

PubMed

Transforming growth factor-β1 functional polymorphisms in myel

Format: Abstract

Full text links



See 1 citation found by title matching your search:

Bone Marrow Transplant. 2017 May;52(5):739-744. doi: 10.1038/bmt.2016.355. Epub 2017 Jan 30.

## Transforming growth factor-β1 functional polymorphisms in myeloablative sibling hematopoietic stem cell transplantation.

Berro M<sup>1</sup>, Palau Nagore MV<sup>2</sup>, Rivas MM<sup>1</sup>, Longo P<sup>1</sup>, Foncuberta C<sup>3</sup>, Vitriú A<sup>3</sup>, Remaggi G<sup>4</sup>, Martínez Rolon J<sup>4</sup>, Jaimovich G<sup>5</sup>, Requejo A<sup>5</sup>, Feldman L<sup>5</sup>, Padros K<sup>6</sup>, Rodríguez MB<sup>6</sup>, Shaw BE<sup>7</sup>, Larripa I<sup>2</sup>, Belli CB<sup>2</sup>, Kusminsky GD<sup>1</sup>.

### Author information

### Abstract

**Hematopoietic stem cell transplantation (HSCT)** with **sibling** donors (s.d.) is a life-saving intervention for patients with hematological malignancies. Numerous genetic factors have a role in transplant outcome. Several **functional polymorphisms** have been identified in TGF-β1 gene, such as single-nucleotide polymorphism (SNP) at +29C>T within exon 1. Two hundred and forty five patient/donor pairs who underwent a s.d. HSCT in our centers were genotyped for this SNP. In the **myeloablative** cohort, +29CC donors were associated with an increase in severe chronic GvHD (32% vs 16%, hazard ratio (HR) 9.0, P=0.02). Regarding survival outcomes, +29CC patients developed higher non relapse mortality (NRM) (1-5 years CC 28-32% vs TC/TT 7-10%; HR 5.1, P=0.01). Recipients of +29TT donors experienced a higher relapse rate (1-5 years TT 37-51% vs TC 19-25% vs CC 13%-19%; HR 2.4, P=0.01) with a decreased overall survival (OS) (1-5 years TT 69-50% vs TC/CC 77-69%; HR 1.9, P=0.05). Similar to previous **myeloablative** unrelated donors HSCT results, we confirmed that +29CC patients had higher NRM. In addition we found that +29TT donors might be associated with a higher relapse rate and lower OS. These results should be confirmed in larger series. Identification of these SNPs will allow personalizing transplant conditioning and immunosuppressant regimens, as well as assisting in the choice of the most appropriate donor.

PMID: 28134923 DOI: [10.1038/bmt.2016.355](https://doi.org/10.1038/bmt.2016.355)

[Indexed for MEDLINE]

Publication type, MeSH terms, Substances



**Publication type**

Multicenter Study

**MeSH terms**

Adult

Donor Selection/methods

Female

Genotype

Graft vs Host Disease/genetics

Hematologic Neoplasms/complications

Hematologic Neoplasms/mortality

Hematologic Neoplasms/therapy

**Hematopoietic Stem Cell Transplantation/methods\***

**Hematopoietic Stem Cell Transplantation/mortality**

**Hematopoietic Stem Cell Transplantation/standards**

Humans

Male

**Myeloablative Agonists/therapeutic use**

Polymorphism, Single Nucleotide

Recurrence

Siblings

Survival Analysis

Tissue Donors\*

**Transforming Growth Factor beta1/genetics\***

**Transplantation Conditioning/methods**

Treatment Outcome

**Substances**

**Myeloablative Agonists**

**Transforming Growth Factor beta1**

---

**LinkOut - more resources**

