

FEV1 decline and COPD and this agreed with Wang *et al.*, (2009) who detected that the intrinsic Q-1 SNP may influence the splicing of the ss-variant and disturb the growth of *ADAM33*. Subsequent results on protease activity may cause a defect in tissue repair after inflammation-induced damage. This may lead to progressive damage of alveolar tissue and thereby enhance accelerated decrease in lung function [9]. In a Dutch population, the SNPs S1, S2, and Q-1 were associated with FEV1 decline, and the SNPs S1, S2, F+1, and T2 were associated with the presence of COPD while paper of Simpson *et al.*, (2005) on European children showed that SNPs F+1, M+1, T1, and T2 significantly associated with lower FEV1 and COPD [13]. Current research in line with Xiao *et al.*, (2005) who point out there is a relationship between *ADAM33*-V4 polymorphism and COPD in Tibetan population of china [17] but inconsistent with study of Pabst, *et al.*, (2009) who show no genetic association between polymorphic variants in *ADAM33* and the onset or course of COPD [18,21]. Finally, only present study in Iraq are detected that *ADAM33*-V4 and Q-1 SNPs have role in development of COPD and other researches on genetics of COPD should be completed to determine the causative factors of COPD in this population.

CONCLUSION

COPD not causes by smoking or other environmental factors only but also strongly associated with genetic polymorphism. *ADAM33*/V4 and Q-1 SNP polymorphisms significantly correlated with COPD patients and this mean that individual who has *ADAM33*/V4 and Q-1 SNP polymorphisms more susceptible to COPD in this population.

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