Transnational Access Report

1. General Information

Project Acronym (ID):	TOMATO P4Hs
Project Title	The role of prolyl 4 hydroxylases in tomato fruit development.
Installation used	MicroCT UNOTT, UK
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2. Duration of access

Begin of the project	End of the project
10/12/2014	11/12/2015

3. Project summary (max. 250 words)

Proline hydroxylation is a major post-translation modification of hydroxyproline-rich glycoproteins (HRGPs) such as arabinogalactan proteins (AGPs) and extensins (EXTs) that is catalyzed by prolyl 4-hydroxylases (P4Hs). Tomato genome comprises at least nine unigenes encoding putative P4Hs (Fragostefanakis *et al.* 2012), and their involvement in plant growth and development has been demonstrated in Arabidopsis, Tobacco and Carnation (Vlad *et al.* 2010). The hypothesis that HRGPs play significant roles on cell wall structure and function and their implication in root and shoot tissues while in cell division and expansion phases has been shown in Tomato (Fragostefanakis *et al.* 2014). In addition to that Velasquez *et al.* (2011) reported that polysaccharides and HRGPs that include EXTs and AGPs are able to alter individual root cells and Seifert and Roberts (2007) showed an involvement of AGPs in early embryonic patterning by the observation that certain AGP carbohydrate epitopes are differentially expressed during embryogenesis which indicates that AGPs are involved in inhibitory signaling, leading to alterations in embryo size. In this content, the novelty of the current project is to exploit how P4H genes are involved in fruit ripening noticing the plethora of HRGPs, proteoglycans and glycopeptides as structural components of the cell wall. This is achieved by the production of stable transformed plants that they silencing the gene of interest, causing alterations in fruit cell division and expansion phases.

4. Main achievements (max. 250 words)

Tomato seeds (*Solanum lycopersicum*) c.v. Ailsa-Craig of the transgenic line RNAi-PH43 and the empty vector control will be examined under the High Resolution X-ray micro-Computed Tomography, in order to determine alterations in the outer layer of the seed, as well as differences in the embryo morphology. The seed structure exhibits major alterations in embryo size and shape, as well as the outer morphology, requiring further detailed morphological analysis. Such an imaging analysis is a requirement, in addition to the transcriptomic and metabolomic analysis that needs to be performed to understand these alterations. In addition, alterations were observed in the germination efficiency of the transgenic lines.