

38 Eukaryotic PCNA

protein sequences

ensemble

Partner protein

also collected

from ensemble

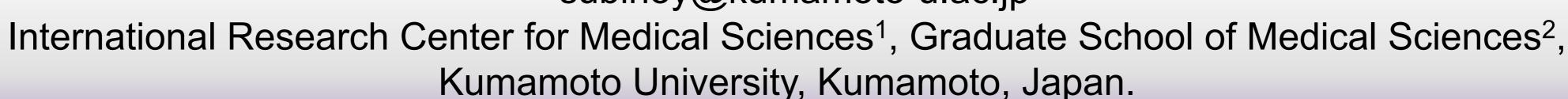
sequences were

PCNA

were collected from

Co-evolving residue network analysis of proliferating cell nuclear antigen PCNA indicates few mutations among residues of high betweenness

Subinoy Biswas¹, Christian Schönbach^{1,2} *subinoy@kumamoto-u.ac.jp





Introduction

- ❖ PCNA is a core protein of DNA replication process and has multiple interacting partner.
- ❖ PCNA proteins involved in DNA repair, recombination and cell cycle regulation
- There is no information of mutational effects of PCNA and its partner protein in human cancers
- Also no information how coevolving residues of PCNA and its interating proteins formed the underlying networks

MSA of partners

• FEN1

• RFC1

POLD1

Is there any key residues that holds a higher importance in those networks or there is no such clear information?

POLD2

POLD3

POLD4

• RFC3

• RFC4



Objectives:

- 1. To investigate the evolutionary constraints in residue-residue interaction by network topology and other network properties like betweenness, degree distribution.
- Mutational impact of coevolving residue on PCNA and its partner proteins at structural and functional levels.
- The relationships of hub residues in context of cancer-associated mutations.

PCNA

3

229

517

Materials and Methods

141

Col2

Col1

32

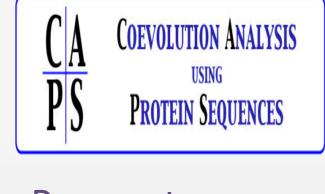
Col1

Col1

Coevolving

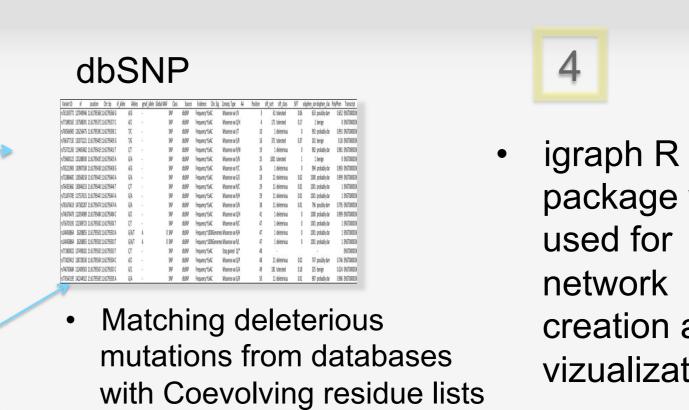
residue lists

MSA of PCNA and partners were used in separate sets for determining coevolving residues



Parameters

- Bootstrapped value 3000
- Correlation cut-off >= 0.8
- Alpha < 0.01



COSMIC

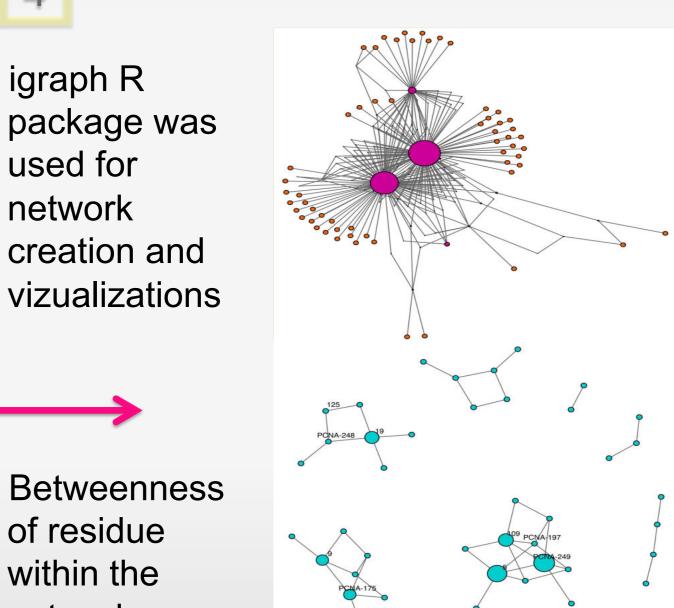
Betweenness

used for

network

of residue within the network were highlighted with size of the node

Inter & Intra Network construction



Identifying key High Betweenness residues (HBR) with mutation which **linked with Cancer**

