Phenotypic and Genetic Dissection of Maize Internode Length

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INTRODUCTION

Plant height (PH) is among the most studied traits in maize, and is a function of two component traits, internode length (IL) and node number (NN). NN has been associated with the timing of vegetative to reproductive transition (i.e. flowering time). With the growing interest in utilizing maize as a source of biomass for biofuel production, it is desirable to alter the maize ideotype to enhance not only grain yield but also biomass yield without altering maturity. This could be achieved through the development of plants with superior PH, given the strong association of this trait with biomass yield. The objectives of this study were to: (1) characterize the phenotypic diversity and the relationships among PH, IL, below and above the uppermost ear IL (BEIL and AEIL, respectively) and NN, and (2) map quantitative trait loci (QTL) for these traits using phenotypically and genetically diverse maize populations including two recombinant inbred line populations (RILs): intermated B73 x Mo17 and Oh43 x W64A population, and two diverse populations, the Wisconsin Diverse Association Panel and the Nested Association Mapping population.

MATERIALS & METHODS

Intermated B73 x Mo17 (IBM)[1]
- 282 RILs grown in Arlington, WI in 2009 and 2010 in a randomized complete block design (RCBD) with two replications each year.
- 8,224 recombination bins markers (*see poster 241-8 for more details*).

Oh43 x W64A (OW)
- 255 RILs grown in Arlington, WI in 2011 in a single replication.
- 5,683 recombination bins markers (*see poster 241-8 for more details*).

Wisconsin Diverse Panel (WiDiv)[2]
- 607 inbred lines grown in Arlington, WI in 2008, 2009, and 2010 and in West Madison in 2011 in a RCBD with two replications each year.
- Genotyped with 203,049 SNPs generated from seedling RNA-sequencing.

Nested Association Mapping (NAM)[3]
- 3,707 RILs from 25 families grown in Arlington, WI in 2009 in a single replication.
- Genetic markers: 1,106 SNPs for joint-linkage mapping, 1.6 million SNPs for genome-wide association (GWAS)[4].

RESULTS: Phenotypic Dissection

Figure 1. Phenotypic variability for internode length (IL), below ear IL (BEIL) and above ear IL (AEIL) in four populations. Comparatively, the two association panels had genotypes with lower values than those observed in the RIL populations, whereas the RIL populations had genotypes with higher values than the association panel populations.

