performed using GraphPad Prism 7 software. The significance of obtained results was calculated using the unpaired student’s t-test. \( P \)-values \( \leq 0.05 \) were considered significant.

**Results:** Differential analysis revealed significant changes in the expression of 220 genes \( (P<0.005) \), representing a diverse response pattern. qPCR analysis on biopsies collected from apical (a), middle (m) and periphery (p) of expanders showed that expression of mechanosensitive genes depends on magnitude of mechanical forces. The highest increase of \( \text{MMP1} \) expression \( (\text{FC}=41-787, P>0.001) \) was detected in the apical biopsies, exposed on the highest pressure. In biopsies “m” the increase in \( \text{MMP1} \) expression was 4-8 times smaller than in biopsies “a”, but still significantly higher than in control \( (\text{FC}=52-175, P>0.001) \). In biopsies “p” the \( \text{MMP1} \) expression was not significantly changed. The evaluation of \( \text{SFRP2} \) expression at 3 days after fill with 30ml saline revealed 5 times higher response \( (P=0.001) \) when additional injection with the same volume was performed 7 days earlier, suggesting that multiple injections stimulate the molecular response of skin in TE more effectively. The opposite effect was observed for double injection with 60ml saline, indicating that when pressure is too high this can negatively affect the molecular response and limit skin growth and regeneration.

**Conclusions:** RNA-seq analysis revealed numerous genes responding to tissue expansions that are involved in a variety of biological processes including homeostasis, proliferation, differentiation, and inflammation. To achieve the most effective stimulation of skin growth, real-time evaluation of pressure within the expanders will be incorporated in subsequent studies. Understanding the correlation between time of expansion, magnitude of pressure and molecular response of skin in TE may help to optimize clinical outcomes, leading to the most efficient recruitment of new skin and make expansion feasible even in compromised tissue beds.

**QS21**

**Exome Mutations In Sun-exposed Skin And Basal Cell Carcinoma**

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Exome Mutations In Sun-exposed Skin and Basal Cell Carcinoma

**Purpose:** Basal cell carcinoma (BCC) is the most common non-melanoma skin cancer and occurs more frequently on the nose. \(^1\) Several tumor suppressor genes and others have been implicated in the pathogenesis of BCC. Known involvement of the Hedgehog pathway, tumor suppressor TP53 and RAS family have been reported and now with advances in sequencing technology other associated mutations have been identified. Many BCCs carry ultraviolet (UV) somatic point mutations. In our study the entire exome was sequenced in non-UV exposed skin, UV exposed skin, and invasive basal cell carcinoma from one patient. We have identified mutations that are unique to non-UV exposed skin, UV-exposed skin, and invasive basal cell carcinoma.

**Methods:** The entire genome was sequenced using Agilent’s Clinical Research Exome kit and the Illumina NextSeq 500 sequencer. Broad’s Genome Analysis ToolKit (GATK) was used to identify the variants. The skin of one patient was examined at 3 sites: UV-exposed, non UV-exposed skin, and invasive basal cell carcinoma for comparison. Examination was performed using a multigene panel including such genes as PTCH 1 and 2 and TP53.

**Results:** Exome sequencing with informatics reveals 5 mutations unique to BCC, overlap of 1 mutation between BCC and UV-exposed skin, and 3 unique mutations in UV-exposed skin. The three unique mutations in UV-exposed skin are TP53 mutations. One TP53 mutation is in common between BCC and UV-exposed skin. Our previous proteomics on this patient displayed increases in DNA-dependent protein kinase catalytic subunit and basement membrane- specific heparin sulfate proteoglycan in his invasive basal cell carcinoma. This finding correlates with mutations seen in these 2 genes.

**Conclusions:** Involvement of TP53 occurs in many cancers. Using exome sequencing three TP53 mutations are associated with UV exposure. There is one TP53 mutation in common between UV-exposed skin and BCC. BCC has 5 specific gene mutations in HSPG2, PRKDC, and ITGB1. The proteins for HSPG2 and PRKDC were increased in this patient’s BCC. These mutations and others can be confirmed with sanger sequencing. RNA sequencing can be performed to confirm that there is upregulation of these genes in BCC. In summary, exome sequencing will be useful in the molecular diagnosis of BCC and its subtypes. Exome sequencing reveals 5 mutations unique to BCC.

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**QS22**

**Defining Enhanced Recovery Pathway With Or Without Liposomal Bupivacaine In Diep Flap Breast Reconstruction**

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**Purpose:** Enhanced Recovery After Surgery (ERAS) are multivariate interventions which have yielded positive outcomes in multiple surgical fields, although its function in reconstructive breast surgery has not been extensively explored. The authors aim to evaluate whether an ERAS protocol and its subsequent addition of liposomal bupivacaine affect patient outcomes.

**Methods:** Patients who underwent breast reconstruction with DIEP flaps from January 2016 to August 2019 were retrospectively reviewed. The ERAS protocol was implemented midway through 2017, and halfway through 2018, intraoperative TAP blocks with liposomal bupivacaine were added to the protocol. Such interventions allowed for comparison of 3 patient groups: pre-ERAS, ERAS, and ERAS + liposomal bupivacaine. Primary outcomes observed were postoperative opioid consumption and length of stay. P-values were obtained using the Wilcoxon test for pairwise comparisons.

**Results:** After adjusting for ERAS compliance, 202 patients were analyzed. The pre-ERAS group was composed of 67 patients, ERAS of 69, and the ERAS + liposomal bupivacaine of 66. Postoperative opioid consumption was reduced when comparing the pre-ERAS and ERAS groups (275 to 146; p < 0.0001), and additionally reduced with the addition of liposomal bupivacaine (124; p = 0.09). Furthermore, hospital length of stay was decreased from 3.6 in the pre-ERAS group to 3.2 (p = 0.0029) in the ERAS, and to 2.6 (p < 0.0001) in the ERAS + liposomal bupivacaine groups.

**Conclusion:** ERAS protocols decrease postoperative opioid consumption and hospital length of stay in DIEP flap breast reconstruction. Addition of liposomal bupivacaine further strengthens the impact of the ERAS protocol.

**QS23**

**Combined Microvascular Breast And Lymphatic Reconstruction With Deep Inferior Epigastric Perforator Flap And Gastroepiploic Vascularized Lymph Node Transfer For Postmastectomy Lymphedema Patients**

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**Purpose:** The combination of microvascular breast reconstruction (MBR) and vascularized lymph node transfer (VLNT) in a single-stage procedure is a surgical option for women who desire breast reconstruction and postmastectomy lymphedema surgery. In this study, we present a series of patients who underwent simultaneous lymphatic and MBR with the gastroepiploic lymph node transfer (GE-VLNT) and the deep inferior epigastric perforator (DIEP) flap respectively.

**Methods:** Between 2018 and 2019, all consecutive patients diagnosed with lymphedema stage IIb - III International Society of Lymphology who underwent simultaneous MBR with DIEP flap and GE-VLNT were included in this study. Patient demographics, comorbidities, prior radiation therapy, operative characteristics, surgical outcomes and complications were collected and analyzed.

**Results:** Six patients underwent simultaneous unilateral MBR with DIEP flap and GE-VLNT. The mean age was 48 ± 10.5 years and mean body mass index was 28.2 ± 4.5 kg/m2. The mean circumference reduction rate was 30.0 ± 5.1% (p<0.001). One patient required re-exploration due to