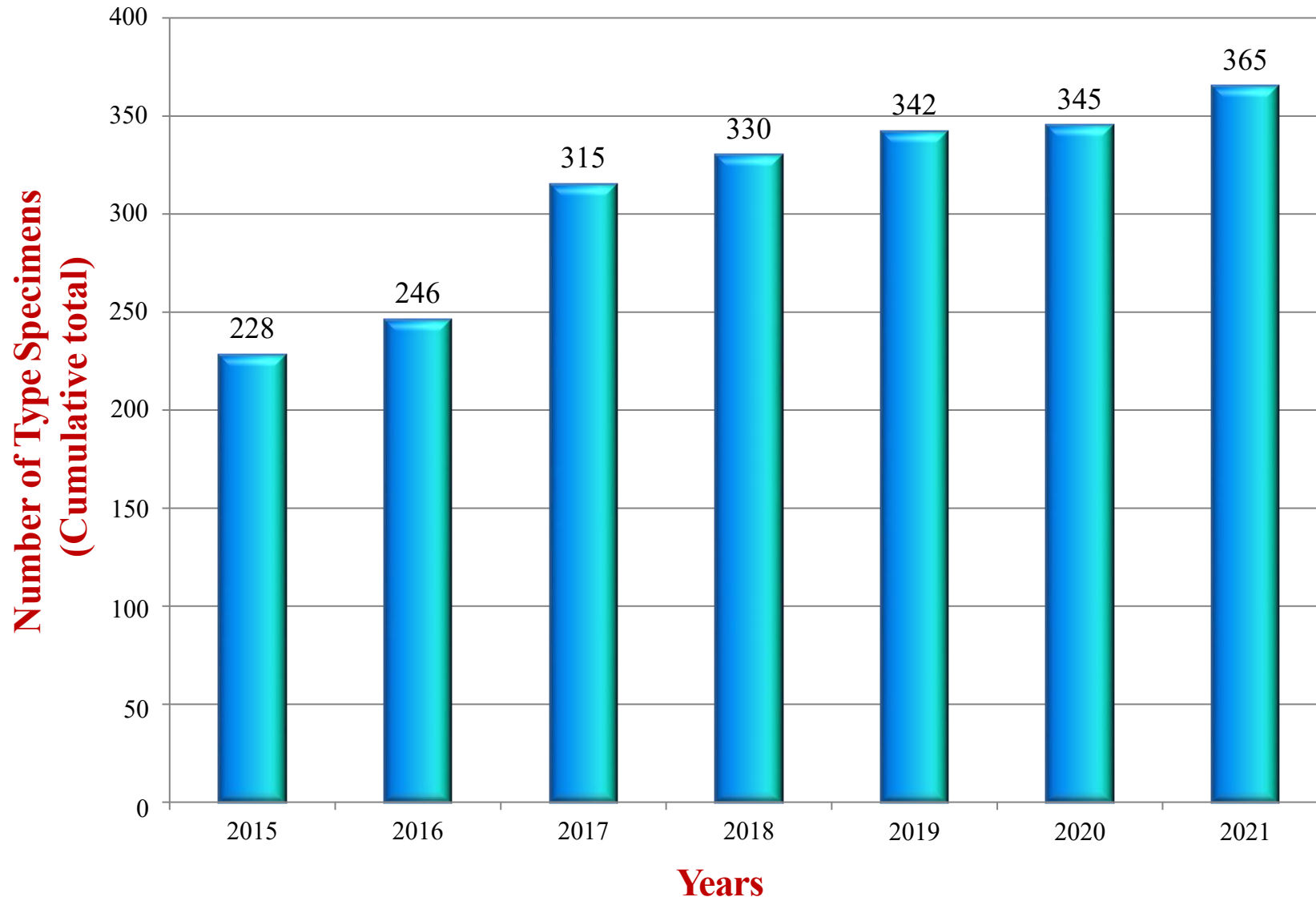
