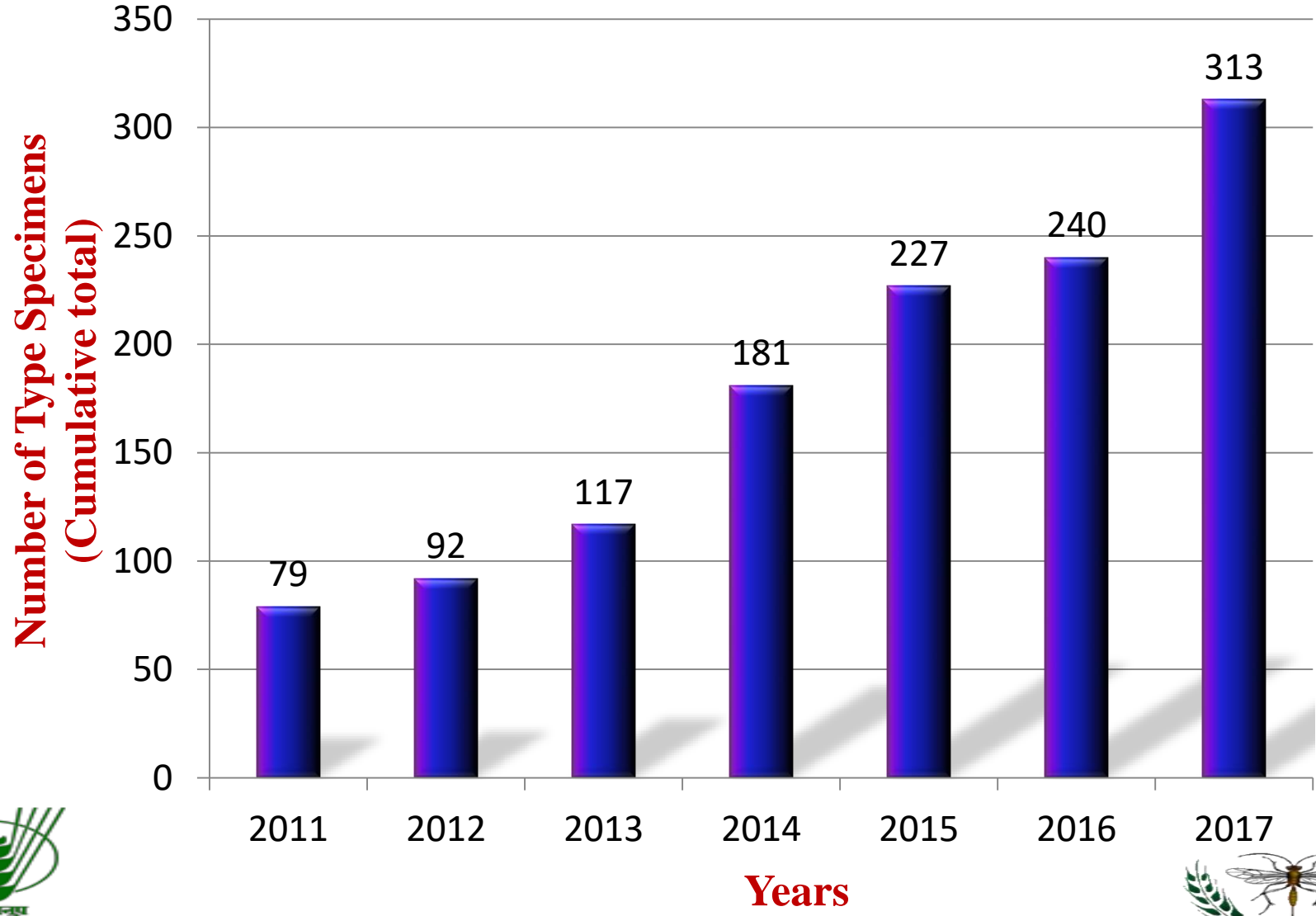
