

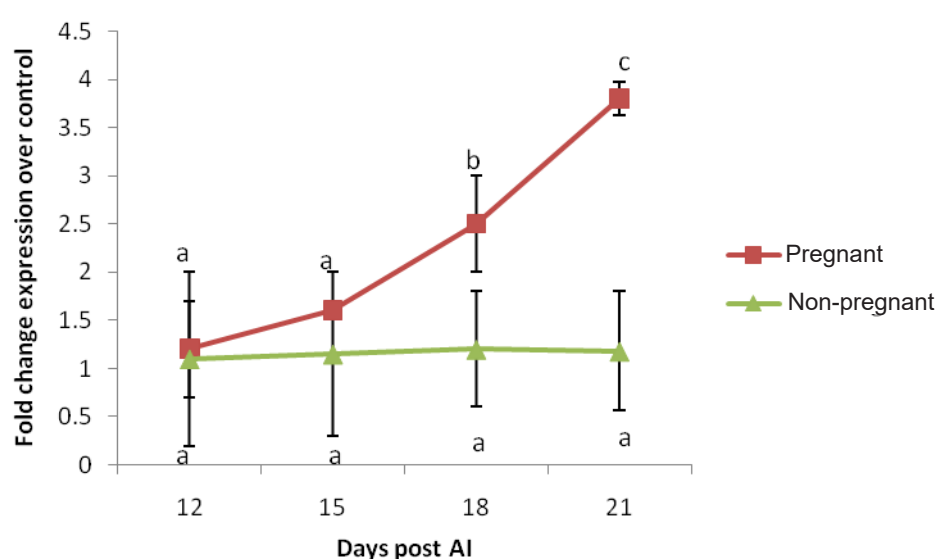


Expression dynamics of ISGs and chemokines in maternal whole blood as an indicator of healthy embryonic implantation in buffalo

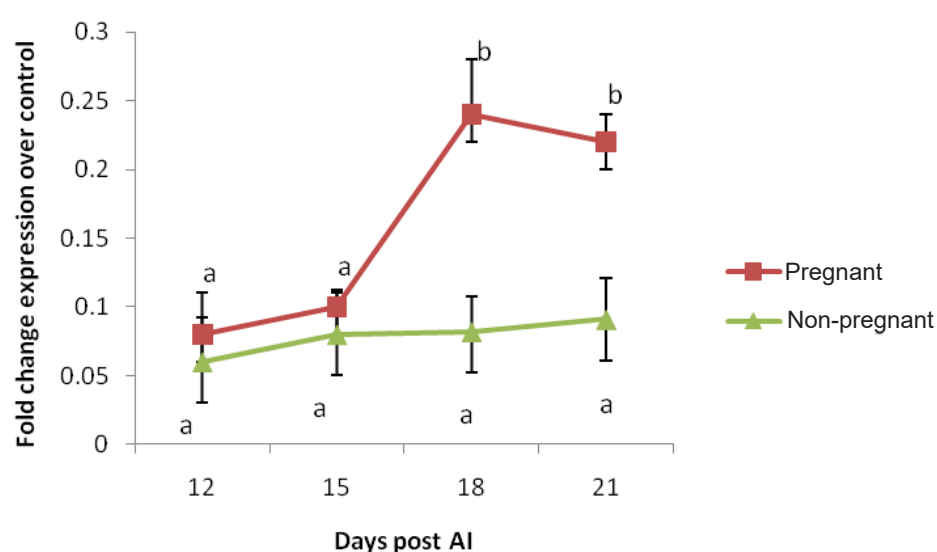
RAJNI KUMARI^{1✉}, SHANKER DAYAL¹, ROHAN KUMAR RAMAN¹, P C CHANDRAN¹, SANJAY KUMAR²
 PRADEEP KUMAR RAY¹, REENA KAMAL¹, JYOTI KUMAR¹, AMITAVA DEY¹, KAMAL SARMA¹ and
 UJJWAL KUMAR¹

ICAR Research Complex for Eastern Region, Patna, Bihar 800 014 India

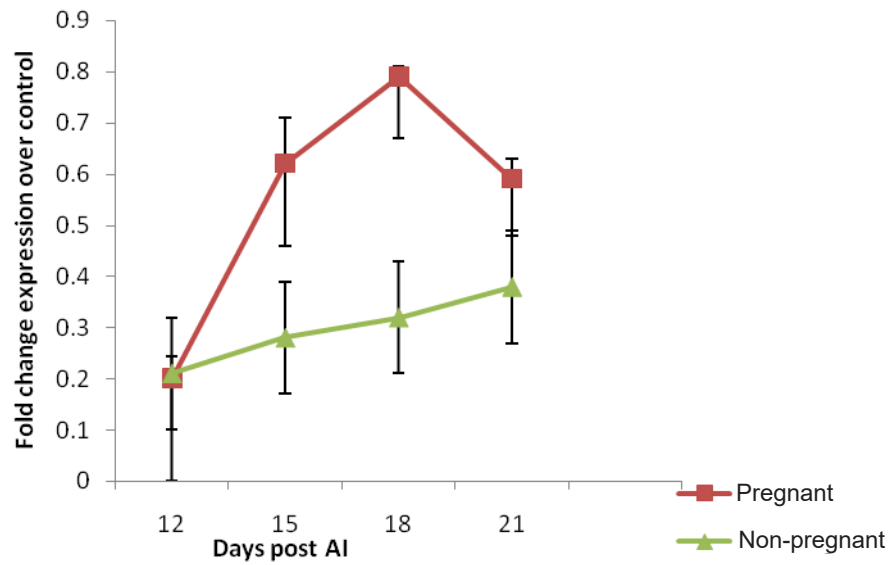
Received: 12 July 2022; Accepted: 12 September 2022



