Association of methylenetetrahydrofolate reductase C677T CT gene polymorphism with a non-dipping blood pressure pattern in morbidly obese patients

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KEYWORDS: MTHFR C677T polymorphisms, arterial hypertension, non-dipper.

CITATION: Cardiol Croat. 2021;16(1-2):38-39. | https://doi.org/10.15836/ccar2021.38

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Introduction: Region near the gene encoding methylenetetrahydrofolate reductase (MTHFR) is associated with blood pressure. CT and TT genotype of the C677T MTHFR gene are more common in obese hypertensive patients with BMI>29 kg/m^2.[1,2] The aim of this study was to prove the connection between C667T polymorphism of MTHFR gene and non-dipping pattern in 24h ambulatory blood pressure monitoring (ABPM) in obese patients.

Patients and Methods: We included 33 patients from a multidisciplinary weight management program in which genetic analysis on MTHFR gene polymorphism was tested and 24h ABPM was performed. Patients were divided into 3 groups: 12 patients with MTHFR C677T healthy genotype CC (9 W, 3 M, age 48.83±9.82y, BMI 44.39±9.69 kg/m^2), 14 patients with MTHFR C677T heterozygous mutation CT (11 W, 3 M, age 47.93±8.74y, BMI 40.9±5.96 kg/m^2), 7 patients with MTHFR C677T homozygous mutation TT (6 W, 1 M, age 43.43±12.22y, BMI 37.46±5.79 kg/m^2). In each group 24h ABPM results were analyzed, and dipping status was determined according to percentage of night systolic blood pressure drop and divided into 4 groups: inverse dipper (<0%), non-dipper (0-10%), dipper (10-20%), extreme dipper (>20%).

Results: Patients with MTHFR C677T: CT had the lowest average night blood pressure drop (8.51±5.9%), comparing to MTHFR C677T: TT (10.17±4.72 %) and MTHFR C677T: CC (10.53± 6.07%). Patients with MTHFR C677T:CT (**Figure 1**) were the only group with inverse dipper pattern present, but also with significant non-dipping pattern (inverse dipper 7.1%, non-dipper 35.7%, dipper 57.1%) comparing to patients with MTHFR C677:TT (non-dipper 28.6%, dipper 71.4%) (**Figure 2**). Patients with MTHFR C677T:CC (**Figure 3**) had the highest level of dipper pattern, but also extreme dipper patter was present (non-dipper 25%, dipper 66.7%, extreme dipper 8.3%).

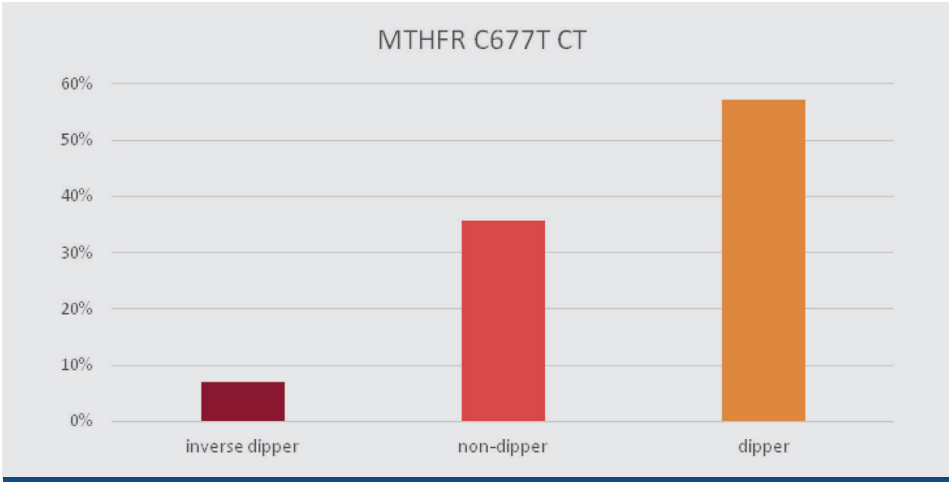

FIGURE 1. Dipping status distribution in patients with MTHFR C677T heterozygous CT mutation.

RECEIVED:
December 4, 2020
ACCEPTED:
December 18, 2020

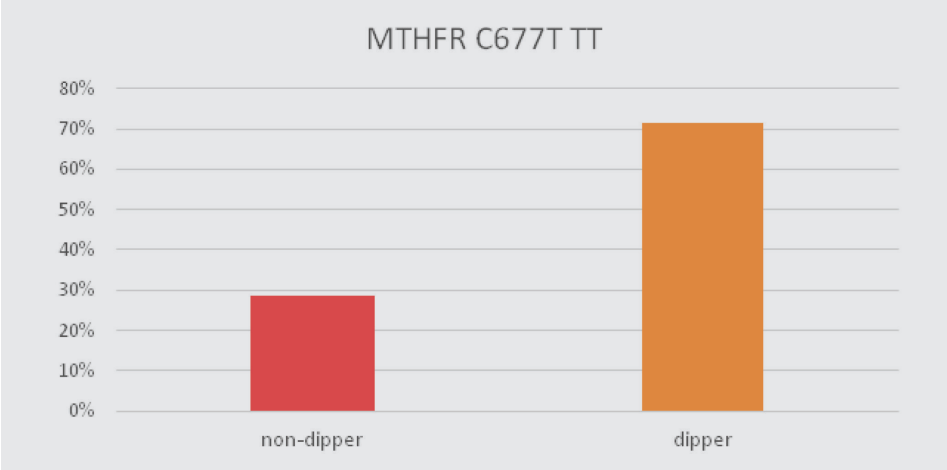

FIGURE 2. Dipping status distribution in patients with MTHFR C677T homozygous TT mutation.

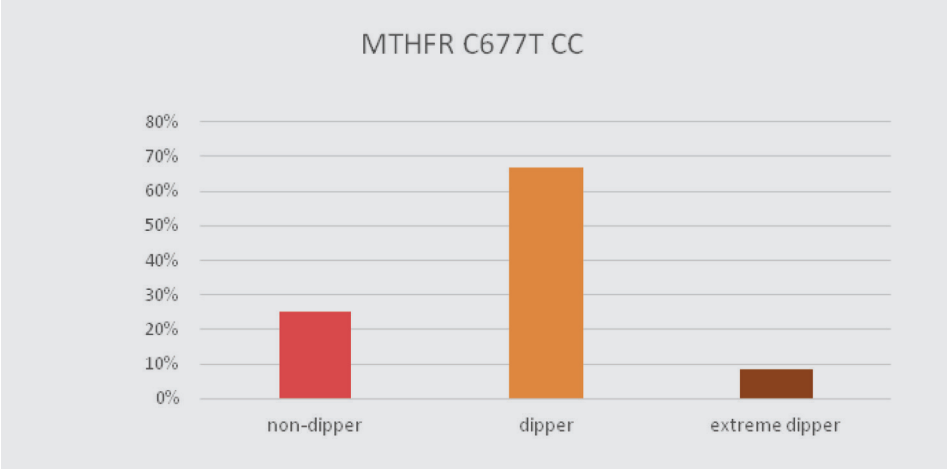

FIGURE 3. Dipping status distribution in patients with MTHFR C677T healthy CC genotype.

Conclusion: MTHFR C677T:CT polymorphism is the most associated with pathological patterns in dipping status; non-dipper and inverse dipper status, more than MTHFR C677T:TT, what indirectly indicates higher cardiovascular risk.

LITERATURE

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