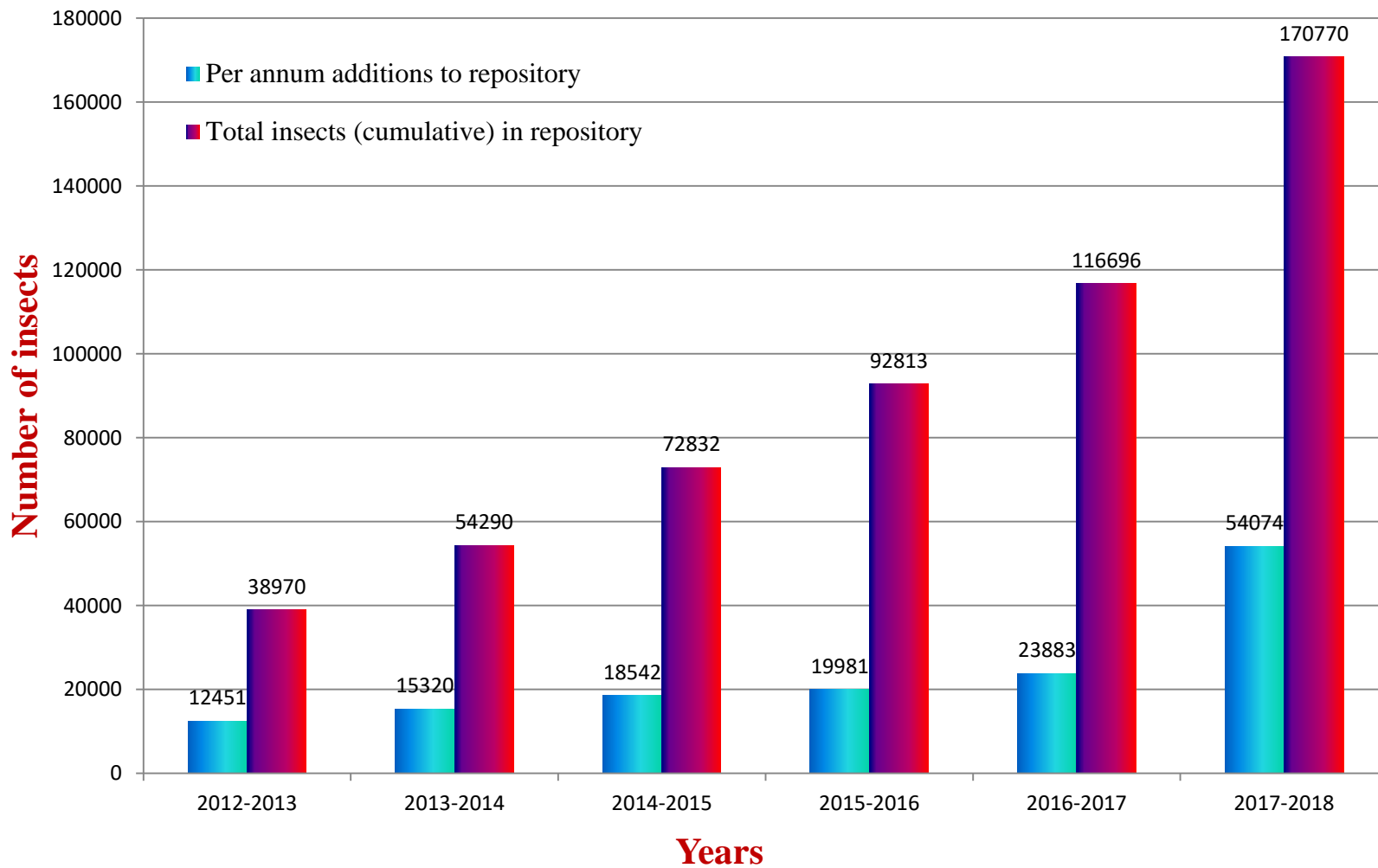


