

Functionality Assessment of Kanha-Pench Corridor

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Abstract: Kanha-Pench corridor is historically widely distributed in 2552 sq. km of Satpura Maikal Range. We identified critical tiger habitat holds 439 sq. km area out of 2552 sq. km forest area of K-P corridor. Where 11 female tigers hold their ground on TCPUs and one male tiger presence noticed in pinch point barrier of connecting linkage under threat environ-anthropogenic conditions. There are 19 tigers were identified on individual basis DNA genotype polymorphism at different 13 microsatellite locus. The mean observed heterozygosity was found to be 0.6102. The relatedness analyses showed that tigers from Kanha –Pench corridor population share more relationships with tigers from Kanha and Tadoba-Nagzira-Brahmapuri complex rather than from Pench Tiger Reserve. We found evidences that a reproducing stable population exists within corridor. Therefore, restoration of Tigers was identified in historically existing critical habitat patches of corridor. Corridor functionality has been proven by findings of adjoining protected areas tiger's genetic signatures in corridor population as Ist and IInd degree of relationship derived from ML-Relate analysis. Therefore potential habitat was identified for effective management and needs of tigers was prescribed to include in regional strategic development plans. We relied on MaxEnt of species distribution modeling to predict tiger distribution based on a suite of environmental variables to determine TCPUs. Potential corridors linkage identified on the basis of least cost path, circuitscape, linkage mapper and their ground truthing was done to assess inference accuracy. Conservation of tigers does not necessarily have to obstruct economic development, when “tiger friendly” management guidelines included in development plans.

Keywords: K-P Corridor- Kanha-Pench Corridor, TCPUs- Tiger Conservation Prioritization Units, BMLR-Binomial Multiple Logistic Regression, LCP analysis- Least Cost Path Analysis, SFRI-State Forest Research Institute Jabalpur, Madhya Pradesh.

1. INTRODUCTION

The Tiger (*Panthera Tigris*, Linnaeus) is the national animal of India. As the national animal of India, tiger symbolizes India's wildlife wealth. The combination of grace, strength, agility and enormous power has earned the tiger great respect and high esteem. Out of the eight races of the species known, the Indian race, the Royal Bengal Tiger is found throughout the country (except the north-western region) and also in the neighboring countries like Nepal, Bhutan and Bangladesh. The Government of India, under its "Project Tiger" program, started a massive effort to preserve the tiger population in 1973. Today, the tiger advances as a symbol of India's conservation of itself and its wildlife heritage.

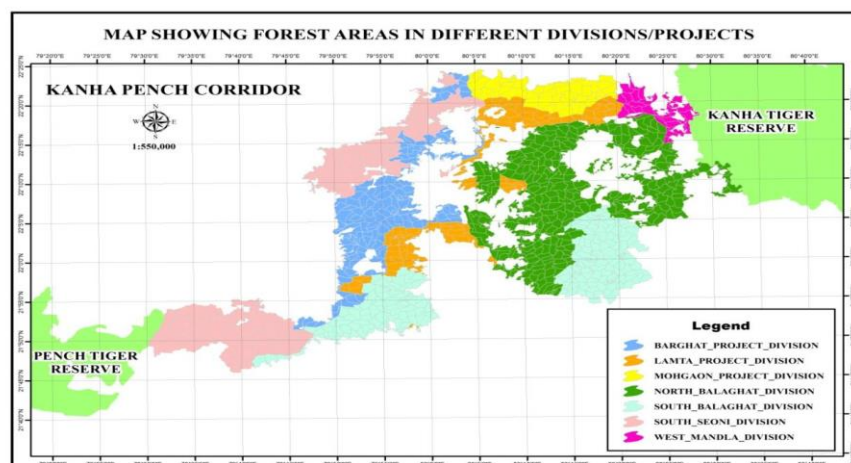
The tiger was adopted as the National Animal by the Indian Board for Wildlife in 1972 in place of the lion. It was selected as a national animal because of its presence in larger parts of the country. It is found in 16 states while the lion is found only in one state. Also, because of the worldwide importance of the animal, and the need to protect it. Tiger as the National Animal of India symbolizes the power, strength, elegance, alertness, intelligence and endurance of the nation. Tiger has also been long part of Indian mythology and folklore.

Tigers are crucial for the ecosystems in which they live. As top predators of the food chain, tigers keep populations of prey species in check, which in turn maintains the balance between herbivores and the vegetation upon which they feed. Balanced ecosystems are not only important for wildlife, but for people too – both locally, nationally and globally. People rely on forests, whether it is directly for their livelihoods or indirectly for food and products used in our daily lives. Tigers not only protect the forest by maintaining ecological integrity, but also by bringing the highest levels of protection and

investment to an area. Tigers are an “umbrella species”, their conservation also conserves many other species in the same area. They are long-ranging and require vast amounts of habitat to survive. Large areas of intact forest therefore must be preserved for tiger conservation. Due to the illegal wildlife trade, tigers also bring robust enforcement against poaching and habitat encroachment, as well as systematic biological monitoring. Despite conservation efforts since the 1970s, wild tiger populations did not stop declining. Tiger range governments came together and decided that business-as-usual approaches were not working. All 13 tiger range governments committed to the ambitious conservation goal set for a tiger – to double the number of wild tigers by 2022. This involves increasing protection where the tigers are currently, maintaining wildlife corridors and connectivity between areas and then boosting resources and protection for where tigers can be in the future, when their numbers have increased. Doubling wild tigers is possible with full commitment from the tiger range countries. World tiger population is now estimated to be around 3900. “The Tx2 commitment is the best chance we have at securing the future of wild tigers and their habitats – tigers may not get a second chance in the wild, and neither may we,”– Mike Baltzer, Leader of Tigers Alive, WWF [1]

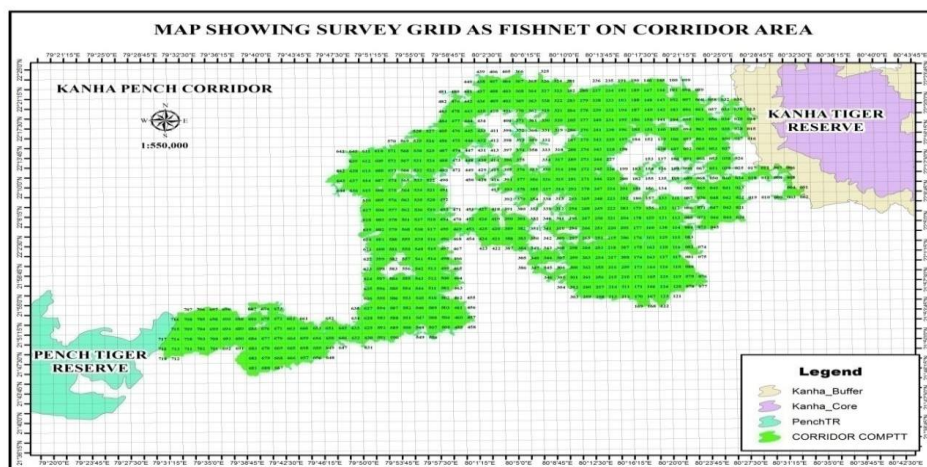
In India, as per WII tiger census report 2014, current Tiger population is 2226. That is a sharp rise of almost 60 per cent from 2006, when the first scientific and independent estimate delivered a shocking statistic that only 1411 tigers left in India. The latest tiger count marks a 30 per cent rise since the last estimate as 1706 in 2010. Presently, we have now 2226 tigers in 47 tiger reserves. In the same line Madhya Pradesh state tiger population dynamics showed 300, 257 and 308 numbers in 2006, 2010 and 2014 respectively. That is clear indication of non substantial population growth of tigers in Madhya Pradesh although country level tiger population sharply grown, while the protection measures were near to equal. This fact compels to examine the carrying capacity of protected areas, when tiger presence and frequently movement were regularly reported in K-P corridor by the regional territorial forest divisions therefore ground truthing and reason for the presence of tigers in K-P corridor was studied under source-sink dynamics model. Therefore we have performed two years DNA based monitoring in K- P corridor by indirect way to know dispersal situation in connecting corridor. Kanha-Pench corridor is historical natural corridor and situated in the geospatial location of Satpura Maikal range in central highland India. Our study finding indicating presence of minimum 19 tigers outside of protected areas including 11 tigresses, most of them were found with their cubs. Genetic evidences of generational movement from adjoined source population were found by genetic relatedness analysis. It compelled us to focus on identification of suitable habitat for safe dispersal of tigers in corridor from adjoined of PAs. The present knowledge of tiger presence and their habitat outside protected areas is inadequate and this lacuna was addressed to make possible better management of the vast forest cover available in Kanha-Pench corridor. This study was designed to addressing lack of accurate and reliable information of tiger presence and their critical habitat outside of PAs by DNA based monitoring of tigers in historical Kanha-Pench corridor.