Recombinant Inbred Lines
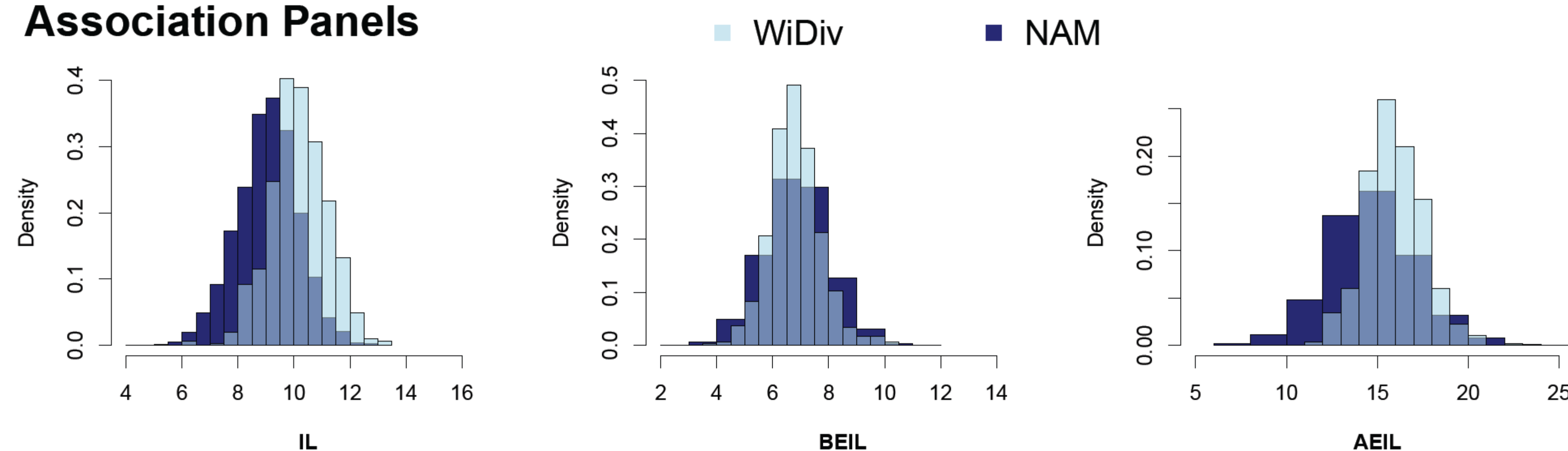IBM   OW
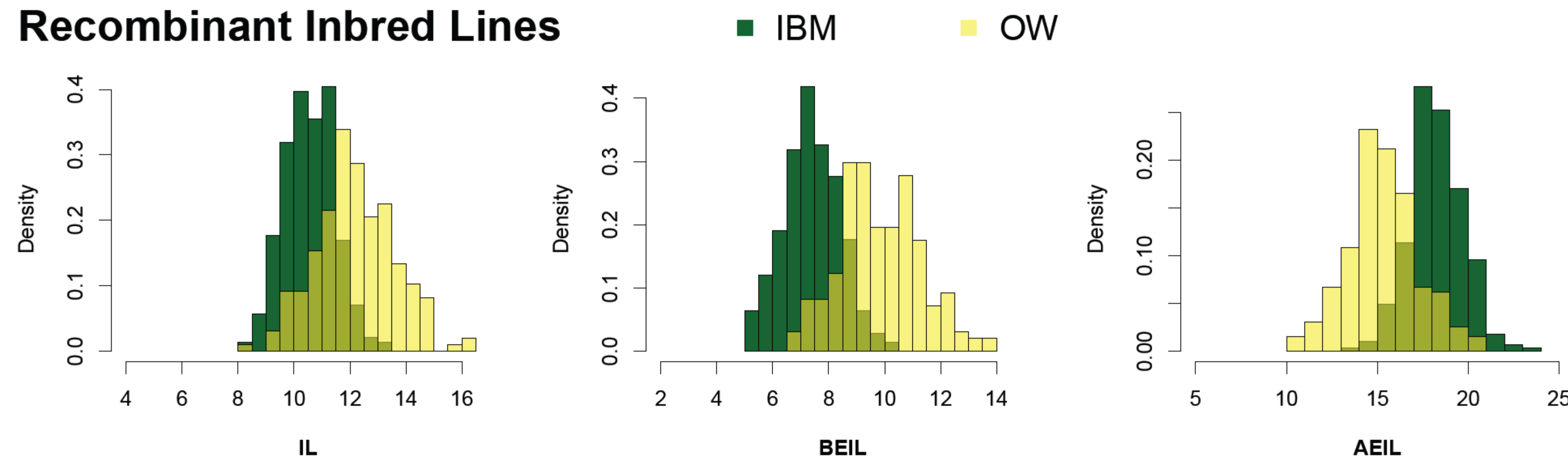
Association Panels
WiDiv   NAM

Figure 2. Spearman's rank correlations ($p<0.001$) and clustering analysis (dendogram) among IL, BEIL, AEIL, PH and NN evaluated in the combined total of 4,851 inbred lines across all four populations.

Interestingly, NN and IL have similar association to PH, but are negatively correlated to each other. Remarkably, BEIL was weakly correlated to NN, but showed the strongest correlation with PH and IL. The large heritabilities observed for all traits indicates that these associations have a strong genetic basis.

Figure 3. Maize stalk. The first three above-ground and the compressed below-ground internodes are shown.

