattern recognition receptors that are able to detect "non-self" microbe-associated molecular patterns (MAMPs) such as bacterial flagellin. In Arabidopsis thaliana the bacterial flagellin epitope flg22 is a potent elicitor of the Pattern-Triggered-Immunity (PTI) response which converts the leaf intercellular space into a defensive compartment as the end point. The introduction of the otherwise virulent pathogen Pseudomonas syringae pv. tomato DC3000 (Pto) into PTI-activated leaf tissue results in an extended period of non-virulent stasis in which Pto fails to deliver type III secretion system effectors (T3Es) into host cells, does not proliferate, and fails to cause disease associated symptoms. The molecular mechanism(s) by which the PTI response induces non-virulent stasis are not understood. To determine the physiological changes associated with the non-virulent stasis of Pto in PTI-activated leaves, we have conducted preliminary dual RNA-seg transcriptome profiling of Arabidopsis and Pto inoculated into flg22 pre-treated leaves. Using the Pto RNA-seq results as a guide, we generated mutant and over expression bacterial strains to attempt to either reproduce or alleviate PTI-induced stasis. We also used various peptide/amino acid co-infiltration treatments to alleviate non-virulent stasis. Preliminary RNA-seq profiling revealed that PTI may be associated with reprograming the expression of Pto virulence genes. Overexpression of the virulence regulating sigma factor HrpL in *Pto* could delay the restriction of Type III effector translocation but only temporarily. However, we also found that co-infiltration of *Pto* with 1% tryptone (enzymatic digest of casein) was sufficient to partially alleviate non-virulent stasis even in leaves with fully established PTI. These results indicate that (i) restriction of Type III effector translocation and (ii) altered amino acid/nutrient status could be key components of the elusive PTI-induced non-virulent stasis. These observations are important clues towards a mechanistic understanding of the highly effective innate immune defenses of plants.