Chart 1: Number of Type Specimens of insects at ICAR-NBAIR museum



**Chart 2: Number of preserved insects in the ICAR-NBAIR museum:
Annual additions and cumulative figures**



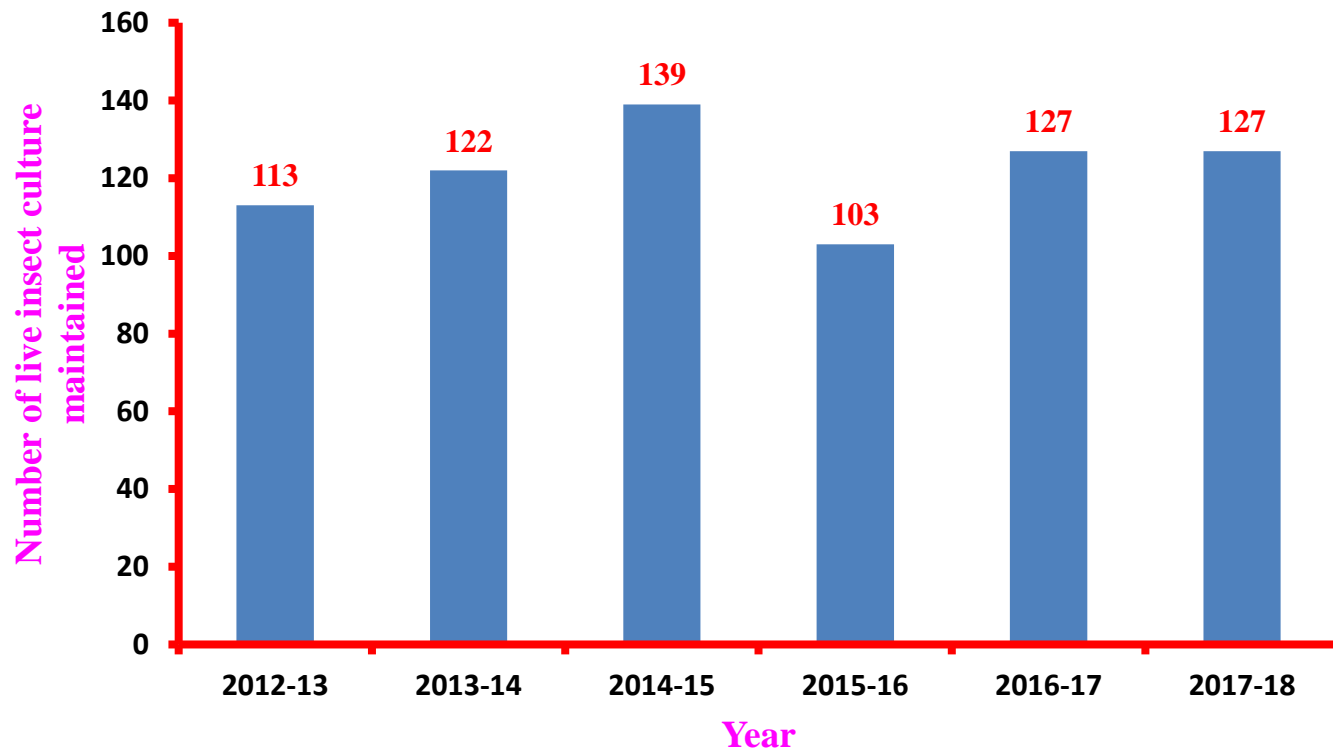


Chart 3: Total number of live insect cultures continuously maintained in the largest live insect repository in Asia (ICAR-NBAIR)

