Coral reefs are vital marine ecosystems which are declining due to pressures such as elevated temperature, ocean acidification, nutrient loading, and increased incidence of disease. It is thought that these pressures have a negative effect on corals' innate immune systems driving a stress induced inflammatory immune response, as well as bleaching. In this study, the coral Pocillopora damicornis was investigated for tumor necrosis factor receptor associated factors (TRAFs). Thirty-seven TRAF proteins were identified in P. damicornis. When compared to the TRAF proteins seen in other animals, P. damicornis seems to possess a very diverse and expansive repertoire of TRAF proteins. The large and diverse repertoire of TRAF like proteins seen in P. damicornis may be indicative of the diverse molecular mechanisms behind their ability to tolerate a high level of stress.

Mammalian immunological cascades which utilize TRAFs in the activation of transcription factors. The pathways pictured are relevant to known receptors in coral immunology. Signaling cascades included are toll-like receptor/interleukin receptors, NOD-like receptors, and tumor necrosis factor receptors present in coral innate immune. Black arrows represent initiation of cascade, red arrows represent inhibition, and blue arrows represent the movement of transcription factors into the nucleus. Adapted from Dhillon et al., 2018. O’Neill et al., 2001. Chung et al., 2002. and Xie et al., 2013. TRAF proteins compared to TRAF proteins identified in Homo sapiens, Drosophila melanogaster, Hydra vulgaris, Suberites domuncula, Stylophora pistillata, and Acropora digitifera. Neighbor joining tree computed with 1000 bootstrap replicates to show evolutionary divergence of different TRAF proteins. Thirty-one potential TRAF homologs were identified in the P. damicornis genome through local alignment searches and protein domain identification. Evident phylogenetic separation of the TRAF proteins is observed across vast phyla, though variability in the placement of the Zn RING domain or the coiled-coil domain hits with cutoff e-10 was included. The thirty-seven TRAF proteins were run through HMMERSCAN against a database to identify the protein domains and their amino acid coordinates within the protein. Pfam domain hits with cutoff e-10 were used as probable domains. The proteins are organized based on grouping in the phylogenetic tree (Figure 2).