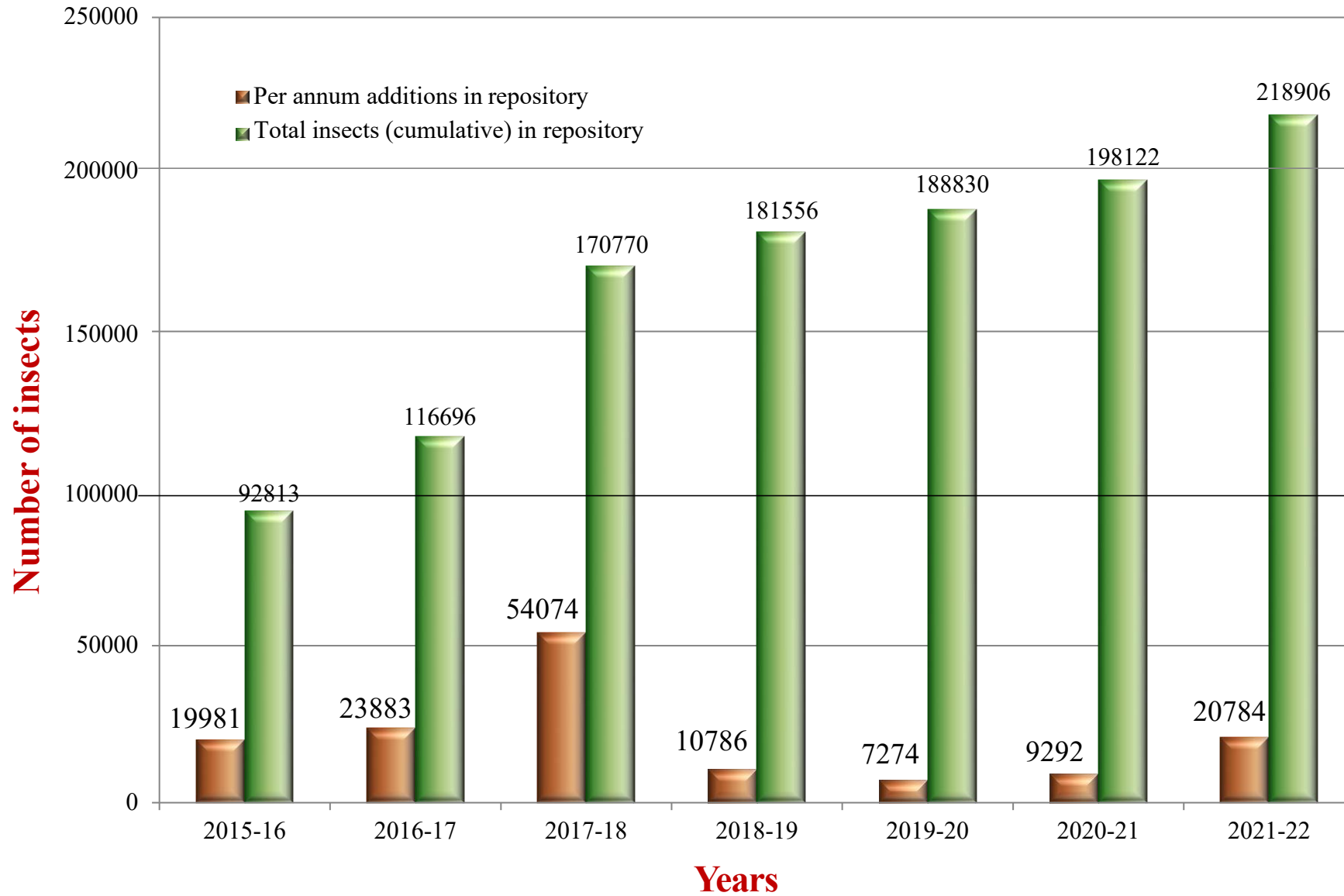