STUDY SITE: The Kanha-Pench corridor area in the satpura-maikal hill ranges in the satpura- Maikal hill ranges is a part of one of the most crucial tiger conservation units of the world as it is still a contiguous forest patch. (Wikramanayake et al.1998) [2]. The study covered the forest tract falling in seven forest divisions. The length of the corridor is 140 km. and lies between 21° 46’05” to 22°24’10” North and 79°30’03” to 80° 32’55” East. Four territorial forest divisions and three forest Development Corporation divisions areas are falling under Kanha-Pench Corridor area as shown in map no. 1



Map no.1

SURVEY DESIGN: We carried out the Corridor functionality survey for tigers in Kanha– Pench corridor (KPC) to determine tiger prioritization area and connecting links within KPC areas in during Dec 2012 to May 2015. We initially superimposed 5sq. km sized 719 numbers of grids on the Geo referenced land-cover map of KPC as shown in map no. 2, out of which all 719 grids were sampled for tigers and other wildlife presence and habitat use; we have done 100 % ground truthing of tiger presence and their habitat related variables. We carried out sign survey in spatially replicated segments within each of the 719 grids. A total of 2552 km² was intensively surveyed which consisted of 25 forest Ranges. There are two major linkages suggested namely Kanha – Pench direct link via Sarekha Ghat– Latgaon–Nainpur–Khatiya–Mocha and outside the corridor Boda–Khapa – Jalgaon – Pandiyachhapara link (Sen 2007) [3]. Although insurgency problems are in lougur range yet we surveyed because of its critical role to connect Tadoba-Nagzira-Brahmapuri complex. Ecological predictions about tiger presence were confronted with sign detection data generated from only presence location by MaxEnt model. We also surveyed the area for ungulate prey presence, human disturbance, and habitat status. We used a presence survey method that explicitly accounted for spatial correlation recently designed to assess large scale Species Distribution Modeling of tigers.



2. METHODOLOGY

FIELD PROTOCOL: The survey was conducted in the pre and post monsoon seasons during Dec 2012 to May 2015 to minimize variations in animal detection probabilities induced bioclimatic factors. Typically, tigers move along forest trails to hunt or to locate, avoid of deter conspecifics (Karanth and Sunquist 2000) [4]. Their passage is marked by tracks and occasional scat deposits (Smith et al. 1989) [5]. Fresh signs of tigers, leopards, dholes, and major ungulate prey species in KPC were identified and recorded by trained observers. Only unambiguously identified signs were recorded. Overall, the number of spatial replicates in a grid (sampling effort) were 3 fixed, We collected fresh fecal sample of carnivore and recorded signs of tigers, leopards, dholes, and ungulate prey species, as well as signs of livestock or human presence. Each type of sign detection was assigned only once to each 100 m trail segment, thus yielding the standard “1” (detection) or “0” (nondetection) histories required for habitat suitability analyses. These sign detection data were aggregated at 1 km length to form “spatial replicates”.

Surveys were not random, but instead conducted along features that were likely to have tiger sign (e.g. dirt roads, dry water courses, and animal trails along with opportunistic cattle kill sites) so as to maximize detections. Surveys were conducted by the local guard and a local assistant who had intimate knowledge of the forest and were trained to observe and record tiger sign in pre-designed datasheets. All encounters of tiger pugmark track sets and scats were recorded. These were distinguished from those of other carnivores based on criteria described by Jhala et al. (2014) and Karanth and Nichols (2010) [6,7]. A total of 719 grids were sampled by sign detection of carnivore, omnivore, herbivore and livestock. It was critical to presence of water within a 2.5x2.5 km area to sustain the population of herbivore. The size was relevant for fine scale and site specific subsequent administrative and managerial inputs.

GENETIC APPROACH:

- Identification of Tiger and Leopard Fecal Samples: DNA was isolated from the above described samples except the ones found not suitable for isolation or ones which had fungal growth. This was done in a dedicated room free of

PCR products to minimize contamination. DNA was extracted from sets of ten samples along with an extraction control to monitor for contamination at the time of isolation. DNA obtained was subjected to PCR amplification with TIG 490 primers (Mukerjee et al. 2007) [8] and with tiger-specific cytochrome b primers, TIF and TIR (Bhagavatula et al. 2006) [9] to identify samples of tiger or leopard origin.

- **Quantification of Tiger Positive Samples:** Fecal samples yield unpredictable amounts of low quality DNA, which can lead to subsequent genotyping errors. Therefore we quantified the amount of DNA in each tiger-positive sample by real-time PCR (Reddy et al. 2012) [10].
- **Microsatellite Genotyping:** Tiger DNA extracts were genotyped at 13 microsatellite loci (Menotti Raymond et al. 1999 and Bhagavatula et al. 2006) [11,9]. DNA was amplified, electrophoresed and analysed as described in (Reddy et al. 2012) [10]. All PCR steps, except addition of template DNA, were performed in a hood that was UV-irradiated before and after use to avoid contamination. All PCR reactions included positive and negative controls. PCR products were electrophoresed on an ABI 3730 Genetic Analyser and alleles were sized relative to an internal control (500 L1ZTM, Applied Biosystems) using GeneMapper software version 3.7 (Applied Biosystems).
- **Individual Identification:** Allelic data were analyzed in Microsoft Excel spreadsheets and genotypes were scored manually. Allele frequency analysis, estimates of probability of identity (PID) and PIO (sib) were carried out in CERVUS version 3.0 (Marshall et al. 1998; Kalinowski et al. 2007) [12]. Individuals were identified by the Identity Test in CERVUS. After PID analysis, minimum number of loci required to match a pair of genotypes was kept at 7. Genotypes which mismatched at 2 or lesser number of loci were reexamined manually at the mismatching loci, in order to rule out scoring or entry errors, and in ambiguous cases, the concerned loci were genotyped again. PCR was also repeated in triplicates at the unamplified loci to obtain complete genotypes. Genotypes with less than 7 loci were not considered for further analysis.
- **Sex Identification:** Sex of putative individuals was determined by typing zinc finger locus and randomly a few samples were rechecked with amelogenin locus (Pilgrim et al. 2005) [13].
- **Genetic Diversity:** Consensus genotypes, constructed from matching pairs of genotypes, were used to determine observed and expected heterozygosities in POPGENE (Yeh et al. 1999) [14].
- **Relatedness Analysis:** We used ML-RELATE to calculate maximum likelihood estimates of relatedness (r) and to establish relationships from co-dominant genetic data (Kalinowski et al. 2006) [15]. Maximum likelihood estimates of relatedness are usually more accurate than other estimators and are useful to discriminate between four common pedigree relationships: unrelated (U), half-siblings (HS), full-siblings (FS) and parent-offspring (PO). Values of r range between 0 and 1, and are indicative of the proportion of shared alleles which are identical by descent between pairs of individuals (Kalinowski et al. 2006) [15]. Forty-three individual tigers from Kanha tiger reserve, 21 from Pench tiger reserve and 26 individuals from Tadoba-Nagzira-Brahmapuri complex were included in the relatedness analysis along with Kanha-Pench corridor samples.

HABITAT SUITABILITY APPROACH:

Tiger Conservation Prioritization Unit (PTCUs) Demarcation: BMLR analysis (SPSS 19), MaxEnt (species distribution modeling), Circuitscape (Resistance theory), LCP (Least Cost path), linkage mapper (Matrix analysis) were performed on Arc GIS platform for Identification of Tiger conservation prioritization units and their connecting linkage with pinch point barrier. The work was initiated with the Grid wise information collection of vegetation, Faunal, geographical, physical, anthropological and climatic factors. Functionality survey of Kanha-Pench corridor was performed during 2012 to 2015.

