

GENETIC AND BIOMECHANICAL PREDICTORS OF SPORTS INJURY RISK: ADVANCING PERSONALIZED TRAINING AND REHABILITATION STRATEGIES

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ABSTRACT:

Sports injury susceptibility is influenced by complex interactions among genetic, anthropometric, and prior-injury characteristics. This study examined whether ACTN3 rs1815739 polymorphism contributes to musculoskeletal injury occurrence and burden and whether its effects remain evident after accounting for selected participant-level risk factors. A quantitative observational analysis was conducted among 80 participants classified as RR, RX, or XX genotypes. Age, body weight, height, body mass index, body-fat percentage, previous injury history, injury phenotype, cumulative injury burden, and injuries across four observation periods were evaluated. Group differences were assessed using one-way ANOVA, Pearson's chi-square test, and the Kruskal-Wallis test, while multivariable binary logistic regression identified independent predictors of injury occurrence. Overall, 60.0% of participants experienced at least one injury. Injury prevalence was highest among XX carriers (73.3%), followed by RR (61.5%) and RX (53.8%) participants, although genotype differences were not statistically significant. XX carriers demonstrated an adjusted injury odds ratio of 2.18 relative to RR carriers, whereas previous injury history produced the strongest non-genetic association (OR = 2.44). Anthropometric variables were not significant independent predictors. A significant genotype difference was observed only for injury burden in Period 4. These findings indicate that ACTN3 genotype may contribute to injury susceptibility within a broader multifactorial framework. Personalized prevention and rehabilitation strategies should therefore integrate genetic information with previous injury, longitudinal monitoring, and future biomechanical assessment.

KEYWORDS: ACTN3 rs1815739; musculoskeletal injury; genetic susceptibility; personalized rehabilitation; injury risk

1. INTRODUCTION

Sports injuries result from a combination of genetic risk factors, physical attributes, training loads, previous injury and movement factors. Modern sports medicine is thus progressing from general injury-prevention models to individualized models considering both biological and performance data. The use of omic technologies combined with recent developments in genetics has boosted the capacity to identify individual susceptibility profiles in athletes and develop specific training and rehabilitation strategies.

The potential to identify individual susceptibility profiles in athletes using genetics, omic technologies, and digital health has increased (Juginovic et al., 2025). The combination of genomic, biochemical, nutritional and pathophysiological data has also been suggested as a way to enhance sports performance and limit sport-related limitations (Spanakis et al., 2025).

There is genetic variation that can affect structural integrity, muscle function, recovery ability and susceptibility to musculoskeletal injury. There has been a growing interest in the variants of genes related to muscle phenotype, tendon and ligament properties, and exercise responsiveness, especially in the context of sport-related muscle injuries (Leonska-Duniec, 2025). Recent studies increasingly suggest using multi-trait genetic profiling instead of single polymorphisms to inform training prescription, rehabilitation and long-term health management (Imperatore et al., 2025).

ACTN3 is one of the most studied exercise-related genes, as it is involved in the fast-twitch skeletal muscle function, physical performance, and potential susceptibility to injury. Soccer populations have suggested that

genetic makeup can play a role at the same time in determining what athlete they are, what their capacity is, and what their injury risk is (Murtagh et al., 2023). Thus, the use of genetic tests in the context of the clinical and physiological profile has been proposed as a potential use in individual sport-training plans (Naureen et al., 2020).

Genetic variation, however, is not the only factor that can account for the susceptibility to injury. The risk of injury is likely to vary significantly based on biomechanical loading, asymmetry, muscle control, and previous tissue damage of everyone. There has been an increasing interest in the use of data-driven approaches that combine biomechanics with wearable monitoring to detect early warning signs and assist in preventive interventions (Sufian et al., 2024).

Applications of AI in sports biomechanics have also allowed for the individual-level analysis of motion patterns, outputs from the various wearable sensors, and the movement characteristics of injuries (Souaifi et al., 2025). The combination of multidimensional information for performance monitoring and injury prevention (Dergaa & Chamari, 2024) has therefore been increasingly relevant to the field of sports medicine, where big-data approaches have become increasingly relevant. Additionally, machine-learning methods have been applied to investigate biomechanical features related to injury prevention and rehabilitation in physically active individuals (Wang & Pei, 2024).