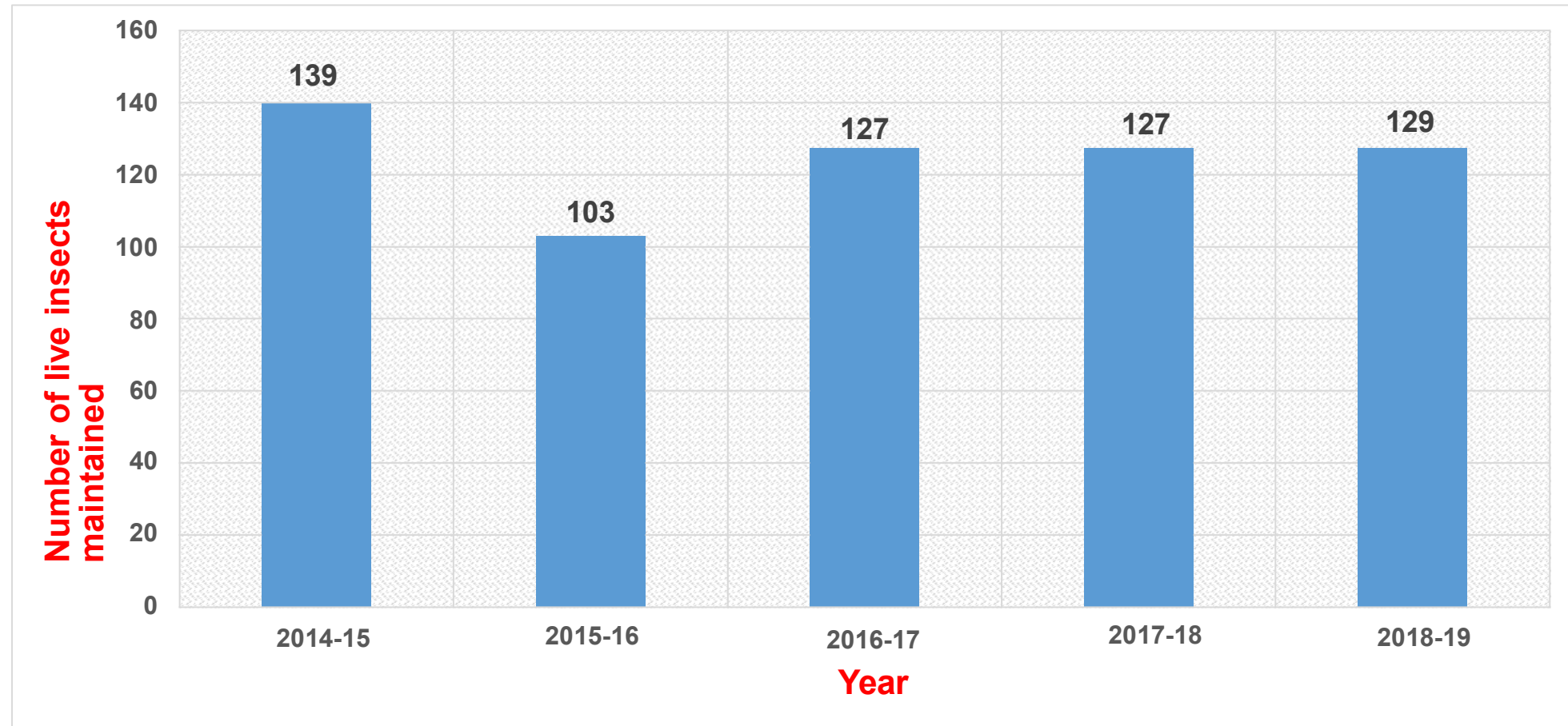