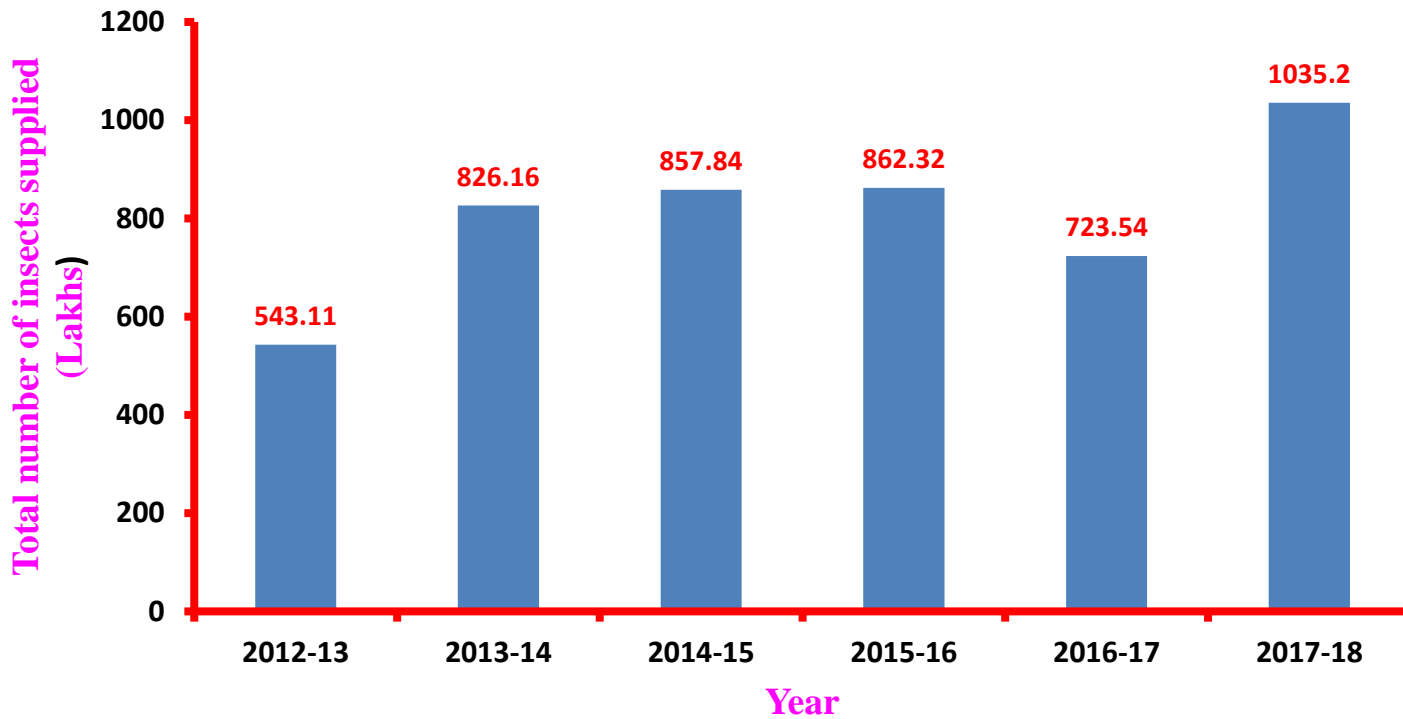


Chart 4: Total number of live insects supplied to different parts of the country (in lakhs)

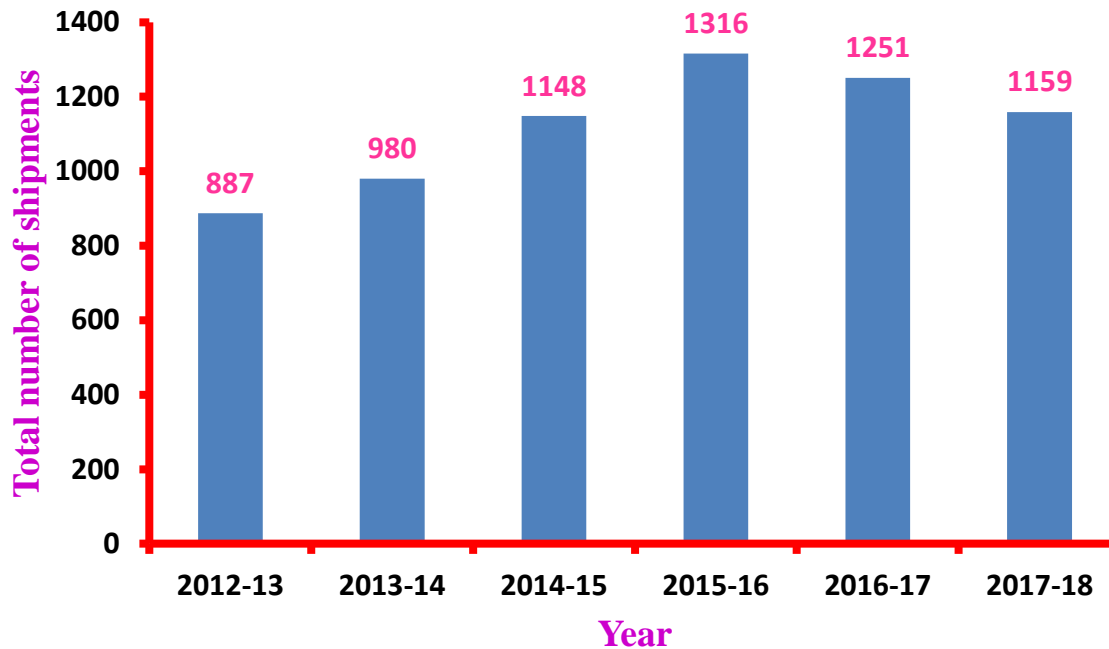


Chart 5:Total number of shipments of insects & insect resources supplied to different parts of the country

