I couldn't get the full model (incorporating both interaction term and nested terms) to work when I tried to get lsmeans::lsmeans NOR doBy::lsmeans.

I ended up dropping the interaction term and compared the full model with the working model (without interaction term) and got a really high p-value and called it good.

########## FULL MODEL

FullModel <- lm(Ylw.Lesion.Proportion ~ Experiment  + GrowingFlat%in%Experiment + AgarFlat%in%GrowingFlat%in%Experiment + Plant + Isolate + Plant:Isolate, data = Phenos)

########## WORKING MODEL #####   drop Plant:Isolate, keep all nested terms

WorkingModel <- lm(Ylw.Lesion.Proportion ~ Experiment  + GrowingFlat%in%Experiment + AgarFlat%in%GrowingFlat%in%Experiment + Plant + Isolate, data = Phenos)

#compare full and fuller models

anova(FullModel, WorkingModel) # new model dropping Plant:Isolate seems to be best reduced model, and can get lsmeans from this model. p-value is .9992, RSS is 105.85 vs. 116.38 for reduced model lacking interaction term.

#lesson: doBy can't handle interaction term, lsmeans can't handle nested terms

#therefore, neither can handle full model lsmeans