- **Primary Data –** Carnivore, Omnivore and Herbivore presence data. Water availability in water hole survey data, salt lick survey data, canopy density, silviculture working circle data, grazing status data.
- **Secondary Data-** village location (SOI), prey density (WII Census 2010), village population (Census 2011), elevation (SRTM DEM), Climatic data (BioClim), Cattle kill Data (M.P. Forest Department)
- **Remotely sensed Data,** Forest cover (LISS-3), land use (World View Imaginary-2)

We have examined the corridor viability on three aspects namely, genetic, habitat and physical, therefore we developed genetic database and GIS raster's of tiger presence locations along with its surroundings all significance correlated variables.

3. RESULT AND DISCUSSION

As DNA of each individual tiger is unique, DNA based method is more accurate for arriving at tiger numbers, distribution, sex ratio and Genetic relationship with source population as degree of relatedness within population of corridor and with source population. As the source of DNA is only fecal matter, it can be used even in remote areas and with creating minimum disturbance to the animals. Two problems were examined through this study.

1st problem is non substantial growth of tiger population in Madhya Pradesh. After the first scientific census of wild life in 2006. In Madhya Pradesh, tiger population dynamics showed clear indication of non substantial population growth of tigers in Madhya Pradesh as shown in fig.no.1, although country level tiger population has grown sharply, while the protection measures were near to equal.

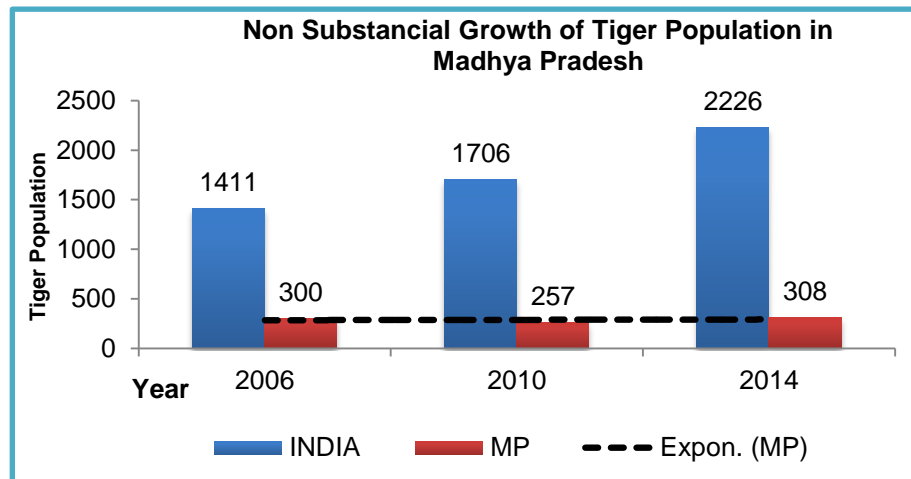
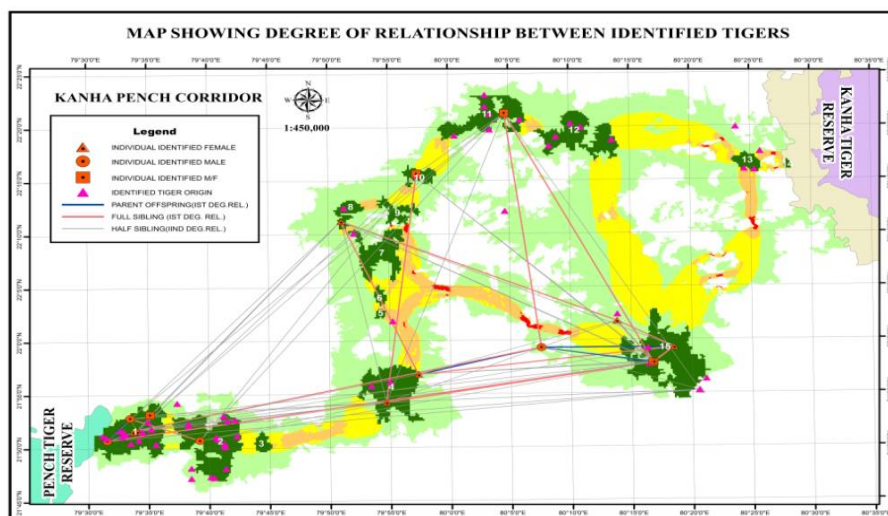


Fig. no. -1

Genetic approach: We have identified the presence of minimal nineteen tigers in corridor areas during our studies. Out of which eleven were females and four were male tigers. The presence of female tiger in critical tiger habitat clearly indicates that these patches have the capacity to support small population. Relatedness analysis in ML-RELATE Programme indicates about the fact that the populations present in corridor have first degree relationship with thirteen tigers of Kanha, 12 tigers of Tadoba-Nagzira-Brahmapuri complex and three tigers of Pench adjoining protected areas. These genetics signatures present in corridor have proof of generational movements from adjoined source population and evidence of restoration ecological process in corridor areas.

All of these above described scientific facts saying aloud about the spillover of tigers due to saturation of carrying capacity of the protected areas as shown in map no. 2



Map no. 2

On the basis of above described work we found 83 were positively of tiger origin and 13 were of leopard origin out of 157 scat samples were collected from Kanha-Pench Corridor, Madhya Pradesh from January 2013 to January 2015. After the PID (Probability of identity) analysis, minimum number of loci required to match a pair of genotypes was kept at 7. We identified a total of nineteen individuals of which 11 were females and 4 were males. We could not establish the sex of 4 individuals.

Fig. 2: Graphical representation of probability of identity values of individuals (Ind)

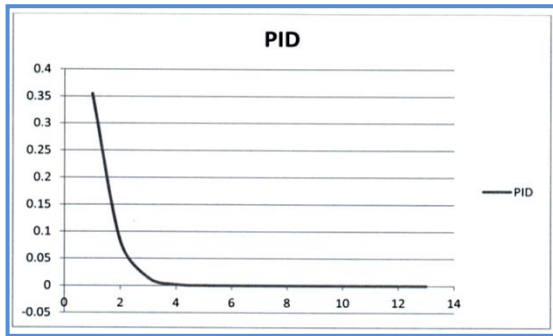


Fig. 3: Graphical representation of probability of identity values of siblings (Sib)

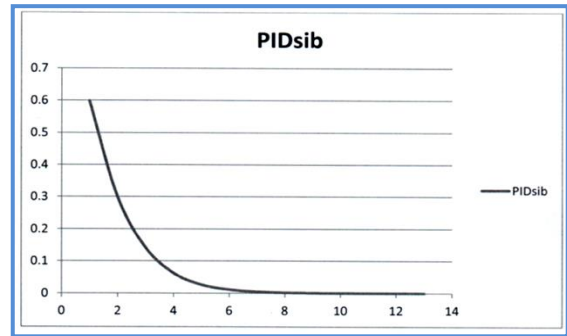


Table no. 1: Description of final Genotypes and Sex of Kanha-Pench Corridor Individuals.

Animal Id	F37a	F37b	F42a	F42b	F53a	F53b	Fca96a	Fe.96b	F115a	F115b	F124a	F124b	F141a	F141b	F146a	F146b	Fca391a	Fca391b	Fca424a	Fca424b	Fca441a	Fca441b	E6a	E6b	E7a	E7b	Sex
PKC20	0	0	230	238	172	176	203	203	187	193	0	0	267	279	0	0	202	210	154	174	148	156	153	156	143	153	-
PKC46	227	227	206	230	0	0	0	0	183	183	0	0	263	271	0	0	210	210	162	162	148	152	141	156	141	153	-
PKC50	227	235	206	234	184	184	201	203	187	187	216	216	267	271	0	0	214	222	0	0	0	0	147	147	143	153	F
PKC56	227	227	230	230	0	0	201	205	0	0	208	216	267	271	0	0	0	0	162	162	144	148	150	150	143	143	M
PKC102	223	223	230	234	0	0	0	0	183	191	0	0	271	279	0	0	206	206	162	170	148	152	147	156	141	153	M
PKC103	223	223	238	238	0	0	205	205	191	191	0	0	271	271	0	0	202	202	170	170	144	148	156	162	151	151	F
PKC108	0	0	226	230	0	0	203	203	183	183	216	216	0	0	0	0	0	0	162	166	144	148	150	153	143	153	F
PKC111	223	223	234	234	160	162	203	203	183	191	0	0	271	275	0	0	206	214	170	174	148	156	156	159	141	157	F
PKC122/123	227	227	218	226	0	0	203	205	183	187	0	0	0	0	0	0	214	214	162	162	148	152	0	0	141	143	M
PKC132	227	227	230	234	0	0	201	203	183	185	208	216	0	0	0	0	198	206	162	170	148	156	150	156	141	143	F
PKC127/133	227	227	230	234	0	0	203	205	183	187	208	216	263	263	154	158	218	226	158	162	148	156	147	150	143	149	F
PKC136	227	227	230	234	172	172	197	205	183	187	208	216	263	263	0	0	218	226	162	170	148	156	147	150	143	145	F
PKC139/143	227	227	226	230	160	164	203	205	183	187	208	212	263	271	158	158	210	214	158	162	148	152	150	150	141	143	M
PKC157	223	223	230	238	168	168	203	205	0	0	0	0	259	271	0	0	0	0	170	170	148	156	156	162	141	157	F
PKC49	227	237	230	234	184	184	201	203	185	187	208	208	271	271	0	0	210	222	158	162	148	148	147	147	143	153	F
PKC98	0	0	0	0	0	0	205	205	183	183	0	0	0	0	0	0	198	206	162	162	144	148	156	162	141	141	-
PKC113	227	227	226	230	0	0	179	181	183	183	0	0	0	0	0	0	0	0	0	0	148	148	162	162	143	149	-
PKC120	0	0	218	230	0	0	0	0	0	0	0	0	271	275	0	0	202	202	162	170	144	148	156	159	143	143	F
PKC99	0	0	218	238	0	0	209	209	183	183	0	0	0	0	0	0	0	0	170	170	148	148	147	162	157	157	F

