PLOS ONE

CORRECTION

Correction: Discrimination of Deletion and Duplication Subtypes of the Deleted in Azoospermia Gene Family in the Context of Frequent Interloci Gene Conversion

The *PLOS ONE* Staff

The following information is missing from the Funding section: 5) Spanish Ministry of Health (FIS grant PI14/01250) to CK.

Additionally, a portion of the caption for Table 1 is incorrectly displayed in the Results section. Please see the complete, correct Table 1 caption here. The publisher apologizes for the errors.

Table 1. Relationship between a sample's AZFc partial deletion/duplication status and its horizontal variant ratio distribution.

AZFc partial deletion/duplication status	Type of SFV positions (#specific variant: #non-specific variant)						
	0:2x	2x:0	x:x	1:3	1:5	2:4	4:2
No partial rearrangement (x = 2)	+	-	+	+	-	-	-
Partial deletion affecting two DAZ family members (x = 1)	+	+	+	-	-	-	-
Partial deletion affecting two DAZ family members followed by duplication (x = 2)	+	+	+	-	-	-	-
Partial duplication affecting two DAZ family members (x = 3)	+	-	+	-	+	+	+

A + sign means that the corresponding type of SFV position may be present in a sample with the relevant deletion/duplication status. A – sign means that the corresponding type of SFV position is not expected in a sample with the relevant deletion/duplication status. The value of x is the function of the deletion/duplication status.

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Supposing pairwise deletion and duplication of the DAZ family members, one of seven different variant ratios (0:2x, 2x:0, x:x, 1:3, 1:5, 2:4 and 4:2) can be assigned to an SFV position on the basis of its electropherogram picture. Except for 2x:0 and x:x, those ratios directly show the copy number of the family member-specific variant at their respective position. The horizontal variant ratio distribution means the distribution of the different types of SFV positions of a sample. The AZFc partial deletion/duplication status can be determined from the horizontal variant ratio distribution. The electropherogram picture of type 0:2x (0:2, 0:4 or 0:6), type 2x:0 (2:0 or 4:0) and type x:x (1:1, 2:2 or 3:3) sites appears identical, respectively. Their exact variant ratio and, in turn, the copy number of the specific variant at the 2x:0 and x:x type positions can be obtained from the AZFc partial deletion/duplication status of the sample. Subtyping uses both the AZFc partial deletion/duplication status and the copy number of the specific variant (s) at each SFV position as the starting point. [There are positions, such as position 1964 in Fragment II, which comprise more than two variants in certain samples; therefore, their

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description is necessarily more complex. For example, in the view of DAZ3, the integers in the formula 1:(1+2) mean one specific C, one non-specific A (which, at the same time, is specific to DAZ4) and two non-specific Gs. Overall, it refers to a 1:3 type position. Under the same considerations, 1:(0+3) is identical with 1:3; 0:(2+2) and 0:(1+3) with 0:4; and 2:(0+2) with 2:2.]

Based on variant ratios only, no distinction can be made between partial deletion and partial deletion followed by duplication. Therefore, samples found to carry partial deletion must be checked using a dosage test to determine if they also underwent duplication. In a similar way, the identification of samples with the entire AZFc region duplicated requires to subject partially-non-rearranged samples to a dosage test. However, the lack of knowledge of the exact DAZ copy number of samples belonging to these two categories does not influence subtyping.

Reference

1. Vaszkó T, Papp J, Krausz C, Casamonti E, Géczi L, Olah E (2016) Discrimination of Deletion and Duplication Subtypes of the Deleted in Azoospermia Gene Family in the Context of Frequent Interloci Gene Conversion. PLoS ONE 11(10): e0163936. doi: 10.1371/journal.pone.0163936 PMID: 27723784