PUBLICATION VERSION?

p12 "no specific molecular insights arose largely because the majority of genes had no annotation".  Are genes without annotation enriched?  In general, filamentous fungus-specific genes involved in niche adaptation or development, those not found in yeasts, are largely unannotated.  You may want to check if genes with signal peptides for secretion are enriched.  Many effectors and plant cell wall degrading enzymes are secreted.

[http://www.cbs.dtu.dk/services/SignalP/](http://www.cbs.dtu.dk/services/SignalP/" \t "_blank)

Genes for secreting proteins and those expressed in planta are often enriched in subtelomeric regions and/or gene sparse high-speed regions (I think Cuomo et al., Science 2007; Raffaele et al., Science 2010), which are discussed later.

P15 "it would predict clustering of the great majority of eGWA hits to a few locations" Isn't it also possible that not eQTL but their downstream genes are in the high-speed genomic regions?