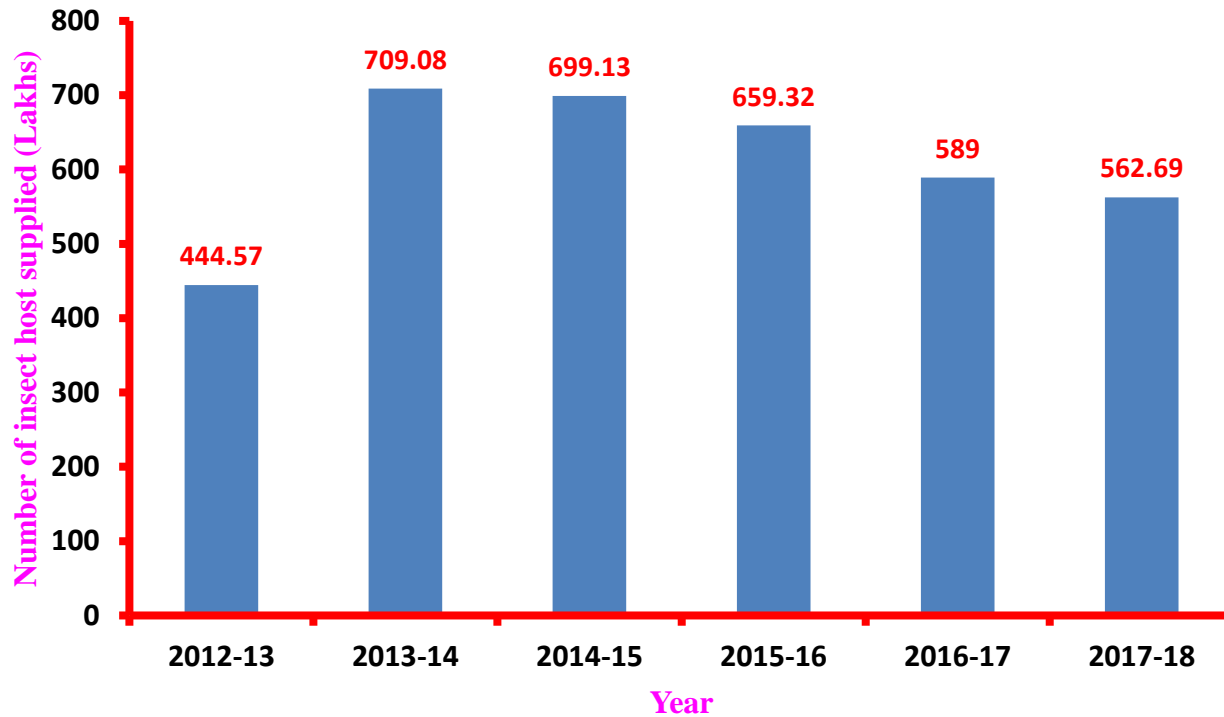


Chart 6: Total number of live insect host supplied to different parts of the country (in Lakhs)