Table no. 1 shows the measures of genetic variation at 13 studied microsatellite loci in genotyped individuals of Kanha-Pench corridor. Number of alleles observed across the microsatellite loci used for all individuals varied from 2 (L8) to 8(L9) with an overall mean of 5.4615±1.7614. Observed number of alleles (5.4615) across the loci was more than effective number of alleles (3.5668). Shannon's information index showed that most of the loci were highly informative, with an overall mean polymorphism across the loci for Shannon's information index at 1.3547 ±0.4085. Expected heterozygosity (He) ranged from 0.5000 to 0.8791 with mean of 0.7064±0.1251; and observed heterozygosity ranged

from 0.1429 to 0.8333 with mean of 0.6102 ± 0.1832 . Average expected gene diversity within the population ranged from 0.3750 to 0.8520 with an overall mean of 0.6718 ± 0.1367 as shown in Table no. 2.

Table no. 2: Measures of Genetic Variation at studied Microsatellite Loci in Kanha-Pench Corridor

Locus	Sample Size	Observed number of alleles	Effective number of alleles*	Shannon's information Index [†]	Observed heterozygosity	Expected ^a heterozygosity	Nei's heterozygosity	Heterozygote deficiency ^b
L1	28	4	2.0103	0.8800	0.1429	0.5212	0.5026	-0.72582502
L2	36	6	4.1274	1.5875	0.8333	0.7794	0.7577	0.069155761
L3	14	7	5.4444	1.8095	0.4286	0.8791	0.8163	-0.51245592
L4	32	7	3.5068	1.4876	0.6250	0.7379	0.7148	-0.15300176
L5	32	5	2.7380	1.2241	0.5625	0.6552	0.6348	-0.14148352
L6	16	3	2.2456	0.8815	0.6250	0.5917	0.5547	0.05627852
L7	26	6	3.4141	1.4643	0.6923	0.7354	0.7071	-0.05860756
L8	4	2	1.6000	0.5623	0.5000	0.5000	0.3750	0
L9	28	8	6.7586	1.9846	0.6429	0.8836	0.8520	-0.27240833
L10	34	6	2.9490	1.3081	0.5882	0.6809	0.6609	-0.13614334
L11	36	4	2.5019	1.1314	0.8333	0.6175	0.6003	0.349473684
L12	36	6	4.8000	1.6472	0.7222	0.8143	0.7917	-0.11310328
L13	38	7	4.2722	1.6431	0.7368	0.7866	0.7659	-0.06331045
Mean	28	5.4615	3.5668	1.3547	0.6102	0.7064	0.6718	-0.13618347
St. Dev		1.7614	1.4808	0.4085	0.1832	0.1251	0.1367	0.464428457

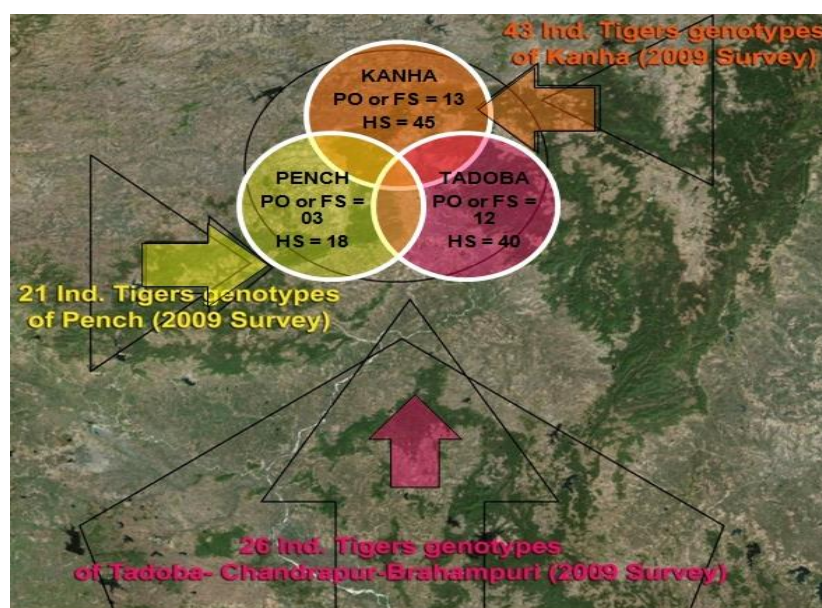
* Effective number of alleles (Kimura and Crow, 1964) [16]

[†] Shannon's Information index (Lewontin, 1972) [17]

^a Expected heterozygosities were computed using Levene (1949) and Nei's (1973) expected heterozygosity [18]

^b Heterozygote deficiencies were expressed as $D = (H_o - H_e) / H_e$

PULATION RELATEDNESS WITH ADJOINING PROTECTED AREAS: Maximum likelihood estimates of



relatedness in ML-RELATE showed twenty-three 1st degree (PO or FS) relationships and forty-five 2nd degree relationships (HS) among the tigers genotyped from the Kanha-Pench Corridor. When we compared 43 Kanha individuals with tigers from Kanha-Pench Corridor, we got thirteen 1st degree relationships and forty-five 2nd degree relationships. Similarly we got three 1st degree relationships and eighteen 2nd degree relationships among tigers from Pench and Kanha-Pench Corridor, and twelve 1st degree relationships and forty 2nd degree relationships among tigers from Tadoba-Nagzira-Brahmapuri complex and Kanha-Pench Corridor as shown in table

no. 3. (1st Degree relationship (PO= PARENT OFFSPRING, FS= FULL SIBLING) IInd Degree relationship (HS= HALF SIBLING))

Table no. 3: Maximum likelihood relationships among genotyped tigers from the Kanha-Pench corridor