Results and Discussion

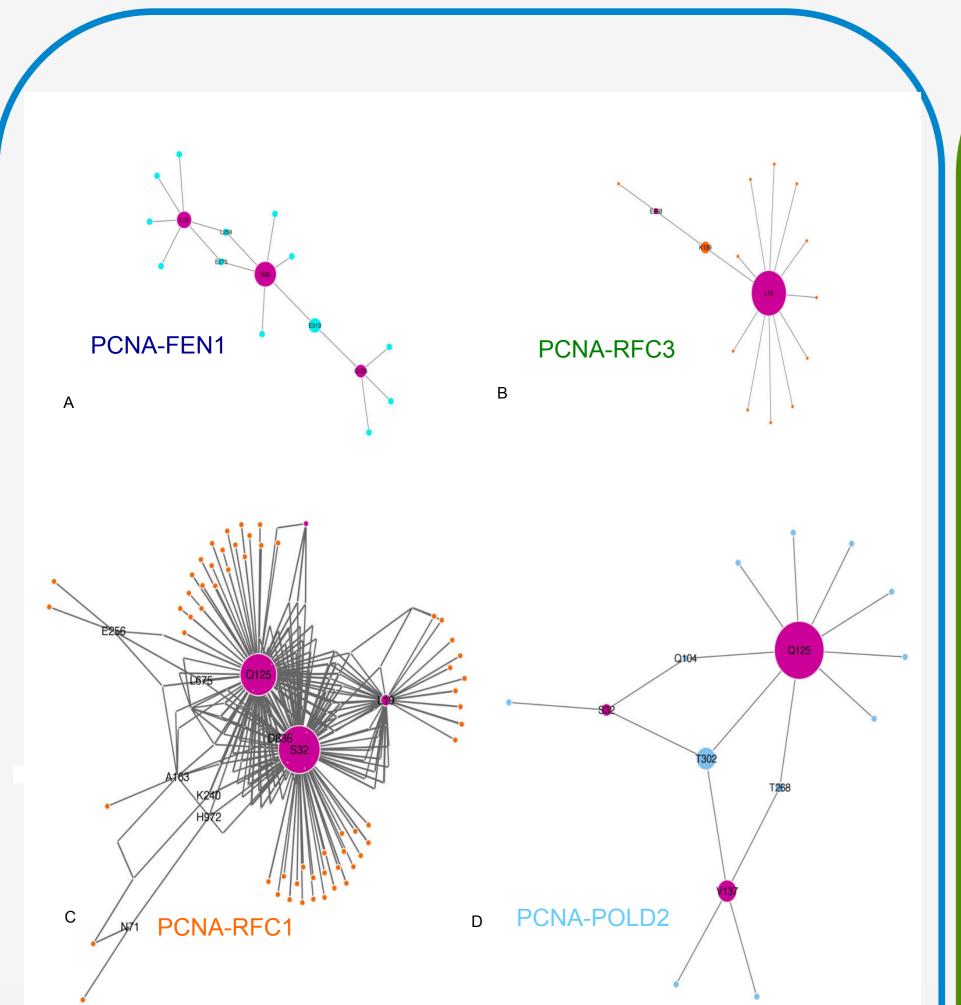


Fig 1: PCNA-inter coevolving residue networks. Pink color representing PCNA nodes. Node size representing betweenness of residues in that network.

- Biggest cluster in each PCNA-inter coevolving residue network are shown
- ❖ In three networks the residue Q125 of inter-domain connecting loop region appeared among HBR and strongly connected with coevolving residues from partner proteins