← internode →
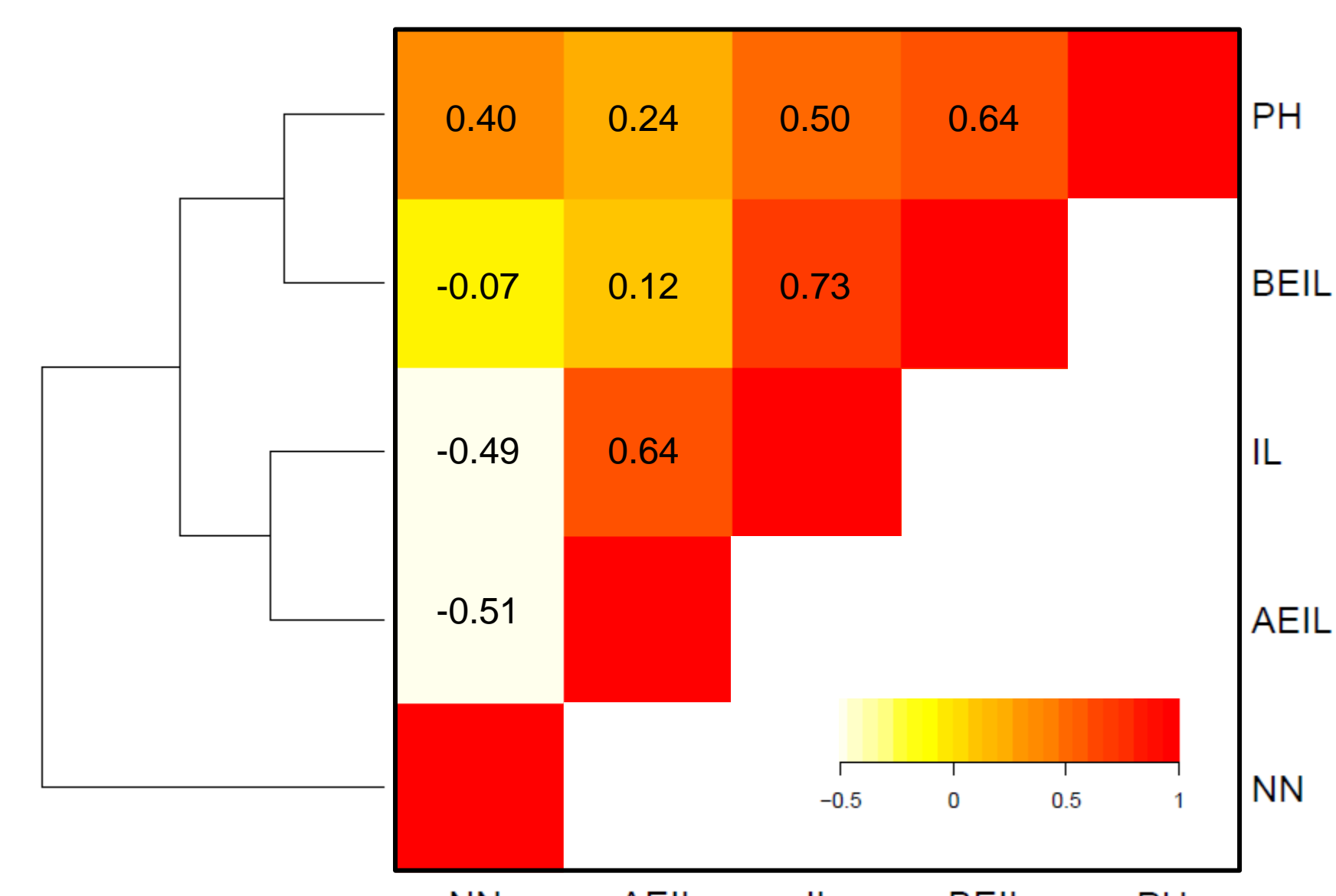
RESULTS: Genetic Dissection

Table 1. WiDiv and IBM broad-sense heritability (H^2) and percent of variance explained (QTL model R^2) by the IBM QTL. Despite the large traits heritabilities observed, the QTL models explained less than 50% of the variance in the IBM population.