More generally, biomechanical assessment can help identify movement strategies that create excessive mechanical stress and can help identify modifiable variables that can be focused on during training (Jabara & Ati, 2025). Restriction of movement and asymmetry in the body are also new-found features that have been examined in the context of sports injury prediction, highlighting the need for functional assessment on a person-by-person basis (Zhou & Liu, 2025).

They are all signs that future injury-risk models will rely on a combination of fixed biological and modifiable physical and training-related factors. Although there have been significant advances, there are important challenges to overcome in practice, such as the fact that the process of injury development is multifactorial and the value of any one genetic marker is likely to be quite limited. Also, there is a need to consider genetic information in conjunction with anthropometric factors, history of previous injuries, and longitudinal injury trends rather than as a deterministic factor. This is particularly the case for genes like ACTN3 where genotype tendencies are more easily learned when considered alongside non-genetic factors and subsequent injury histories.

The purpose of the present study was to examine participant- and genetic-level risk factors for musculoskeletal injuries. The scope encompassed genotype distribution, anthropometric characteristics, history of previous injuries, overall injury occurrence, injury phenotype, cumulative injury burden, and period-specific injury patterns. The aims were to identify if there were differences in injury occurrence or burden between the ACTN3 genotypes, explore the influence of past injury and anthropometric factors and to explore whether these factors could be incorporated into a more individualized approach to injury prevention, training and rehabilitation.

2. MATERIALS AND METHODS

2.1 Study Design, Participants, and Variables

A quantitative observational design was employed to explore the association between ACTN3 rs1815739 polymorphism, anthropometric profile and musculoskeletal injuries and injury burden. Analytical sample consisted of 80 persons with a unique identification code. Duplicate records, coding inconsistencies and missing observations were identified during pre-analysis of the records, resulting in no duplicate participant records (Muniz, 2026).

The genotype of ACTN3 (rs1815739) was the most important genetic factor. The three genotypes CC, TC, and TT were represented in the conventional ACTN3 R577X coding using the same nomenclature RR, RX, and XX, respectively. 26 RR, 39 RX and 15 XX participants were included in the study sample. The genotype frequencies were used for the calculation of the corresponding R- and X-allele frequencies, each participant providing two alleles.

A Hardy-Weinberg equilibrium test was also performed by chi-square goodness-of-fit test to examine genotype distribution. Age in years, body weight in kg, height in cm, BMI in kg/m², body-fat percentage were the participant characteristics. BMI was calculated from measured weight and height. There were no previous musculoskeletal injuries recorded in the dichotomous variable. The dichotomous variable of previous musculoskeletal injury (or no injury) is a history of musculoskeletal injury prior to the observation period.

2.2 Injury Outcomes and Phenotype Classification

Information on musculoskeletal injuries was available in four successive observation periods (Periods 1-4). Injuries were identified and recorded individually for each period. All injuries were counted for each participant over the 4 periods to calculate the overall injury burden per participant. Overall, 86 injury events were recorded in all participants. A binary variable called any injury was created for the primary injury-risk analysis. Those who experienced at least one injury in the four observation periods were considered injured, whereas those who reported no injuries were considered non-injured.

As a result, 48 participants suffered one or more injuries, and 32 participants suffered no injuries. The phenotypes of injuries available were divided into three groups: joint injury, muscle injury, non-traumatic

injury, and traumatic injury. A binary variable (presence or absence) was used for each phenotype. All 80 participants had data on muscle-injury and non-traumatic-injury. The two phenotypes' analyses (joint-injury and traumatic-injury) were performed on 79 observations available for the one participant with insufficient information. The denominator for joint and traumatic injuries was 14 rather than 15 in the XX-genotype group.

2.3 Descriptive, Genetic, and Group Comparison Analyses

Mean $\pm$ standard deviation (SD) was used for continuous variables, and frequency and percentage for categorical variables. Descriptive statistics were used to determine genotype frequencies and the frequencies of the R- and X-allele. One-way analysis of variance (ANOVA) was used to determine age, weight, height, BMI and body-fat percentage differences among RR, RX, and XX genotype groups.

The frequency of previous injury was compared between the genotype groups by using Pearson's chi-square test. The prevalence of any injury was calculated in each group (RR, RX, XX) using the denominator of 26, 39 and 15 participants, respectively. Pearson's chi-square test was used to evaluate association between ACTN3 genotype and overall injuries occurrence. The genotype associations with each joint, muscle, non-traumatic and traumatic injuries phenotypes were also studied separately by Pearson's chi-square tests. Percentages were reported based on the number of participants for each phenotype that were available. The cumulative and period-specific injury counts were both discrete and had non-normal distributional characteristics, which required differences among the three genotype groups to be evaluated using the Kruskal-Wallis's test.