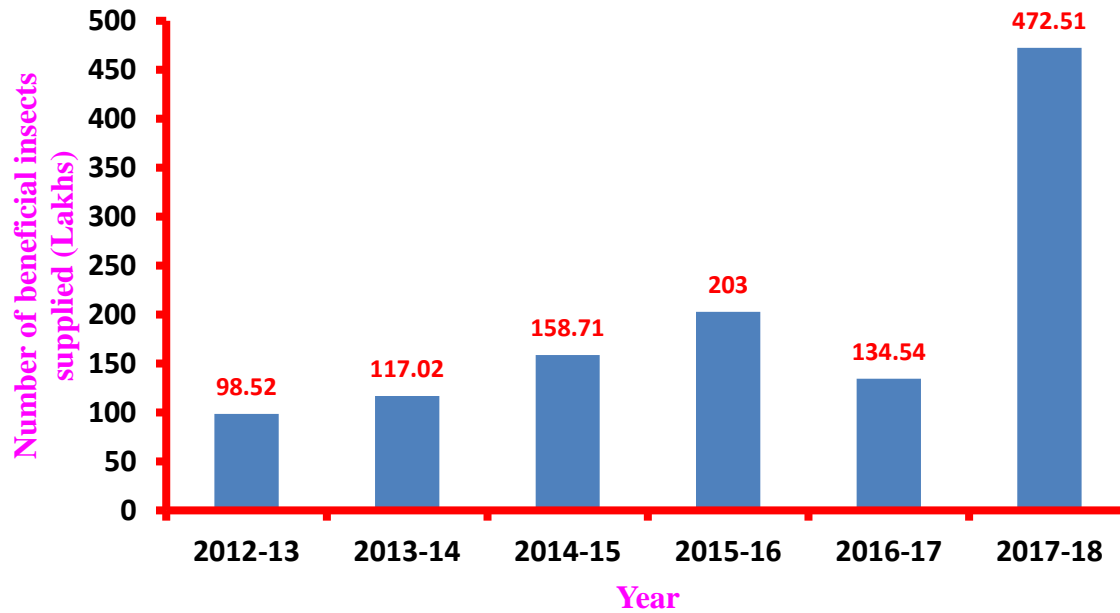
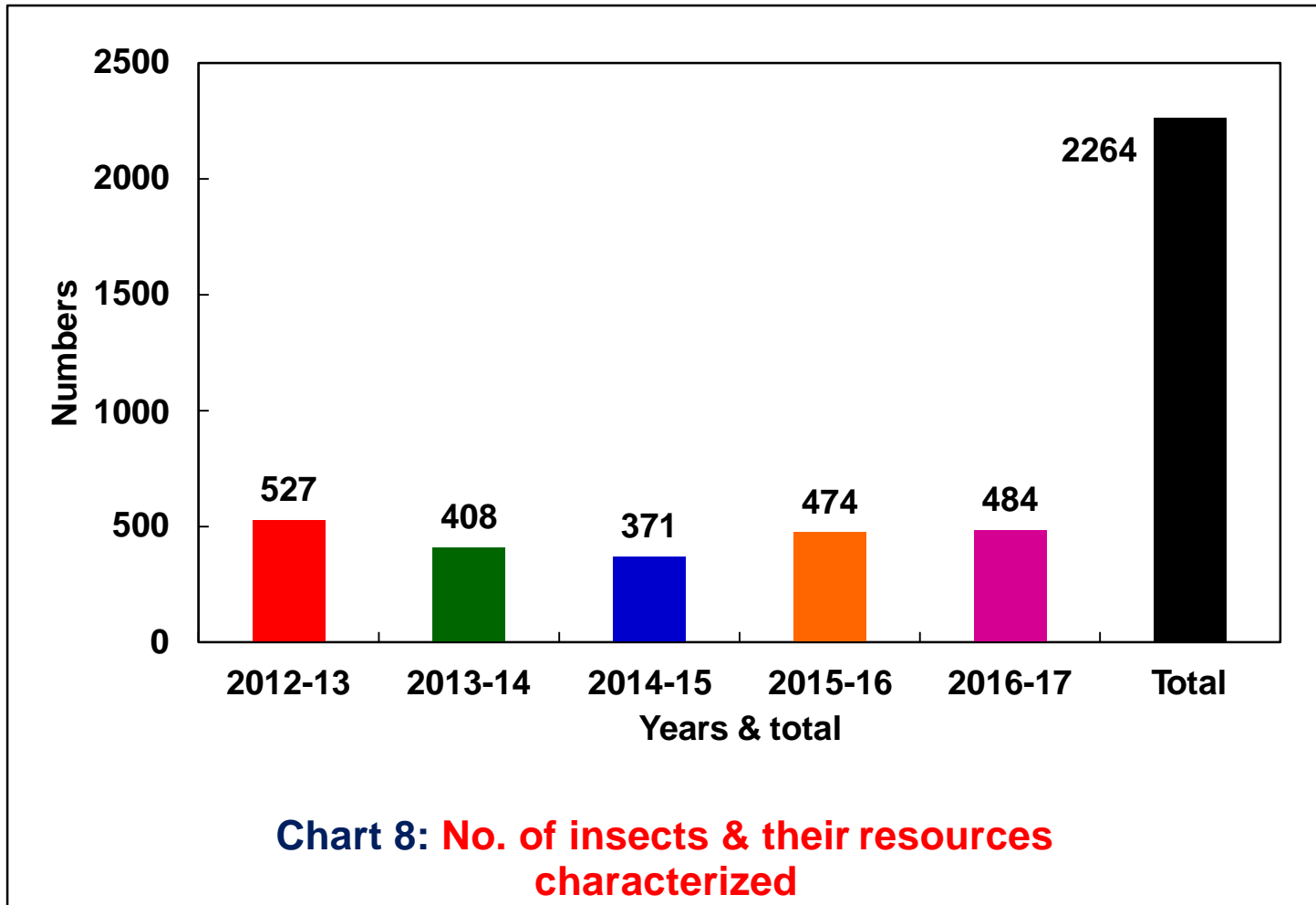


