Title

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THE USE OF DYNAMIC OPTICAL COHERENCE TOMOGRAPHY AND 3D IMAGE PROCESSING TO EXAMINE MORPHOLOGY IN PORT-WINE BIRTHMARK MICROVASCULATURE

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Background: Dynamic optical coherence tomography (D-OCT) allows for 3D in vivo imaging of cutaneous blood vessels and facilitates assessment of vascular patterning, modal vessel diameter, superficial plexus depth, and vessel density for cutaneous vascular conditions like capillary malformations (Port Wine Birthmark or PWB) and rosacea. The goal was to determine if vessel characteristics as measured by D-OCT differed in these two conditions.

Study Design/Materials and Method: Subjects with PWB or rosacea involving the cheek, temple, or jawline were recruited to this multi-institutional prospective study. D-OCT images were captured for lesional and for either adjacent uninvolved or contralateral, anatomically matched uninvolved control skin. D-OCT images were processed with ImageJ and AngioTool to create a morphometric analysis of number of vessel branch points. A two-tailed *t* test was performed for statistical analysis.

Results: The cohort included 27 with PWB and 10 subjects with rosacea. Average vessel diameter in PWBs was 93.3 μm and larger than control vessels ($p = 0.0003$), and 126.7 μm in rosacea, also larger than control vessels ($p = 0.00006$). Neither PWBs nor rosacea displayed larger number of vessel branches (PWB, $p = 0.75$; rosacea, $p = 0.5$) or longer length (PWB, $p = 0.98$; rosacea, $p = 0.31$) as compared to control. On inspection, PWB images displayed serpiginous, bulbous branching and loss of vessel hierarchy, organization, and regularity. Rosacea images displayed straight branching at near 90-degree angles, and normal vessel hierarchy, and regularity.

Conclusion: The superficial vessels in PWB and rosacea were larger than control vessels and differences were noted in morphology of PWB as compared to rosacea vessels. Additional detail about vessel size at different depths and range of vessel diameters would likely be helpful in guiding treatment. Future work will stratify data by genotype to help develop therapies with enhanced outcomes.