The procedure was performed on the total injury burden and then separately on the number of injuries reported in each of the four periods (Periods 1, 2, 3 and 4). Event totals and mean injury count by period also were calculated descriptively.

2.4 Multivariable Injury-Risk Analysis

A multivariable binary logistic regression model was utilized, and predictors of overall musculoskeletal injury occurrence were identified independent of the other variables. Any injury (coded 0 = none and 1 = at least one) was considered the dependent variable. Genotype ACTN3, previous injury history, age, BMI and body-fat percentage were simultaneously entered as predictors.

The ACTN3 genotype was entered as a categorical variable and compared separately to RR (as a reference group) and to XX (as a reference group). All the previous history of injury was entered as a binary predictor, and age, BMI and body-fat percentage as continuous covariates. Adjusted odds ratios (ORs) with 95% confidence intervals (CIs) and p-values were presented for regression results. All 80 participants were part of the regression model because the dependent variable and all predictors were available for these individuals. All tests were two-tailed and $P < 0.05$ was deemed statistically significant.

2.5 Ethical Considerations

Data was secondary, participant level, with none of the data being personally identifiable information. The participant codes were not introduced as a variable in statistical models but were only used to verify the registration. The information available to the researchers was used to carry out all analyses and results are presented only in summary form to ensure participant anonymity and research integrity.

3. RESULTS

3.1 Participant Characteristics and ACTN3 Genetic Distribution

A total of 80 participants, with full demographic, anthropometric, injury-history and ACTN3 rs1815739 genotype data, were included in the analysis. The mean age of the overall sample was 27.11 ± 1.74 years, with a mean body weight of 78.79 ± 9.13 kg, mean height of 178.75 ± 6.66 cm, mean BMI of 24.64 ± 2.34 kg/m², and mean body-fat percentage of $13.12 \pm 3.91\%$.

Thirty-six participants (45.0%) reported having been previously injured in their musculoskeletal system. The ACTN3 genotype distribution comprised 26 RR (32.5%), 39 RX (48.8%), and 15 XX (18.8%) participants. The frequencies of the R and X alleles were 56.9% and 43.1%, respectively. The distribution of the genotypes was in Hardy-Weinberg equilibrium (chi-square = 0.003, $p = 0.956$). Age, body weight, height, BMI and body-fat percentage were similar among the genotype groups with no statistically significant differences as shown in Table 1. Further, there was no significant difference in the previous injury history by genotype (chi-square = 3.346, $p = 0.188$).

Table 1. Demographic, Anthropometric, and Injury-History Characteristics According to ACTN3 Genotype

Characteristic	RR (n = 26)	RX (n = 39)	XX (n = 15)	p-value
Age, years	27.00 $\pm$ 1.67	27.10 $\pm$ 1.71	27.33 $\pm$ 1.99	0.841
Weight, kg	77.83 $\pm$ 9.31	78.69 $\pm$ 8.52	80.72 $\pm$ 10.63	0.624
Height, cm	177.35 $\pm$ 6.17	179.10 $\pm$ 6.86	180.27 $\pm$ 6.91	0.364

Characteristic	RR (n = 26)	RX (n = 39)	XX (n = 15)	p-value
BMI, kg/m ²	24.72 +/- 2.53	24.52 +/- 2.15	24.81 +/- 2.60	0.902
Body fat, %	13.53 +/- 3.89	12.73 +/- 3.85	13.41 +/- 4.28	0.686
Previous injury, n (%)	11 (42.3)	21 (53.8)	4 (26.7)	0.188
Total injuries, mean +/- SD	1.15 +/- 1.16	1.00 +/- 1.19	1.13 +/- 0.99	0.692*

Values mean +/- SD or n (%). Continuous anthropometric characteristics were compared using one-way ANOVA; previous injury was assessed using Pearson's chi-square test. *Kruskal-Wallis's test was used for total injury counts.

The occurrence of injuries by genotype is shown in Figure 1. The highest prevalence of injuries was found in XX genotype; however, this was not the only pattern that resulted in a statistically significant genotype effect.