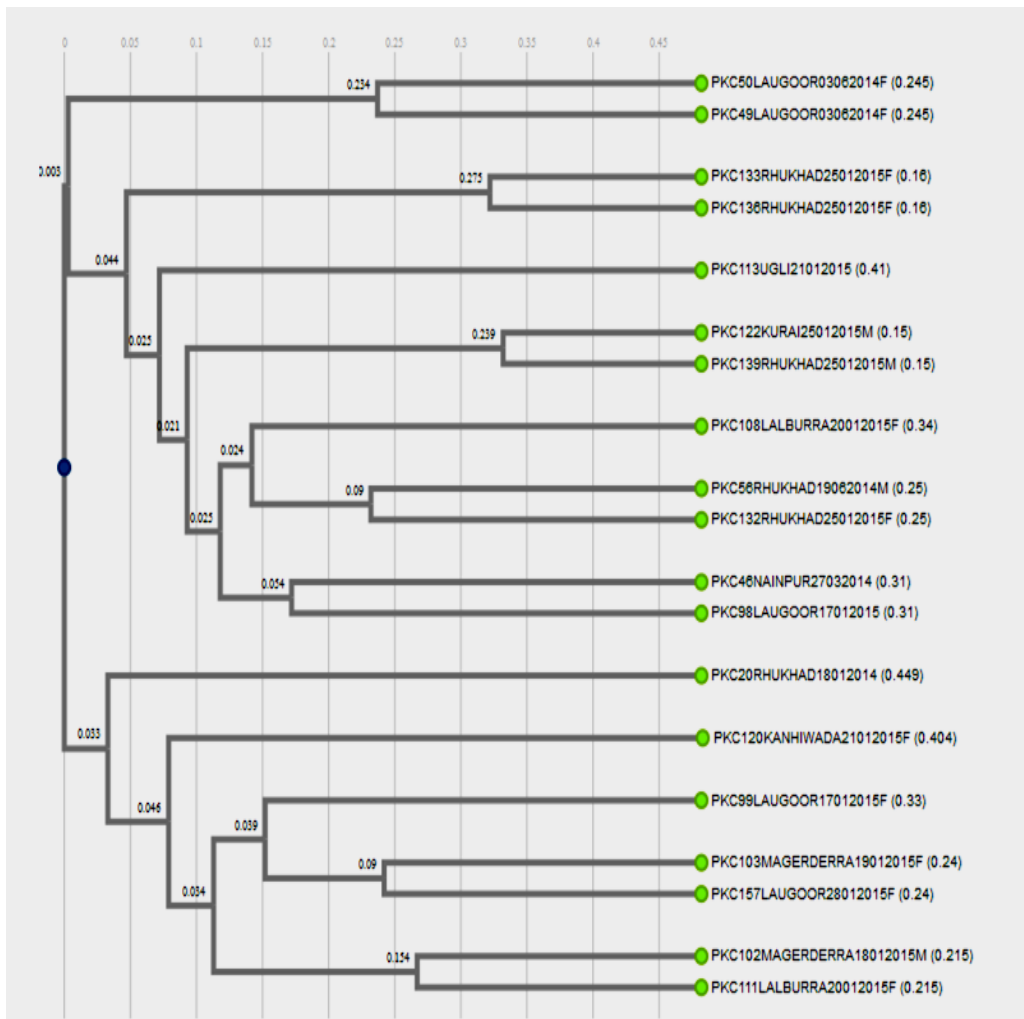
	P K C2 0	P K C4 6	P K C5 0	P K C5 6	P K C1 02	P K C1 03	P K C1 08	PK C11 1	PK C12 2	PK C13 2	PK C13 3	PKC 136	PK C13 9	PK C15 7	PK C49	PK C98	PK C11 3	PK C12 0	PK C9 9
PKC2 0	-																		
PKC4 6	U	-																	
PKC5 0	U	U	-																
PKC5 6	U	U	HS	-															
PKC1 02	U	FS	U	U	-														
PKC1 03	U	U	U	U	HS	-													
PKC1 08	HS	HS	HS	HS	HS	U	-												
PKC1 11	U	U	U	U	PO	HS	U	-											
PKC1 22	U	HS	U	U	U	U	HS	U	-										
PKC1 32	U	HS	U	PO	FS	U	HS	HS	U	-									
PKC1 33	U	U	U	HS	U	U	HS	U	U	FS	-								
PKC1 36	U	U	U	HS	U	U	HS	U	U	FS	FS	-							
PKC1 39	U	HS	U	PO	U	U	HS	U	FS	U	HS	U	-						
PKC1 57	U	U	U	U	PO	FS	U	FS	U	HS	U	U	U	-					
PKC4 9	U	HS	FS	HS	HS	U	U	U	U	HS	U	U	U	U	-				
PKC9 8	U	FS	U	FS	PO	FS	FS	HS	HS	HS	U	U	HS	FS	U	-			
PKC1 13	U	HS	U	U	U	U	FS	U	HS	U	HS	U	U	U	U	HS	-		
PKC1 20	HS	U	U	HS	U	FS	HS	FS	U	HS	U	U	U	HS	U	HS	U	-	
PKC9 9	U	U	U	U	HS	HS	U	HS	U	U	U	U	U	FS	U	HS	HS	HS	-

Four common pedigree relationships: unrelated (U), half-siblings (HS), full- siblings (FS) and parent- offspring (PO)

UPGMA ANALYSIS:

UPGMA(Unpaired Group Mean Algorithm) Similarity Matrix UPGMA is a simple agglomerative (bottom up) hierarchical clustering method. The UPGMA method (Sneath and Sokal, 1973) [19] is a simple agglomerative hierarchical clustering method. The UPGMA method employs a sequential clustering algorithm, in which local topological relationships are inferred in order of decreasing similarity and a dendrogram is built in a stepwise manner. That is, first the two closest data points are identified and grouped in the dendrogram as shown in fig. no. 4.

Fig. 4 Similarity Denrogram Created by using Upgma Software on Similerty Matrix



HABITAT SUITABILITY APPROACH:

MAXENT ANALYSIS: Replicated MAXENT model for TIGER_PRESENECE Variable selected on the basis of significance value derived from BMLR analysis in SPSS 19.

Fig. 5, ROC Curve, Mean AUC 0.889

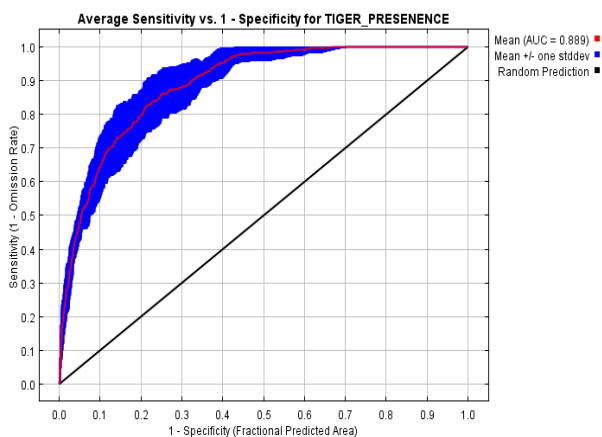
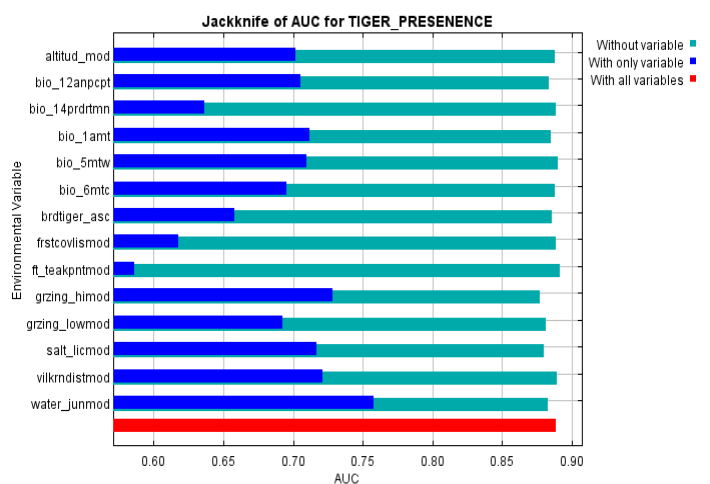
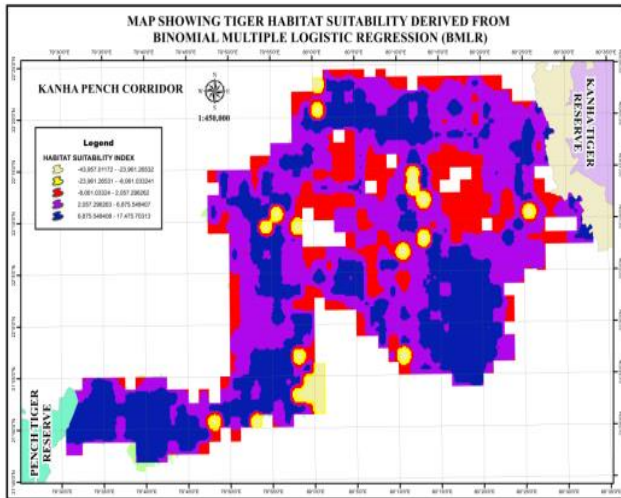


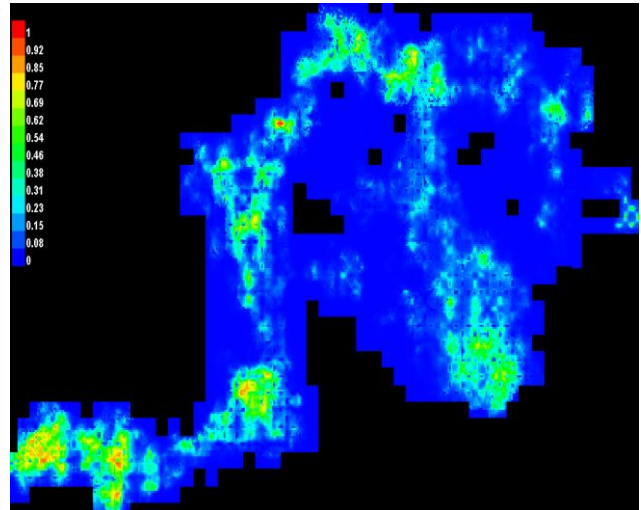
Fig. 6 Jackknife Test



Tiger Habitat Suitability Map: Researcher relied on two scientific approaches i.e. BMLR and MAXENT analysis to find out habitat suitability map on GIS environment. Both of the approaches approximately classified the same area according to their suitability for tiger presence. Here BMLR is supportive approach to justify the inference of MAXENT findings as shown in map no 3 and 4.