Trait	IBM H^2	IBM QTL R^2	WiDiv H^2
IL	0.87	0.35	0.92
BEIL	0.90	0.46	0.85
AEIL	0.74	-	0.75
PH	0.95	0.43	0.90
NN	0.96	0.48	0.93

Figure 4. QTL identified in the IBM and OWRI RILs and SNPs detected in the WiDiv association panel.
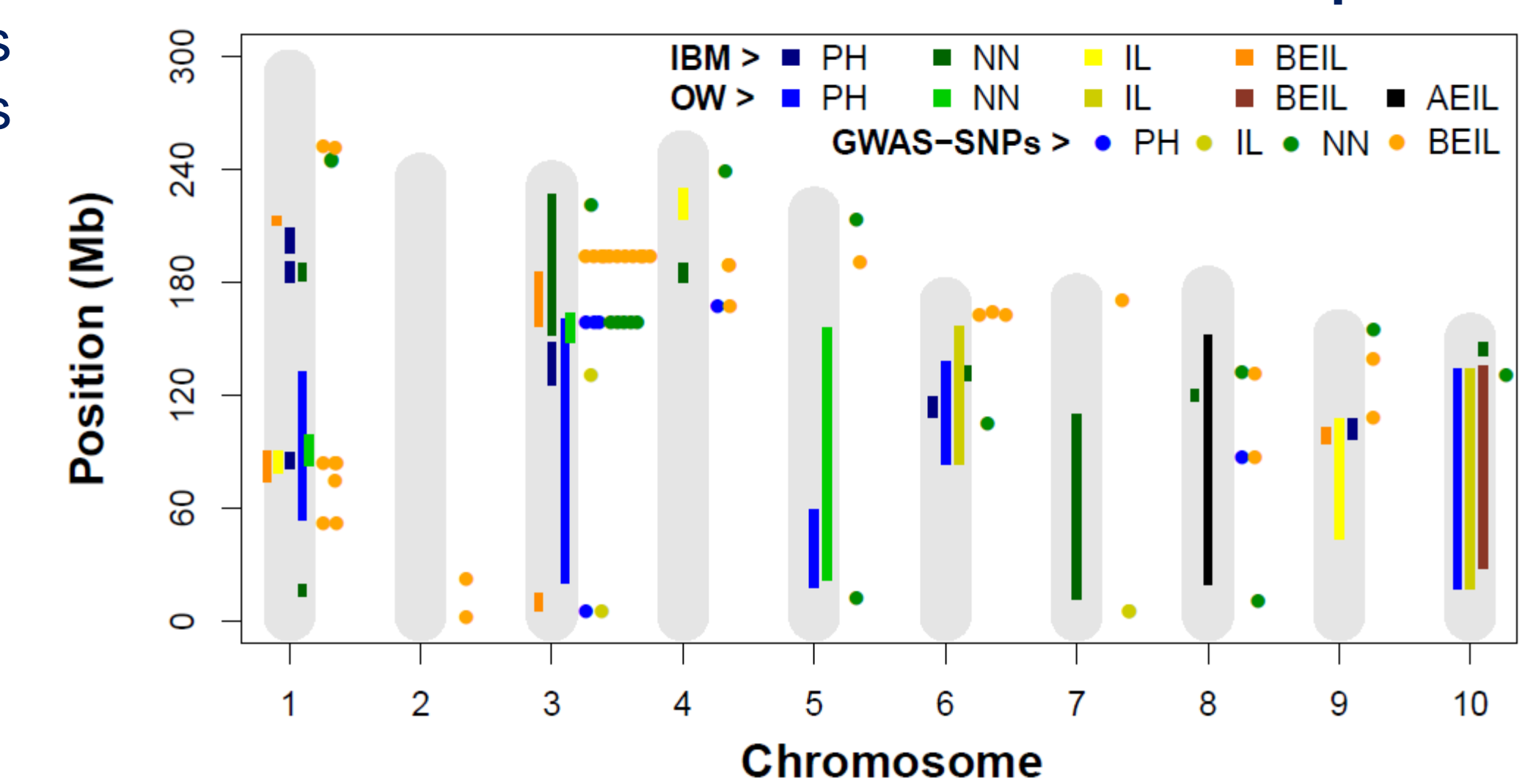
QTL hotspots were identified in the RILs. WiDiv-GWAS allowed to identify several other QTL and enabled to narrow-down several QTL to few candidate genes. The same was observed in the NAM, in which QTL detected through joint-linkage overlapped with SNPs detected through GWAS. Interestingly, a QTL in chromosome 9 affecting BEIL (and also PH and IL in IBM and NAM) was detected in the IBM, WiDiv and NAM. This region was not associated with NN.