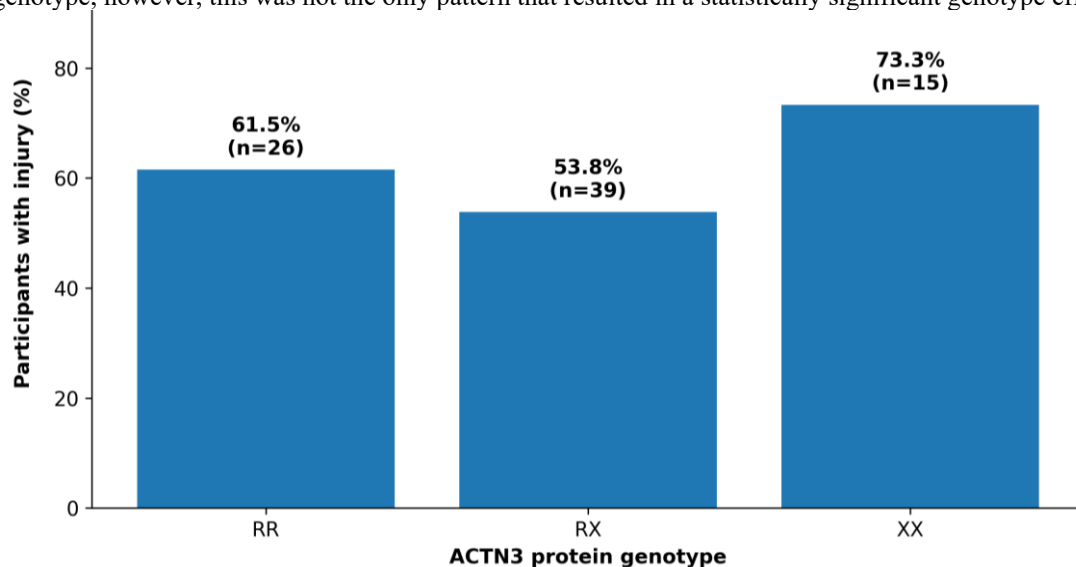


Figure 1. Musculoskeletal Injury Prevalence by ACTN3 Genotype

3.2 ACTN3 Genotype and Musculoskeletal Injury Occurrence

In all, 48 of 80 participants (60.0%) suffered one or more musculoskeletal injuries in the observation periods. Injury prevalence was 61.5% in RR, 53.8% in RX, and 73.3% in XX participants. Hence, most of the injured people were found in the XX group, which was about 19.5 percentage points more than the RX. However, the relationship of ACTN3 genotype to injury was not statistically significant (chi-square = 1.752, $p = 0.416$).

The mean cumulative injury burden was also generally similar between the genotypes: 1.15 +/- 1.16 injuries for RR genotype, 1.00 +/- 1.19 injuries for RX genotype, and 1.13 +/- 0.99 injuries for XX genotype and was not significantly different by the Kruskal-Wallis's test ($H = 0.735$, $p = 0.692$). The prevalence of injuries by injury phenotype analysis showed that there was no difference across the three genotypic groups for muscle injuries, but the prevalence of joint injuries and non-traumatic injuries were highest for the XX group. RR participants had the highest rate of traumatic injury (38.5%). The results of these phenotype distributions were not statistically significant and are displayed in Table 2 and Figure 2.

Table 2. Injury Occurrence and Injury Phenotype According to ACTN3 Genotype

Injury outcome	RR	RX	XX	chi-square	p-value
Any injury, n (%)	16/26 (61.5)	21/39 (53.8)	11/15 (73.3)	1.752	0.416
Joint injury, n (%)	9/26 (34.6)	12/39 (30.8)	7/14 (50.0)	1.677	0.432
Muscle injury, n (%)	8/26 (30.8)	12/39 (30.8)	4/15 (26.7)	0.098	0.952

Injury outcome	RR	RX	XX	chi-square	p-value
Non-traumatic injury, n (%)	9/26 (34.6)	14/39 (35.9)	7/15 (46.7)	0.673	0.714
Traumatic injury, n (%)	10/26 (38.5)	11/39 (28.2)	4/14 (28.6)	0.833	0.659

Percentages were calculated using available observations for each phenotype. One observation was unavailable for joint and traumatic injury classification.