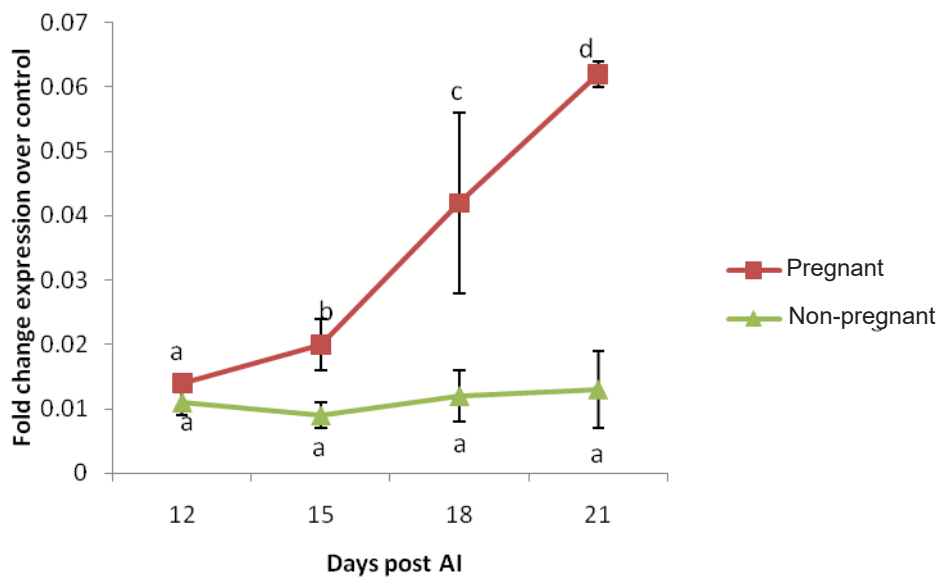
Supplementary Fig. 1. Transcriptional abundance of ISG15 gene in pregnant and non-pregnant samples on different days post AI. Minimum level of significance was set at 95%. Each point represents Mean±SEM. Points with different superscript denotes significant difference (P<0.05).



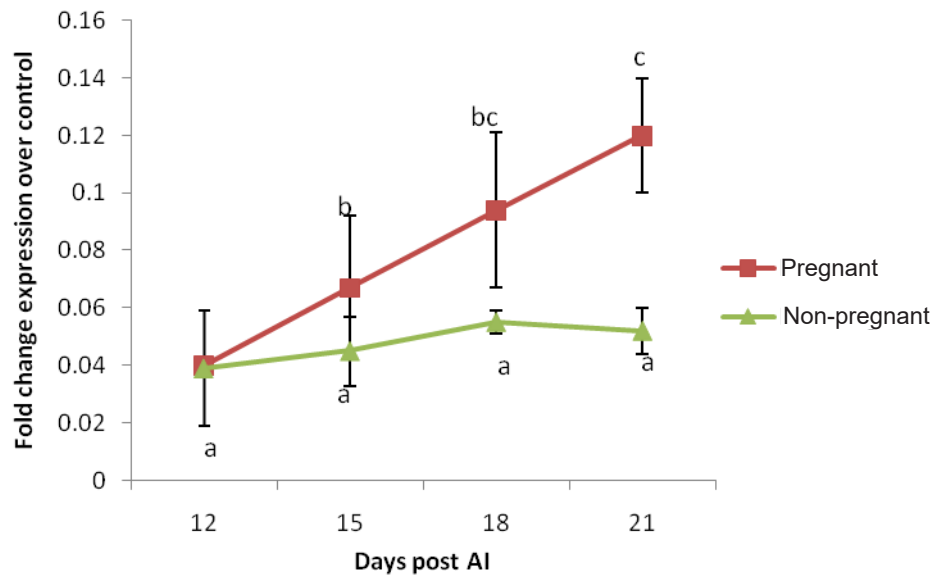
Supplementary Fig. 2. Transcriptional abundance of MX2 gene in pregnant and non-pregnant samples on different days post AI. Minimum level of significance was set at 95%. Each point represents Mean±SEM. Points with different superscript denotes significant difference (P<0.05).



Supplementary Fig. 3. Transcriptional abundance of MX1 gene in pregnant and non-pregnant samples on different days post AI. Minimum level of significance was set at 95%. Each point represents Mean±SEM. Points with different superscript denotes significant difference ($P<0.05$).



Supplementary Fig. 4. Transcriptional abundance of CCL8 gene in pregnant and non-pregnant samples on different days post AI. Minimum level of significance was set at 95%. Each point represents Mean±SEM. Points with different superscript denotes significant difference ($P<0.05$).



Supplementary Fig. 5. Transcriptional abundance of CXCL10 gene in pregnant and non-pregnant samples. Minimum level of significance was set at 95%. Each point represents Mean±SEM. Points with different superscript denotes significant difference ($P<0.05$).