Number of Type Specimens digitized at National Insect Museum (ICAR-NBAIR)

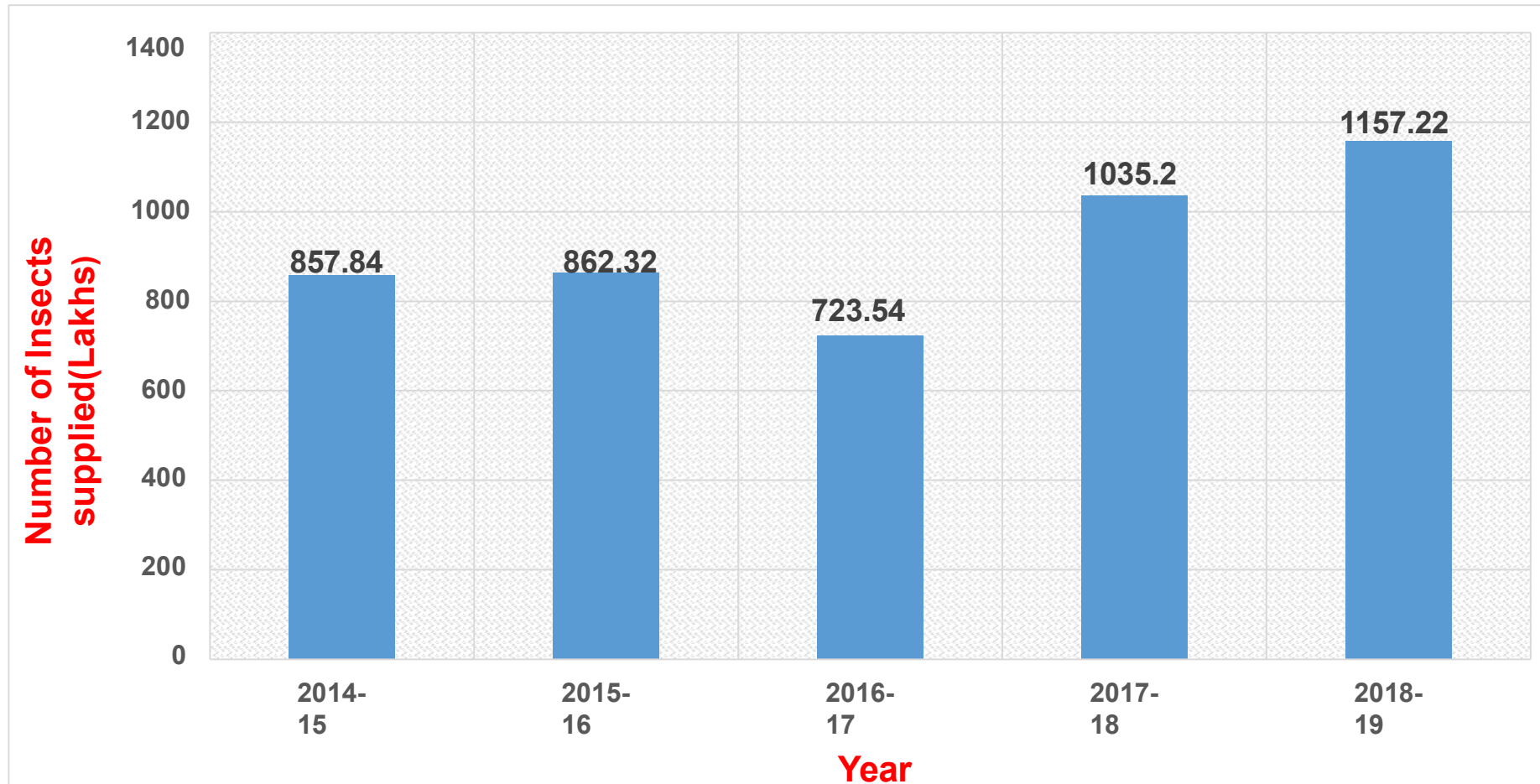


Number of preserved insects in the ICAR-NBAIR museum: Annual additions and cumulative figures

