1. The study comprised of 84 chronic hepatitis C patients and 75 healthy controls. The mean±S.D age of the healthy group was 33.36±0.753 years and that of chronic hepatitis C group was 34.76±1.245 years. The frequency of HCV genotype-1 was 28 (33.33%), genotype-3 50 (59.52%) and genotype-4 6 (7.14%). The mean±S.D. of baseline HCV RNA viral load was 2057334.45±4243232.025 copies/ml. Out of the total number of 84 patients undergoing peg interferon + Ribavirin therapy there were 50 (59.52%) responders and 34 (40.48%) non-responders.

2. The C4 SNP rs2857009 CC genotype is significantly associated with chronic hepatitis C. Subjects carrying the rs2857009 CC genotype is 2.6 times increased risk of chronic hepatitis C as compared to non CC genotype carriers.

3. The CC genotype of rs2857009 is significantly associated with poor outcome to treatment. The rs2857009 CC genotype carriers are 57 times increased risk of not responding to treatment as compared to non CC genotype carriers.

4. The serum C4 level was significantly higher in control group when compared to CHC group. The CC genotype of rs2857009 is associated with reduced levels of serum C4 levels.

5. The C4 mRNA levels were also significantly higher in control group when compared to CHC group. rs2857009 ‘C’ copy is associated with reduced C4 mRNA levels when compared to carriers with no copy of ‘C’ allele.
6. Increased levels of serum C4 was associated with positive response to treatment. By logistic regression a model for predicting the response to treatment which is given by the equation

\[ P_x = \frac{1}{1 + e^{-z}} \]

where \( P_x \) = probability of positive response;

\[ z = -446.87 + 0.291x \text{ Baseline C4 levels in mg/dl} \]

7. From the above equation a cut-off level of \( >-147.521 \) was found to predict positive response to treatment with 80% sensitivity and 94.12% specificity. It had a positive predictive value of 95.24%, a negative predictive value of 76.19% and a diagnostic accuracy of 85.71%.

8. A logistic regression analysis revealed that age, rs2857009 polymorphism and HCV genotype was independent predictors of ‘Moderate + high Fibrosis’ when compared to ‘Absent-Fibrosis’ & ‘Mild fibrosis’ groups. Increased age, rs2857009 CC & CG genotype were associated with increased risk of Moderate fibrosis when compared to young and rs2857009 GG genotype carrier patients; Whereas HCV genotype 1 carrier patients had lower risk of progressing to Moderate fibrosis than non genotype 1 carrier patients.

9. CFH SNP rs4658046 TT genotype carriers are at 2.21 times increased risk of CHC when compared to non TT genotype carriers. The rs4658046 is not associated with treatment outcome. The rs10922103 was not associated with CHC but AA genotype of rs10922103 was associated with negative outcome of treatment whereas GA genotype carriers had 15 times likelihood of positive response to treatment.
10. The CFH mRNA expression level of healthy was significantly higher than the CHC group. Neither rs4658046 nor rs10922103 was associated with the mRNA expression levels.

11. There was no significant difference in the CFH mRNA levels between the responders and non-responders. Neither rs4658046 nor rs10922103 was associated with the mRNA expression levels.

12. There was no significant difference in the levels of serum CFH levels between the healthy and disease group. Neither rs4658046 nor rs10922103 was associated with the CFH serum levels.

13. There was no significant difference in the levels of serum CFH levels between the responders and non-responders. Neither rs4658046 nor rs10922103 was associated with the CFH serum levels.

14. rs4658046 TT genotype carriers had 2.51 fold increased risk of chronic hepatitis C than non TT genotype carriers. Decreasing CFH level was associated with an increased likelihood of CHC.

15. rs4658046 polymorphism was not associated with the LFT. The GG genotype of rs10922103 was associated with increased ALP levels.

16. Age, and HCV genotype were independent predictors of ‘Moderate Fibrosis’ when compared to ‘Absent-Fibrosis’ & 'Mild fibrosis’ groups. Neither CFH level nor the rs4658046 and rs10922103 polymorphisms are associated with disease progression.

17. The C3 polymorphism rs7951 and rs2230201 was not associated with CHC. rs7951 was also not associated with treatment outcome. However rs2230201
CC genotype was associated with positive response to treatment and CT genotype with poor outcome.

18. The C3 level was significantly higher in healthy when compared to CHC. The genotypes of rs7951 were not associated with serum C3 levels whereas CC genotype of rs2230201 was associated with increased levels of serum C3 levels.

19. The C3 level was significantly higher in responders when compared to non-responders. The genotypes of rs7951 were not associated with serum C3 levels in the responder and non-responder group. However CC genotype of rs2230201 was associated with increased levels of serum C3 both in responders and non-responders.

20. The mRNA expression in healthy group was 1.54 times that of CHC group. The genotypes of rs7951 and rs2230201 were not associated with C3 mRNA expression.

21. There was no difference in C3 mRNA expression levels between responder and non-responder group. The genotypes of rs7951 and rs2230201 were not associated with C3 mRNA expression in both the responder and non-responder.

22. Age, C3 level and rs2230201 were associated with positive response to treatment. By logistic regression a model for predicting the response to treatment which is given by the equation

\[
P_x = \frac{1}{1 + e^{-z}}
\]

\[
z = -21.394 + (0.602 \times \text{C3 levels}) - (0.152 \times \text{Age}) - (9.58 \times V)
\]

where \( V = 0 \), if CC genotype and \( V = 1 \) if non-CC genotype.

23. From the above equation a cut-off level of >10.48 was found to predict positive response to treatment with 70% sensitivity and 97.1% specificity. It had a
positive predictive value of 94.54%, a negative predictive value of 68.08% and a diagnostic accuracy of 67.06%.

24. Rs2230201 CC & CT genotypes are associated with increased risk of progressing to fibrosis when compared to TT allele. Increased age of patients was associated with increased risk of higher fibrosis when compared to young.