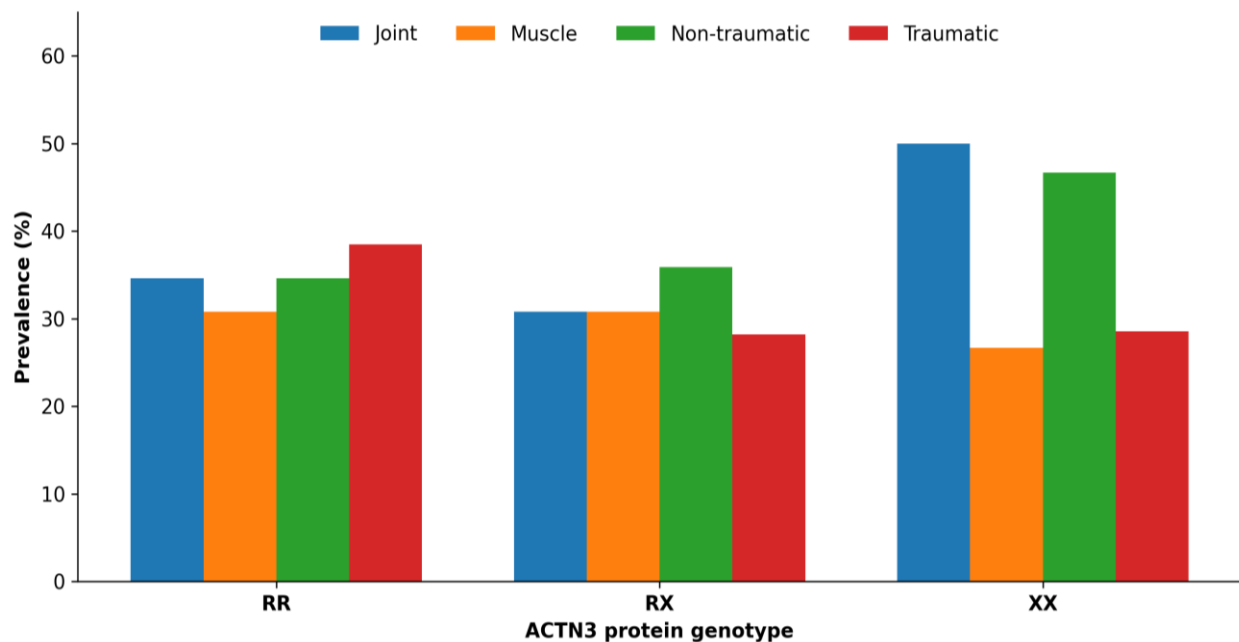


Figure 2. Injury Phenotype Prevalence Across ACTN3 Genotypes

3.3 Temporal Patterns of Injury Burden

There were 86 individual injury events observed during the four observation periods. The highest burden of injuries for the entire game occurred in period 1 with 32 injuries, followed by period 4 with 20 injuries, then periods 2 and 3 with 17 injuries each. The average number of injuries per participant was thus 0.40 in Period 1, 0.21 in Period 2, 0.21 in Period 3, and 0.25 in Period 4. Toward or away from the infection, the temporal pattern varied between genotypes in magnitude and direction.

The highest mean injury burden was in Period 1 (0.60 +/- 0.63), which dropped to 0.07 +/- 0.26 in Period 4. RR participants demonstrated the opposite trend with an increase in the number of injuries in Period 4 (0.46 +/- 0.65 injuries per participant). Intermediate pattern was relatively stable among RX carriers. There were no significant differences between the genotypes during Periods 1-3 as reported in Table 3. There was a significant difference between the genotypes in Period 4 ($H = 7.334$, $p = 0.026$). The different temporal profiles are also clearly visible in Figure 3.

Table 3. Period-Specific Injury Burden According to ACTN3 Genotype

Observation period	RR, mean +/- SD (events)	RX, mean +/- SD (events)	XX, mean +/- SD (events)	H	p-value
Period 1	0.31 +/- 0.47 (8)	0.38 +/- 0.54 (15)	0.60 +/- 0.63 (9)	2.447	0.294
Period 2	0.19 +/- 0.49 (5)	0.21 +/- 0.47 (8)	0.27 +/- 0.46 (4)	0.677	0.713

Observation period	RR, mean +/- SD (events)	RX, mean +/- SD (events)	XX, mean +/- SD (events)	H	p-value
Period 3	0.19 +/- 0.40 (5)	0.23 +/- 0.48 (9)	0.20 +/- 0.41 (3)	0.031	0.985
Period 4	0.46 +/- 0.65 (12)	0.18 +/- 0.45 (7)	0.07 +/- 0.26 (1)	7.334	0.026

Values represent mean number of injuries per participant +/- SD; values in parentheses indicate total injury events. Group comparisons used Kruskal-Wallis's test.