Chart 7: Total number of beneficial insects supplied to different parts of the country (in Lakhs)

Insect Genomic Resources



Insect Genomic Resources

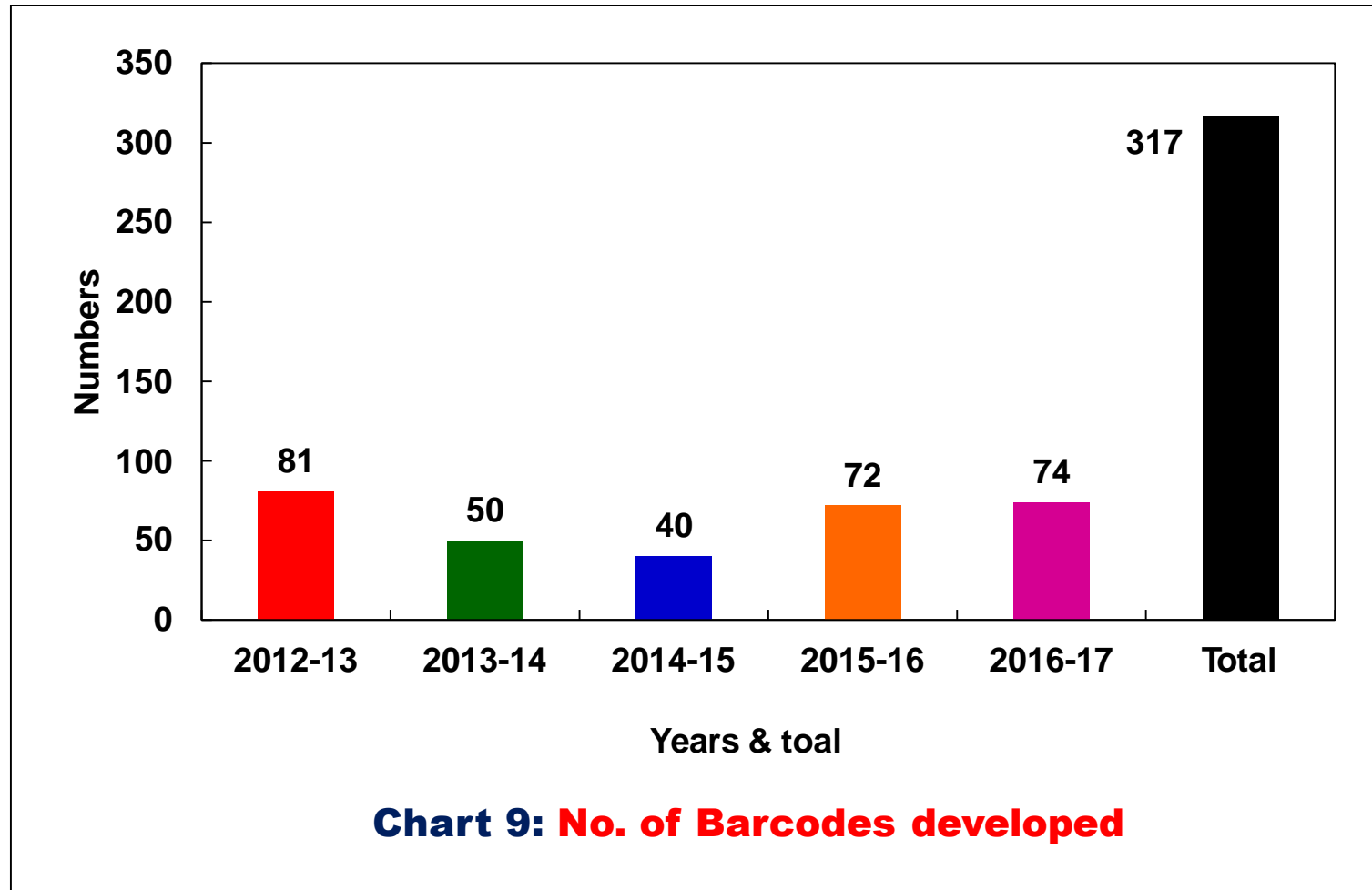


Chart 9: No. of Barcodes developed

Transcriptome analysis of insects

Leucinodes orbonalis

- **Platform:** Illumina 2500 (1T upgrade)
- **Total transcript length:** 73476635bp
- **Total number of transcripts:** 52279
- **GC%:** 46-50%
- **N50:** 2220
- **Q30:** >95%
- **SSRs:** 13047
- **E-value= 0:** 31.8%
- **Genes in databases:** >7000 genes were found in nr, kog, GO and pfam database
- **Genes up-regulated:** 12398
- **Genes down regulated:** 8068
- **SNPs:** >71K
- **Genes involved in signal transduction:** 1465
- **BioSample accessions:** SAMN05991854, SAMN05991855, SAMN05991856, SAMN05991857
- **BioProject:** ID PRJNA352591



About 20-40 rounds of insecticide sprays are given for control of this pests.

Whole Genome sequence of insects and their resources

Leucinodes orbonalis

- **Platform:** Illumina HiSeq2500 (1T Upgrade System). PacBio RSII (P6C4)
- **Estimated Genome Size (Flow cytometry):** 980MB
- **Paired end libraries:** 350 and 550bp
- **Mate pair:** 5Kb and 10Kb
- **Paired end Nzero rate:** 99%
- **Mate pair Nzero rate:** 99.66%
- **Paired end GC rate:** 35%
- **Mate pair GC rate:** 37%
- **Paired end Q30:** 93%
- **Mate pair Q30:** 86%
- **Illumina assembly:** First level assembly complete
- **PacBio:** Sequence run is on progress

