

Transport analysis of a DTT negative triangularity scenario

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Plasmas with cross section featuring positive triangularity (PT) have historically been preferred to those with negative triangularity (NT), due to their better magnetohydrodynamic stability properties [1]. Recently, the NT option has gained more interest, since it could allow to achieve H-mode levels of confinement in L-mode, avoiding detrimental edge localised modes (ELMs). As long as experimental evidences add up (TCV: [2], DIII-D: [3], AUG: [4]), the NT option is now studied as a possible viable option for a future fusion reactor [5]. Within this framework, a NT scenario is under investigation for the divertor tokamak test (DTT) facility [6]. Here, the results of the transport analysis of the DTT reference full power scenario with Ne seeding are presented, comparing a NT option with the PT reference one. The analysis consists of transport simulations, gyrokinetic and quasi-linear runs. The transport runs are carried out with the ASTRA code [7], coupled with the quasi-linear model TGLF SAT2 [8]. Larger temperature gradients are predicted by ASTRA for NT, but not sufficient to recover the loss due to the lack of pedestal in NT L-mode. The difference of PT and NT profiles is mainly due to the different boundary conditions rather than to the geometry itself. Flux-tube gyrokinetic runs are performed with the GENE code [9] at fixed radius to characterise the turbulence and to evaluate the associated flux levels. The variation of the temperature stiffness, i.e. the degree to which the temperature profiles respond to changes in the applied heat fluxes, is also investigated when going from PT to NT. The GENE results indicate ITG dominant turbulence at larger radii. A strong (>50%) stabilising effect is observed when the triangularity is reversed, both on linear growth rates and nonlinear heat fluxes. This effect is partially compensated by the high temperature stiffness, that limits its impact on logarithmic gradients. TGLF stand-alone runs are ongoing, to be compared with GENE. This work is performed within the TSVV-02 EUROfusion task.

References

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