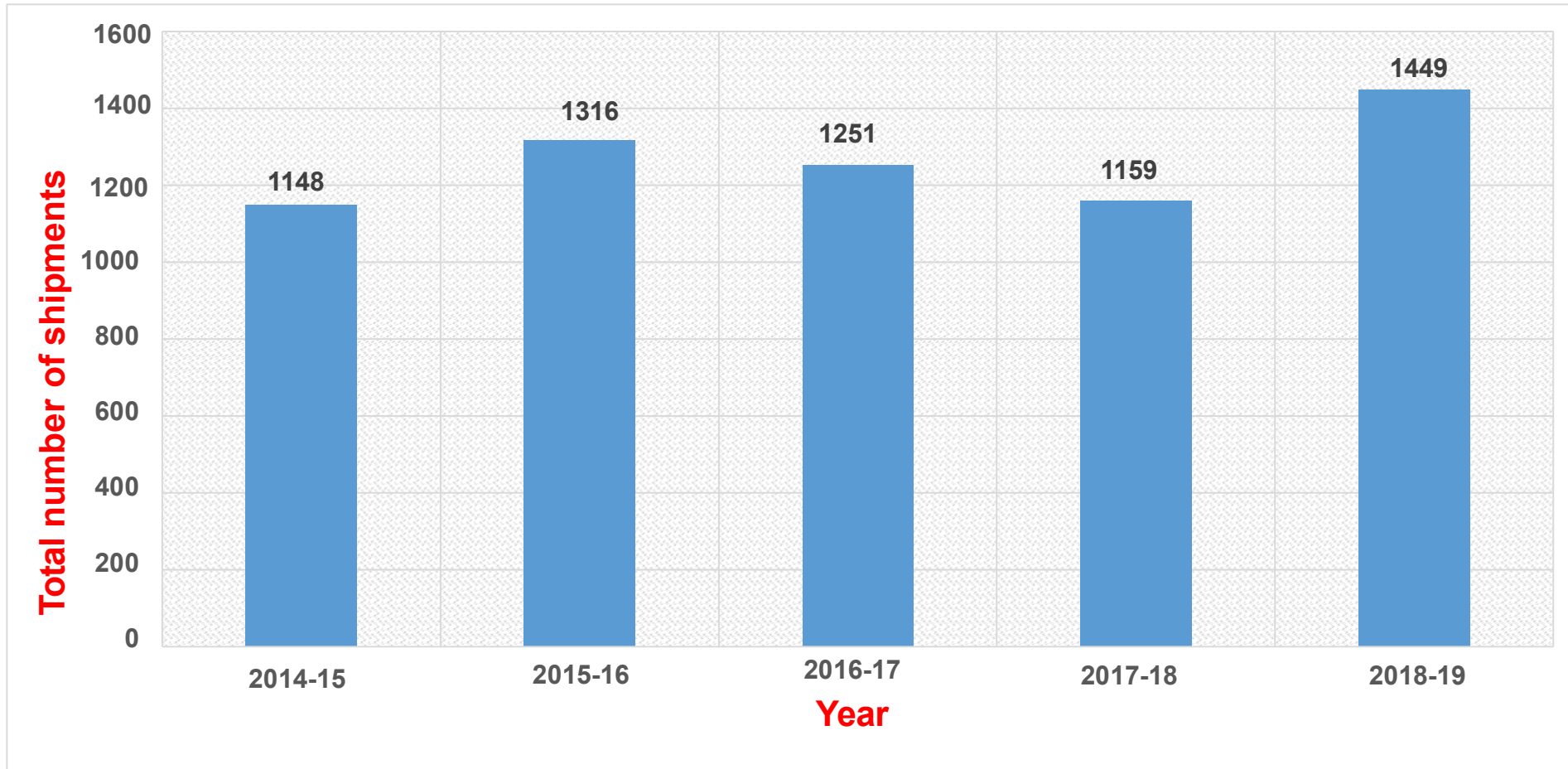




Number of insect live cultures maintained at ICAR-NBAIR



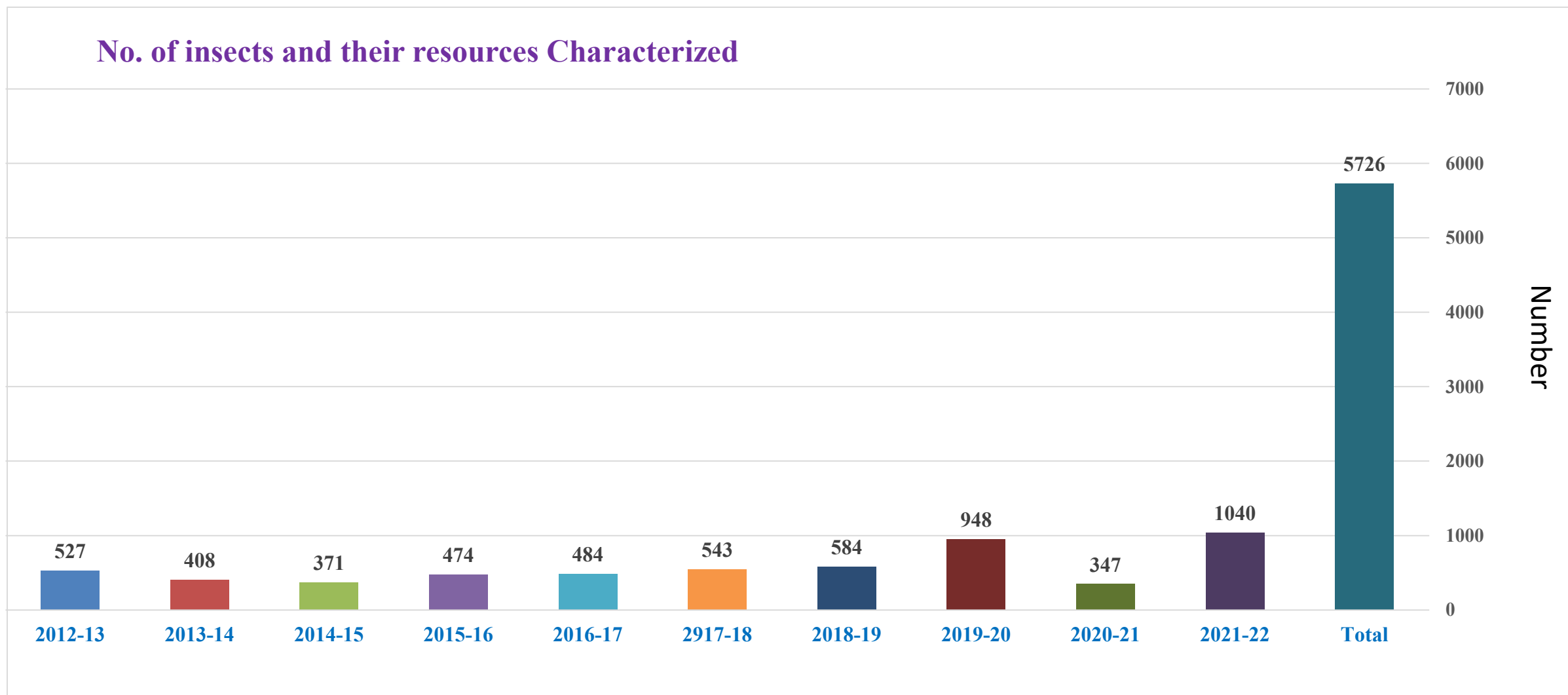
Total number of insects supplied during last 5 years



Total no. of shipments(Host insects and natural enemies) supplied to different organizations.