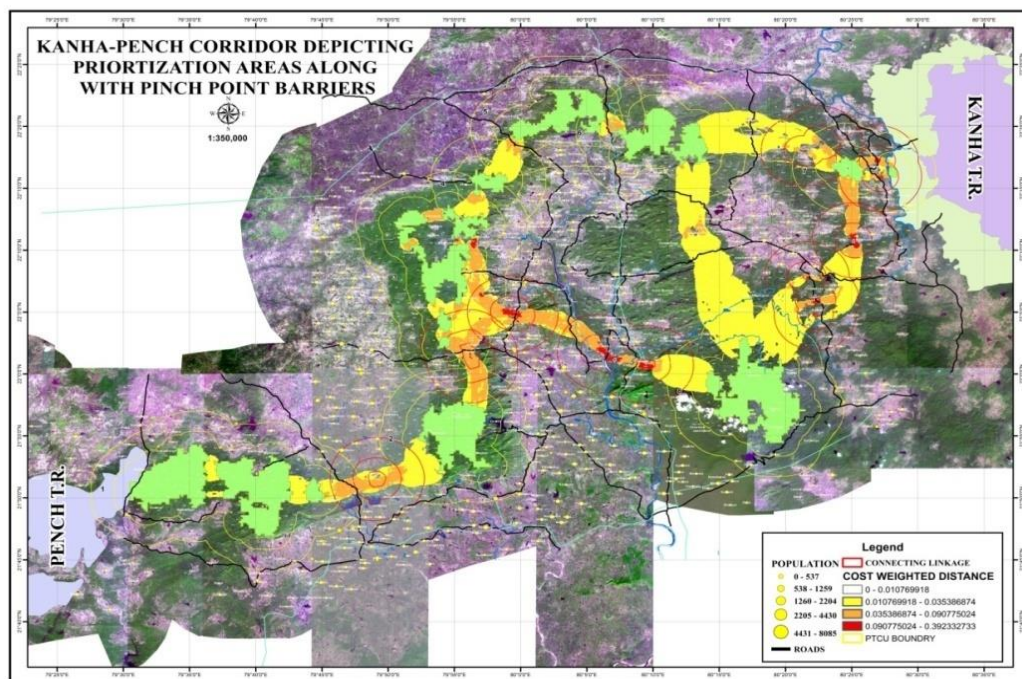
Map no. 3: BMLR Analysis



Map no. 4: MaxEnt Analysis

The probability of occurrence as presence of tiger as shown above map clearly demarcated the areas of critical tiger habitat. These areas are also serving as stepping stone of corridor for tiger movement. The eleven female tigress presences were noticed in these critical tiger habitat through this study is a concrete scientific evidence to keep these areas as tiger conservation prioritization areas. Thus on the basis of MaxEnt result, we identified eight TCPUs as shown below in world view 2 imaginary map. After corridor mapping, we run Pinch point Mapper (McRae 2012) [20], based on circuit theory by using the program Circuitscape (McRae and Shah 2009) [21] to identify pinch points within the least-cost corridors as shown in above map.

The details of prioritization tiger conservation units as inference from MaxEnt analysis were described below. Table indicating details of Tiger conservation units had shown below in map no 5.



Map no 5: Kanha-Pench corridor depicting prioritization areas along with pinch point barriers

After the GIS mapping of the corridor total area 2500 sq. km area was found most suitable as tiger habitat. Identified 429 sq. km area is demarcated in eight Tiger conservation prioritization units as shown in table no.4 Among of them fifteen forest area are now working as stepping stone. Conservation practices are only immediate requirement of these Tiger Conservation Prioritization Units. The conservational step can prevent the timely fall in the quality of the tiger area. The Kanha-Pench corridor is a stepping stone type of corridor now established by current study.

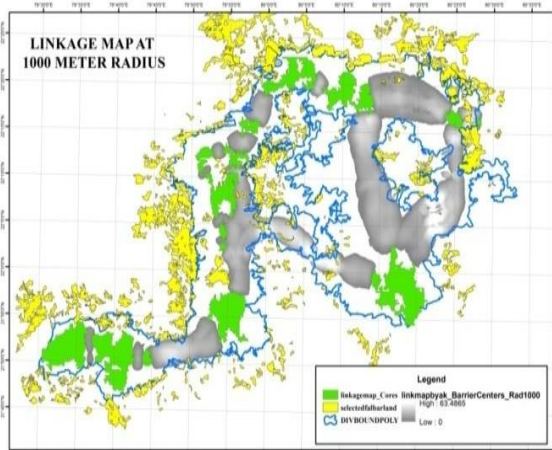
Pinch point barriers were located under the total 8 weak links were also been identified by utilizing software's like Fragstrat, linkage mapper. Whereas the highest risk compared to the entire corridor area has been calculated for tigers.

Table no. 4: Details of Prioritization Tiger Conservation Units (PTCUs)

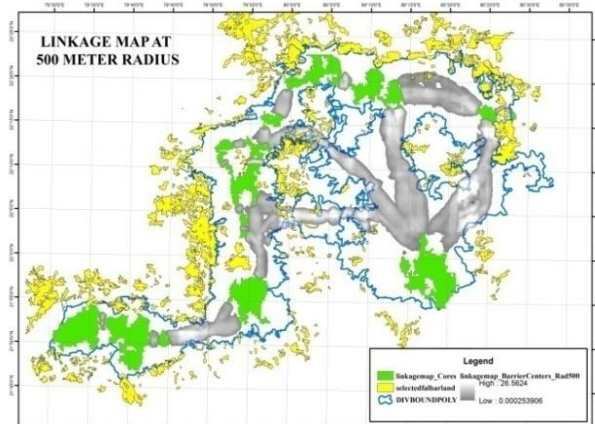
PTCU No.	Stepping Stone Core Area (In ha.)	Village Area (In ha.)	Forest Area (In ha.)
1	13388	423.33	12964.67
2	5393	146.72	5246.28
3	6055	117.5	5937.5
4	956	0	956
5	4112	0	4112
6	4553	0	4553
7	1015	0	1015
8	8502	802.60	7699.39
Total	43974	1490.15	42483.84

Two routes were generated by linkage mapper analysis, when one KM width of corridor was kept as condition. While three routes were generated when half km width was a condition as shown in map no. 6 and 7. Reciprocating availability of water, grasses, prey, fodder and bamboo in weak links and enhances safety measures so that safe movement can be ensured by weak links of tigers.

Map no. 6: If we kept 1000 meter width of corridor in linkage mapper then it derived only two routs rather than three as shown below in map.



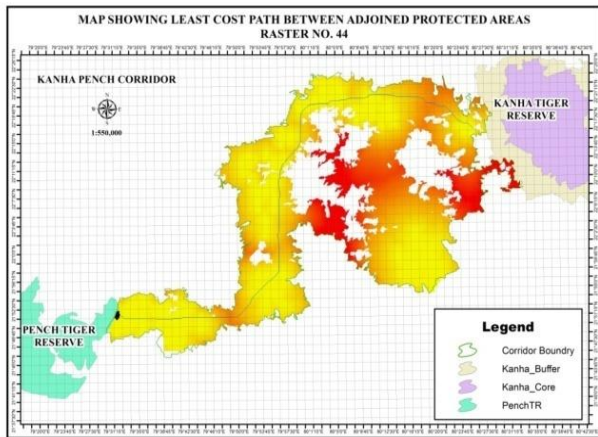
Map no. 7: If we kept 500 meter width of corridor in linkage mapper then it derived three routs rather than three as shown below in map.