Figure 5. Manhattan plots for WiDiv GWAS. Analyses were performed using a mixed linear model controlling for familial relatedness based on kinship values and population structure based on principal components[5]. The dotted line represents the Bonferroni-corrected threshold based on effective number of independent tests. Red dots are SNPs with false discovery rate ≤ 0.05. The analyses were performed using the GAPIT package implemented in R[6].
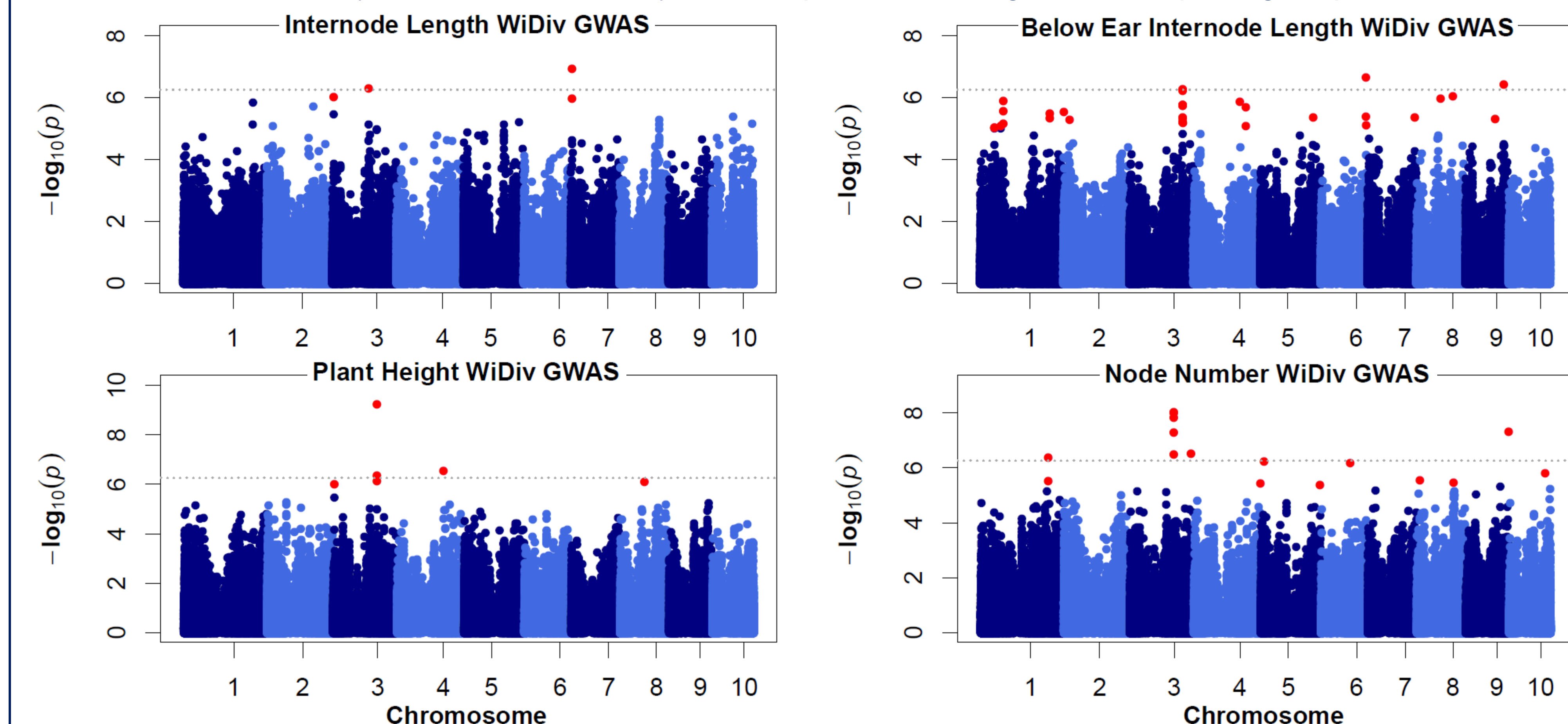
Figure 6. Joint linkage-mapping and GWAS in NAM. The width of the shaded rectangles correspond to the 1.0-LOD support interval and the height of the shaded rectangle represents the LOD score of the joint-linkage mapping QTL. Symbols correspond to single SNPs associations (GWAS) and their resample model inclusion probability (RMIP). Chromosomes 4, 5 and 9 were selected because they contain QTL hotspots for different traits.