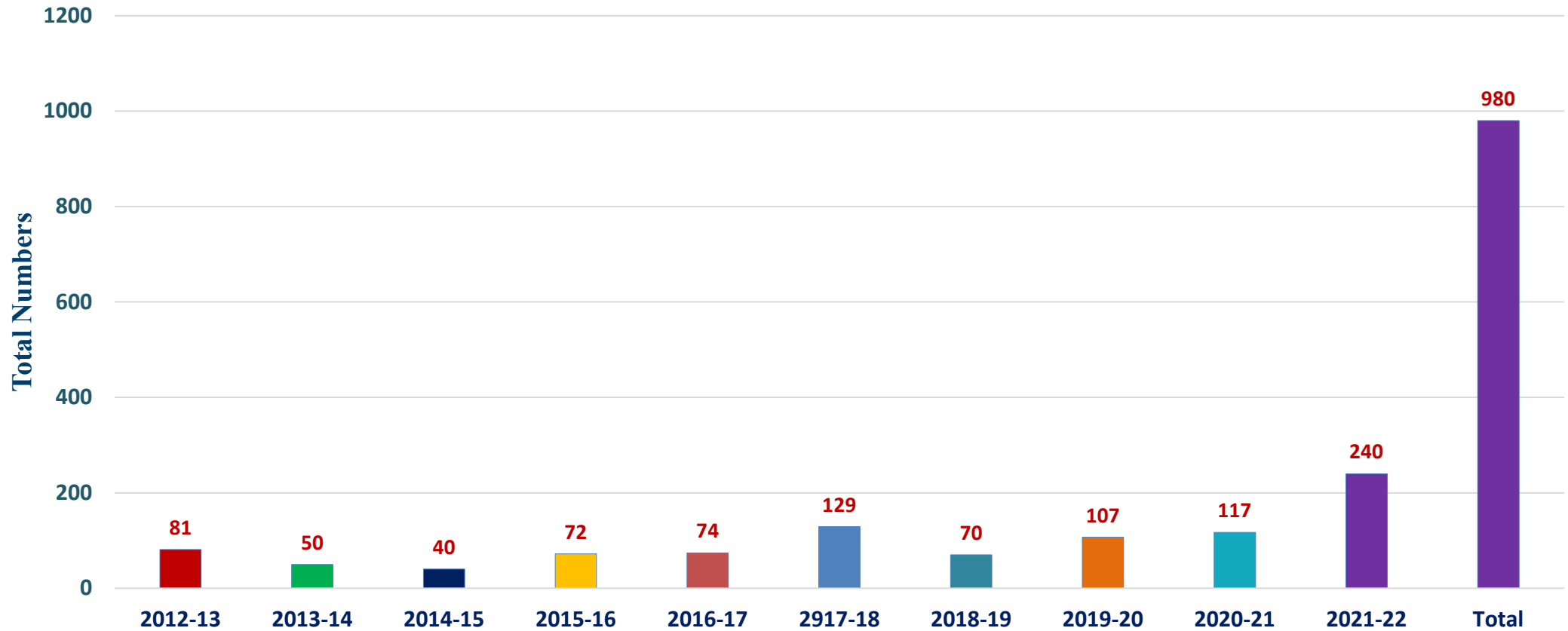
Insect Genomic Resources

No. of insects and their resources Characterized



Insect Genomic Resources

Number of Insects DNA Barcoded



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 read 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

nucleopolyhedrovirus (NPV)

- **Platform:** Illumina NextSeq500 (2
- **Samples:** L1 (Ludhiana: 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*

Whole Genome sequence of insects and their resources

Amrasca biguttula biguttula

- Whole genome sequencing, de novo assembly and annotation
- Genome size 1128 Mb
- No. of protein coding genes: 26223
- Repeat content 24.2%
- Stage specific transcriptome sequencing, assembly and annotation
- Expression profiling of genes related to insecticide resistance and RNAi validation

Polyphagotarsonemus latus

- Whole genome sequencing, de novo assembly and annotation
- Second smallest Arthropod genome: 49.1 MB
- 10,263 protein coding genes
- Low repeat region: 6.59%
- 24 novel CYP genes

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