systemic sclerosis (SSc) and mesenchymal transformation of the major event for microvascular dysfunction. Recent studies have shown epigenetic regulation of long non coding RNAs (IncRs) in different disease pathophysiology.

**Objectives:** To study the differential expressions of IncRs in patients with SSc and to study their associations with regulatory molecules of fibrosis

**Methods:** Peripheral Blood were collected from 15 diffused cutaneous SSc patients (dSSc) [ACR, 2013] and 10 age-sexes matched healthy controls. RNA was isolated from the peripheral blood & cDNAs were prepared and the relative mRNA expressions were measured with respect to an endogenous control gene by real-time PCR. Protein expressions were measured by ELISA.

**Results:** Increased expression of MEG3, MALAT1 and NEAT1 (3.5, 3, 4fold respectively) has been found in SSc patients with respect to healthy individuals and they are mutually correlated (MEG3 and MALAT1: r=0.7, p<0.0001; MEG3 and NEAT1: r=0.7, p<0.0001). The expression of NEAT1 is significantly higher (p=0.0009) in case patients with disease duration (DD) >5 years compare to the patients with DD≤5 years. No significant difference was found in the expression of MEG3 and MALAT1 between these two subpopulations. Modified Rodnan’s skin score (mRDSS); the clinical parameter of measuring fibrosis, was significantly up regulated (p=0.004) in patients with long disease duration (>5 years) and also have a positive correlation with DD(r=0.2, p=0.02) and the regulatory RNAs: MEG3 (r=0.4, p=0.003), MALAT1 (r=0.2, p=0.02), and NEAT1( r=0.3, p=0.009).

The master regulator of fibrosis TGFβ which is significantly up regulated at both transcriptional (p=0.0001) and translational (p=0.0009) level has significant positive correlation with MEG3 (r=0.3, p=0.02), MALAT1 (r=0.5, p=0.0005), and NEAT1( r=0.3, p=0.006). MEG3, MALAT1 and NEAT1 also have significant high correlation (r=0.7, p<0.0001; r=0.6, p<0.0001 and r=0.7,p<0.0001 respectively) with cSMA: the marker of fibroblast activation and the collagen-I (r=0.3, p=0.03; r=0.3, p=0.03 and r=0.3, p=0.03 respectively).

In multivariate analysis MEG3 and NEAT1 together could explain 37.5% variability of fibrotic marker and NEAT1 alone could explain 35.5% of the same.

**Conclusion:** mRDSS probably does not reflect the underlying fibrotic process occurring sub-clinically, as no significant correlation was observed either with the disease duration or with the pro-fibrotic molecules (TGFβ, cSMA, and collagen1). The strong inter-correlation of NEAT1, MALAT1 and MEG3 suggest that any one of them might well be studied as specific marker of sub-clinical fibrosis. The long non coding RNAs (MALAT1, MEG3, NEAT1) better reflects the sub-clinical fibrosis occurring in the patients, suggested by strong correlation with fibrotic markers (TGFβ, cSMA, collagen1). The linear regression values suggest that NEAT1 could be an important biomolecule in SSc pathogenesis.