Abstract

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Haemonchus contortus is a blood-sucking nematode found mainly in livestock. This nematode causes a disease called haemonchosis. During its evolution, it has developed emerging resistance to anthelmintics, a is growing global problem despite good strategies. Aldo-ketoreductases (AKRs) belong to the super family of NADPH-dependent oxidoreductases catalyzing oxidation-reduction reactions of aldehydes and ketones in various organisms from bacteria to mammals. In mammals, they are abundantly expressed in various tissues. Their essential role is mainly in the metabolism of hormones, xenobiotics, eobiotics, oxidative molecules or a role in drug resistance. Some species, such as aldosareduktasa (ADR), are also capable of damaging the organism. Unfortunately, very little has been described about these enzymes in *H. contortus*, and therefore this thesis deals with the investigation of putative AKR genes in this nematode. Genome sequencing identified 22 genes from the AKR superfamily. Expressions of all AKRs were detected in eggs, larvae and adults. Furthermore, the expression of AKR in the developmental stages of the drug-susceptible strain (ISE) and the benzimidazoleresistant strain (IRE) of H. contortus was compared. AKR1, AKR3 and AKR10 were expressed the most in all stages, while the other AKRs were only marginally expressed. When expression was compared between ISE and IRE strains, two AKRs appeared in the IRE strain with very high expression in adults. These are AKR17 and AKR19, which may be associated with drug resistance. According to the results, it would be interesting to pay more attention to selected AKRs in the future.