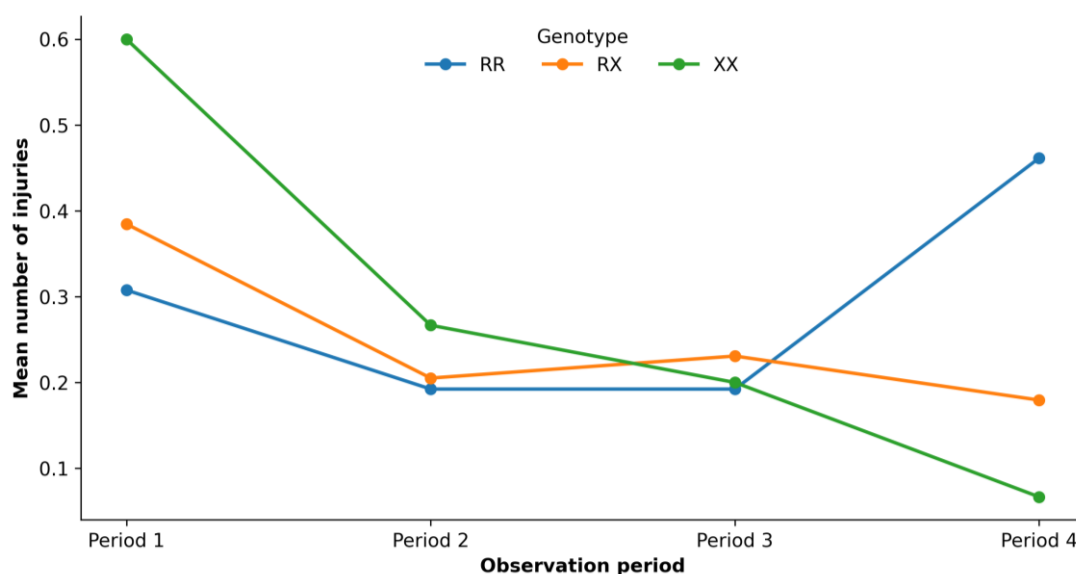


Figure 3. Temporal Distribution of Injury Burden by ACTN3 Genotype

3.4 Multivariable Predictors of Musculoskeletal Injury Risk

To assess ACTN3 genotype as a predictor of at least one musculoskeletal injury, multivariable binary logistic regression was used, controlling for previous injury history, age, BMI and body-fat percentage. The RR genotype was used as the reference group. The estimated odds of injury were found to be lower for RX than RR (adjusted OR = 0.72, 95% CI: 0.25-2.08, $p = 0.546$), but higher for XX than RR (adjusted OR = 2.18, 95% CI: 0.51-9.23, $p = 0.290$) after adjustment. The XX estimate is associated with a wide confidence interval, suggesting that the small size of the XX subgroup is a large source of uncertainty.

The non-genetic risks factors that had the highest risk estimates in the model were previous injury history, with previously injured participants having an adjusted odds of subsequent injury of about 2.44 (95% CI: 0.88-6.73, $p = 0.085$). No age, BMI or body-fat percentage were independently linked to injury occurrence. The full regression results are given in Table 4 and adjusted odds ratios, and 95% CIs are displayed in Figure 4.

Table 4. Multivariable Logistic Regression for Predictors of Musculoskeletal Injury Occurrence

Predictor	Adjusted OR	95% CI	p-value
RX vs RR genotype	0.72	0.25-2.08	0.546
XX vs RR genotype	2.18	0.51-9.23	0.290
Previous injury	2.44	0.88-6.73	0.085
Age, per year	0.83	0.62-1.12	0.228

Predictor	Adjusted OR	95% CI	p-value
BMI, per kg/m ²	1.05	0.83-1.33	0.666
Body fat, per 1%	1.10	0.96-1.26	0.181

OR = odds ratio; CI = confidence interval. RR genotype was the reference category. The dependent variable was occurrence of at least one injury during the observation period.

