Thyroid cancer has been considered as one of highest familial risk carcinomas among all kinds of cancers. Recently, five thyroid cancer significantly associated genetic variants (rs965513, rs944289, rs116909374, rs966423 and rs2439302) have been discovered and validated in two independent GWAS and numerous Case-Control studies in different populations. In present study, we estimated the familial relative risk of thyroid cancer attributable to these five single nucleotide polymorphisms (SNPs) in Han Chinese population and established 9 machine-learning prediction models based on these SNPs in 845 primary thyroid cancers and 1005 normal controls. We found that four SNPs were significantly associated with thyroid cancer in Han Chinese population while no polymorphism was observed for rs116909374. Small familial relative risks (1.02-1.05, p-value<10-16) and limited power to predict thyroid cancer (AUCs: 0.54-0.60) were observed which indicate limited clinical potential in thyroid cancer risk estimation. These results suggest prediction model based on few significant association SNPs have limited prediction ability for thyroid cancer.