Least Cost Path: Least cost path analysis was used to determine optimal corridor paths between the Kanha and Pench tiger reserve. Considering the area between the points between which connectivity is being explored, it computes a composite 'cost of movement' score for every cell in the intervening landscape grid by considering factors that would promote or impede movement of Tiger.

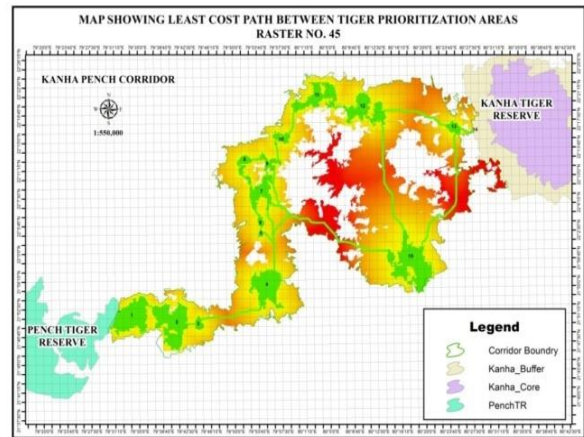
When we ran least cost path analysis tools in ARCGIS software between the K-P source populations, the derived least cost path depicted as maps on shown below

Map no. 8 LCP between the PAs



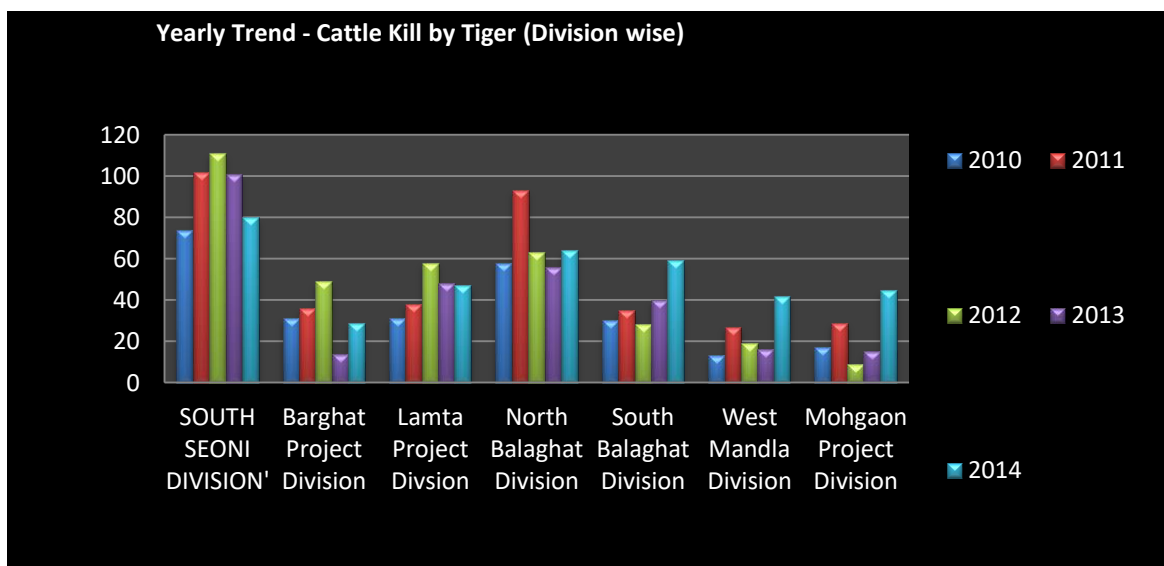
There are eight tiger prioritization conservation units are serving as stepping stone for tiger movements are now connected by least cost path analysis as shown map below.

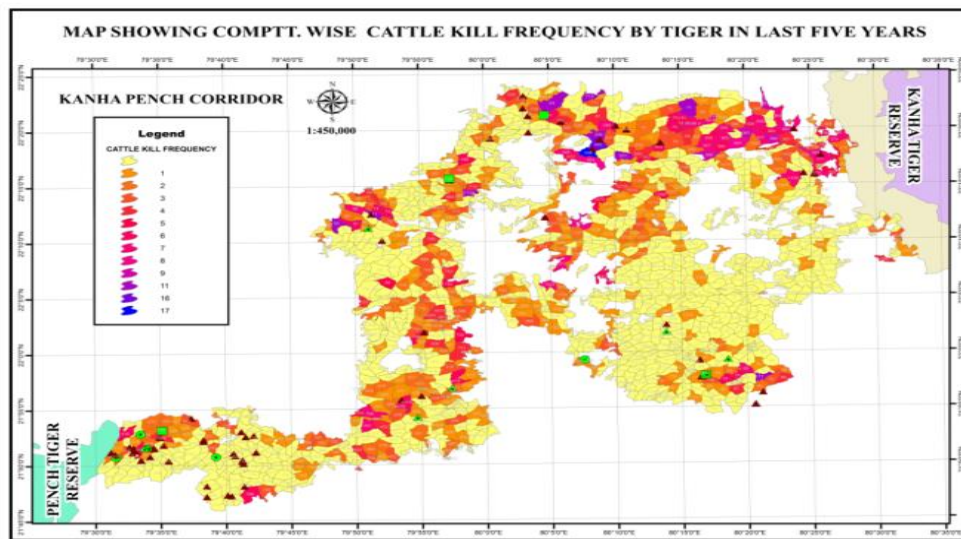
Map no.9 LCP between TCPUs constituting stepping stones



2nd Problem: Human animal conflict is common in corridor area. At present, approx avg. 321 livestock are killed by tiger every year in the Kanha-Pench corridor. Cattle killed data were procured from concerned territorial forest divisions along with their relevant compartments. Data was analyzed on GIS platform afterward conditions were depicted regarding the tiger- human conflict as shown on below map no. 10 shown below. These cattle kill evidences of corridor area clearly indicating about the dependency of tiger on livestock for predation. This fact was verified by ungulate encounter rate data obtained by WII wild life census data 2010. GIS map indicate about prey density of corridor area is nearly half rather than adjoining protected areas. This reason is a root cause of human tiger conflict. These events are also an evidence of corridor is utilizing by the tiger. Conditions are alarming, however corridor is historical and has potential to support tiger population but due to human population expansion, agriculture extension and uncontrolled grazing, poaching, now tigers are under threat conditions utilizing these connecting linkages for movement. In other words, it can be say safely; Kanha-Pench corridor is functional on the cost of cattle kill

Map no. 10, Map depicting compartment wise cattle kill frequency by Tigers in 2010 to 2014 (five years)





4. RECOMMENDATIONS

Feeling of revenge against the cattle kill and human injury or death of forest dwellers generally found in corridor. The excessive pressure is visible in the forest areas due to the settlement of the village around weak linkages. On the paths of movements of tigers, the symptoms of aggression in behavior of wild animals seen as conflict or multiple kill due to human disturbances such as road construction coup felling works, grazing etc. As a result cases of fatal attack during the binning of Mahua (*Madhuca indica*) flower on villagers by sloth bear are common and recorded in document of the division. Leopards are roaming around the villages for predation of small domestic ungulate due to insufficient prey density in forest area of corridor. Low prey density in forest area creates conflict between human and carnivore. Occasionally leopard entre in villages for predation of live domestic animals in night also documented. Therefore it is necessary that the area of grazing should be delineated and the availability of the grass and bamboo should be insured throughout the year in forest areas for optimum prey base. So that passage of wildlife will not be fall on the side of human settlements.