***Helicoverpa armigera* nucleopolyhedrosisvirus (NPV)**

- **Platform:** Illumina NextSeq500 (2)
- **Samples:** L1 (Ludhina: most virulent), F1 (Faridkot: least virulent)
- **L1 genome size:** 136760bp
- **F1 genome size:** 113631bp
- **L1 putative ORFs:** 40
- **F1 putative ORFs:** 47
- **L1 & F1 hrs:** 5-5
- **L1 & F1 bro genes:** 4-4
- **L1 unique ORFs:** 18 (300bp), 19 (401bp)
- **L1 GenBank Accession number:** KT013224
- **F1:** Draft genome
- **L1 Gene validation by PCR:** *pol-h*, *iap-2*, *dbp* and *pif-1*

Genetic diversity analysis of populations of insects

Plutella xylostella

- **Sample collection:** 13 states of India
- **Geographic area:** ~ 12250000km²
- **Gene used:** *mtCOI*
- **Haplotypes:** 9
- **Polymorphic sites:** 11
- **Transitional sites:** 5
- **Transversional sites:** 6
- **Phylogenetic analysis method:**
Maximum likelihood (GTR model in MEGA v7.0)
- **Population from Shillong India clubbed with Australian populations of DBM**
- **Monophyletic clade:** 9 populations (All Indian populations)

Leucinodes orbonalis

- **Sample collection:** 18 States (32 places) of India
- **Gene used:** *mtCOI*
- **Haplotypes:** 17
- **Polymorphic sites:** 34
- **Transitional sites:** 20
- **Transversional sites:** 14
- **Phylogenetic analysis method:**
Maximum likelihood (GTR model in MEGA v7.0)
- **Majority of haplotypes were related to Solan, Himachal Pradesh, India**
- **Monophyletic clade:** All the populations were monophyletic, out group population was from CANADA, GenBank HQ953004