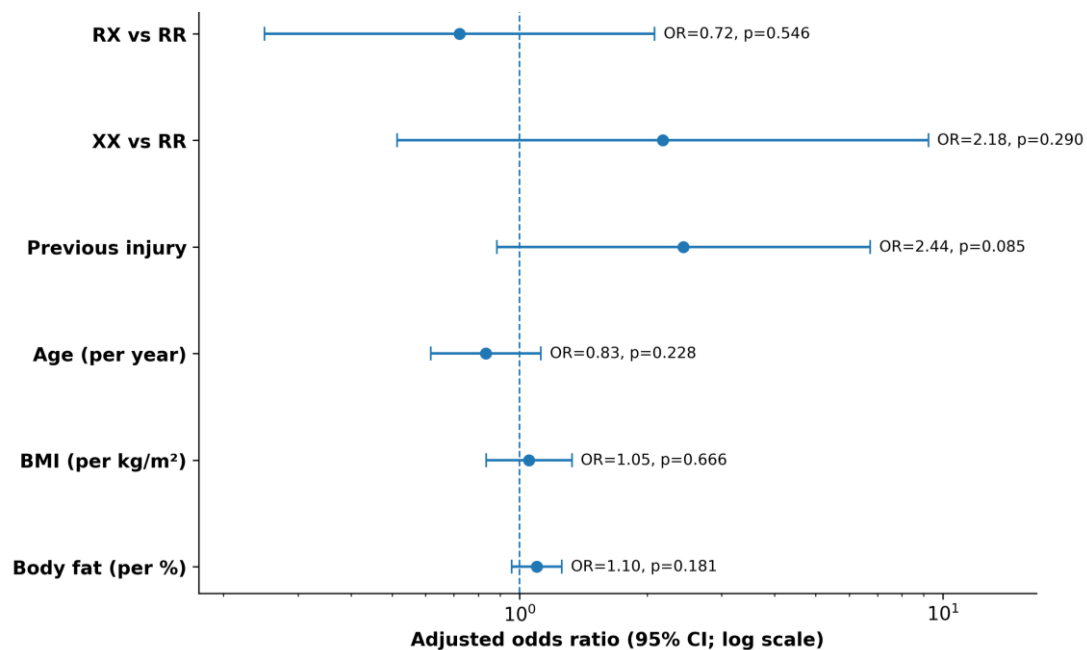


Figure 4. Multivariable Predictors of Musculoskeletal Injury Occurrence

3.5 Integrated Injury-Risk Profile

The findings together suggest that the ACTN3 rs1815739 genotype was not independently significantly associated with the overall incidence of musculoskeletal injuries or cumulative injuries at the 5% significance level. However, there were a few interesting directions. The highest crude injury prevalence was seen among XX carriers (73.3%) and a relatively high ratio of injury odds relative to RR carriers (more than 2 relatives) was found, whereas a relatively high proportion of joint injuries and non-traumatic injuries were observed. Otherwise, the overall injury prevalence was lowest among the RX participants. The results also indicate that susceptibility to injury may be a combination of genetic and previous injury exposure.

Previous injury history had the strongest adjusted Nongenetic effect (OR = 2.44) and was close to statistical significance ($p = 0.085$). Temporal analysis also showed that there is significant genotype variation in Period 4, even though there were no genotype differences in cumulative injury burden. These observations alone provide support for interpretation of ACTN3 not as a standalone predictive marker to drive the risk of injury but as a component in a multifactorial system and also serve as a quantitative basis for subsequent training and rehabilitation personalization studies.

4. DISCUSSION

In this study, the ACTN3 rs1815739 variation was investigated alongside anthropometric factors and injury history, as potential musculoskeletal injury risk factors. The overall rate of injury occurrence did not significantly differ between RR, RX and XX genotypes, though the crude prevalence of injury was highest in the XX group (73.3%) than the RR (61.5%) or RX (53.8%) groups. This directional pattern is consistent with the general principle that inherited characteristics of the muscles could play a role in inter-individual variations in injury susceptibility, but genetic factors are rarely the only factor. The escalating body of evidence related to the genetic risk factors for non-contact soft tissue injury also highlights the difficulty of translating individual polymorphisms into a practical risk assessment tool (Borzemska et al., 2024).

The second analysis also showed that the risk of injury was about 2.18 times higher in the XX than the RR group, but this difference was not statistically significant, and the confidence interval was rather broad. This uncertainty aligns with the prevailing evidence currently available that in most cases genetic injury-risk markers

need to be validated in larger populations for them to be used in clinical and training decisions. Therefore, combinations of injury-associated genes (IA genes), such as structural and connective-tissue markers, have been the subject of more research, and a broader genetic profile is becoming more accepted than the single gene interpretation (Abed et al., 2024).