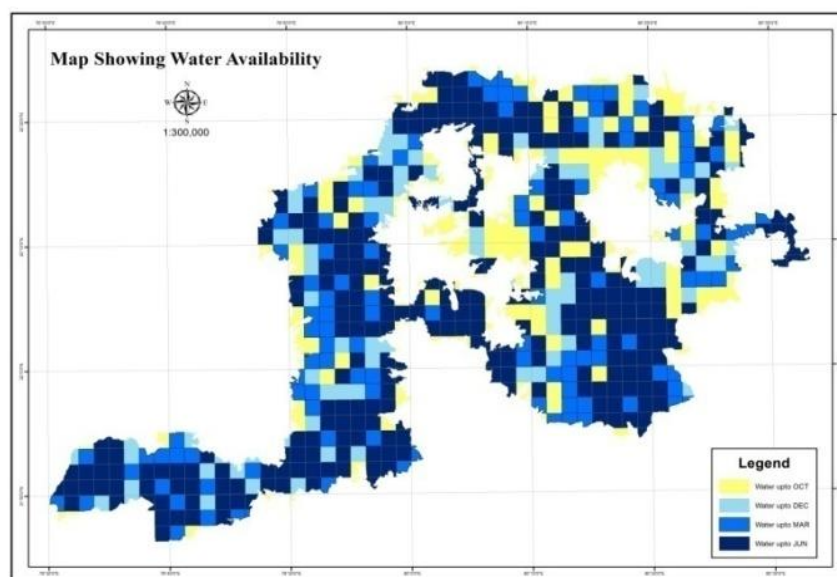
Among of 2500 sq.km area of corridor 429 sq. km area is identified as critical tiger habitat by MaxEnt Species Distribution modeling, in which 19 Tigers presence were confirmed by DNA test. The presence of 11 female tigress performed successful restoration of tigers in the corridor region. This restoration has been possible by generational movements from protected areas, therefore its proofs have been obtained by inter population genetic correlates. Result of DNA analysis clearly indicate about continuous displacement from source population. The allele of Kanha, Tadoba-Nagzira-Brahmapuri complex and Pench sub meta population has been found in corridor population. Therefore Kanha-Pench corridor population of Tigers is admixed population of Kanha Pench and Tadoba-Nagzira-Brahmapuri adjoining PAs. The Genetic heterozygosity was found 0.61 with no sign of genetic bottleneck, that's proving functional status of corridor by indicating good genetic variability. Although, now linkage habitat of corridor has become less suitable because of human disturbance. *Bos gaurus* sensitivity is more compared to tigers for habitat fragmentation noticed during occupancy survey. Conditions prevail naturally in tiger prioritization area; low grazing pressure; low human interruptions; water availability during hot summer days; natural creatures such as caves; large size rocks; undulating topography; low biotic pressure; abundant availability of palatable grasses and far distance from human settlement.

While uncontrolled grazing, excessive human disturbance, high biotic pressure, low density forest cover, plain topography, water scarcity during hot summer days and easy availability of domestic cattle are the universal conditions of connecting linkages present everywhere. Tigers are moving under threat due to these conditions prevail in connecting linkages. Although the easy diet available through easy access to them receives constant food along with this biological pressure by less distance from the villages. Villagers are constantly facing the consequences of the loss of livestock and their agricultural crops. Conflict severity increases during water scarcity in summer days when wild animals migrate from forest area to manmade water structure for quench the thirst. Its notable that the above reasons promote easy poaching.

Teak plantations were done at a macro level under Forest Development Corporation within the corridor habitat. The fact remarkably came out by habitat suitability analysis that monocrop plantation raised by MPRVVN through clear felling of miscellaneous fruit bearing forest were found least suitable for tiger occurrence. While the habitat suitability for tiger was found optimum where natural miscellaneous forest left untouched under protection circle area. Therefore it was recommended that before the allotment of forest area for teak mono crop plantations, it should be insured that allotted forest area is not falling under the least cost pathway for movements of tigers. However, if the monocrop teak plantation is required due to the economic benefits of the state then plantation area should not be selected more than 25 ha. as one set of plantation and between the two sets of plantation a minimum 2.5 km ridiculous distance should be kept so that type of miscellaneous bamboo forest remain intact. Water is a basic need of life for wild life and its availability is necessary in home range area of herbivore for functional niche of ecosystem healthy ecosystem works on survival of herbivore in unit forest area. Availability of herbivores wild animal depends on availability of water and grasslands. Presence of water during the whole year period is essential component for the viable ecological system in the home range of ungulate. Kanha Pench corridor is falling under 5 sq. sized 719 grids. While 122

grids of them have not sustain water till the month of June. Therefore seasonal movement of wild animal centered toward available source of water. That phenomenon also creates assessable opportunity becomes available for the purpose of poaching. Conflict incidence increases between the wild creatures such as bears and tigers to occupy the water source. Therefore it is necessary to ensure the availability of water throughout the year in all 719 grids (5 sq.km size) through creation of medium sized micro water shade so that there is neither seasonal movement required nor easy opportunity for snail possible as shown in map no. 11

Map no. 11 showing water availability in different extent of months



Only fifteen % area is blank area out of 2500 sq. km area of KP corridor. Most of the orange area is available in West Mandla forest division, where grassland and silvipasture development work can be undertaken on priority. Bamboo regeneration was found minimum in West Mandla forest division area falling under corridor because of bamboo plantation with soil moisture conservation work required for wild life survival. In order to make the regeneration of bamboos become possible. Generally it has been observed that the work of teak gap plantation in less than 5 ha. open area is prevalently in priority. It is recommended by the present study below than five ha. open area treated under grass land management through palatable seed broadcasting along with regular weed eradication.

In addition to the above facts, unemployment and economic degradation are also fatal in the protection of wild animals. Therefore the deployment of ecotourism and the active participation of the villagers living around weak links should be ensured during allocation of ecotourism works under wildlife conservation programme. Many of the natural sites have capacity to be developed as ecotourism centre like Jhangul, Jhanghghoghra, Gangulpara Dam, Laugor FV, Sonawani FV, Amodagarh FV, Thawr Wainganga river junction, Dhuty Dam, Kopijhola FV, Nahelesarra dam, Sakata FV and Rookhad

FV have enormous possibility as eco tourism centre. Where tourist can see the wild animals in their natural habitat and also experience the natural variants of wildlife. As it is known, only 20 % area of PAs is being kept available to tourists because of that many tourists are not allowed to enter park in favorable season of ecotourism. If tourist pressure is being diverted towards buffer and corridor areas. Neither tourist will be disappointed nor does deficit of creating opportunities for the employment of forest dwellers in weak links of corridor.

5. CONCLUSION

Corridor is functional on the cost of cattle kill. Kanha-Pench corridor is stepping stone type of corridor. This corridor has 8 prioritization conservation units and majorly 8 weak links within its extents. This corridor is now restored by generational movement of tiger from adjoining protected areas. The relatedness analysis indicates about gene flow is greater from Kanha and Tadoba-Nagzira-Brahmapuri complex comparatively Pench source population. All the critical tiger habitats are occupied by the female breeding tigers. Many of them are breeding tigress. This fact conveys us about its historical existence and viability to support the connecting meta population. Genetic study also confirmed generational dispersal movement from source population through their blue print of genetic signature in genotype of corridor population.

After the identified prioritization conservation units and pinch point barrier within connecting linkage should be taken for immediate action for betterment of conservation and mitigation. A conservation measure is a current need of prioritization units and silvipasture development, control grazing, habitat improvement, intensive patrolling in pinch point barrier are the basic needs of connecting linkage for conducive habitat development. Involvement of local stakeholders in eco tourism, diversion of ecotourism pressure towards corridor areas from core area of PAs are the basic points should be critically analyzed and adopted further for better scientific management of corridor.

HYPOTHESIS TESTING: Hypothesis of the study “Kanha Pench Corridor is not functional for genetic exchange” - is rejected since all the output indicators of the study reveal that 19 tigers (11 females included) were present with genetic signatures of first degree (PO, FS) relationship, second degree relationship (HS) between individual tigers belongs to adjoining source population and within corridor population. However; *Corridor is functional on the cost of cattle kill.*

ACKNOWLEDGEMENT: We thank Dr. H.S. Pabla, Ex. Chief Wildlife Warden for inspiration to initiate the study. I express my deep sense of gratitude to Shri Narendra Kumar, Ex. PCCF, Head of Forest Force & Ex. Chief Wild Life Warden for granting permission to carry out the research study on dispersal Tigers. My sincere thanks also goes to Shri Jitendra Agrawal Ex. CWLW Madhya Pradesh for his insightful comments and encouragement, but also for the hard question which incited me to widen my research from various perspectives. We thank Dr. Dharmendra Verma, Ex. Director State Forest Research Institute for providing technical guidance. We thank Shri Sunil Agrawal Ex. WPO Kanha-Pench corridor for encouragement to initiate the study. We thank Dr. P. Anuradha Reddy, Scientist, CCMB, Hyderabad for providing support in DNA Analysis. We also thank Mr. Amrendra Sinha for GIS work. We are thankful to all the field staff of Forest Department, Government of MP for their support in field work.

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