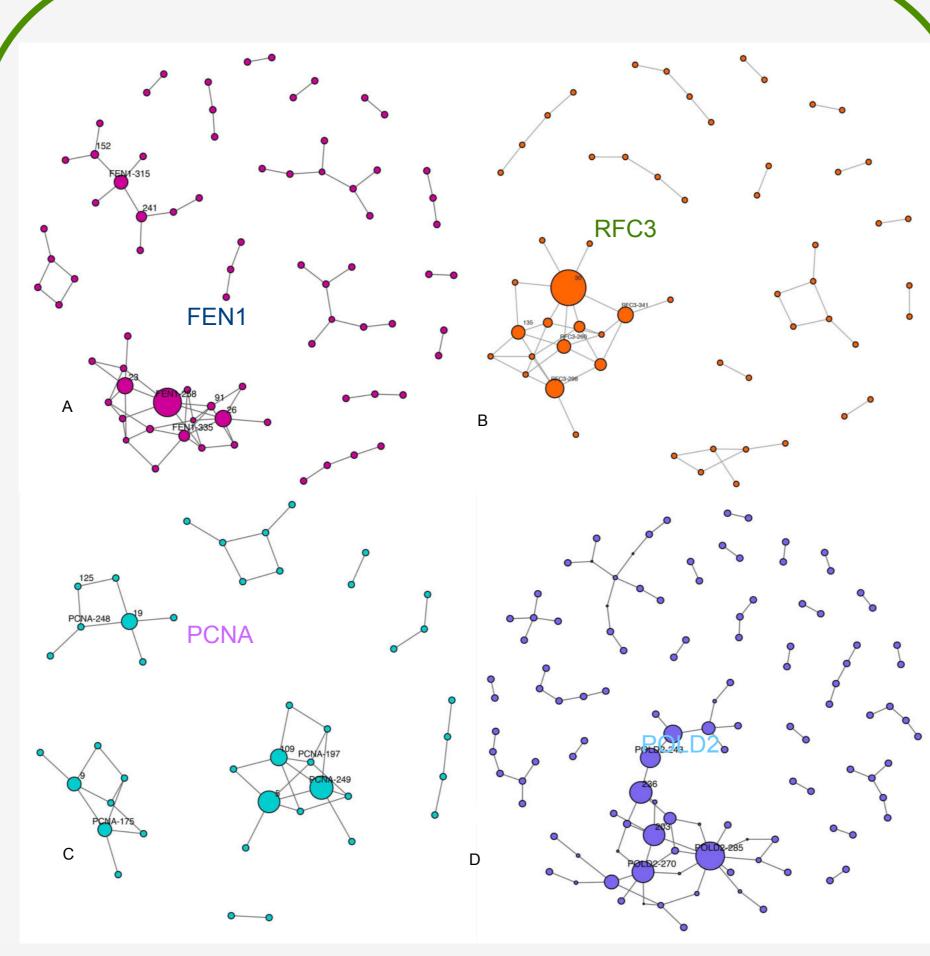


Fig 2: Intra-coevolving residue networks. Node size representing betweenness of residues in that network.

- Full intra-coevolving network are shown for each protein
- ❖ Residue 125 of PCNA also appeared in intracoevolving network
- ❖ HBR residue 125 and 19 appear in the same cluster in PCNA intra-coevolving network

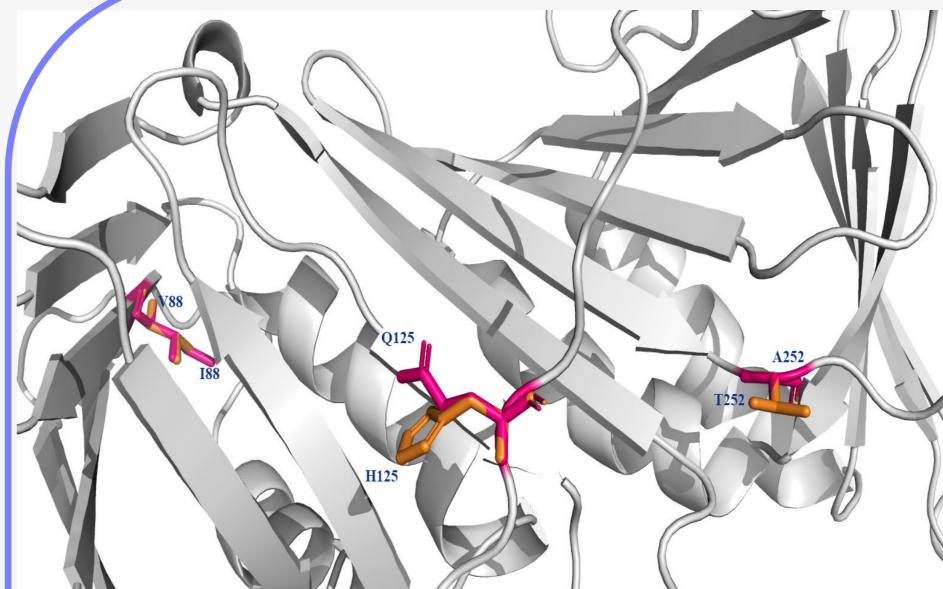


Fig 3: PCNA inter coevolving residues mutations overlay (pink residue mutated to orange) Q125H, I88V and A252T.

- Q125 of PCNA inter-domain connecting loop strongly coevolved (total degree 128) with residues of RFC1 (117), POLD2 (9), FEN1 (4) and RFC3 (2)
- ➤ Glutamine (Q125) residue of PCNA mutated to Histidine (H) which is shown in Fig 3. Such drastic structural change from neutral-polar amino acid to basic amino acid predicted to negatively affect interaction and may results in a major disruption in function of PCNA and interaction with its partner protein

One such example of functional disruption may be due to mutations reported in cancer samples (COSM5777338)

- Similarly, may be due to mutation of 188 of PCNA to V leads to cancer(COSM21734, also matched in cancer samples)
- High Betweenness residues often formed the hub in the network like Q125 of PCNA in present study, and deleterious mutation of hub residue causes fatal consequences of protein functions and human health

Key High Betweenness Residues of PCNA

PCNA-FEN1 inter network		PCNA-POLD2 inter network		PCNA-RFC1 inter network	
PCNA Residue No	Betweenness	PCNA Residue No	Betweenness	PCNA Residue No	Betweenness
32	74.5	125	68.33	32	8138.19
19	50.5	POLD2-302	26.83	125	7148.19
FEN1-313	44	137	26.17	19	1965.60
125	39	32	14.50	RFC1-972	433.28

Conclusion

- PCNA coevolving residue network analysis suggest that residues of high betweenness and degree seem to be selected against disease-associated mutations
- PCNA residue Q125 of inter-domain connecting loop predicted in this study to play a crucial role in protein-protein interactions with other interacting partners
- Q125 residue of PCNA present both in intra coevolution and therefore predicted any mutation on that key residue has drastic effect on human health