The current results confirm this conservative stance and indicate that ACTN3 could better be used as a part of a polygenetic risk profile. The non-genetic adjusted effect of previous injury history was most pronounced, with an odds ratio of 2.44, but at a level that was not statistically significant. This is clinically significant as the tolerance of the tissues, movement strategies, and the exposure to re-injury will be altered from previous musculoskeletal injuries. Similarly, research into personalized injury-management has highlighted the significance of an individual's injury history for the designing of recovery and return-to-activity procedures (Aldanyowi & AlOraini, 2024).

The finding also bolsters the importance of using non-modifiable genetic traits along with modifiable clinical and training-related factors. There were no significant differences found between the two groups for age, BMI, percentage body fat, weight or height and none of these variables significantly accounted for the occurrence of injury in the multivariable model. This implies that the observed genotype pattern was not due solely to sizeable anthropometric imbalance between the groups. The importance of incorporating these participant factors with biomechanical and computational data has been increasingly supported by contemporary injury-risk research, which targets the simultaneous consideration of multiple variables and doesn't cancel the value of biomechanical or computational data (Cao & Chen, 2025). The integration of various athlete attributes has also been shown to be a valuable approach in developing injury-prediction systems, especially via machine-learning applications (Cao & Liu, 2025).

Temporal analysis identified another finding: not only was there no significant difference in the cumulative burden, but there was also a significant difference in injury burden by genotype in Period 4. The XX participants had a decreasing number of injuries throughout the observation periods, while the RR participants had the greatest number of injuries in the late period. This is a good example of how the risk of injury varies over time and therefore should not be considered a static characteristic of the athlete. Monitoring systems that rely on data and are increasingly proposed to change the risk profile of athletes and to adapt rehabilitation strategies over time (Sediri et al., 2025). The modern sports medicine approach, which is focused on technology, also prioritizes ongoing monitoring of training, recovery, and injury indicators to optimize personal interventions (Qin & Pourkhamisi, 2025).

One of the major limitations of the present analysis is the lack of direct biomechanical measures. Future models may be improved by incorporating joint mechanics, efficiency of movement, asymmetry, muscle activation, or external loading using biomechanical data. Specific research on biomechanical data on injuries has highlighted the importance of these measurements as tools to identify modifiable risk mechanisms (Khosravi, 2025). Similarly, adaptive decision systems that integrate both physical-performance and injury-related parameters are possible with AI-based training analytics, thereby improving prevention (Mishra et al., 2024). Individualization of recovery monitoring and return-to-play decision making through technology-based rehabilitation practices is also emerging (Ogbemudia, 2025).

In general, the results indicate that genotype of ACTN3 should not be considered a determinative factor for injury. Instead, its potential significance is in the context of a broader system that includes past injury, longitudinal injury burden, anthropometric factors, and future biomechanical factors. This is in line with the continuity of the trend of multidimensional, athlete-specific assessment in sports physiology that aids in enhancing sports performance and minimizing injury risk (Saadati, 2023). This is a better way to base personalized training and rehabilitation than on any single genetic or physical marker it is possible to identify.

5. CONCLUSION

This study aimed to investigate the contribution of ACTN3 rs1815739 polymorphism, anthropometric traits and previous injury history to the risk of musculoskeletal injury. Within overall injury occurrence and cumulative injury burden, there were no significant differences between RR, RX and XX genotypes, but the crude prevalence of injuries was highest in the XX genotype (73.3%) with an odds ratio greater than 2 relative to the RR genotype. The results indicate a potential directionality of genetic influences however; the broad confidence intervals and lack of significant associations mean that it is not considered as a stand-alone or determinant injury susceptibility gene. Perhaps most important, previous injury history was the strongest non-genetic predictor, with about 2.44 times greater adjusted odds of subsequent injury. This discovery underscores the need for the importance of including prior injury exposure in individual risk assessment. No anthropometric characteristics were significantly associated with injury occurrence and only a significant genotype difference was found in the last observation period, suggesting that susceptibility to injury can change over time. In summary, the results are in favor of a multi-factorial approach for predicting and rehabilitating sports injuries for the individual. Genetic data may offer more value when used in conjunction with injury history, long-term monitoring, anthropometric data, and future biomechanical data. Vigorous and larger prospective studies that include more genetic markers, muscle function, and workload and movement mechanics are needed to create more effective, individual training, injury prevention, and rehabilitation programs.

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