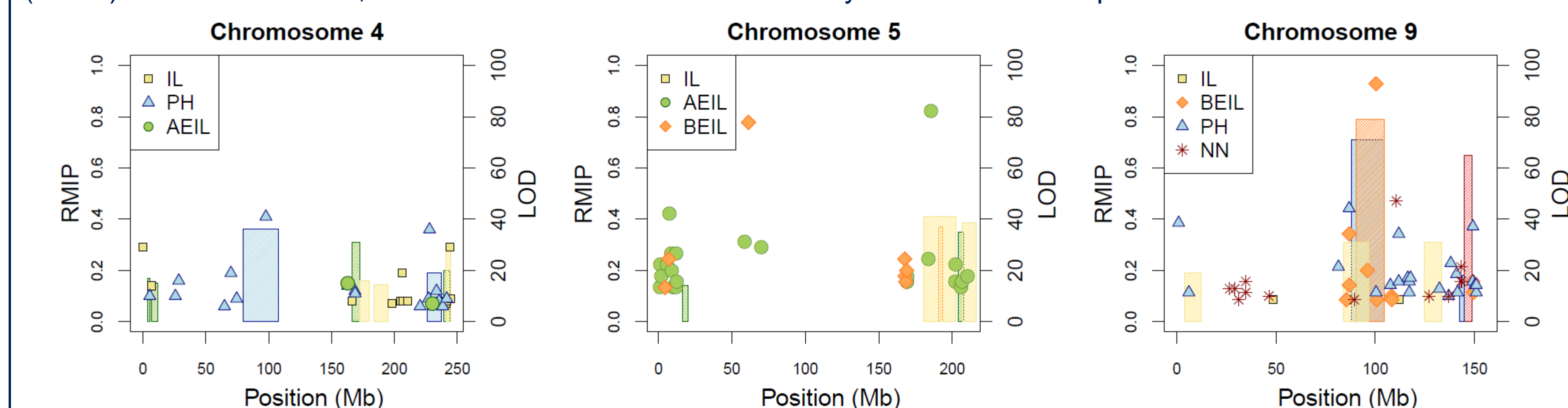
CONCLUSIONS

PH can be phenotypically and genetically dissected into NN and IL. Subsequently, IL can be further partitioned into BEIL and AEIL. Large levels of phenotypic variation were observed for all traits in the populations analyzed. BEIL showed a strong association with PH and IL, but not with NN. Several QTL and SNPs were associated with BEIL. QTL-hotspots were identified for PH, IL and BEIL. GWAS allowed enhancing the resolution of a number of the QTL identified. The information provided in this study constitutes an important step towards the characterization of the genetic architecture of internode length, a key trait in maize breeding and genetics.

References
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